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DEVELOPMENT OF AN *IN SILICO* KIR GENOTYPING ALGORITHM

AND ITS APPLICATION TO POPULATION AND CANCER

IMMUNOGENETIC ANALYSES

by

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DEVELOPMENT OF AN *IN SILICO* KIR GENOTYPING ALGORITHM AND ITS APPLICATION TO POPULATION AND CANCER IMMUNOGENETIC ANALYSES

A

DISSERTATION

Presented to the Faculty of

The University of Texas

Health Science Center at Houston

and

The University of Texas

MD Anderson Cancer Center

Graduate School of Biomedical Sciences

in Partial Fulfillment

of the Requirements

for the Degree of

DOCTOR OF PHILOSOPHY

by

Howard Rosoff, B.S.

Houston, Texas

August 2016

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DEDICATION

To my family for the love and support.

ACKNOWLEDGEMENTS

I would like to thank my supervisor, Dean Lee, for his help and for the opportunity to conduct my research in his lab.

I also thank my fellow lab members who offered assistance during my training as I acquired experience in scientific experimentation and various immunology bench methods.

I thank the members of my advisory, candidacy exam, and supervisory committees for volunteering their time to help me meet the requirements for graduation.

Finally, I would like to express my appreciation to the organizers of the Rosalie B. Hite Graduate Fellowship in Cancer Research and the American Legion Auxiliary Fellowship for their financial support of my work.

DEVELOPMENT OF AN *IN SILICO* KIR GENOTYPING ALGORITHM AND ITS APPLICATION TO POPULATION AND CANCER IMMUNOGENETIC ANALYSES

Howard Rosoff, B.S.

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Gene content determination and variant calling in the complex KIR genomic region are useful for immune system function analysis, pathogenesis and disease risk factor elucidation, immunotherapy development, evolutionary investigations, and human migration modeling. Sequence-specific oligonucleotide and sequence-specific primer PCR methods are the *de facto* standards for KIR presence/absence identification, but the current platforms are unsuitable for SNP calling, impractical for KIR typing large cohorts of DNA samples, and inapplicable for typing repositories in which sequence data, but not cells or cell analytes, are available. Alternative typing methods, such as *in silico* sequence-based typing, can address the problems associated with amplicon-based approaches. However, common next generation sequencing technologies that map short reads to a reference genome exhibit high rates of read mismapping in regions containing loci that are homologous, polymorphic, and variable in content. I developed a novel approach for rescuing KIR genotyping function from sequence read alignment data files exclusively, with no requirement for additional DNA or amplification reactions. This Sequence Read Remapping And Motif Counting (SeRRAMC) approach utilizes a pattern-matching algorithm to select mapped reads containing oligomotifs that uniquely discriminate the variants of a single KIR gene and remap the selected reads to the consensus coding sequence of the respective KIR. The process dramatically reduces read mismapping to near zero, thereby enabling high confidence KIR typing and variant calling from short sequence reads. I used this approach for an analysis of KIR variation in 2535 modern humans across 26 populations

from around the world, plus three Neandertals and a Denisovan. The results identified 175 unique KIR genotypes, the four most frequent of which vary significantly across modern humans, and found 36 population-associated nonsynonymous single base polymorphisms. On average, African and Far Eastern genomes encode fewer KIR genes but a greater number of population-correlated variants, while South Asians have higher gene content with moderate variation. Archaic humans match European and South Asian genotypes at some key polymorphic sites and African genotypes at others. I also applied the SeRRAMC method to an analysis of 5489 germline exomes from cancer patients spanning 22 disease groups. After stratifying the samples by race and ethnicity, the results show no significant correlations between KIR gene content and cancer but did identify a transmembrane domain polymorphism in the KIR3DL3 framework gene associated with melanoma and another variant in the KIR3DP1 pseudogene associated with prostate adenocarcinoma. The analysis also revealed significant batch effects due to disparities in the lengths of sequence reads produced by different sequencing centers. SeRRAMC processing is the first approach to enable these types of immunogenetic analyses. It also offers the first solution for quantifying KIR-specific gene transcripts from RNAseq data and for calling structural variants from *de novo* sequence assemblies generated by third generation single molecule or synthetic long read sequencing technologies.

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Abbreviations

BAM: Binary Alignment/Map

BWA: Burrows-Wheeler Aligner

HLA: Human Leukocyte Antigen

INDEL: Insertion or Deletion

IPD: Immuno Polymorphism Database

KIR: Killer Immunoglobulin-like Receptor

LRC: Leukocyte Receptor Complex

NGS: Next Generation Sequencing

OKG: One Thousand Genomes Project

OR: Odds Ratio

SAM: Sequence Alignment/Map

SBT: Sequence-Based Typing

SeRRAMC: Sequence Read Remapping And Motif Counting

SNP: Single Nucleotide Polymorphism

SSO: Sequence-Specific Oligonucleotide

SSP: Sequence-Specific Primer

TCGA: The Cancer Genome Atlas

VCF: Variant Call Format

WGS: Whole Genome Sequence

WXS: Whole Exome Sequence

Chapter 1: Background

1.1 NK cell attributes and function

NK cells are large granular lymphocytes that play a central role in antiviral and antitumor immunity. They carry the same payload of perforin and granzyme B as cytotoxic T cells but function primarily as a component of the innate immune system. Therefore, they do not express a somatically recombined receptor with exquisite target specificity (the hallmark of an adaptive lymphocyte). Instead, they express members from multiple families of germline-encoded receptors, each one with broader specificities. Diversity in sequence and expression of activating receptors results in an NK cell repertoire capable of recognizing and killing a wide range of pathogens, while multiple inhibitory receptors provide checkpoint redundancy to prevent self-reactivity. The net balance of activating and inhibitory signals determines whether or not an NK cell will reach its threshold of activation, and set points vary from one cell to another.

An NK lymphocyte putatively functions by synapsing with a target cell and interrogating it to ascertain whether it is in a steady state or a stressed state. A cell can be stressed due to viral infection or malignant transformation. The mechanism of interrogation comprises a complex set of receptor-ligand engagements, each one with a binding affinity independent of other interactions. If the target exhibits a sufficiently stressed state, the NK cell is prompted to take action. Depending on the particular NK cell, this can include polarization and degranulation, release of cytokines, or both.

1.2 KIR structure and organization

The Killer Immunoglobulin-like Receptors (KIR) constitute one of the major families of surface proteins expressed by NK cells (and some T cells) that play a significant role in lymphocyte activation and inhibition[1]. Each KIR receptor has either two or three extracellular Ig-like domains (2D or 3D) and either a long or short cytoplasmic tail domain (L or S)[2]. Long-tailed KIRs contain one or two ITIM domains and propagate inhibitory signals that contribute to lymphocyte self-tolerance[3]. Short-tailed KIRs associate with the intracellular DAP12 adaptor protein, which contains two ITAM domains that transduce activating signals to promote lymphocyte responses against target cells in a stressed state[4]. Gene duplication and conversion events during the evolution of primate germlines have resulted in 14 coding genes within the KIR family (five KIR2DL, five KIR2DS, three KIR3DL, and one KIR3DS gene)[5-7]. In addition, two translationally-inactive pseudogenes, KIR2DP1 and KIR3DP1, derived from a KIR2DL and a KIR3D locus respectively[8].

The KIR family is encoded within a short (~143 kb) genomic region towards the 3' end of the broader Leukocyte Receptor Complex (LRC), which is itself located towards the telomeric end of the human chromosome 19q arm[9]. The KIR region is organized into centromeric and telomeric subregions that are demarcated by four framework KIRs[10]. The centromeric section is bound by KIR3DL3 at the 5' end and the inner framework KIR3DP1 gene, while the inner KIR2DL4 and KIR3DL2 (the most 3' gene) flank the telomeric region. KIR genotyping of over 18,000 individuals around the world has revealed 100% positive linkage between 3DL3, 3DL2, and 2DL4 and 98% positive linkage between 3DP1 and the other three framework genes[11,12]. KIR genes are highly polymorphic, encompassing over 700 known alleles across the family, ranging from 15 2DS3 variants to over 100 known 3DL3 alleles (Figure 1)[13]. Additional variation across the human population results from differential gene

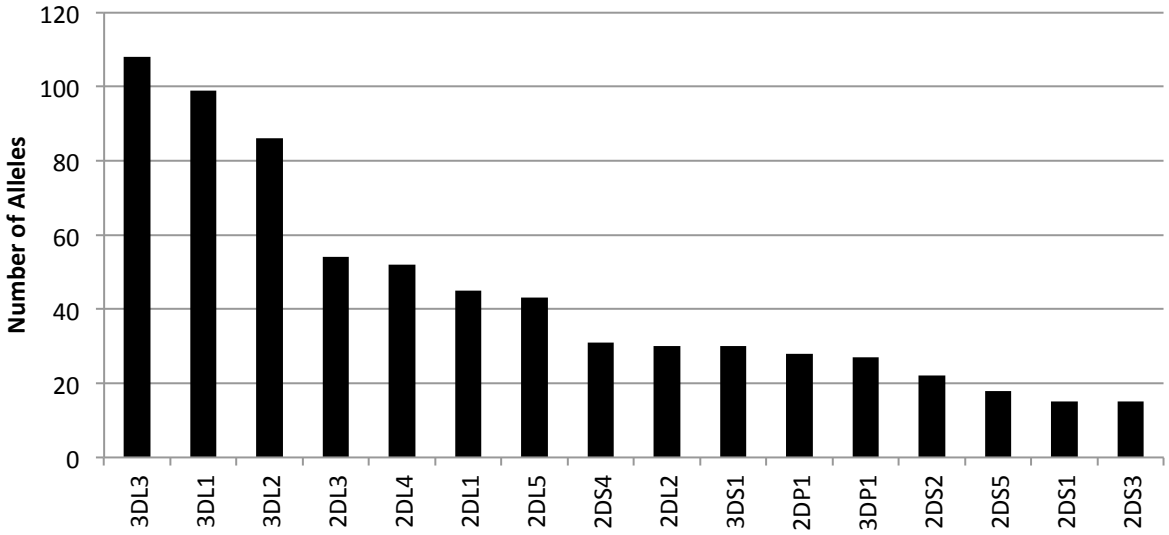


Figure 1 KIR gene polymorphism. 703 alleles across 16 KIR genes.

content within the KIR region[14]. Each haploid oocyte and spermatocyte gamete carries a subset of the 16 KIR family members, and the combination of the two haplogroups determines the total KIR content encoded within a single diploid genome. The centromeric 2DL2 and 2DL3 are mutually exclusive within an individual KIR haplotype, as are the telomeric 3DL1 and 3DS1 genes. The set of KIR2DL5 alleles is subdivided into 5A (telomeric) and 5B (centromeric) groups, and both (or neither) can exist within a haplotype. KIR2DS3 and 2DS5 may each be encoded within the centromeric and telomeric regions, and they are mutually exclusive in each subregion. The highest frequency haplotype (designated type A) is a low gene content group consisting of the four framework KIRs plus a $2DL3^{+}2DP1^{+}2DL1^{+}3DL1^{+}2DS4^{+}$ non-framework motif[15]. Therefore, type AA is the most common genotype. Other KIR combinations containing higher gene content are broadly categorized as B haplotypes, which are incorporated into BX genotypes. Furthermore, 14 of the 31 known KIR2DS4 alleles contain a 22 nucleotide deletion in the extracellular D2 domain (exon 5) that results in secretion of the receptor rather than retention in the plasma membrane[16]. Since 2DS4 is the only activating KIR encoded within the A haplotype, individuals with an AA genotype that is homozygous for 2DS4

deletion alleles express no activating KIR on the surface of their NK cells and must rely on other receptors to reach lymphocyte activation thresholds.

1.3 KIR and KIR ligand contribution to NK cell repertoire variation and disease

KIR genes are major contributors to variation in NK cell phenotype and function for several reasons. In addition to receptor allelic and gene content heterogeneity, lymphocyte variation results from diversity of KIR ligands. The known ligands for the major inhibitory KIR receptors are alleles of the Human Leukocyte Antigen (HLA) Class I major genes (HLA-A. B, and C), which are extremely polymorphic, with thousands of variants across the three loci[17]. Furthermore, there is stochastic and/or regulated expression of whichever KIR alleles are present within the genome, as well as variation in expression of members from other families of leukocyte receptors, resulting in an immensely heterogeneous population of innate lymphocytes within the NK cell repertoire[18]. Combinations of KIR gene content, KIR allelic variants, and HLA allelic variants are implicated in a number of disease conditions, including the containment/clearance of virally-infected cells[19,20], autoimmune disease[21,22], pregnancy-related disorders[23,24], and cancer susceptibility[25,26] or protection[27]. Therefore, the identification of KIR genotypes is a critical component in understanding the function of NK cells and their role in pathogenesis.

1.4 Issues with *de facto* KIR genotyping approaches

Sequence-specific primer (SSP)[28-31] or sequence-specific oligonucleotide (SSO)[32,33] assays are currently the most commonly used methods for KIR typing. However, the major repositories of genetic sequences that have become publicly available in recent years, such as The Cancer Genome Atlas (TCGA) collection, are exclusively retrospective in the sense that they only offer access to sequence read alignment files and variant calling information. They do

not make cells or cell analytes available for PCR-based genotyping. Even if biological materials were available for these samples, it would be impractical, time-consuming, and expensive to perform very large numbers of PCR assays. Furthermore, several probes for amplicon-based typing do not have specificity for the alleles of a single KIR gene, thereby limiting the utility of these platforms for variant calling. Therefore, it is useful to develop *in silico* sequence-based typing (SBT) approaches that only require sequence data for genotyping.

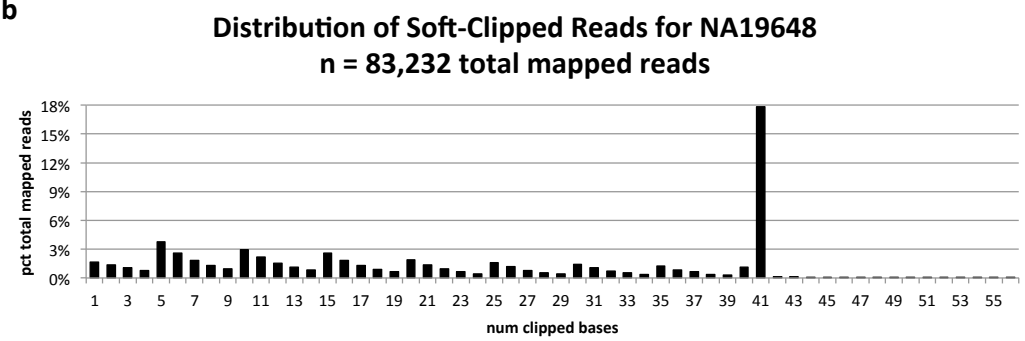
Sequence-based typing for complex genomic regions such as the KIR cluster presents unique challenges that do not exist for other areas of the genome. The homology between KIR loci results in a large degree of short sequence read mismapping for a resequencing (i.e. not *de novo*) project aligned to the human reference genome (Figure 2). Mismapped reads typically have a significant number of bases soft-clipped by the aligner in order for the remaining portion of the read to map to the reference sequence (Figure 2a,b). Any discrepancies between the aligned portion and the reference will provide false positive evidence during variant calling (Figure 2a). Consequently, the mismapped reads also fail to produce evidence of variation within the true gene of origin, resulting in false negative variant calling. For the KIR region, read mismapping results in errors not only in variant calling, but in gene content calling as well.

a

alignment file: NA19648.mapped.ILLUMINA.bwa.MXL.exome.20120522.bam
reference: GRCh37
aligner: BWA

SAM field	value	description
1	SRR099389.24681047	read ID
3	19	reference name
4	55285007	reference position
5	0	Phred map quality
6	41S35M	CIGAR
10	CTTCTCCATCAGTCGCATGAAGCAAGACCTGGCAGGGACCTACAGATGCTACGGTTCTGTTACCCACTCCCCCTAT	sequence
optional	NM:i:1	edit distance
optional	MD:Z:22T12	mismatching positions

b



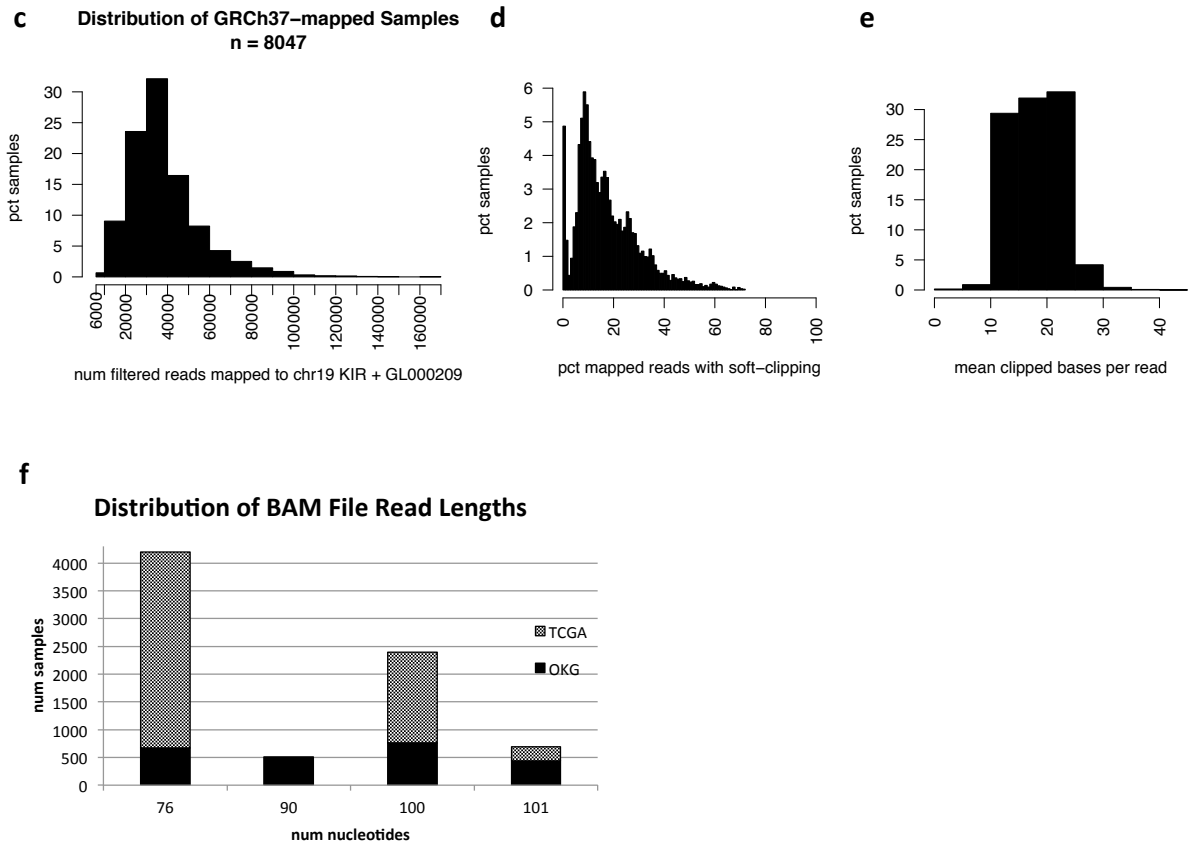


Figure 2 Mapping quality for NGS reads mapped to the human reference genome KIR regions. (a) Individual read level. A single read from the WXS BAM file for 1000 Genomes Project sample NA19648 is mapped within the genomic coordinates annotated as KIR2DL1 (19:55281265-55295778) with Pr(wrong mapping position) = 1.0, and 53.9% of the read is soft-clipped from the 5' end. Nucleotide 23 of the mapped portion deviates from the reference. (b) Sample level. 55.0% of all mapped reads for sample NA19648 have at least 10% soft-clipping. (c,d,e,f) Cohort level. For 2535 OKG and 5512 TCGA WXS BAM files, the median number of KIR-mapped reads per file (after filtering for duplicates and failed QC reads) is 34,435 (c), and a median 14.6% of all mapped reads are soft-clipped (d) with a mean 18.1 soft-clipped bases per read (e). (f) Most BAM files within the cohort contain 76 or 100 nucleotide paired-end reads. 254 of the BAM files each contain reads of two different lengths (not shown).

Several of the problems associated with genotyping regions containing loci that are homologous, polymorphic, and variable in content can be addressed by recent third generation technologies that produce long-range sequence reads. These platforms use single molecule approaches (e.g. Pacific Biosciences SMRT sequencing[34], Oxford Nanopore MinION[35]) or create synthetic long reads by partitioning and barcoding DNA during library prep for sequencing by short read instruments (e.g. 10x Genomics GemCode[36], Illumina TruSeq[37]). Long read sequencing enables the assembly of *de novo* genomes that can be used for short

variant calling along coding and noncoding regions, as well as for haplotype phasing and calling of structural variants, including CNVs, gene fusions, and gene recombinations. However, short read instruments still dominate the sequencing market, and labs with an existing investment in these instruments will continue to generate massive volumes of short read data. Therefore, it is necessary to develop methods that salvage as much genotyping information as possible from current and future short read sequence data repositories.

Chapter 2: The SeRRAMC KIR Genotyping Algorithm

2.1 Introduction

In order to rescue KIR gene content and variant calling function from short sequence reads, it is necessary to include additional processing steps within a conventional read mapping and genotyping pipeline. An attempt to call variants from reads mapped to the human reference genome without performing these additional steps will result in high false positive rates. The Sequence Read Remapping And Motif Calling (SeRRAMC) algorithm was developed to enable accurate read mapping and subsequent high confidence gene content and variant calling in complex genomic regions. This approach iterates through the reads in a sequence alignment file stored in the BAM format, selects the specific reads that can be uniquely discriminated as belonging to the variants of a particular gene, and remaps those reads to the consensus coding sequence for that gene. The algorithm is implemented as a software tool that can batch process large numbers of BAM files to rapidly identify the presence or absence of KIR genes within each genome and to generate remapped BAM files containing vastly improved read alignment qualities that can be used as inputs for established variant calling pipelines.

2.2 Algorithm development

2.2.1 Identification of oligomotifs unique to each KIR gene

The nucleotide CDS sequences for all KIR alleles within the Immuno Polymorphism Database (IPD) release 2.6.0 (January 19, 2015) were downloaded (https://www.ebi.ac.uk/ipd/), and a list of all exons from all alleles was compiled. Following removal of identical exon sequences, a variable-sized sliding window iterated through each exon sequence to generate all possible oligomotifs of a specified size range. A minimum window size of seven nucleotides was arbitrarily selected to ensure motifs would be specific to the alleles of a single KIR gene. A

maximum window of 50 nucleotides was selected on the basis that it is half the size of a commonly used read length for paired-end NGS sequencing (100 bases). Each generated motif was queried against the list of total exons. Any motif common to at least one allele of two or more KIRs was discarded. Oligomotifs unique to one or more variants of a single KIR were appended to an initial list of candidate motifs. From these candidates, motifs common to 50% or more of the alleles for one KIR were selected. For example, there are 52 KIR2DL4 variants listed in IPD 2.6.0, so any motifs common to 26 or more 2DL4 alleles were selected for the final motif list. This list of motifs is used by SeRRAMC to select the KIR region-mapped sequence reads within BAM files aligned to the human reference genome and to create new BAM files containing reads mapped to the CDS consensus sequence for a specific KIR gene.

2.2.2 Selection of high frequency oligomotifs for KIR gene content calling

Following the generation of KIR-specific remapped BAM files, the SeRRAMC utility produces a count of sequence reads containing a single high frequency motif for each KIR gene. Selection of these high frequency motifs from the list of all KIR-specific motifs was determined by empirical analysis of over 8000 whole exome sequences (WXS). 5512 WXS BAM files containing reads synthesized from normal blood-derived germline DNA and mapped to the GRCh37/hg19 reference genome were downloaded from the cohort of TCGA sequences stored in the CGHub repository (https://cghub.ucsc.edu/)[38]. Another 2535 germline WXS BAM files (also mapped to GRCh37) were retrieved from the 1000 Genomes Project FTP site (ftp-trace.ncbi.nih.gov/1000genomes/ftp/phase3/data/<sample>/exome_alignment/)[39,40]. For each BAM file, reads mapped to the KIR region genomic coordinates within the chromosome 19 primary assembly (19:55235984-55378670), as well as reads mapped to the GL000209.1 unlocalized genomic contig were parsed and compiled into a smaller BAM subset file using SAMtools 0.1.18[41]. These BAM subset files were filtered for PCR/optical duplicates, failed QC

reads, and duplicate query sequences (SAM field 10). This filtering step increases the stringency of KIR presence/absence calls, as all reads within a filtered BAM file differ by a minimum of one nucleotide. Reads within the filtered BAM files that contain the motifs specific to a given KIR were selected and remapped to the consensus coding sequence for that KIR using BWA 0.5.9[42]. A count of reads containing zero soft-clipped bases was produced for each motif. For each KIR, the one motif that yielded the highest read count for the greatest number of samples was chosen for SeRRAMC KIR typing (Table 1). Some motifs generated few or zero read counts from all 8047 BAM files, even though these motifs were common to most or all of the alleles of a particular KIR gene. These ultra low frequency motifs were removed from the list of all oligomotifs in order to increase the performance of the remapped BAM file creation for variant calling.

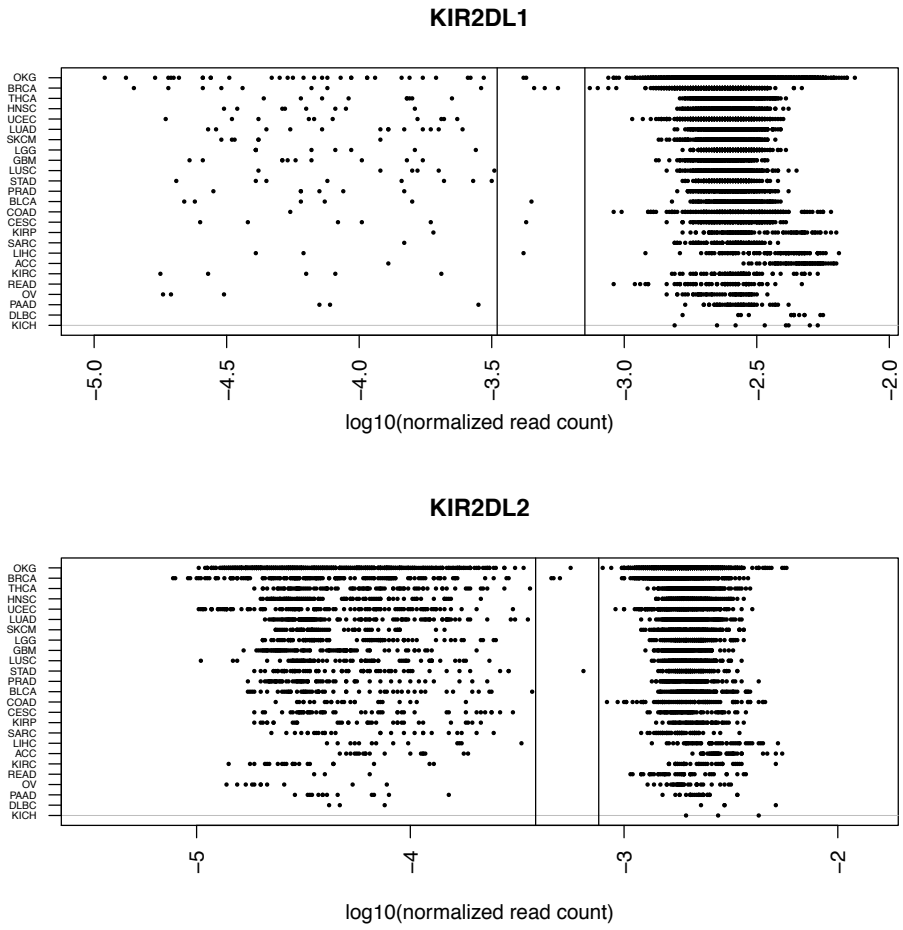
gene	exon	motif	length	numAlleles
3DL3	4	GCTTTGGT	8	108
2DS2	4	AGTATAAG	8	22
2DL2	4	AAGCCAAC	8	28
2DL3	9	TGCACAGTTGA	11	52
2DP1	4	GAAGACCT	8	28
2DL1	4	CGCAAGACCTG	11	45
3DP1	4	CGCAAGACCTT	11	27
2DL4	5	AGCTCCTT	8	52
3DL1	4	GCTTGCCC	8	98
3DS1	7	CATTCTGATTGGGACCTCAGTGGTCAA	27	30
2DL5	5	TTGACATG	8	43
2DS3	4	GGTCGCATGAG	11	15
2DS5	4	CCAAGGGCA	9	18
2DS1	4	AAGCAAGAC	9	14
2DS4FUNC	5	AGGCAGGAGAGAATGTGACCTTGTCCTGCAGCTCCCGGAGCTC	43	17
2DS4DEL	5	TCCATCTATC	10	14
3DL2	4	GTTATGGT	8	86

Table 1 List of high frequency oligomotifs for calling presence or absence of KIR genes.

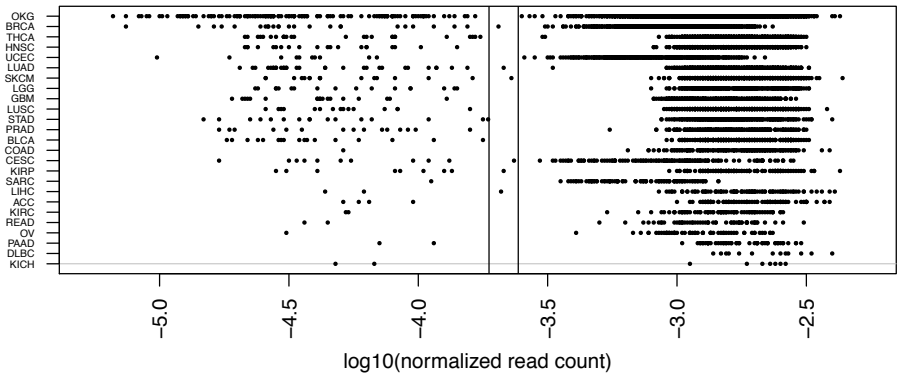
2.2.3 Calling presence or absence of KIR genes

In order to account for the large variation in read coverage between BAM files, the raw read count for each KIR gene (Table A1) was normalized by dividing by the total number of reads mapped to the KIR regions within the filtered BAM files (Table A2). The normalized

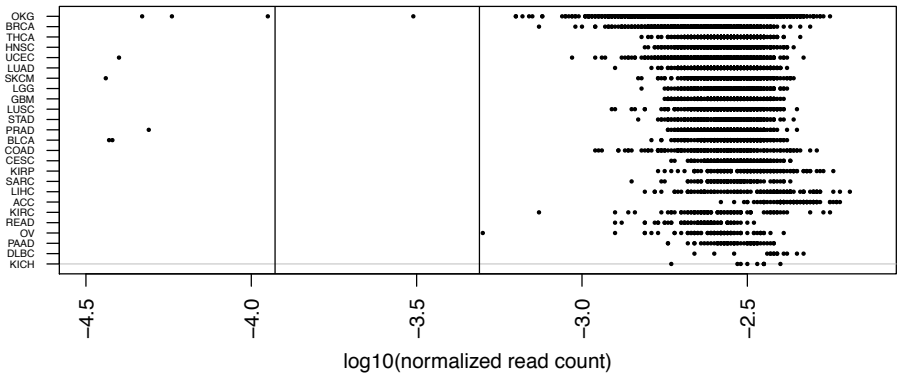
read counts were segregated by TCGA disease group and plotted for each KIR, and then low and high cutoff thresholds were determined by the count distribution (Figure 3). For each sample, if the normalized count was greater than the high cutoff, then that KIR gene was called present. If the normalized count was less than the low cutoff or equal to zero, then that KIR gene was called absent. Any normalized count between the high and low thresholds was flagged as ambiguous.



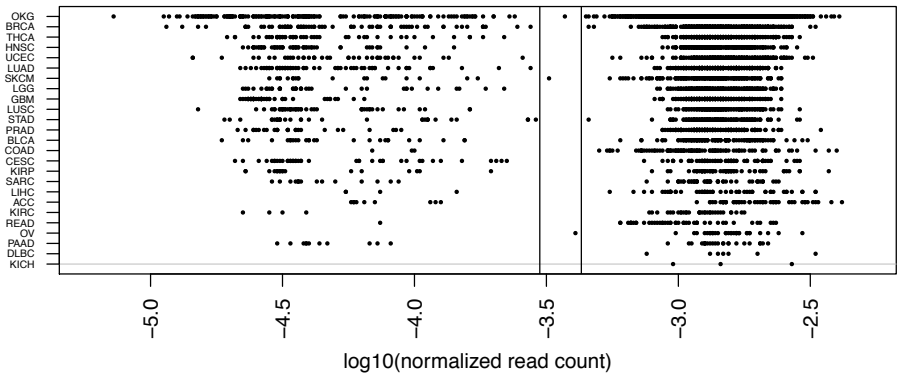
KIR2DL3



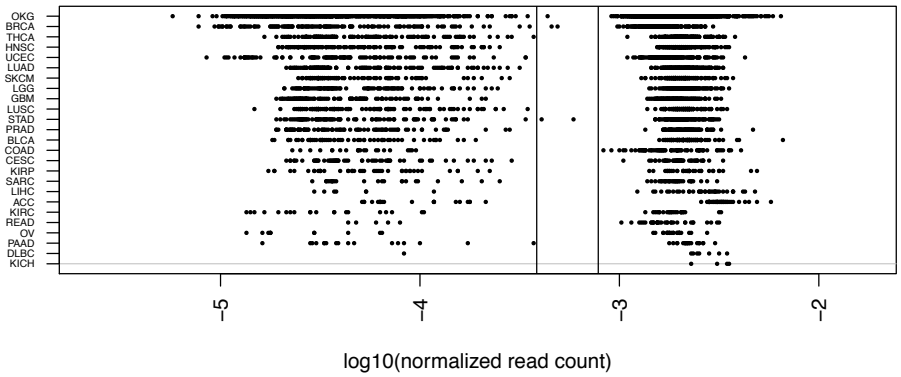
KIR2DL4



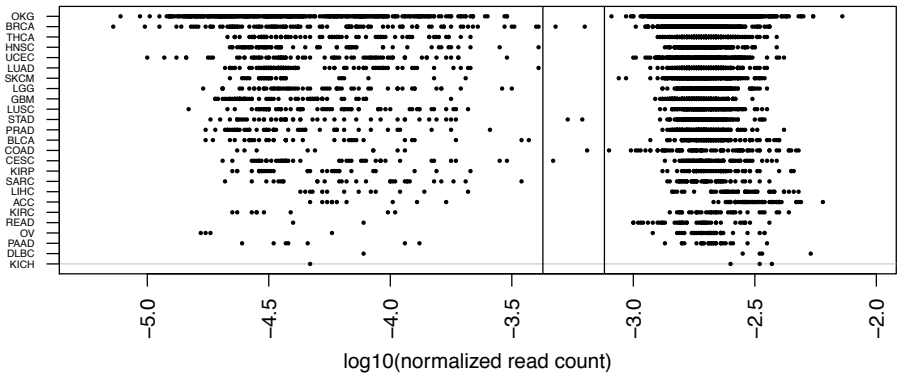
KIR2DL5



KIR2DS1



KIR2DS2



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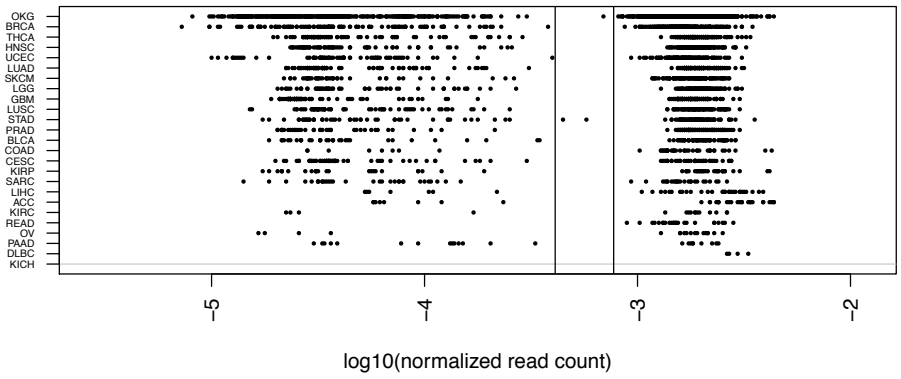
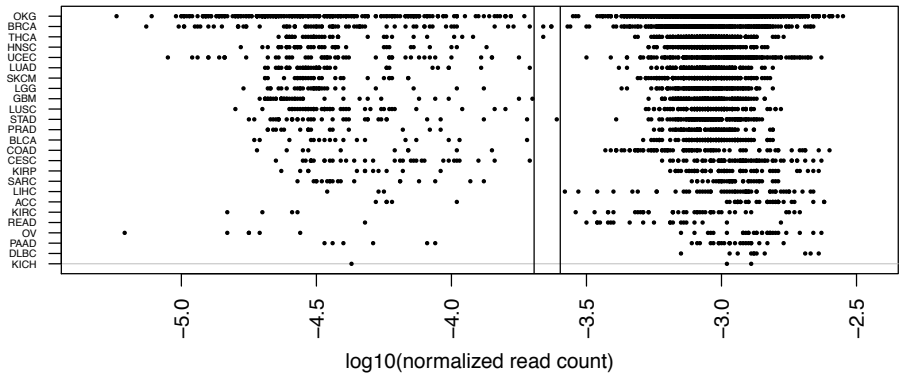
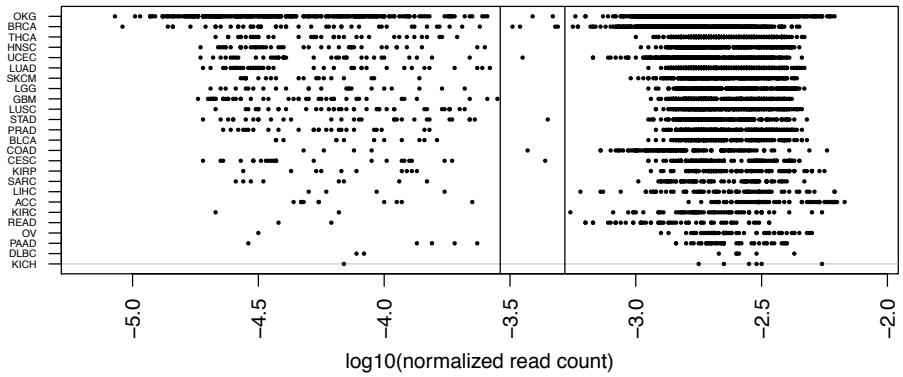


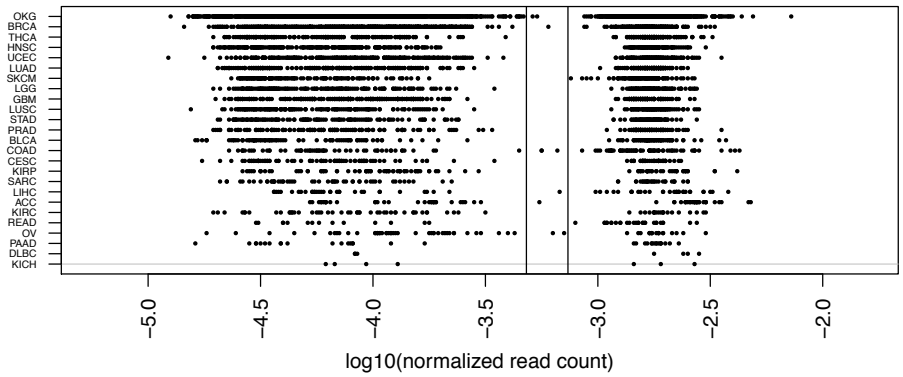
KIR2DS4FUNC



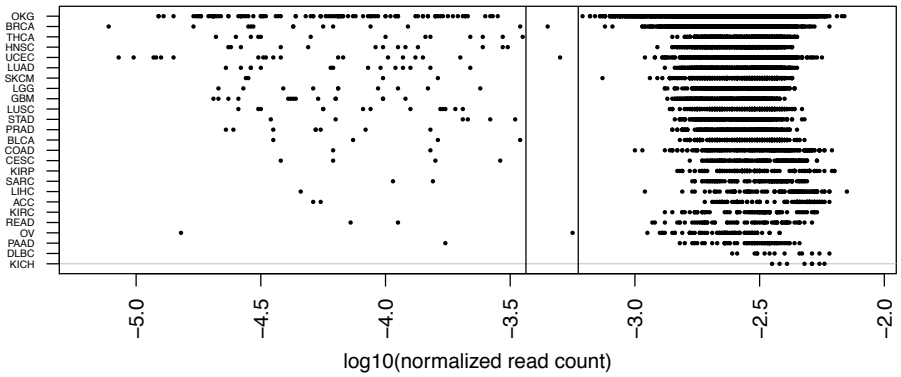
KIR2DS4DEL



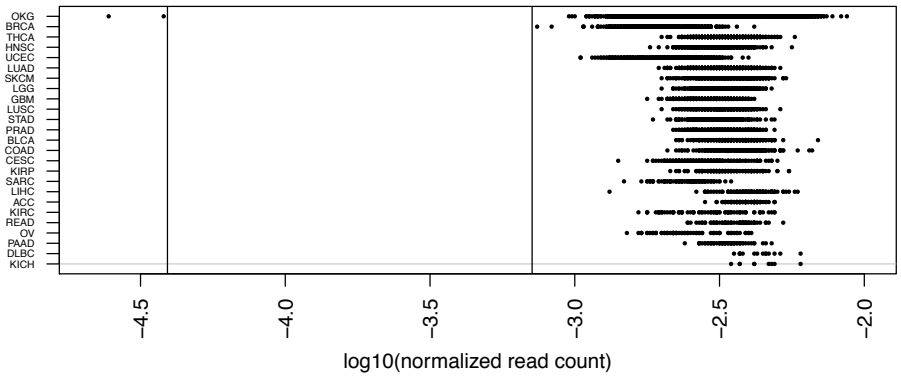
KIR2DS5



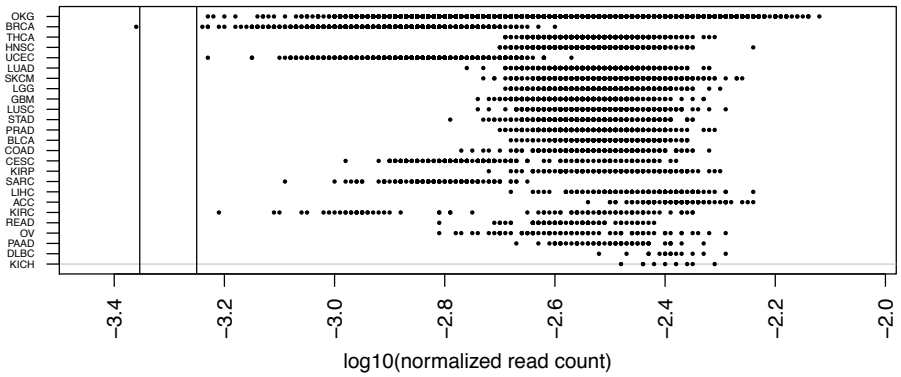
KIR3DL1



KIR3DL2



KIR3DL3



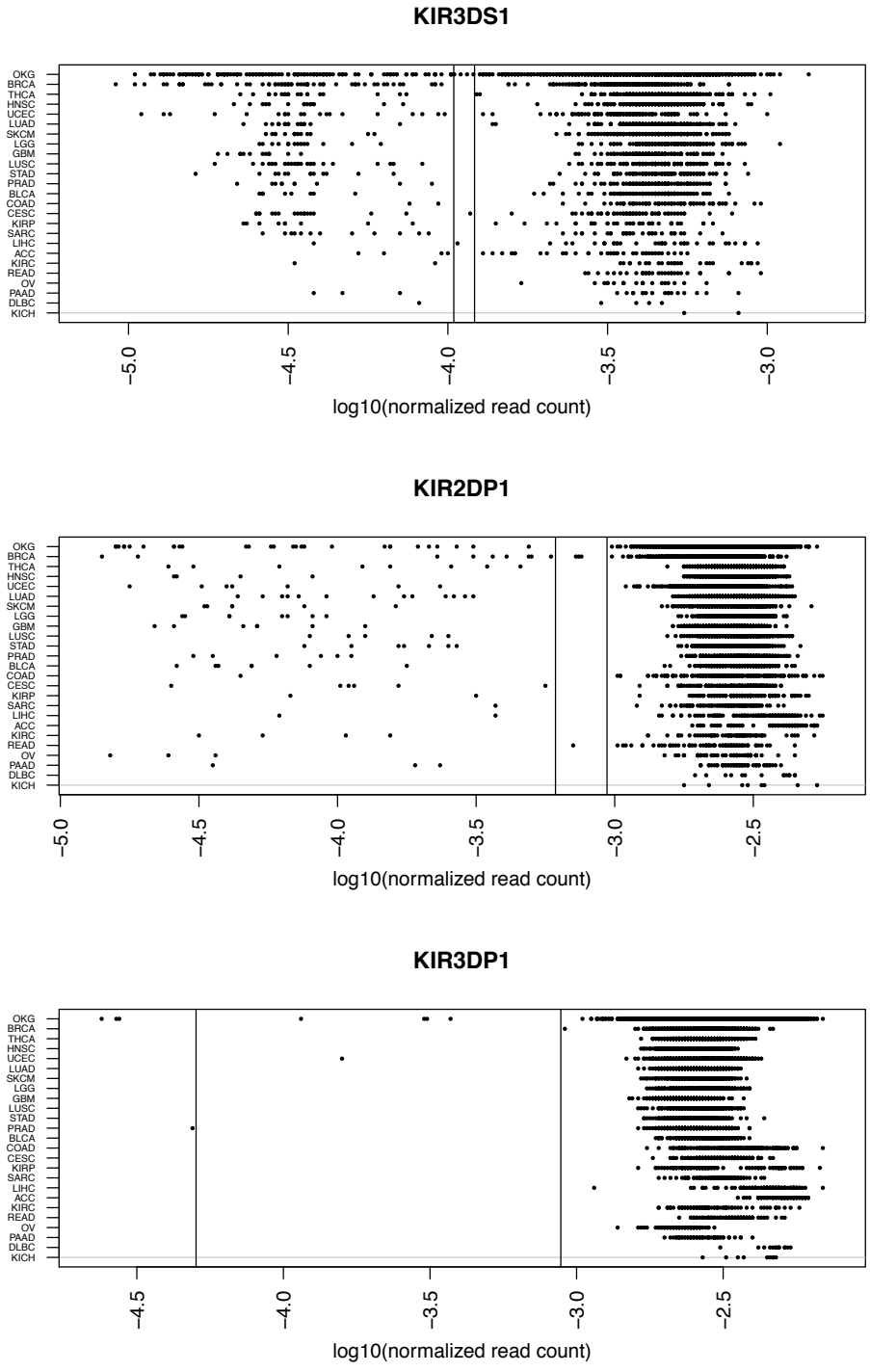


Figure 3 Distributions of normalized KIR-specific read counts and gene presence/absence calling thresholds. 2535 OKG and 5512 TCGA samples. Cutoffs for gene absence (left vertical line) and presence (right vertical line) were determined empirically from the plots and are used to call gene content from future DNA samples. Counts between the cutoffs are flagged as ambiguous for that KIR. Samples with a zero normalized read count (not shown) are also called KIR absent.

2.2.4 Secondary KIR gene content calling method

A visual inspection of the read alignment for some of the remapped BAM files revealed instances in which SeRRAMC called a KIR gene as absent from a sample despite unambiguous remapped read coverage (Figure 4). In order to address this possibility of a misclassification, the algorithm was augmented with a secondary method for KIR presence/absence calling. The number of positions within each remapped alignment file that have a minimum 10x read coverage are counted (Table A3), and if this count meets or exceeds the length of the shortest specific oligomotif for that particular KIR, then the gene is called as present. Otherwise, the gene is called as absent. The two calling methods (normalized read count distribution method and minimum read coverage method) are then resolved according to the following rules: If at least one method calls a KIR as present, the final call is present. If both methods call the gene as absent, the final call is absent. If both methods are ambiguous, then so is the final call. If one method is ambiguous, the final call will default to the other method's call, however a visual inspection of the remapped alignment file is recommended to validate (or reject) the classification. This secondary method is not applicable to the calls for KIR2DS4.

Figure 4 Necessity of a secondary KIR calling method. Remapped KIR3DL3 BAM file for breast invasive carcinoma sample TCGA-AQ-A04L-10A-01D-A12J-09. Thirty-nine remapped reads contain the high frequency 3DL3-specific motif GCTTTGGT (positions 584 to 591), but the normalized read count is beneath the absence cutoff. Visual inspection of the alignment file shows sufficient coverage from reads containing other 3DL3-specific motifs (such as the TTTGACATT motif from 748 to 756) to call the gene as present.

2.2.5 Discrimination of KIR2DS4 functional and deletion variants

Of the 31 KIR2DS4 alleles listed in IPD 2.6.0, 14 contain a 22 base deletion in the exon that encodes the D2 extracellular domain (exon 5), resulting in a disrupted downstream amino acid sequence that causes these receptors to be secreted rather than retained on the lymphocyte surface. During oligomotif selection, a 10 nucleotide motif (TCCATCTATC) containing bases that flank the deletion region was identified as being common to these 14 alleles but not contained within the 2DS4 functional variant sequences or any other KIR sequence. A single 43 base motif (AGGCAGGAGAGAATGTGACCTTGTCCTGCAGCTCCCGGAGCTC) spans the 22 bases common to the 17 functional 2DS4 alleles but is not found within the sequence of any other KIR allele. This enables the SeRRAMC software to call presence or absence of 2DS4 functional and deletion variants separately for each DNA sequence.

2.2.6 Algorithm validation

To test the accuracy of the SeRRAMC algorithm, SSO KIR typing results were compared to *in silico* typing from NGS sequence reads. Blood draws were taken from 14 donors and submitted to the MD Anderson Histocompatibility Laboratory for typing of germline DNA using the KIR SSO Genotyping Test (One Lambda). Two donors whose genomes encode low KIR gene content (D1 and D2, Figure 5) were selected to validate the specificity of the SeRRAMC algorithm, while two other donors with higher KIR content (D3 and D4, Figure 5) were chosen to validate SeRRAMC calling sensitivity. Blood aliquots from these four donors were submitted to the MD Anderson Biospecimen Extraction Facility for isolation of germline DNA, and the DNA samples were sent to the MD Anderson Sequencing and Microarray Facility for Illumina 75 nucleotide paired-end WXS resequencing following SeqCap EZ exome capture (NimbleGen). All four samples were multiplexed on a single Illumina HiSeq2000 flow cell lane, and BAM files were generated from sequence reads mapped to the GRCh37/hg19 reference using CASAVA 1.8.2 (Illumina). These BAM files were then processed for SeRRAMC KIR gene content calling.

A second validation cohort of 10 samples was selected from 66 oral squamous cancer cell line DNA aliquots generously donated by the MD Anderson Department of Head and Neck Surgery. These DNA samples were submitted for SSO typing using the identical procedure from the first cohort. The corresponding Illumina 101 nucleotide paired-end WXS BAM files for the SSO-typed samples were obtained from the Baylor College of Medicine Human Genome Sequencing Center. KIR gene content was called from these BAM files using the SeRRAMC software, and the calls were compared to the SSO typing results.

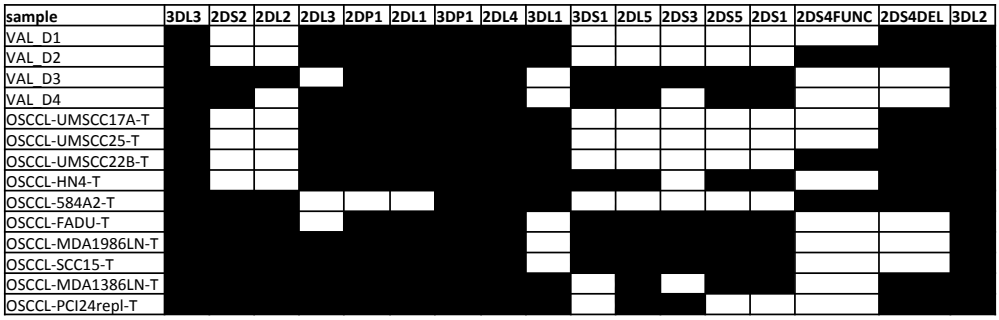


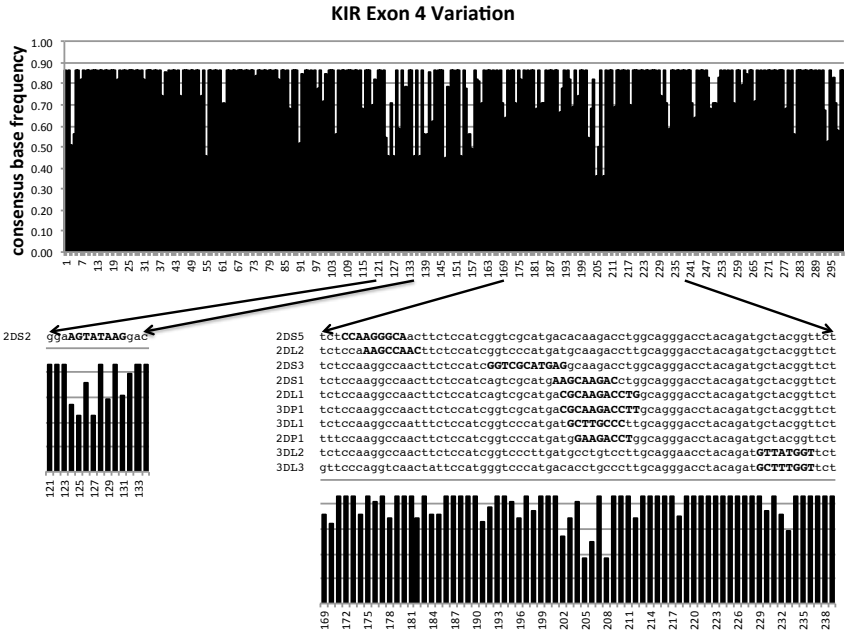
Figure 5 Validation of SeRRAMC KIR calling. Four germline DNA samples and 10 oral squamous cancer cell line samples were SSO KIR-typed and whole exome sequenced by Illumina 75 or 101 nucleotide paired-end sequencing. SeRRAMC KIR presence/absence calls matched SSO calls for all 16 KIR genes for all samples. SeRRAMC discrimination between KIR2DS4 functional and deletion variants was also identical to the SSO results. Two low KIR gene content germline samples (D1 and D2) were selected to validate algorithm specificity, and two samples with greater KIR content (D3 and D4) validated SeRRAMC sensitivity. Black cells = KIR present and white cells = KIR absent as called by both typing methods.

2.3 Results

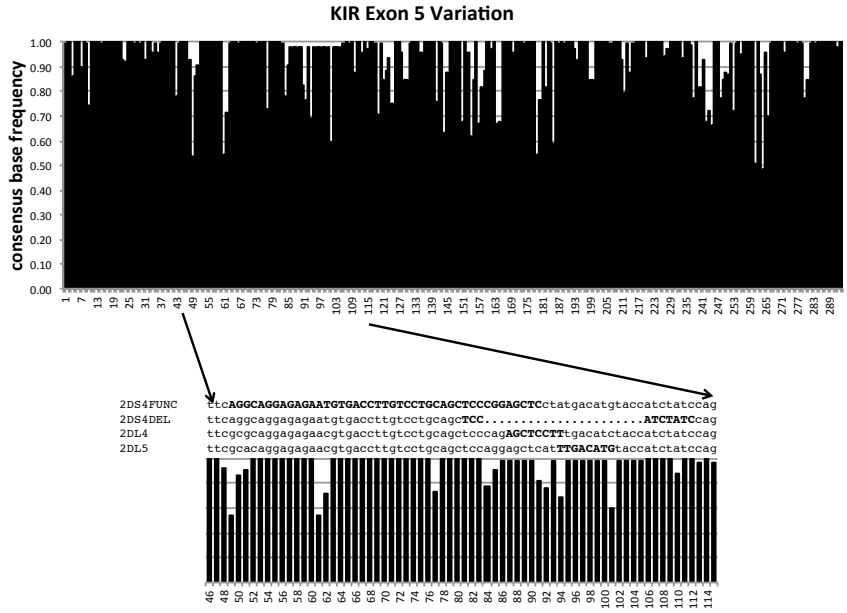
2.3.1 Attributes of oligomotifs for KIR gene content calling

Of the 17 motifs used to call the presence or absence of KIR genes (including separate motifs for KIR2DS4 functional and deletion variants), 15 are between 8 and 11 nucleotides long. The 22 bases within the KIR2DS4FUNC motif that are missing from exon 5 of the 2DS4 deletion variants are common to alleles of other KIR genes. A 43 base oligonucleotide that starts 35 bases 5' of the deletion region and extends eight bases into the deletion region is the only motif that can uniquely discriminate all currently known 2DS4 functional alleles from the deletion variants. Due to the high degree of homology between KIR3DL1 and 3DS1 genes, a 27 base oligonucleotide starting at position 20 of exon 7 is needed to uniquely identify the 30 known 3DS1 alleles. Eleven of the 17 motifs are contained within exon 4 (Figure 6a). In addition to the two KIR2DS4 motifs, the 2DL4 and 2DL5 oligomotifs are also contained within exon 5 (Figure 6b). The 3DS1 and 2DL3 motifs are in exons 7 and 9 respectively (Figure 6c,d).

a


KIR Exon 4 Variation
consensus base frequency
2DS2 ggaAGTATAAGgac
2DS5 tctCCAAGGGCAacttctccatcggtcgcatgacacaagacctggcagggacctacagatgctacggttct
2DL2 tctccaAAGCCAACttctccatcggtcccatgatgcaagaccttgcagggacctacagatgctacggttct
2DS3 tctccaaggccaacttctccatcGGTCGCATGAGgcaagacctggcagggacctacagatgctacggttct
2DS1 tctccaaggccaacttctccatcagtcgcatgAAGCAAGACctggcagggacctacagatgctacggttct
2DL1 tctccaaggccaacttctccatcagtcgcatgaCGCAAGACCTGgcagggacctacagatgctacggttct
3DP1 tctccaaggccaacttctccatcggtcgcatgaCGCAAGACCTTgcagggacctacagatgctacggttct
3DL1 tctccaaggccaatttctccatcggtcccatgatGCTTGCCCttgcagggacctacagatgctacggttct
2DP1 tttccaaggccaacttctccatcggtcccatgatgGAAGACCTggcagggacctacagatgctacggttct
3DL2 tctccaaggccaacttctccatcggtcccttgatgcctgtccttgcaggaacctacagatGTTATGGTtct
3DL3 gttcccaggtcaactattccatgggtcccatgacacctgcccttgcagggacctacagatGCTTTGGTtct

b


KIR Exon 5 Variation
consensus base frequency
2DS4FUNC ttcAGGCAGGAGAGAATGTGACCTTGTCCTGCAGCTCCCGGAGCTCctatgacatgtaccatctatccag
2DS4DEL ttcaggcaggagagaatgtgaccttgtcctgcagcTCC.....ATCTATCcag
2DL4 ttcgcgcaggagagaacgtgaccttgtcctgcagctcccagAGCTCCTTtgacatctaccatctatccag
2DL5 ttcgcacaggagagaacgtgaccttgtcctgcagctccaggagctcatTTGACATGtaccatctatccag

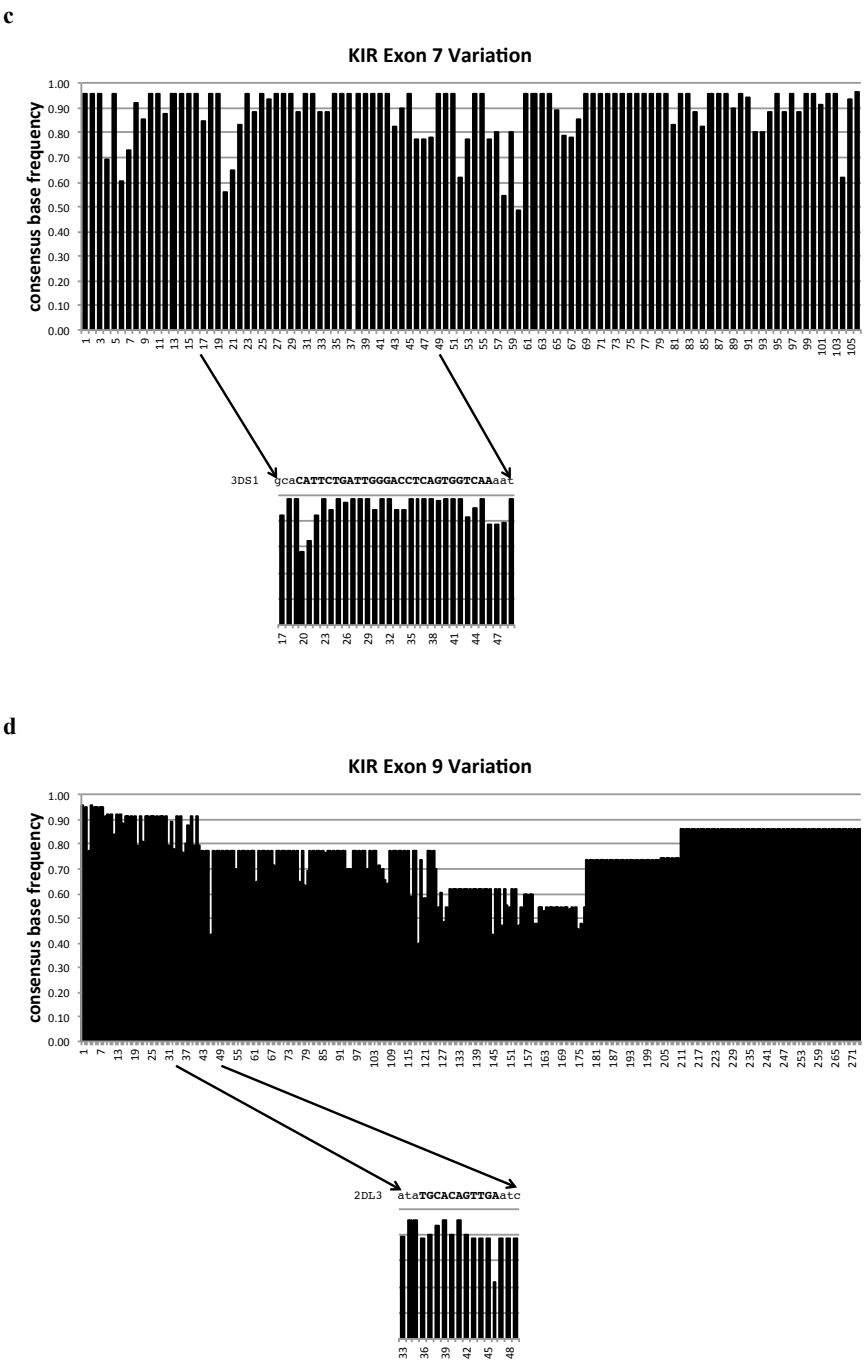


Figure 6 Relative positions of KIR-specific oligomotifs within the exome. Motifs are shown in bold capital letters in the expanded regions. A consensus base frequency < 1.0 indicates that some alleles within the KIR repertoire do not contain that particular portion of the exon.

Of the 703 alleles across all KIR genes listed in IPD 2.6.0, 697 (99.1%) can be uniquely discriminated as members of a single KIR using these 17 oligomotifs. The 2DL2*00303 and

2DL2*004 variants each contain a G in place of an A in position 2 of the 2LD2 motif. The 2DL3*003 and 2DL3*016 alleles each substitute a C for a T in the first motif position, and 2DL3*003 also contains a G to A variation at motif position 2. The 3DL1*054 allele substitutes a G for a T at motif position 3, and the 2DS1*001 variant differs from all other 2DS1 alleles by a G at motif position 2 in place of an A. Of these six alleles that cannot be selected using the SeRRAMC approach, two have no frequency information listed in the Allele*Frequencies database (2DL2*00303 and 2DL3*016), and the other four occur at zero or low frequency within the worldwide populations that have been sampled and typed. The 2DL2*004 allele is found within three of 14 typed populations, with the highest frequency occurring at 4.1% of 50 individuals from a South Africa Xhosa group. The 2DL3*003 allele is found within two of 12 typed populations, with the highest frequency occurring at 4.5% of 154 individuals from a Northern Ireland group. The 3DL1*054 allele is not found within a sample of 162 Han Chinese people from Zhejiang Province, and the 2DS1*001 allele does not occur in any of the 638 individuals spanning seven sampled populations.

2.3.2 Sequence read remapping performance of the SeRRAMC algorithm

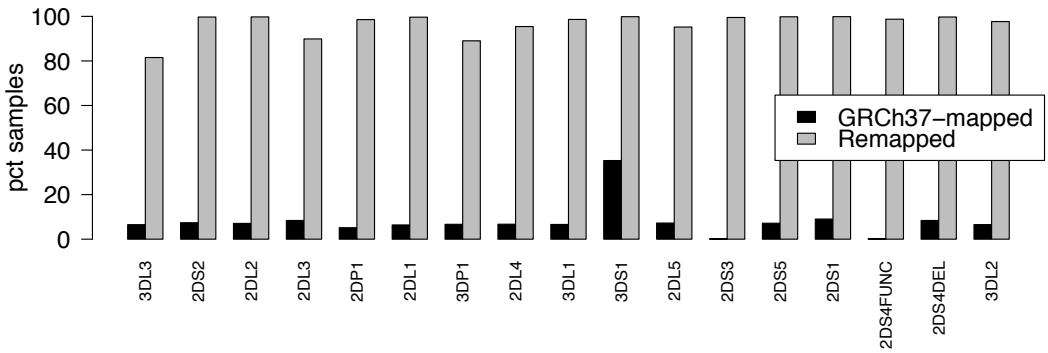
Reads that map poorly to the KIR regions of the human reference genome and that contain a KIR-specific oligomotif exhibit significant improvement in mapping quality following SeRRAMC processing (Figure 7). The majority of KIR-specific reads remap to their respective KIR consensus coding sequences with no soft-clipping and with a dramatic reduction in the probability of an incorrect mapping position (Figure 7a). Remapped BAM files contained either no soft-clipped reads (Figure 7b) or a few at most (Figure 7e). Out of 273.0 ± 278.8 (mean ± s.d.) unique KIR-specific reads per filtered WXS BAM file, the number of clipped reads per sample was reduced from 46.2 ± 83.2 to 0.03 ± 0.20 by the algorithm.

a

alignment file: NA19648.mapped.ILLUMINA.bwa.MXL.exome.20120522.bam
aligner: BWA

SAM field	valueBeforeRemaping	valueAfterRemaping
1	SRR099389.24681047	same
3	19	2DS1Consensus
4	55285007	252
5	0	37
6	41S35M	76M
10	CTTCTCCATCAGTCGCATG**AAGCAAGAC**CTGGCAGGGACCTACAGATGCTACGGTTCTGTTACCCACTCCCCCTAT	same
optional	NM:i:1	NM:i:1
optional	MD:Z:22T12	MD:Z:63T12

b



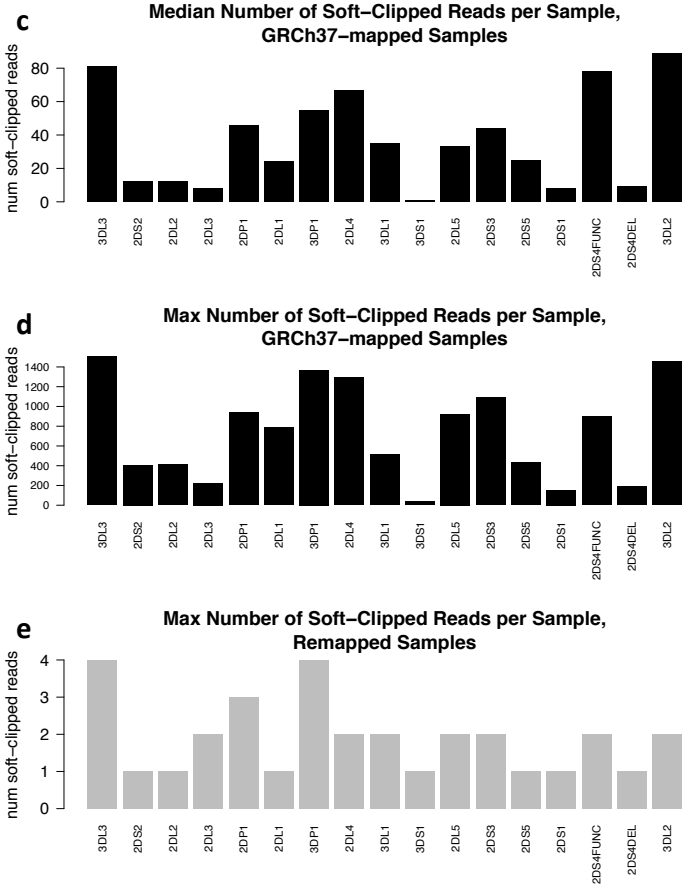


Figure 7 Mapping quality for KIR reads before and after SeRRAMC remapping. (a) Individual read level. The sequence read from Figure 2, partially mapped to KIR2DL1 within the GRCh37 reference, is called a KIR2DS1 read by the SeRRAMC algorithm (motif shown in bold within the read sequence) and remapped to the KIR2DS1 consensus coding sequence. The read remaps with zero soft-clipping (SAM field 6), and Pr(wrong mapping position) decreases from 1.0 to 0.0002 ($10^{-Q/10}$, Q = SAM field 5). (b-f) Cohort level. After remapping KIR-specific reads (as called by the SeRRAMC algorithm) from each TCGA or OKG BAM file to the respective KIR coding consensus sequences, the reads that remapped were compared to the identical set of reads originally mapped to the KIR regions within the GRCh37 reference genome. (b) Before remapping, most BAM files contain mismapped reads. (c) The median number of KIR-specific clipped reads per BAM file before remapping. (d) The maximum number of KIR-specific clipped reads per BAM file before remapping. After remapping, the majority of KIR-specific BAM files contain no mismapped reads (b), the median number of soft-clipped reads per sample is zero for all KIRs (not shown), and the BAM files that do contain any clipped reads have at most a few (e).

2.3.3 Algorithm validation results

The SeRRAMC software correctly called presence/absence of all 16 KIR genes and discriminated between KIR2DS4 functional and deletion variants for all four germline DNA samples and all 10 oral squamous cancer cell line DNA samples.

2.4 Discussion

The SeRRAMC software is currently implemented as a BASH shell script and is compatible with any system capable of running BASH 3.x, SAMtools, and BWA. The program takes reads from whole exome and/or whole genome sequencing stored in the BAM format as input and outputs six sample by KIR gene text files (raw KIR-specific read counts, normalized read counts, presence/absence calls from distribution of normalized counts, number of positions with minimum read coverage, presence/absence calls from minimum coverage, and final presence/absence calls from resolution of the two calling methods). The software allows batch processing of multiple BAM files and defaults to calling all KIR genes but can be restricted to specific KIRs of interest.

For variant calling, the SeRRAMC algorithm remaps reads to all the regions of a KIR consensus coding sequence that are unique to alleles of that KIR gene. The software does not perform variant calling, but rather generates BAM files containing high quality read alignments that can be used as input for any preferred variant calling pipeline (bcftools, GATK, etc.). The portion of a gene where variants can be called with high confidence depends on the degree of sequence homology that particular gene shares with other members of the KIR family. For five KIR genes, over 40% of the coding sequence is unique to the individual KIR, while four KIR genes contain less than 10% nonhomologous consensus sequence (Figure 8). These specific regions, plus any flanking sequence with sufficient read coverage, are suitable for high confidence variant calling. Failure to remap KIR region reads before attempting variant calling will result in a significant likelihood of false positive SNPs and/or INDELS called from mismapped reads. There may also be false negative variants because reads originating from

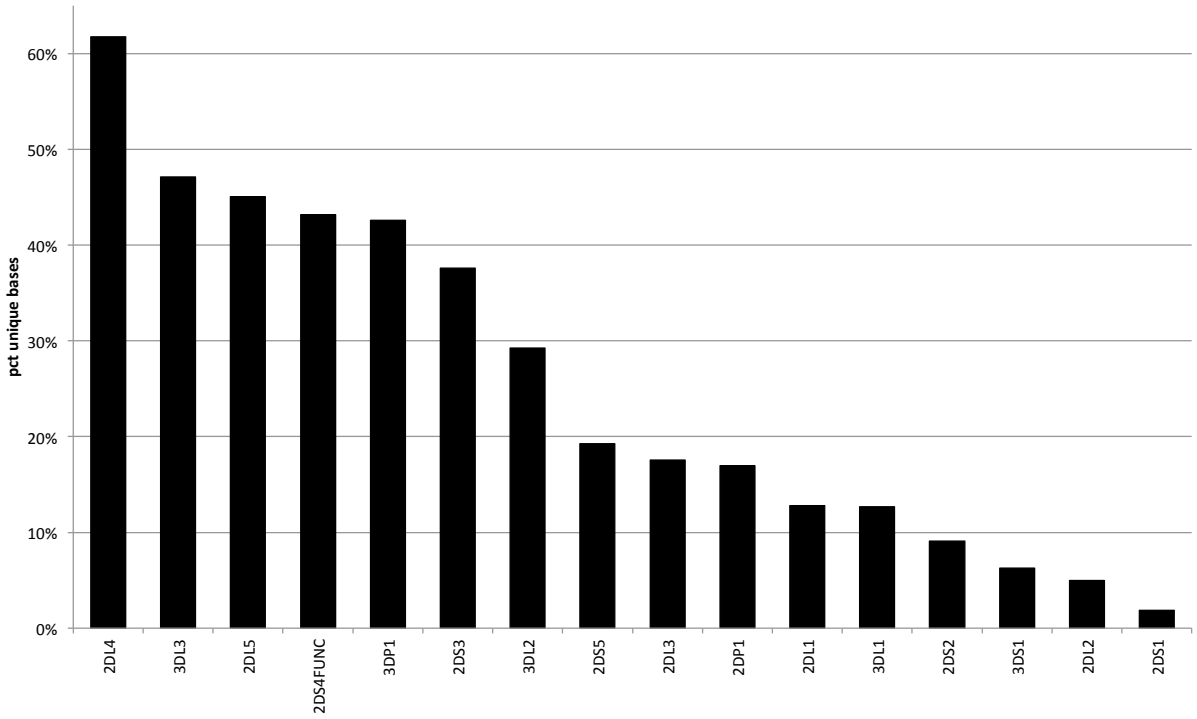


Figure 8 Proportion of each KIR gene containing KIR-specific oligomotifs. The total number of nucleotides within each KIR consensus coding sequence spanned by all KIR-specific motifs divided by the length of the coding sequence.

DNA of a particular KIR are incorrectly mapped to the genomic coordinates of a different KIR gene.

Fifteen of 17 oligomotifs used for gene calling are between 8 and 11 bases in length. 859 of 926 motifs (92.8%) for variant calling range in length from 7 to 20 nucleotides. Therefore, SeRRAMC remapping can be applied to BAM files produced by most short read sequencing technologies. The algorithm can also be adapted for calling KIR content and variation from long-range reads generated by single molecule sequencing or synthetic long read approaches. Illumina 36 nucleotide single-end reads are too short for calling KIR2DS4 functional variants, since those alleles require a 43 base motif for unique identification. Furthermore, if a motif length is close to the read length, then a higher read depth may be necessary in order to ensure a sufficient number of specific reads for accurate KIR calling. For example, identifying the 27 base KIR3DS1 motif within 36 nucleotide Illumina reads or the 43

base KIR2DS4FUNC motif within 50 nucleotide SOLiD reads may require a larger number of reads.

The current version of the SeRRAMC software only remaps sequence reads that contain a KIR-specific oligomotif. For a BAM archive of reads from a paired-end sequencing project, the association between mates is broken, and KIR-specific reads are remapped as single-end reads to their respective KIR reference consensus coding sequences. Since paired-end mates are synthesized from the same DNA fragment template (or from the reverse complement template), it can be inferred that both mates in a pair originated from the same KIR fragment even if only one of the mates contains a KIR-specific motif. Future versions of the software may remap both mates in order to increase the coverage along the reference sequence where variant calling can be performed.

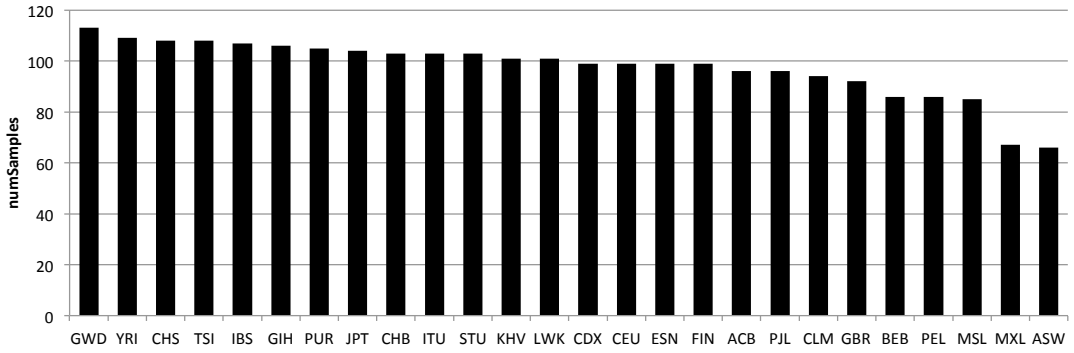
The SeRRAMC approach is also suitable for assessing relative abundance of KIR gene transcripts within RNAseq data sets generated from KIR-expressing NK or T cells. Currently, there are only a few monoclonal antibodies specific to alleles of a single KIR that can be used for cytometric expression profiling at the protein level. KIR-specific oligomotifs enable expression measurements for all KIR genes, albeit at the transcript level.

Performance of the algorithm for each sequenced sample depends on several factors, including read depth of the original WXS or WGS BAM file, enabling of variant calling in addition to gene content calling, the number of KIR genes selected for analysis, and the computer hardware resources.

Chapter 3: Large-scale KIR immunogenetics analysis of modern and archaic humans

3.1 Introduction

Once the SeRRAMC presence/absence classification calls had been validated, the algorithm was used for *in silico* KIR analysis of WXS BAM files from 2535 individuals across 26 human populations within the 1000 Genomes Project catalog (Figure 9 and Table A4). In addition, KIR variants from four archaic human DNA samples were analyzed. Two Neandertal samples were sequenced from bones discovered in the Vindija Cave in northern Croatia and in the El Sidron Cave near coastal northwestern Spain[43,44]. Another Neandertal sample was sequenced using DNA isolated from a female toe phalanx found in 2010 in the Denisova Cave in the Altai Mountains of southern Siberia[45]. The fourth sample was recovered in 2008 from a finger phalanx of a young girl in the same Denisovan Cave but identified as genetically distinct from Neandertals[46,47].



group	description	region
ACB	African Caribbean in Barbados	AFR
ASW	African Ancestry in Southwest US	AFR
BEB	Bengali in Bangladesh	SAS
CDX	Chinese Dai in Xishuangbanna, China	EAS
CEU	Utah residents, North & West European ancestry	EUR
CHB	Han Chinese in Bejing, China	EAS
CHS	Southern Han Chinese, China	EAS
CLM	Colombian in Medellin, Colombia	AMR
ESN	Esan in Nigeria	AFR
FIN	Finnish in Finland	EUR
GBR	British in England & Scotland	EUR
GIH	Gujarati Indian in Houston,TX	SAS
GWD	Gambian in Western Division, The Gambia	AFR

group	description	region
IBS	Iberian populations in Spain	EUR
ITU	Indian Telugu in the UK	SAS
JPT	Japanese in Tokyo, Japan	EAS
KHV	Kinh in Ho Chi Minh City, Vietnam	EAS
LWK	Luhya in Webuye, Kenya	AFR
MSL	Mende in Sierra Leone	AFR
MXL	Mexican Ancestry in Los Angeles, California	AMR
PEL	Peruvian in Lima, Peru	AMR
PJL	Punjabi in Lahore,Pakistan	SAS
PUR	Puerto Rican in Puerto Rico	AMR
STU	Sri Lankan Tamil in the UK	SAS
TSI	Toscani in Italy	EUR
YRI	Yoruba in Ibadan, Nigeria	AFR

region	description
AFR	African
AMR	Americas
EAS	East Asian
EUR	European
SAS	South Asian

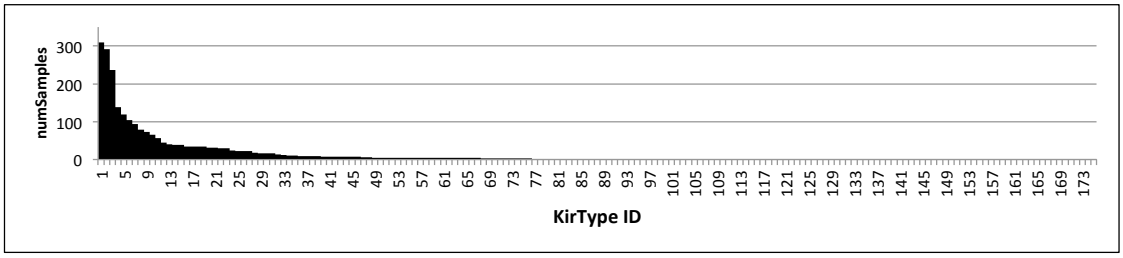
Figure 9 Group distribution of 2535 OKG WXS BAM files.

3.2 Results

3.2.1 KIR genotypes of modern humans

SeRRAMC KIR typing revealed a total of 175 unique KIR genotypes (Figure 10a and Table A5). 2042 samples (80.6%) are clustered within the 25 most frequent KIR types, while the remaining 493 samples (19.4%) are distributed across a long tail of 150 types, 69 of which occur once within the entire cohort (Figure 10). KIR type AA is found within 839 samples (33.1%). When type AA is stratified by functional versus nonfunctional 2DS4, the frequencies of heterozygous, homozygous functional, and homozygous nonfunctional types are 12.2%, 11.5%, and 9.3% respectively. The highest frequency KIR BX genotype - containing all A genes (homozygous for 2DS4 deletion variants) plus 3DS1, 2DL5, 2DS5, and 2DS1 - accounts for 139 (5.5%) of all samples. Linkage between KIR gene pairs closely tracked the

a



b

kirTypeID	count	freq	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
1	310	0.122	■			■	■	■	■	■	■						■		■
2	292	0.115	■			■	■	■	■	■	■						■		■
3	237	0.093	■			■	■	■	■	■	■							■	■
4	139	0.055	■			■	■	■	■	■	■	■	■		■	■		■	■
5	119	0.047	■			■	■	■	■	■	■						■		■
6	104	0.041	■			■	■	■	■	■	■	■	■		■	■	■		■
7	94	0.037	■			■	■	■	■	■	■							■	■
8	79	0.031	■			■	■	■	■	■	■		■	■			■	■	■
9	73	0.029	■			■	■	■	■	■	■	■	■	■	■	■		■	■
10	66	0.026	■			■	■	■	■	■	■	■	■		■	■		■	■
11	57	0.022	■			■	■	■	■	■	■		■	■				■	■
12	45	0.018	■			■	■	■	■	■	■		■	■			■		■
13	40	0.016	■			■	■	■	■	■	■	■	■	■	■	■	■		■
14	39	0.015	■			■	■	■	■	■	■		■		■	■		■	■
15	39	0.015	■			■	■	■	■	■	■							■	■
16	35	0.014	■			■	■	■	■	■	■		■		■	■	■		■
17	35	0.014	■			■	■	■	■	■	■	■	■	■		■	■		■
18	34	0.013	■			■	■	■	■	■	■	■	■	■		■	■		■
19	34	0.013	■			■	■	■	■	■	■	■	■		■	■	■		■
20	32	0.013	■			■	■	■	■	■		■	■		■	■	■		■
21	32	0.013	■				■	■	■	■	■	■	■	■	■	■	■	■	■
22	30	0.012	■			■	■	■	■	■		■	■	■	■	■	■		■
23	30	0.012	■			■	■	■	■	■		■	■		■	■	■		■
24	24	0.009	■			■	■	■	■	■	■	■	■	■		■	■	■	■
25	23	0.009	■		■	■	■	■	■	■	■		■		■		■		■

Figure 10 Distribution of KIR types for 2535 OKG WXS BAM Files. (a) *In silico* typing produced 175 unique KIR genotypes. (b) The 25 highest frequency KIR types represent 2042 (80.6%) of all samples.

linkages reported in the Allele*Frequencies database (Figure 11). Positive linkage concordance is within -3% to +1% for 76.7% of KIR pairs and within -4% to +7% for all pairs (Table A6).

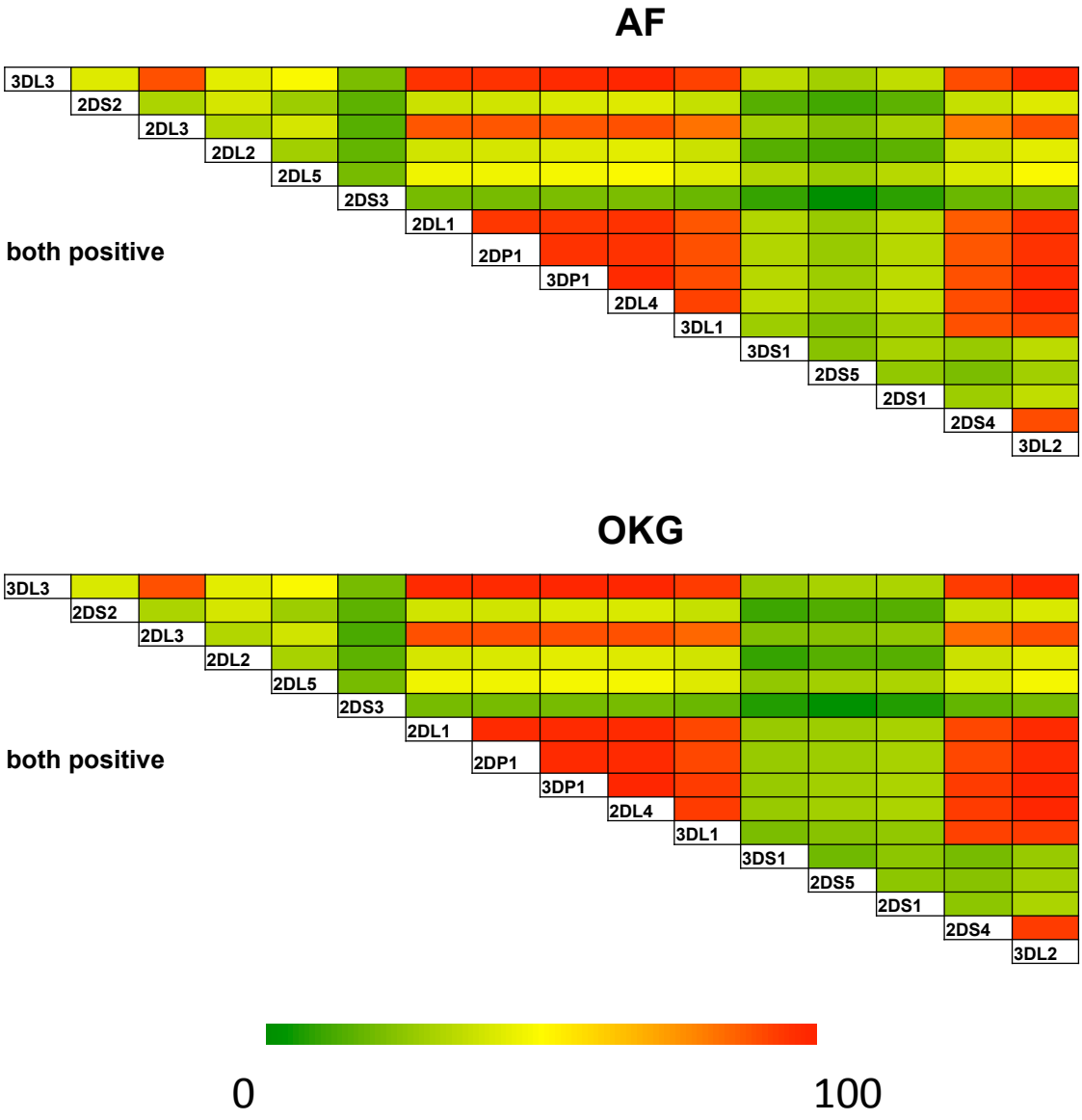


Figure 11 KIR linkage comparison. Positive linkage between KIR pairs from 553 KIR genotypes in the Allele*Frequencies database (AF) and 175 KIR genotypes in the OKG cohort.

3.2.2 KIR genotypes by population

The four most common KIR genotypes showed significant positive or negative association with at least one population when comparing each population to the other 25 groups

in the OKG cohort (Figure 12a,b and Table A7). The KIR AA 2DS4FUNC/DEL heterozygous type is less associated with three South Asian groups (mean OR = 0.23, mean 95% CI = 0.08-0.70) but occurs at a significantly higher frequency within three East Asian groups and the Peruvian group (2.27, 1.40-3.68). KIR type AA 2DS4FUNC/FUNC homozygous is weakly associated with all five European, all five South Asian, and the Puerto Rican populations (0.15, 0.04-0.59) but is significantly associated with two West African, three East Asian, and the Peruvian group (2.90, 1.83-4.61). KIR type AA 2DS4DEL/DEL homozygous is significantly associated with three West European groups and the Puerto Rican group (2.45, 1.47-4.09). The most common KIR BX type is not encoded within a single genome out of 321 individuals from three West African populations (0.00, 0.00-0.00) but is significantly found within the Iberian, Finnish, and Indian Telugu groups (2.82, 1.56-5.12). All other KIR genotypes occur at too low a frequency to identify significant associations with specific populations.

3.2.3 KIR genotypes of archaic humans

All four of the archaic DNA samples are homozygous for KIR2DS4 deletion alleles (Figure 12c). The Altai Neandertal has most other KIR A genes but is missing the 3DP1 framework pseudogene. The two inhibitory KIR B genes (2DL2 and 2DL5), but no activating KIR B genes, are also encoded within the Altai genome. The Vindija Neandertal genome contains all KIR genes identified in the Altai genome plus 3DP1 and 2DS5. The Sidron Neandertal has all Vindija KIRs plus 3DS1 and 2DS3. The Denisovan genome likely has the identical KIR gene content as the Sidron Neandertal, although the presence of 2DL2 is ambiguous due to low read count (only four 2DL2-specific reads were found within the BAM alignment file that maps Denisovan reads to the modern human reference genome). Of the four ancient human KIR genotypes, the Vindija type is the only one found within the 1000 Genomes

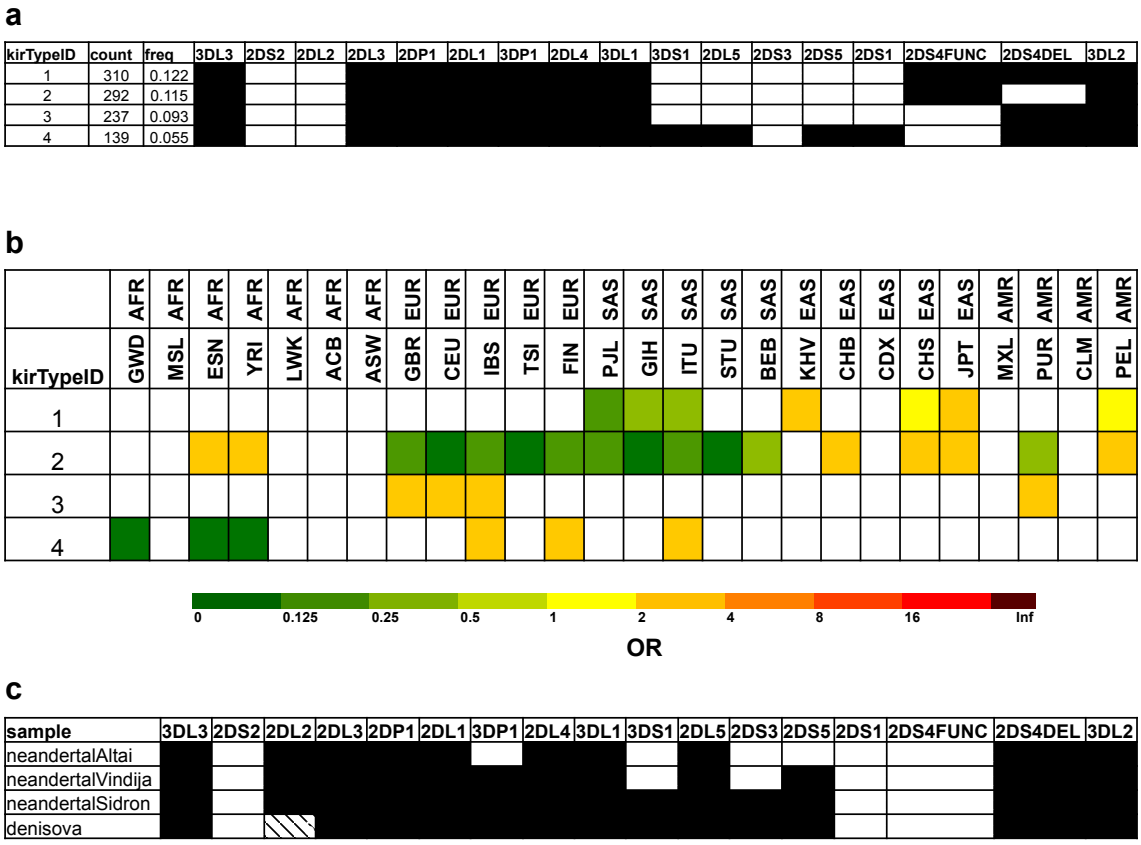
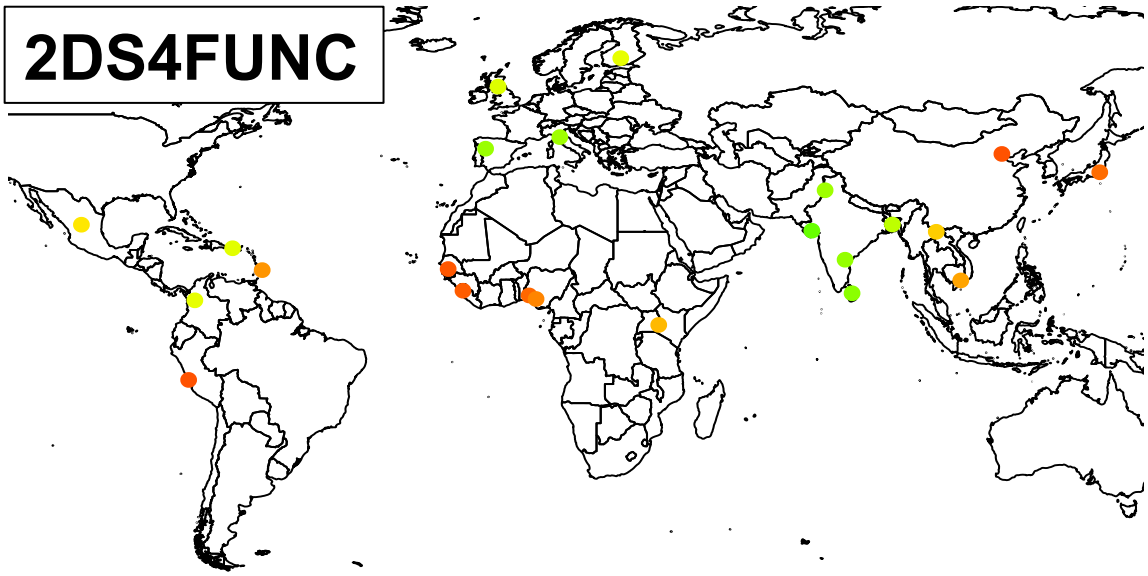


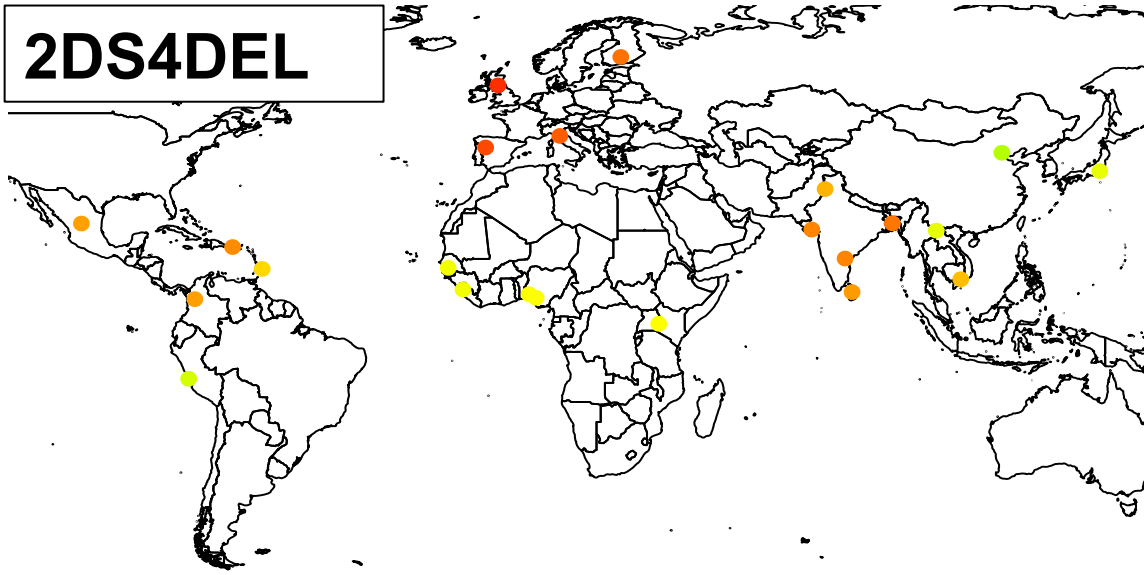
Figure 12 Significant KIR genotypes. (a) Four KIR types associated with OKG groups. (b) Individual OKG populations. OR > 1.0 = genotype significantly associated with population. OR < 1.0 = genotype significantly not associated with population. Blank field = not significant. (c) Archaic human KIR types. The presence of 2DL2 within the Denisovan genome is ambiguous.

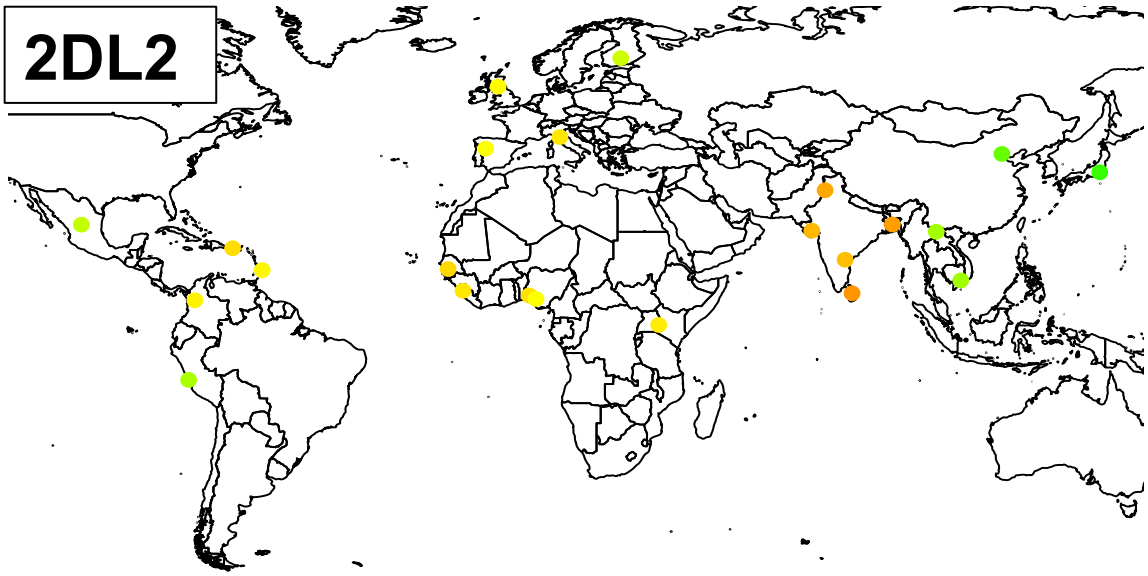
cohort, matching the KIR gene content of two individuals (out of 101) from the Luhya group in western Kenya.

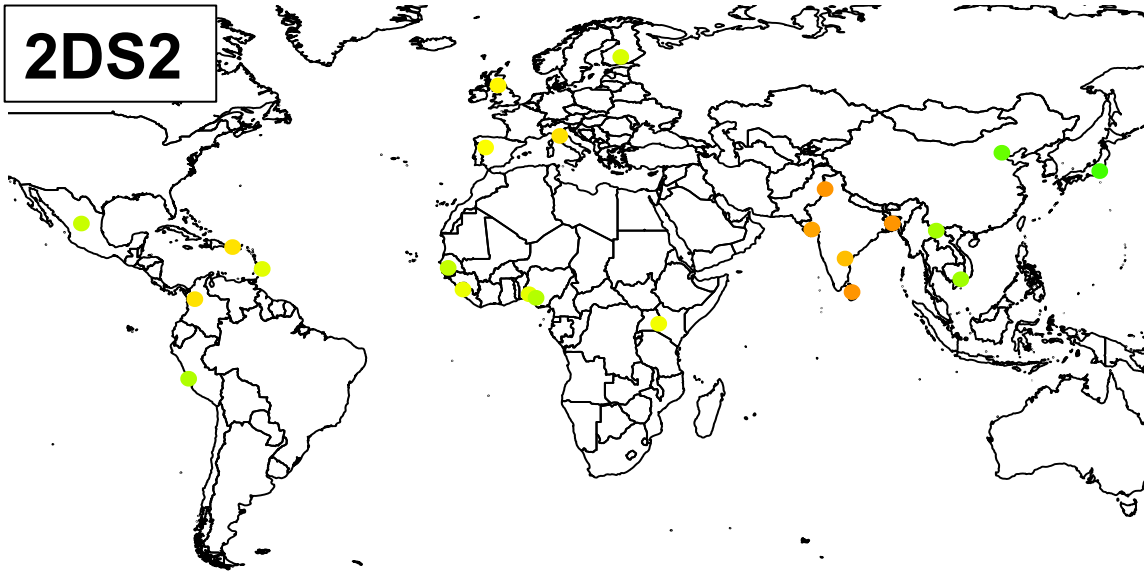
3.2.4 Worldwide distribution of KIR frequencies

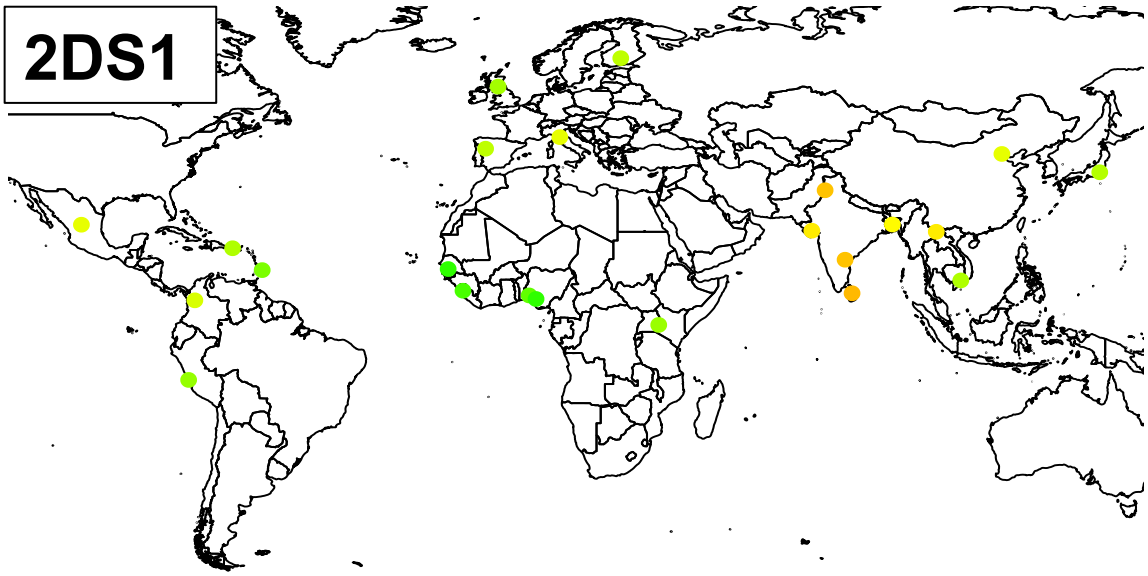
Functional variants of KIR2DS4 occur at very high frequencies within groups from western Africa, Beijing, Tokyo, and Peru (0.819 ± 0.021, mean frequency ± s.d.) (Figure 13). KIR2DS4 deletion alleles are most common in Europe (0.843 ± 0.050) and also common in groups originating from South Asia (0.719 ± 0.048). B content KIR genes occur at lower frequencies throughout the world compared to KIR A genes, but are highest within South Asian groups, particularly 2DL5 (0.741 ± 0.044), 2DL2 (0.667 ± 0.032), and 2DS2 (0.687 ± 0.034).

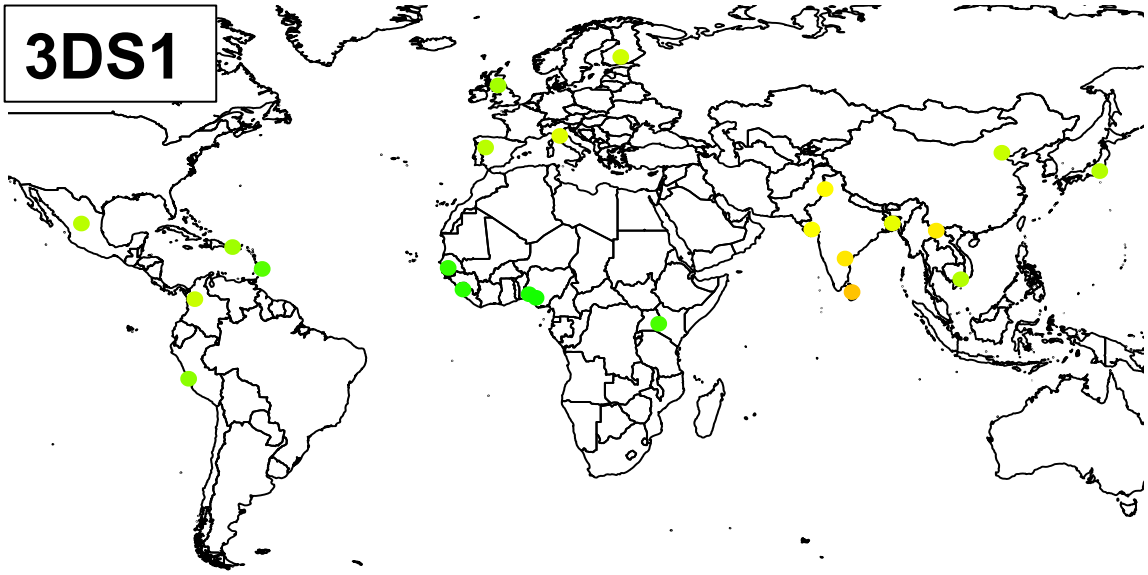

2DS4FUNC

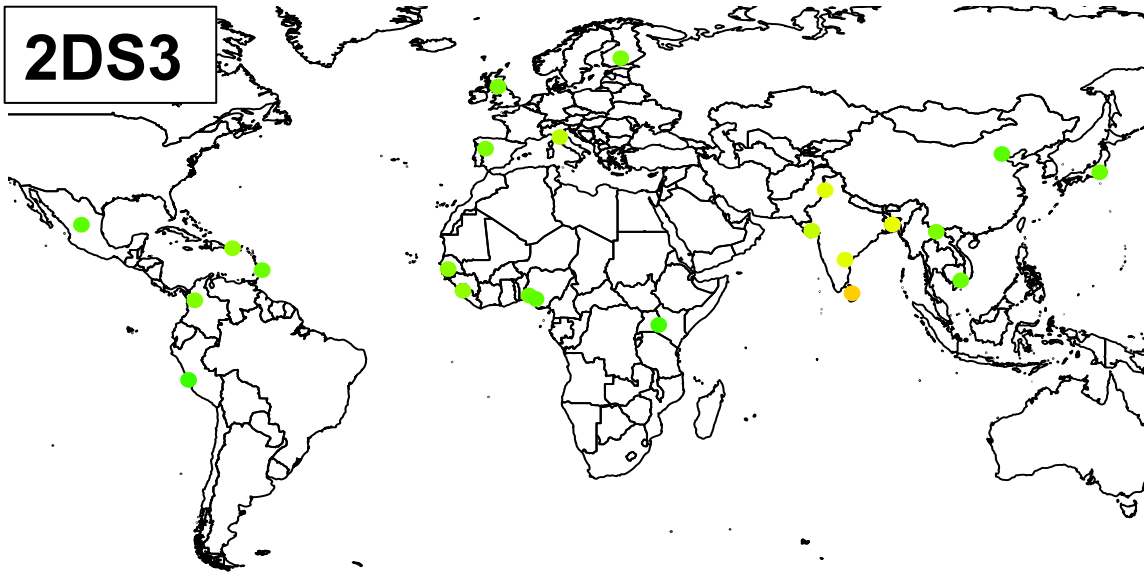

2DS4DEL

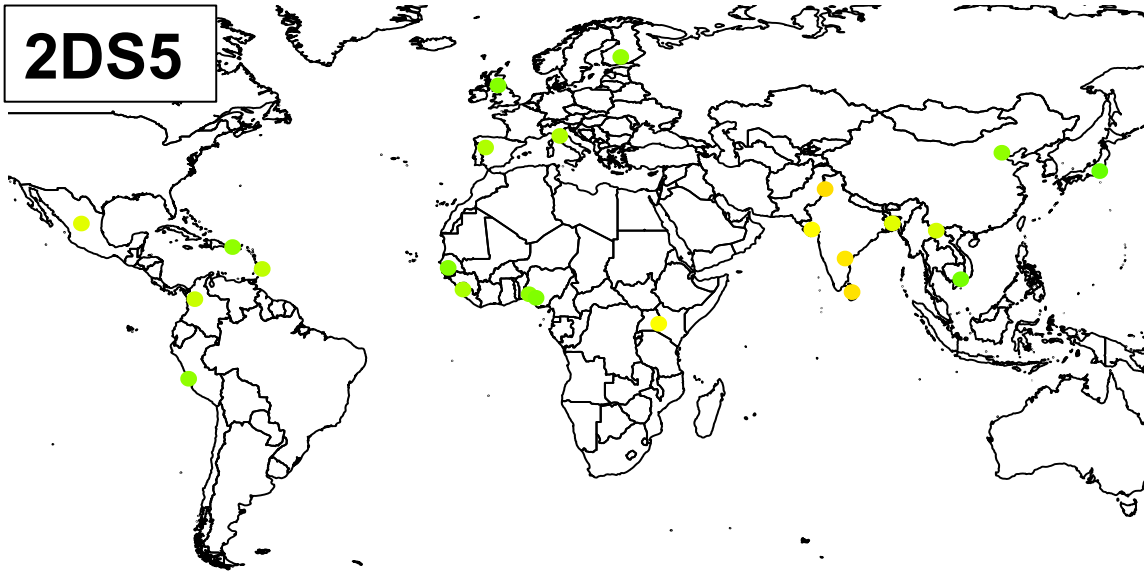

2DL2

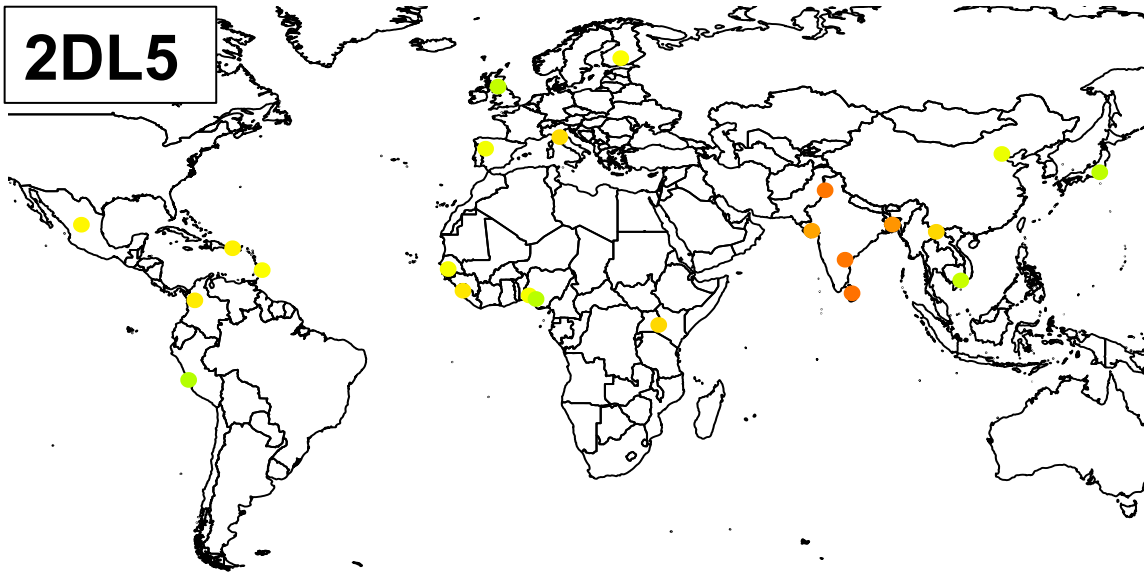

2DS2


2DS1


3DS1


2DS3


2DS5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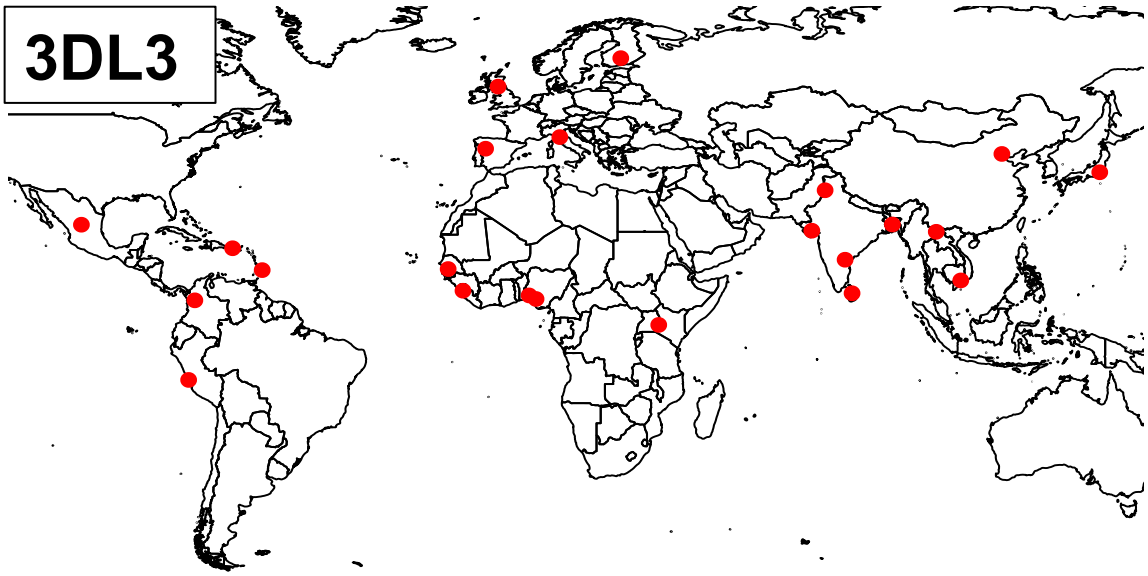
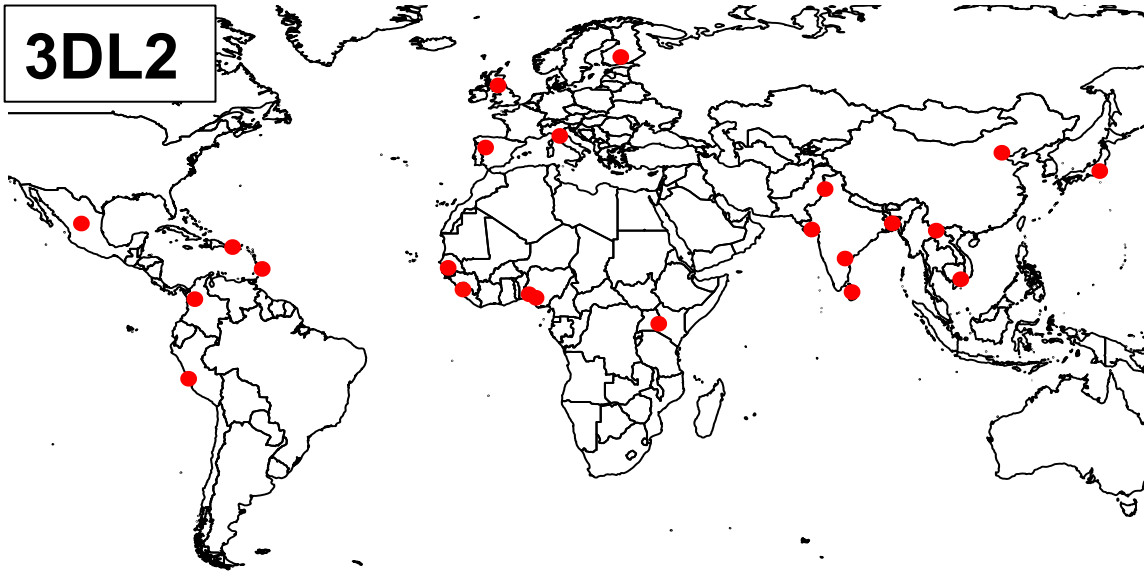
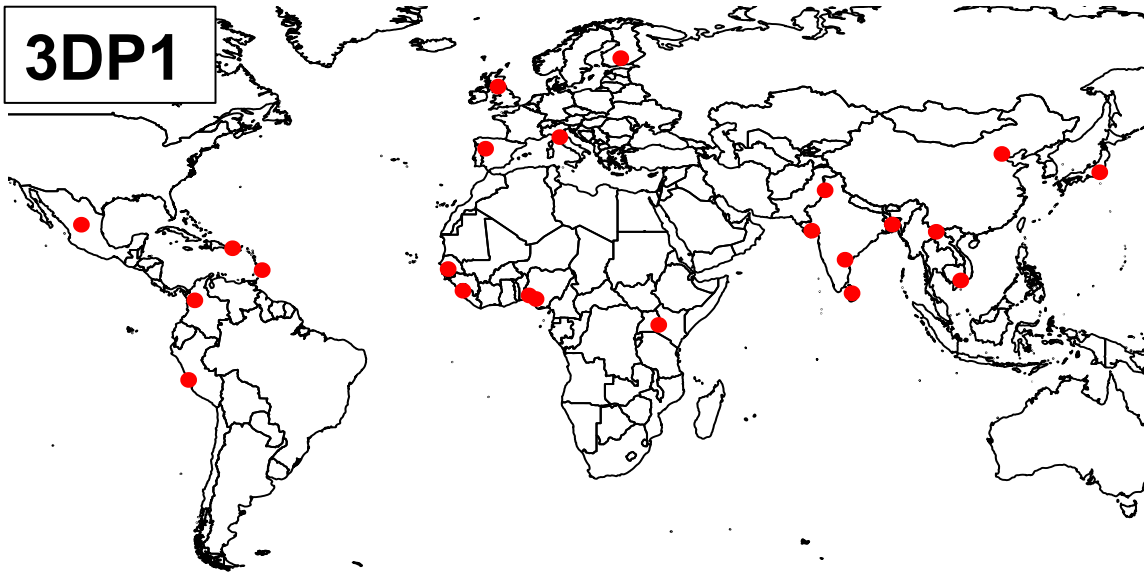
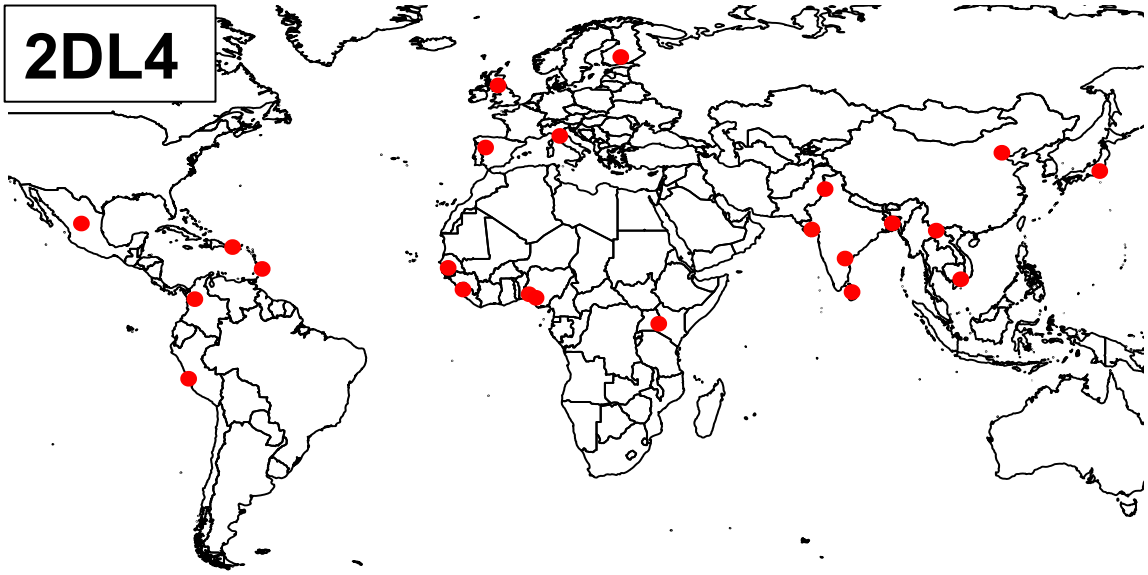
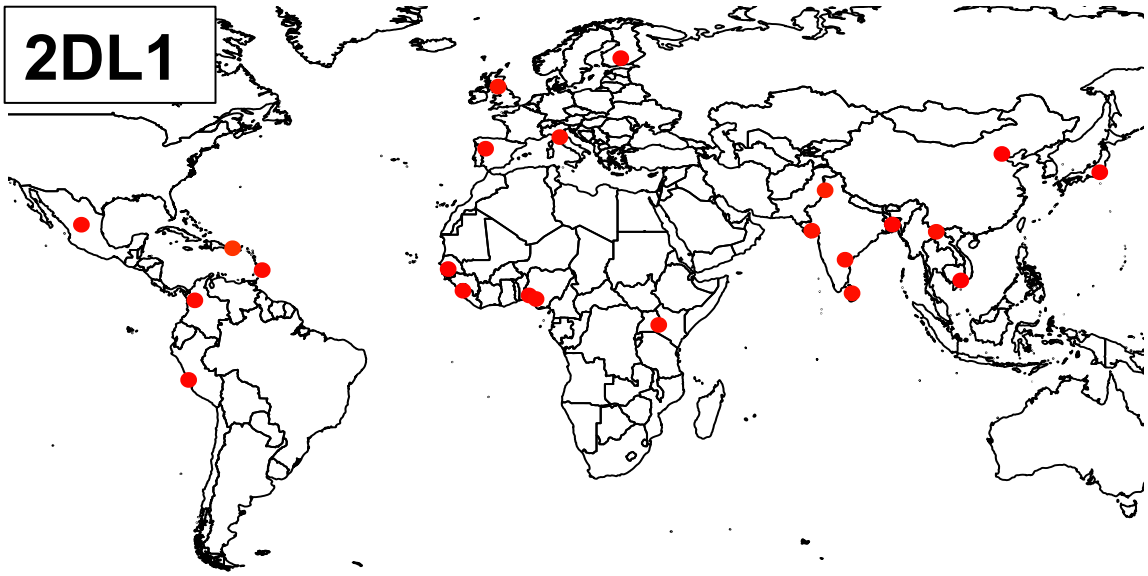
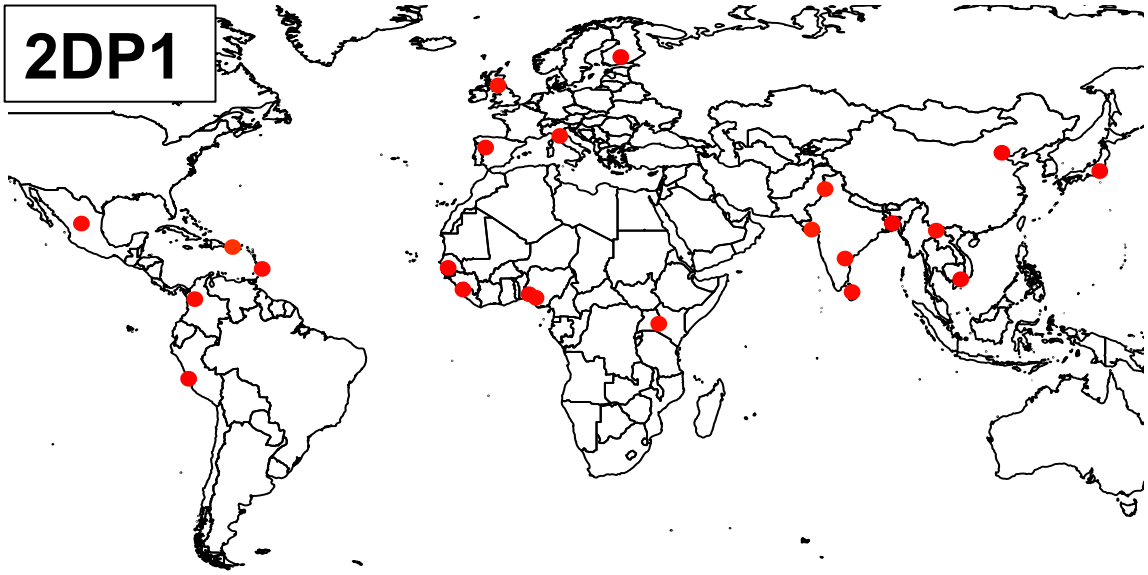

3DL3


3DL2


3DP1


2DL4


2DL1


2DP1

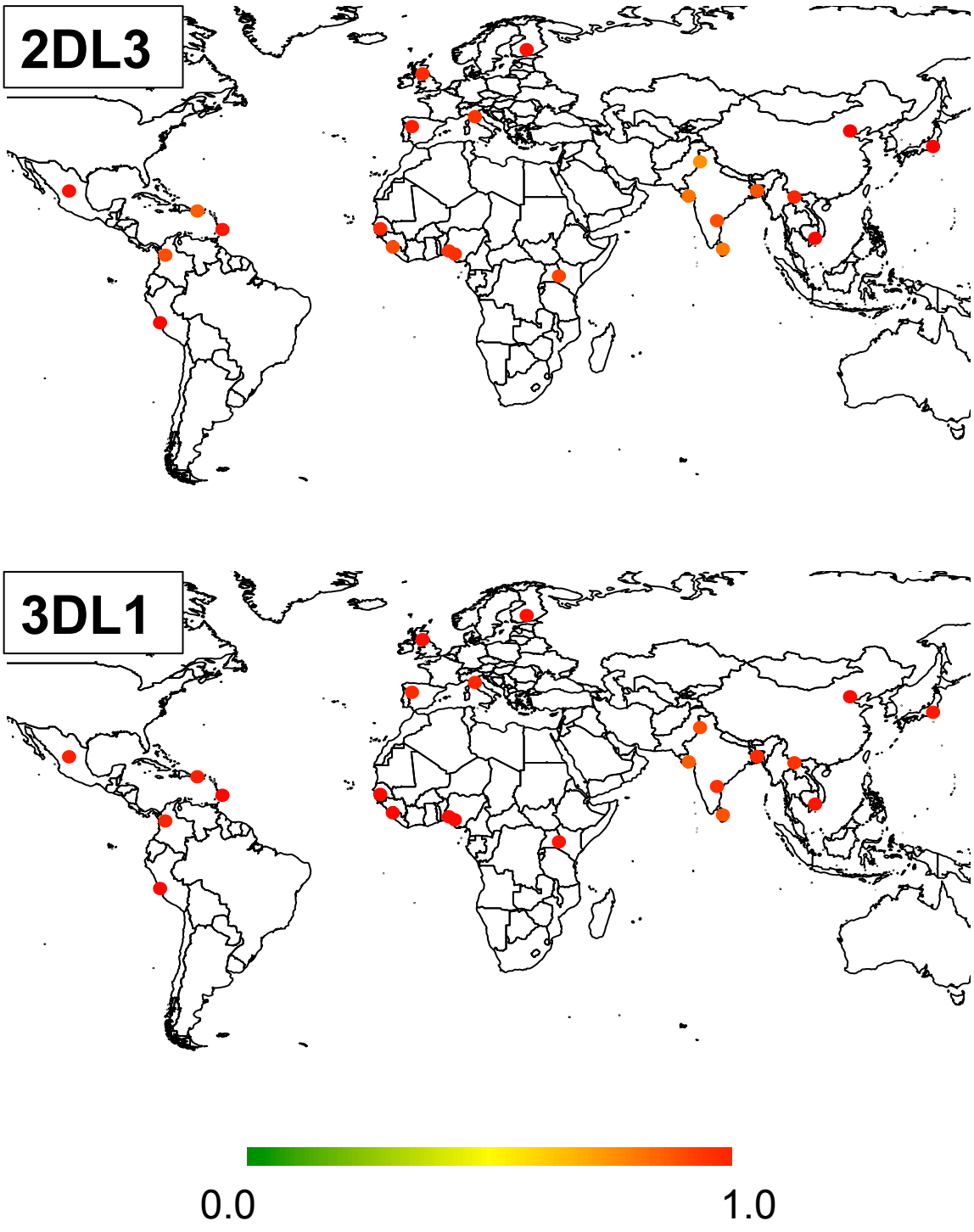


Figure 13 Worldwide gene frequencies for KIR2DS4 variants, KIR B genes, KIR framework genes, and KIR A genes.

3.2.5 KIR short variants by population

Variant calling analysis identified 56 significant single base substitutions across seven KIR genes and both pseudogenes, 36 of which are nonsynonymous (Figure 14a and Tables A8a-c). The most diverse inhibitory KIR variants were found within exon 5 of KIR2DL4, which encodes the extracellular D2 domain. Two nucleotide substitutions within this region (G412A and C625G) result in amino acid residue changes A115T and P186A respectively. The A/A genotype at position 412 and the G/G genotype at position 625 are most common within all groups of African ancestry, three East Asian Groups (Beijing, Southern Han, and Tokyo), and the Peruvian group when comparing each of these groups to all other OKG populations (412 A/A mean OR = 3.52, mean 95% CI = 1.97-6.29 and 625 G/G 3.66, 1.95-6.93). The 412 G/G and 625 C/C genotypes occur most commonly within groups of European and South Asian descent, as well as within the Colombian group (412 G/G 0.26, 0.12-0.56 and 625 C/C 0.23, 0.10-0.55). KIR2DS5 is the only activating KIR containing a significant population-associated SNP, and a G535A nucleotide substitution (producing a G158R codon change in exon 5) exhibits the most extreme variation across the human population out of all KIR variants. All five South Asian groups, as well as the Iberian and Chinese Dai groups, have an A/A genotype exclusively at this position (OR cannot be computed because all 324 individuals spanning these seven populations have the 535 A/A genotype). The other most significant KIR framework variants are a 3DL2 exon 4 G474T SNP (E137D) and a 3DL3 exon 4 G502A SNP (V147I). The 3DL2 474 T/T genotype occurs at very high frequency within all five East Asian groups and the Peruvian group (12.06, 6.64-21.95); while the 474 G/G genotype is much more commonly found in six of seven African groups, four of five European groups, and three of five South Asian groups (0.12, 0.03-0.51). For the 3DL3 variant, the 502 A/A genotype is strongly

a

| | | |

b

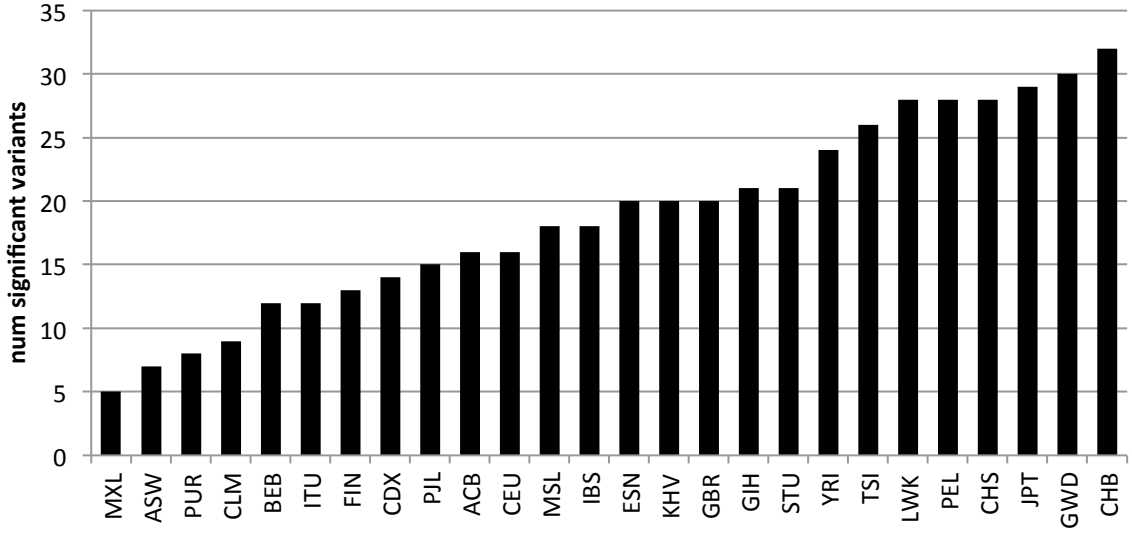


Figure 14 Short KIR variants across human populations. (a) 36 significant nonsynonymous KIR single base substitutions. OR < 1.0 = genotype1 significantly associated with population. OR > 1.0 = genotype2 significantly associated with population. Blank field = not significant. The Altai Neandertal genome does not encode 2DS5 or 3DP1. Purple = less than five reads provided inner coverage of the variant away from the read ends. (b) Number of significant KIR variants per OKG population.

associated with four of five South Asian groups, all five East Asian groups, and the Peruvian group (4.91, 2.20-11.28); while the 502 G/G genotype occurs mostly within all seven African groups and the Toscani and Puerto Rican groups (0.28, 0.15-0.53). Two populations living in the Southwestern United States (Mexican and African origin), as well as the Puerto Rican and Colombian groups, exhibit the fewest number of significant KIR variants (mean = 7.5 variants), while two East Asian groups (Beijing and Tokyo) and the Gambian group have the highest number of population-correlated KIR variants (mean = 31.0 variants) (Figure 14b).

3.2.6 Ancient human KIR variation

For the 2DL4 exon 5 polymorphisms at positions 412 and 625, all four ancient human genomes have the same genotypes that are significantly associated with the European and South Asian OKG populations and significantly less associated with the African and East Asian

populations (Figure 14a). However, three ancient genomes have the same 2DS5 position 535 genotype that is strongly associated with the LWK group in Africa (the Altai Neandertal genome does not encode 2DS5). The genotype of all four archaic genomes at 3DL3 position 502 is also most common within African populations. The Altai and Vindija Neandertal genomes share identical genotypes for 18 of the 19 variants where genotyping information is available for both individuals. They differ only at position 869 within exon 5 of KIR3DL3, where Altai has an A/A genotype that is significantly associated with modern human groups in Beijing and Peru, and Vindija has a C/C genotype that is not significantly found within any of the 26 OKG populations. The Vindija and Sidron Neandertals are identical at 24 KIR variant sites and differ only at 2DL4 position 395 within exon 5, where Sidron has a C/T heterozygous genotype associated with three East Asian groups (Beijing, Southern Han, and Vietnam), and Vindija has a T/T homozygous genotype that is not significantly associated with any OKG groups. Although the Denisovan and Sidron genomes encode the same KIR gene content, five of 24 KIR variants differ between them.

3.3 Discussion

The results indicate that early KIR genes remained prevalent as humans migrated from the African continent into Eurasia. KIR2DL2 and 2DL5 are likely the earliest B content genes and emerged prior to the first archaic human exodus from Africa. Additional migrations out of Africa occurred subsequent to the appearance of 2DS2. The centromeric KIR B genes (2DS2 and 2DL2) are found at low frequencies in East Asia, and the activating B genes in the telomeric KIR subregion are less common for most African groups. KIR B genes occur at their highest frequencies in populations that originated within and around the Indian subcontinent, which may indicate a founder effect from European migrants carrying KIR B content. Deletion variants of KIR2DS4 are found within all of the ancient humans and are more common in European and

South Asian populations. Functional 2DS4 alleles are more prevalent within African genomes and unexpectedly re-emerge in Vietnam, China, and Japan - possibly as the result of a founder migration route from Africa to Southeast Asia to the Far East. African ancestral groups living in Africa are dominated by low KIR gene content and are in the upper half of short variant frequencies that deviate significantly from the rest of the world due to geographic isolation (and, consequently, low genetic admixture) (Figure 15). Europeans also mostly have low gene content but exhibit more moderate variant deviation from the world, while South Asians have higher gene content with moderate variant deviation. Far Eastern genomes encode low KIR content with the least allelic admixture. The individuals with African ancestry living in the Southwestern United States, as well as the Mexican, Colombian, and Puerto Rican groups, have the least divergence from global variant frequencies regardless of specific KIR gene content as a result of population admixture. Peruvians have very low frequencies of B gene content and are the least admixed of groups in the Americas. For the SNPs with the greatest range of diversity across modern humans, the archaic humans match the European and South Asian genotypes at some loci (e.g. 2DL4 pos 412 and 625) and African genotypes at others (e.g. 3DL3 pos 502). Interbreeding between human species may have also contributed KIR content to modern humans.

Due to the unprecedented nature of this research, I emphasized stringency in the data analysis to maximize the likelihood of high confidence calls at the expense of potentially losing the sensitivity to identify findings with smaller effects. For KIR gene content typing, three levels of stringency (duplicate read filtering, minimum expected frequencies, and FDR multiple testing correction) ensured confidence in accurately calling associations between KIR types and populations. Furthermore, the similarity in linkage frequencies between my typing approach and those reported in the Allele*Frequencies database (the world's largest repository of KIR typing information) increases confidence in SeRRAMC gene presence/absence calls and serves

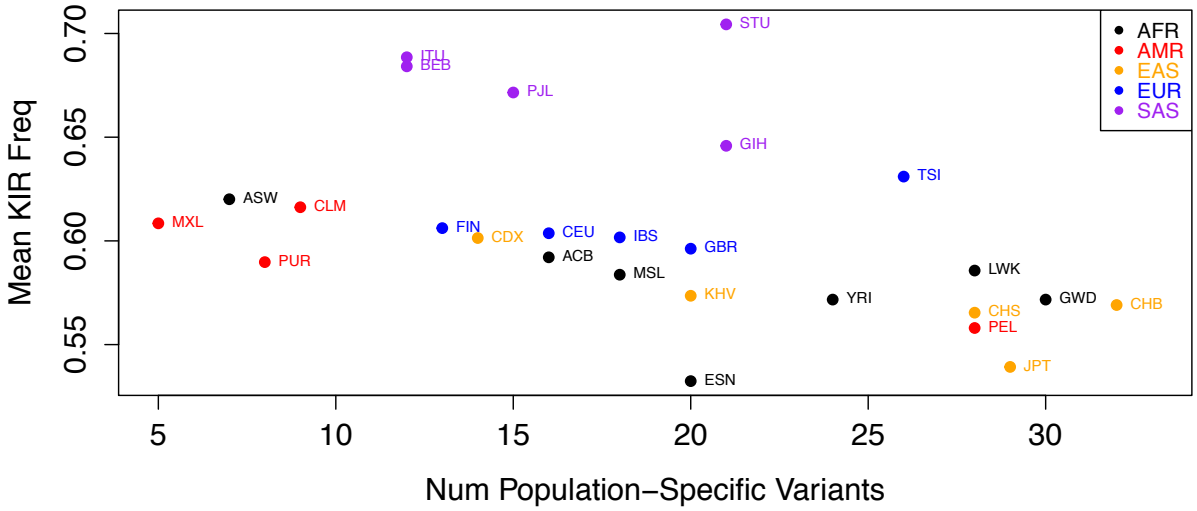


Figure 15 Worldwide KIR gene content and allelic polymorphism. OKG populations clustered by mean KIR frequency (a function of KIR B gene content, since KIR A and framework genes are common across all groups) versus the number of significant KIR variants specific to a population (a function of admixture).

as another level of validation for the typing algorithm in addition to the SSO-PCR validation. For variant calling, an additional three levels of stringency (minimum variant quality, minimum sample genotype quality, and minimum sample read depth) were imposed. Duplicate read filtering also means that all reads providing coverage for any given variant site differ from each other by at least one nucleotide, thereby further increasing the stringency threshold for calling a particular variant.

3.4 Methods

3.4.1 KIR gene content calling

Whole exome BAM files sequenced from the DNA of 2535 individuals spanning 26 human populations were downloaded from the 1000 Genomes Project FTP site and processed with the SeRRAMC algorithm. Heatmaps for individual KIR gene frequencies were plotted on a map of the world using the rworldmap package v1.3-1 in the R statistical computing

environment[48]. Three OKG populations (ASW, CHS, and CEU) were not plotted due to ambiguous geographical origins.

3.4.2 KIR genotype significance testing

For each unique KIR type, chi square testing compared the members of each OKG group to all other members of the cohort in order to identify KIR genotypes significantly associated with specific populations. Because of the large number of ultra-rare KIR types, comparisons were restricted to the 105 statistical tests with an expected frequency of five or greater in each chi square cell. Thirty-eight of these tests had a P-value ≤ 0.05, leaving 34 significant tests after 10% FDR correction. Chi square tests were oriented so that an odds ratio less than 1.0 indicates a genotype occurs at a significantly lower frequency within a given population compared to the rest of the cohort, while an odds ratio greater than 1.0 indicates a higher prevalence of the KIR type within the group.

3.4.3 KIR variant calling and testing

VCF files were generated from remapped BAM files for each combination of KIR gene and OKG population using samtools 0.1.18 mpileup and bcftools 0.1.17. Only short variants with a Phred-scaled quality score of at least 13 (indicating a probability of incorrect alternate base calling ≤ 0.05) for at least one OKG population were selected. To put things in perspective, out of 3715 variant-population combinations, 2166 (58.3%) had a quality score of 999 (the highest score recorded), 3248 (87.4%) had a quality score ≥ 20 (≤ 0.01 probability of wrong alt base call), and only 313 (8.4%) had a quality score < 13. For each of these filtered variants, only those samples with a minimum 10x unique read coverage at the variant site and with a minimum genotype quality score of 13 (≤ 0.05 probability genotype call is wrong, conditioned on the site's being variant) were selected. For each high confidence variant, chi

square testing compared two genotypes for each individual OKG population versus the rest of samples in the cohort that met minimum quality standards. An odds ratio < 1.0 indicates that the first genotype is associated with the specific population, and an odds ratio > 1.0 indicates that the second genotype is associated with the group. The first set of tests compared variants that were homozygous for the reference base to heterozygotes (one reference and one alternate). Out of 1168 statistical tests, 449 had a P-value ≤ 0.05, leaving 406 significant tests after 10% FDR correction. The second test set compared heterozygous to homozygous alternate variants, producing 84 significant tests from 429 total comparisons following multiple testing correction. The third set of tests compared homozygous reference versus homozygous alternate variants, yielding 255 corrected significant tests out of 479 total. The combined significant variants were reduced to the set of 37 SNPs that produced nonsynonymous codons.

3.4.4 Archaic human KIR analysis

The three Neandertal exome and Denisova genome BAM files mapped to GRCh37 were downloaded from the Max Planck Institute for Evolutionary Anthropology web site (http://cdna.eva.mpg.de/neandertal/exomes/BAM/ and http://cdna.eva.mpg.de/denisova/alignments/) and processed with the SeRRAMC algorithm to generate remapped KIR BAM files. However, due to lower read coverage compared to the OKG alignment files, calls for the ancient human samples were made from high quality raw remapped counts rather than from normalized remapped read counts (Table 2). For the Sidron sample, only seven reads remapped to 2DL3. Further analysis showed that four reads containing a 36 nucleotide 2DL3-specific oligomotif and zero edit distance from the 2DL3 reference mapped to exon 4, another two reads containing a 33 nt motif and zero edit distance mapped to exon 7, and one read containing an 11 nt motif and zero edit distance mapped to exon 9. Because reads mapped to multiple exons with no mismatches, and because reads in two of

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
neandertalAltai	207	0	41	23	21	42	0	371	141	0	316	0	0	0	0	232	162
neandertalVindija	558	2	78	19	352	83	469	735	225	1	558	1	238	0	0	491	539
neandertalSidron	180	0	46	7	114	43	164	395	79	7	299	44	83	0	0	135	147
denisova	201	0	4	17	122	30	312	488	59	19	412	108	76	1	0	120	194

Table 2 KIR-specific remapped raw read counts for four archaic human samples.

these regions contain long motifs, the presence of 2DL3 within this genome can be called with confidence. Seven reads also mapped to 3DS1 for Sidron, but a similar analysis resulted in a presence call for the gene. Four reads containing a 27 nt motif and zero edit distance mapped to exon 7, and three reads containing a 9 nt motif mapped to exon 7 (two with zero edit distance and one with a single base mismatch). For the Denisova sample, four reads mapped to 2DL2 exon 5, but the motif they contain is only 10 nt long, and the motif is located towards the end for three of the reads. Therefore, the presence of 2DL2 in this sample was called as ambiguous. All other KIR presence/absence calls for the ancient humans were unambiguous.

For the nonsynonymous variants identified as significantly different across the modern human population, the corresponding genotypes of the four ancient human samples were queried. Because of the lower coverage within these alignment files, the minimum number of reads covering a variant was reduced from 10 for the OKG samples to five for the ancient samples. However, mean read coverages across all significant SNPs were 12.5, 37.8, 14.9, and 18.1 for the Altai, Vindija, Sidron, and Denisova samples respectively. Additional quality control measures were necessary for the Vindija and Sidron exomes, which contain many reads with low quality bases at and near the read ends as a result of errors inherent to sequencing chemically damaged ancient DNA. Deamination of cytosine residues within damaged DNA can produce C → T substitutions near the ends of sequence reads, creating the potential for false variant calls if incorrect bases provide coverage at a given position[49,50]. For this reason, the minimum coverage for these two samples required reads that cover the variant position at least

six bases in from either end. Three variants did not meet this threshold (Vindija 2DP1 pos 1000 and 3DL1 pos 496, Sidron 3DL1 pos 1180) and were flagged as potentially problematic in Figure 14a.

Chapter 4: KIR immunogenetics cancer analysis

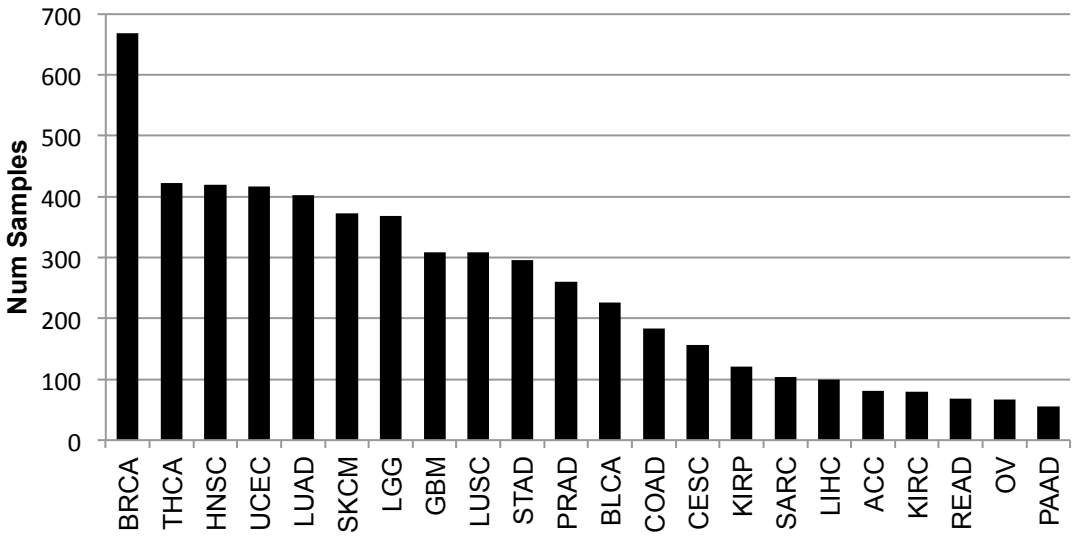
4.1 Introduction

The SeRRAMC algorithm was also applied to a sequence analysis of 5489 WXS BAM files from the TCGA sequence repository for 22 different types of cancer to identify KIR gene content and variation associated with disease (Figure 16 and Table A9). The OKG samples from the population genetics study (individuals not known to have cancer at the time of sequencing) were used as controls for comparison to the TCGA samples (individuals known to have cancer at the time of sequencing). This created the possibility of finding significant results due to KIR gene and allele frequency differences between populations of disparate demographics and not due to cancer. As a measure to prevent this type of confounding effect, the cancer and control sequences were stratified into European, African, and Asian cohorts.

4.2 Results

4.2.1 Similarity between KIR genotypes for stratified TCGA and OKG cohorts

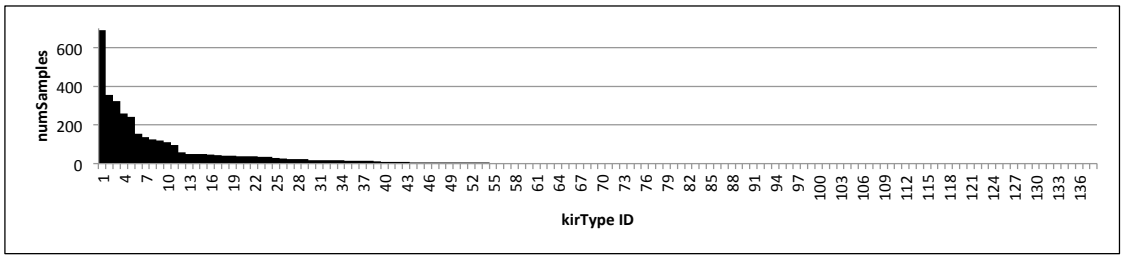
For individuals of nonhispanic European descent, SeRRAMC KIR typing revealed a total of 138 unique KIR genotypes across 3702 samples from the TCGA cohort (Figure 17a and Table A10a). The 23 most common types each account for at least 1% of all samples, and 562 samples (15.2%) are distributed across a long tail of 115 types, 52 of which occur once within the entire cohort. The four nonhispanic OKG populations (CEU, GBR, FIN, and TSI) comprise 52 unique KIR types, and all but four are found within the TCGA samples. KIR type AA homozygous for 2DS4 deletion variants is the most common genotype for both cohorts, representing 18.6% of TCGA samples and 16.1% of OKG samples. KIR type AA with one functional and one deletion 2DS4 allele is the second most common genotype (9.6% and 11.6% of TCGA and OKG respectively). KIR type AA homozygous for 2DS4 functional



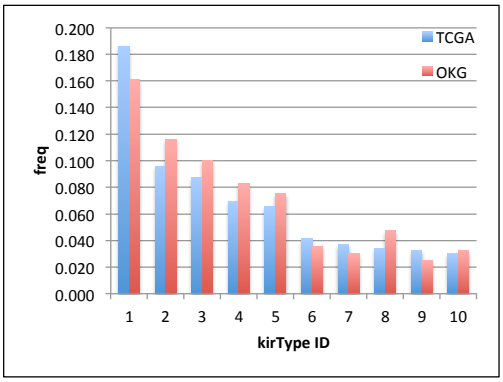
code	disease
ACC	Adrenocortical Carcinoma
BLCA	Bladder Urothelial Carcinoma
BRCA	Breast Invasive Carcinoma
CESC	Cervical Squamous Cell Carcinoma
COAD	Colon Adenocarcinoma
GBM	Glioblastoma Multiforme
HNSC	Head & Neck Squamous Cell Carcinoma
KIRC	Kidney Renal Clear Cell Carcinoma
KIRP	Kidney Renal Papillary Cell Carcinoma
LGG	Lower Grade Glioma
LIHC	Liver Hepatocellular Carcinoma
LUAD	Lung Adenocarcinoma
LUSC	Lung Squamous Cell Carcinoma
OV	Ovarian Serous Cystadenocarcinoma
PAAD	Pancreatic Adenocarcinoma
PRAD	Prostate Adenocarcinoma
READ	Rectum Adenocarcinoma
SARC	Sarcoma
SKCM	Skin Cutaneous Melanoma
STAD	Stomach Adenocarcinoma
THCA	Thyroid Carcinoma
UCEC	Uterine Corpus Endometrial Carcinoma

Figure 16 Disease group distribution of 5489 TCGA WXS BAM files.

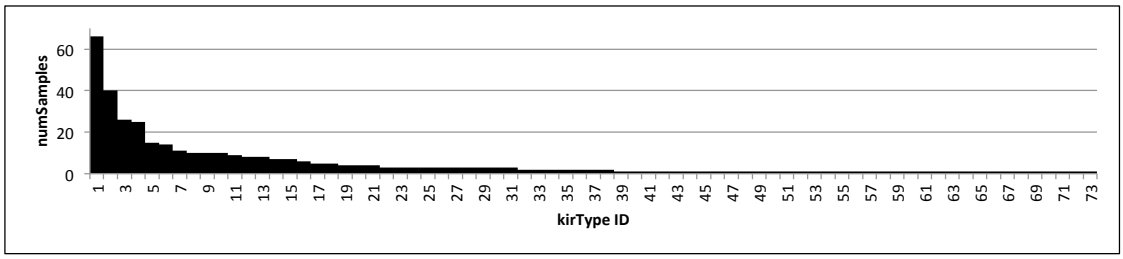
a



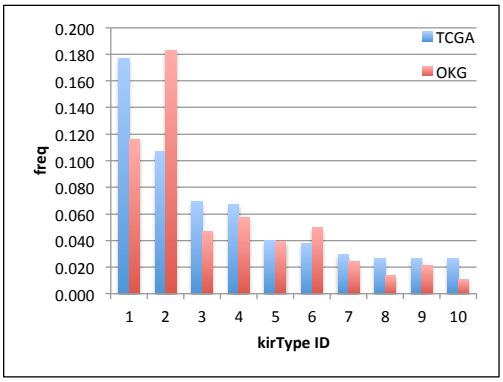
kirTypeID	count	freq	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
1	689	0.186	■			■	■	■	■	■	■							■	■
2	355	0.096	■			■	■	■	■	■	■						■	■	■
3	324	0.088	■			■	■	■	■	■	■	■	■		■	■		■	■
4	258	0.070	■	■	■	■	■	■	■	■	■						■	■	■
5	242	0.065	■	■	■	■	■	■	■	■	■							■	■
6	154	0.042	■	■	■	■	■	■	■	■	■		■	■				■	■
7	136	0.037	■	■	■	■	■	■	■	■	■	■	■		■	■		■	■
8	126	0.034	■	■	■	■	■	■	■	■	■	■	■	■				■	■
9	121	0.033	■	■	■	■	■	■	■	■	■		■	■			■	■	■
10	112	0.030	■	■	■	■	■	■	■	■	■	■	■	■		■		■	■

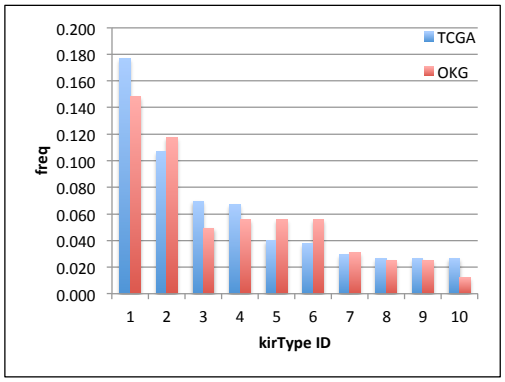


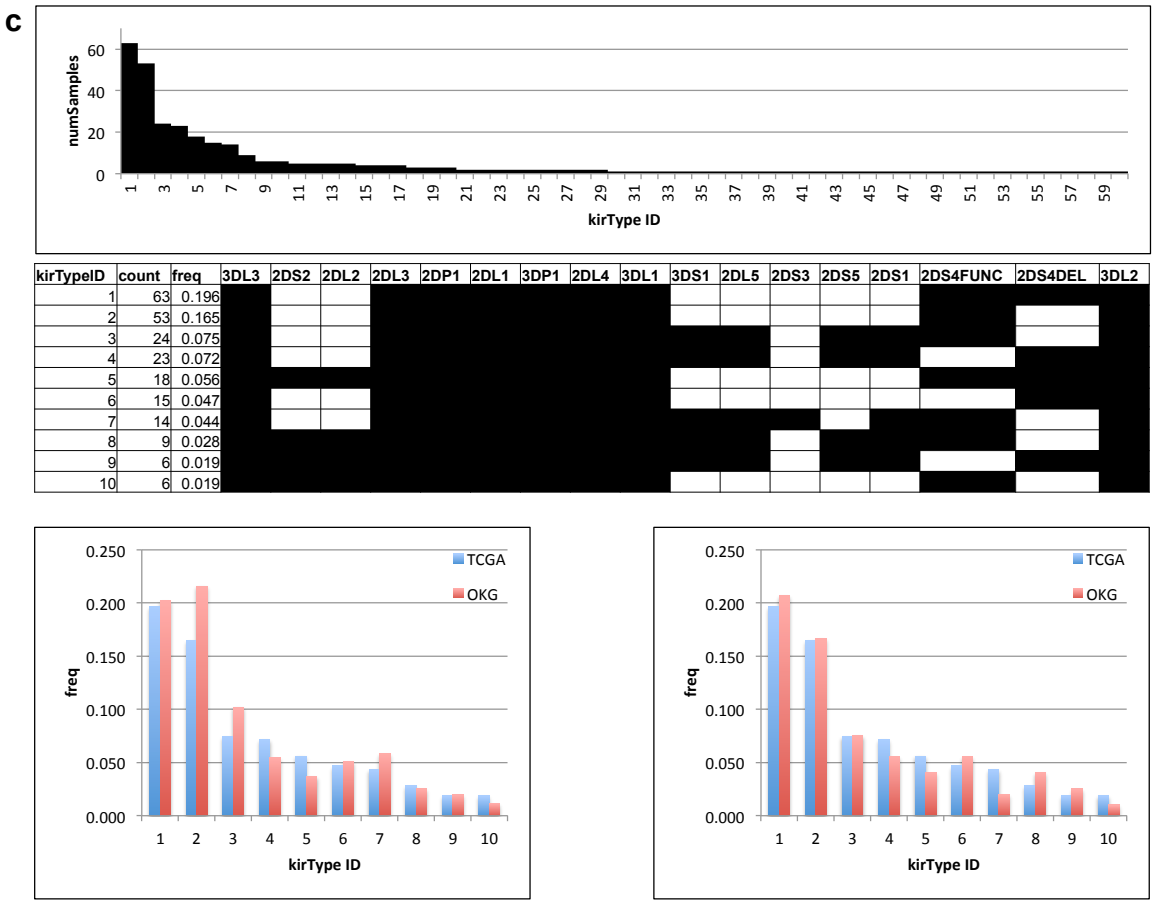
b



kirTypeID	count	freq	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
1	66	0.177	■			■	■	■	■	■	■								■
2	40	0.107	■			■	■	■	■	■	■								■
3	26	0.070	■	■	■	■	■	■	■	■	■		■	■				■	■
4	25	0.067	■			■	■	■	■	■	■							■	■
5	15	0.040	■	■	■	■	■	■	■	■	■						■	■	■
6	14	0.038	■	■	■	■	■	■	■	■	■		■	■			■		■
7	11	0.029	■	■	■	■	■	■	■	■	■						■		■
8	10	0.027	■	■	■	■	■	■	■	■	■		■	■				■	■
9	10	0.027	■	■	■	■	■	■	■	■	■		■		■	■		■	■
10	10	0.027	■	■	■	■	■	■	■	■	■		■		■			■	■







kirTypeID	count	freq	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
1	63	0.196																	
2	53	0.165																	
3	24	0.075																	
4	23	0.072																	
5	18	0.056																	
6	15	0.047																	
7	14	0.044																	
8	9	0.028																	
9	6	0.019																	
10	6	0.019																	

Figure 17 Distribution of KIR types for stratified TCGA WXS BAM Files. (a) The European cohort comprises 138 unique KIR genotypes, with the ten most frequent types representing 2517 (68.0%) of all samples and a maximum frequency difference of 0.025 between the cancer and control samples for the most common type. (b) The African cohort spans 73 unique KIR types, and the top ten types account for 227 (60.9%) of all samples. The maximum frequency difference between the TCGA samples and all African OKG samples is 0.076 (for the second most frequent type), which reduces to 0.010 when comparing the cancer group to two admixed African OKG groups. (c) The Asian cohort spans 60 unique KIR types, and the top ten types account for 231 (72.0%) of all samples. The maximum frequency difference between the TCGA samples and all Asian OKG samples is 0.051 (for the second most frequent type), which reduces to 0.002 when comparing the cancer group to two admixed Asian OKG groups.

variants is only the 17th most abundant genotype (1.2% and 1.8% respectively). The highest frequency KIR BX genotype contains all A genes (homozygous for 2DS4 deletion variants) plus 3DS1, 2DL5, 2DS5, and 2DS1 and accounts for 8.8% of TCGA samples and 10.1% of OKG samples. All other KIR BX types within the top ten genotypes encode the centromeric 2DS2 and 2DL2 genes. For the ten most common TCGA KIR types, the average frequency difference between the two cohorts is 0.012 ± 0.007 (mean ± s.d.) with a maximum difference of 0.025 for the most common genotype.

For the samples of nonhispanic African descent, KIR typing produced 73 unique genotypes across 373 TCGA participants (Figure 17b and Table A10b). The 21 most common types each account for at least 1% of all samples, and 79 samples (21.2%) are distributed across a long tail of 52 types, 35 of which occur once within the entire cohort. The two admixed African OKG populations (ASW and ACB) share 31 unique KIR types in common with the TCGA samples. KIR type AA 2DS4FUNC/DEL heterozygous is the most common genotype for both cohorts, representing 17.7% of TCGA samples and 14.8% of OKG samples. KIR type AA 2DS4FUNC/FUNC homozygous is the second most common genotype (10.7% and 11.7% of TCGA and OKG respectively). KIR type AA homozygous for 2DS4 deletion variants is the fourth most abundant genotype (6.7% and 5.6% respectively). The highest frequency KIR BX genotype contains all A genes (heterozygous for 2DS4) plus 2DS2, 2DL2, 2DL5, and 2DS3 and accounts for 7.0% of TCGA samples and 4.9% of OKG samples. All KIR BX types within the top ten genotypes encode the centromeric 2DS2 and 2DL2 genes, but none contain the telomeric 3DS1. For the ten most common TCGA KIR types, the average frequency difference between the TCGA cohort and all seven African OKG groups (ACB, ASW, ESN, GWD, LWK, MSL, and YRI) is 0.022 ± 0.025 (mean ± s.d.) with a difference of 0.061 for KIR AA 2DS4FUNC/DEL and 0.076 for KIR AA 2DS4FUNC/FUNC. When comparing the TCGA samples to only the two admixed African OKG groups, the mean top ten genotype frequency difference drops to 0.012 ± 0.009 with a maximum difference of 0.029 for the most common KIR type.

For the samples of Asian descent, KIR typing produced 60 unique genotypes across 321 TCGA participants (Figure 17c and Table A10c). The 17 most common types each account for at least 1% of all samples, and 58 samples (18.1%) are distributed across a long tail of 43 types, 31 of which occur once within the entire cohort. The two admixed Asian OKG populations (KHV and CDX) share 31 unique KIR types in common with the TCGA samples. KIR type AA

2DS4FUNC/DEL heterozygous is the most common genotype for both cohorts, representing 19.6% of TCGA samples and 20.7% of OKG samples. KIR type AA 2DS4FUNC/FUNC homozygous is the second most common genotype (16.5% and 16.7% of TCGA and OKG respectively). KIR type AA homozygous for 2DS4 deletion variants is the sixth most abundant genotype (4.7% and 5.6% respectively). The highest frequency KIR BX genotype contains all A genes (homozygous for functional 2DS4) plus 3DS1, 2DL5, 2DS5, and 2DS1 and accounts for 7.5% of TCGA samples and 7.6% of OKG samples. Four of seven KIR BX types within the top ten genotypes encode the centromeric 2DS2 and 2DL2 genes, but only one top ten type contains 2DS3. For the ten most common TCGA KIR types, the average frequency difference between the TCGA cohort and all five East Asian OKG groups (CDX, CHB, CHS, JPT, and KHV) is 0.015 ± 0.015 (mean ± s.d.) with a difference of 0.051 for KIR AA 2DS4FUNC/FUNC. When comparing the TCGA samples to only the two admixed Asian OKG groups, the mean top ten genotype frequency difference drops to 0.010 ± 0.007 with a maximum difference of 0.023 for the seventh most common KIR type.

After stratifying exomes by race and ethnicity, none of the KIR genotypes are significantly more or less associated with the cancer cohort than with the control cohort (Tables A11a-c).

4.2.2 KIR short variants associated with cancer

Variant calling analysis identified five significant single base substitutions across KIR3DL3 and both pseudogenes (Figure 18a-c). The C/C and C/A genotypes at 3DL3 position 961 are significantly more associated with the Caucasian melanoma samples than the A/A homozygous genotype (C/C = 0.37, 0.23 - 0.60, 4.8×10^{-5}; C/A = 0.41, 0.25 - 0.66, 4.0×10^{-4}; OR, 95% CI, P-value). The Caucasian prostate adenocarcinoma samples are significantly associated with two polymorphisms within the 3DP1 pseudogene. The first is an A479C

a

gene	pos	exon	genotype1	genotype2	refAA	altAA	ACC	BLCA	BRCA	CESC	COAD	GBM	HNSC	KIRC	KIRP	LGG	LIHC	LUAD	LUSC	OV	PAAD	PRAD	READ	SARC	SKCM	STAD	THCA	UCEC
3DL3	961	7	C/A	A/A	H	N																						
3DL3	961	7	C/C	A/A	H	N																						
3DL3	971	7	T/T	T/C	V	A																						
3DP1	479	4	A/C	C/C																								
3DP1	774	5	G/C	C/C																								

b

gene	pos	exon	genotype1	genotype2	refAA	altAA	ACC	BLCA	BRCA	CESC	COAD	GBM	HNSC	KIRC	KIRP	LGG	LIHC	LUAD	LUSC	OV	PAAD	PRAD	READ	SARC	SKCM	STAD	THCA	UCEC
2DP1	1313	9	A/A	A/C																								
3DL3	971	7	T/T	T/C	V	A																						

c

gene	pos	exon	genotype1	genotype2	refAA	altAA	ACC	BLCA	BRCA	CESC	COAD	GBM	HNSC	KIRC	KIRP	LGG	LIHC	LUAD	LUSC	OV	PAAD	PRAD	READ	SARC	SKCM	STAD	THCA	UCEC
3DL3	971	7	T/T	T/C	V	A																						

Figure 18 Short KIR variants associated with cancer. (a) European cohort. (b) African cohort. (c) Asian cohort. OR < 1.0 = genotype1 significantly associated with disease group. OR > 1.0 = genotype2 significantly associated with disease group. Blank field = not significant.

substitution in exon 4 (4.89, 2.42 - 9.88, 7.34 x 10^{-6}), and the second is a G774C substitution in exon 5 (4.03, 1.89 - 8.59, 3.56 x 10^{-4}). The breast invasive carcinoma participants of African descent are significantly associated with an A1313C substitution in 2DP1 exon 9 (3.60, 1.72 - 7.52, 8.41 x 10^{-4}).

At first glance, a 3DL3 T971C polymorphism appears to be a highly significant variant in 14 Caucasian cancers, in breast invasive carcinomas of African descent, and in stomach

adenocarcinomas of Asian descent. However, four cancers are associated with a T/C genotype at this position, while the other ten correlate to a T/T genotype. Since there is no biological reason for one variant to create a predisposition to certain cancers, while another variant at the same position represents a risk factor for other cancers, I suspected that these statistical tests were significant due to error and/or some confounding factor. For this reason, I conducted an investigation to determine whether or not batch effects, rather than cancer status, were responsible for the statistical significance of these KIR variants.

4.2.3 Analysis of batch effects within the sequence cohorts

The TCGA samples were sequenced primarily at three Genome Sequencing Centers (Broad Institute = BI, Baylor College of Medicine = BCM, and Washington University School of Medicine = WUSM), and a small percentage of samples were sequenced at the Broad Institute Genome Characterization Center (BI_CGCC) (Figure 19a). A metadata analysis of the samples revealed that read lengths within each TCGA BAM file are dependent on the location where the sequences were generated. All of the BAM files that contain 76 nucleotide paired-end reads were sequenced at BI or BI_GCC, while all WUSM reads are 100 nt paired-end and BCM reads are 101 or 100 nt paired-end (Figure 19b). The populations within the stratified OKG cohorts were each sequenced at multiple sequencing centers (Figure 19c), and read length is dependent on the processing site for these samples as well (Figure 19d). The OKG control cohort remained constant for each disease comparison, therefore the only variable was read length across cancer groups (e.g. each disease group of nonhispanic Caucasian TCGA participants was compared to the same stratified OKG cohort consisting of four nonhispanic European populations).

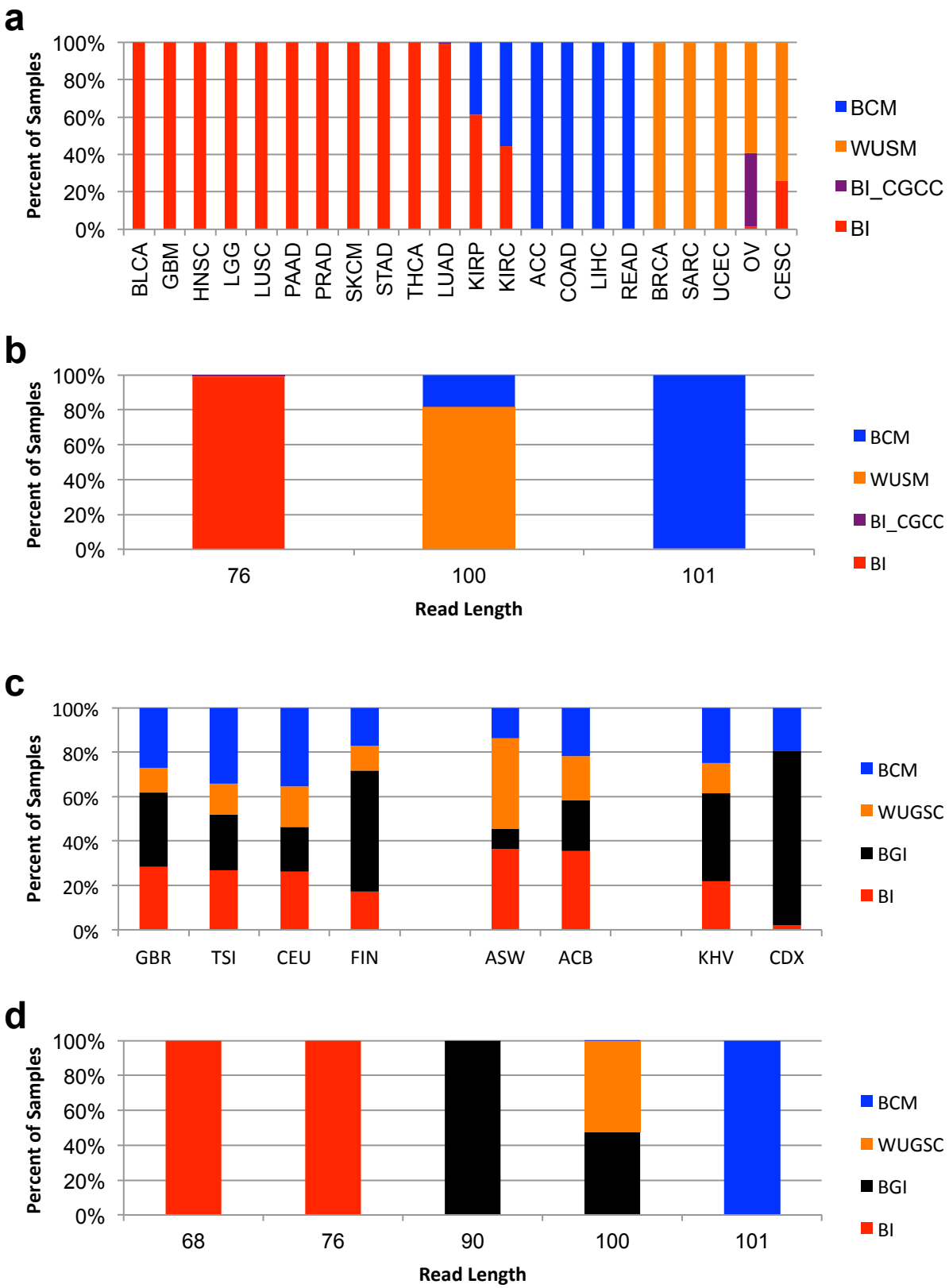


Figure 19 Batch effects metadata analysis of whole exome sequences. (a) TCGA disease groups by sequencing center. (b) TCGA read lengths by sequencing center. (c) OKG populations by sequencing center. (d) OKG read lengths by sequencing center.

For the variant at 3DL3 position 971, the four cancer groups significantly associated with a T/C genotype contain samples sequenced exclusively at 100 or 101 nt reads, while BAM files from the ten cancer groups associated with a T/T genotype all contain shorter reads (76 nt or less). Therefore, these variant calls are an artifact of disparities in sequence read length and are not biologically significant. However, the variant call at 3DL3 position 961 is only significant for the melanoma samples, which were all sequenced at 76 nt. If statistical significance were a result of read length differences, we would expect a similar effect size for one or more additional disease groups that were also sequenced at 76 nt. Since a significant variant call at this position was not observed for any other disease group, I concluded that the null hypothesis is rejected for melanoma due to true biological significance and not due to error. For the same reason, the associations between two 3DP1 variants and prostate adenocarcinoma in individuals of European descent are hypothesized to result from genuine biological significance.

4.3 Discussion

Of the 5489 germline DNA samples within the TCGA cohort, 373 were labeled as nonhispanic African descent, and 321 were labeled as Asian descent. Further stratification by cancer type resulted in groups with small sample sizes that were statistically underpowered to detect significant associations between KIR gene content and disease or between KIR allelic polymorphisms and disease (Figure 20). The two exceptions were the breast invasive carcinoma group, which represented 92 members (24.7%) of the African cohort, and the stomach adenocarcinoma group, which represented 80 samples (24.9%) from the Asian cohort.

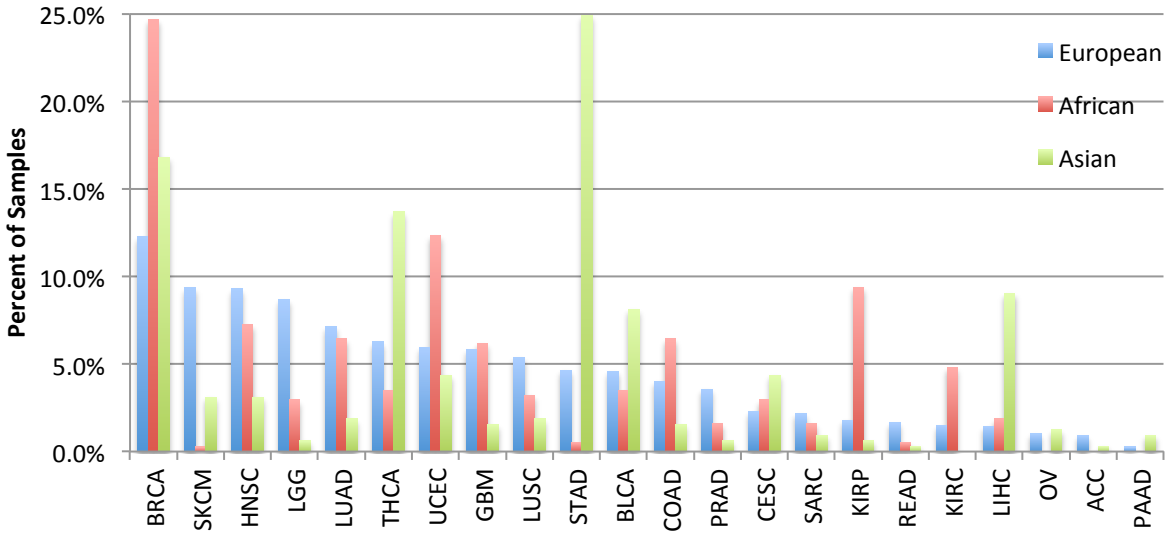


Figure 20 Distribution of TCGA disease groups by stratified cohort.

Both of these groups showed a significant association with a 3DL3 variant at position 971, but the samples of European descent demonstrated that the significance for this variant is the result of a confounding effect from the disparities in read lengths generated by different sequencing centers.

The 3702 samples labeled as nonhispanic European descent produced more statistically powered disease groups for KIR analysis, but melanoma is the only cancer that significantly associated with a 3DL3 variant at position 961. Of the 108 currently known 3DL3 alleles, 23 (21.3%) contain an A at this position, while 51 (47.2%) have a C and 34 (31.5%) have a T at that position. The population genetics analysis showed that A961 alleles occur at much higher frequency within Caucasian genomes, and the cancer analysis showed that individuals with melanoma are respectively 2.4 to 2.7 times more likely to have a C at nucleotide 961 within one or both alleles. An A961C point mutation is a nonsynonymous single base substitution that results in an Asparagine to Histidine change at amino acid residue 300 within 3DL3 exon 7, which encodes the transmembrane domain. A positively charged Histidine in place of a polar uncharged Asparagine within the plasma membrane may alter KIR3DL3 inhibitory receptor

function. The fact that the heterozygous C/A genotype at position 961 produced almost the same effect size as the C/C type provides evidence that an N300H substitution results in gain of function, since a loss of function would not occur if only one allele changed. A gain of inhibitory function may result in impaired or hyporesponsive NK cells with attenuated antitumor activity, but it is unclear why such impairment would correlate to an increased susceptibility to melanoma exclusively. Three other cancers (lower grade glioma, lung squamous cell carcinoma, and bladder urothelial carcinoma) were also significantly associated with a C/A genotype at position 961, but with smaller effects than the one observed for melanoma that did not meet the threshold of significance following multiple statistical testing correction.

KIR2DL4 functions as an activating receptor, despite containing an intracellular ITIM domain, due to a positively charged transmembrane Arginine residue that associates with the FcεRI-γ adaptor protein, leading to activation of MAP kinases and the NF-κB pathway[51-53]. However, there is no evidence that KIRs containing a positively charged transmembrane Histidine can similarly associate with an adaptor protein or that specific 3DL3 alleles can elicit an activating function.

The results also showed that a C/C genotype at 3DP1 position 479 (within exon 4) was nearly five times more likely than an A/C genotype for the prostate adenocarcinoma group, and the population genetics analysis identified C479 alleles as significantly more common within Caucasian groups. The 3DP1*005 and 3DP1*006 alleles are the only two of the 27 known 3DP1 variants that contain a C at cDNA position 479 (Figure 21a). Analysis of the full KIR genomic sequences revealed that these two variants are also the only sequenced 3DP1 alleles with an A at gDNA position 2953 within intron 3.

Previous studies have reported that a pseudogene can effect a regulatory function if its transcripts bind and sequester miRNAs that would otherwise bind to mRNAs transcribed from

a exon 4 intron 3

	480	2960
3DP1*001	AGAGGGGAAG	AATTCGTCCA
3DP1*002	----------	----------
3DP1*0030101	----------	----------
3DP1*0030102	----------	----------
3DP1*0030201	----------	----------
3DP1*0030202	----------	----------
3DP1*0030203	----------	----------
3DP1*0030204	----------	----------
3DP1*0030205	----------	----------
3DP1*0030206	----------	----------
3DP1*00303	----------	----------
3DP1*0030401	----------	----------
3DP1*0030402	----------	----------
3DP1*004	----------	**********
3DP1*005	--------C-	--A-------
3DP1*006	--------C-	--A-------
3DP1*007	----------	----------
3DP1*008	----------	----------
3DP1*0090101	----------	----------
3DP1*0090102	----------	----------
3DP1*0090103	----------	----------
3DP1*00902	----------	----------
3DP1*010	----------	----------
3DP1*011	----------	**********
3DP1*012	----------	**********
3DP1*013	----------	**********
3DP1*014	----------	**********

b

CATACCTTCTGCCAAGGATTCCAAATCGTCCAAAAGAGATTGAACCAGTCTGCTAAGAG
CCTGGACGTGCAGCCTATCCTGGTTCCTCTTCCACCCCCACATAGAAGCAGGAAAGACA
TTAGTTCGAAATAGATACAACAGCCCAAGAGATGAGGCTGAGCCCAGCGGCAAGGGAAT
CAGGAGCTACTAGAGACAGAGGGACAGAGAAGAGGGAGGGAGACAGATGGAAGGACCTG
TACCAGGAGTTATGGGCACAGAAAAGAACATGAAGACACAGAGAGGAAGGAGAGAGATA
AGACACCAGCGAGGGGAAGCCTCACTCATTCTAGGTGCCATGGATGGGATGATAAAGAG
AGATGCCTTCTAAAGTCACAACCTCTCTTCCTAG

c

Figure 21 KIR3DP1 splicing analysis. (a) The 004 and 005 alleles are the only 3DP1 variants with a C at position 479 within the coding sequence. Analysis of the genomic sequence revealed that these two alleles are the only 3DP1 variants with an A at position 2953. (b) The SVM-BPfinder tool does not predict A2953 (red) as a branch point. Green = predicted branch point sequence with highest variable order Markov model score. Yellow = predicted branch point sequence with highest SVM classifier score. (c) The SpliceAid tool does not predict the sequence flanking A2953 (highlighted) as a recognition site for any RNA-binding protein.

the functional version of the gene[54,55]. The reduction in RNA interference results in upregulation of the functional gene expression. If the functional gene is an inhibitory KIR, then less RNAi may produce more inhibited NK lymphocytes that are hyporesponsive against cancer

cells. I hypothesized that the C2953A point mutation within 3DP1 intron 3 created a novel branch point that could be used for alternative RNA splicing, and that the alternative transcripts contained a 3' UTR miRNA binding site not found in canonically spliced 3DP1 transcripts. If true, this might explain why only these two 3DP1 alleles significantly associate with cancer. However, neither the SpliceAid database (www.introni.it/splicing.html) nor the SVM-BPfinder U2 branch point prediction tool (regulatorygenomics.upf.edu/Software/SVM_BP/) identified the sequence flanking A2953 as a branch site (Figure 21b,c)[56,57]. Therefore, the evidence does not support the alternative splicing hypothesis.

It has been previously reported that the 3DP1*004 allele is transcribed, and possibly translated to a secreted receptor protein, as the result of a G16A single base substitution within exon 1 that causes this allele to have the same promoter sequence as the transcriptionally-active 2DL5A variants[58,59]. This allele could have a regulatory effect by competing for miRNAs at the transcript level or by competing for ligands at the protein level. However, 3DP1*005 and 3DP1*006 both contain the G at this position that is associated with the promoter for the transcriptionally-silent 2DL5B alleles. Therefore, there is no evidence that either of these 3DP1 alleles are transcribed, and it remains unclear why the 3DP1 A479C polymorphism exhibits an association with cancer.

After stratifying the TCGA cohort by race and ethnicity, there are no significant differences in KIR genotypes between the cancer samples and the control samples. However, the majority of KIR types are so rare that comparisons are only valid for a few common types. There are also no significant differences between the disease and control groups in the frequencies of individual KIR genes, therefore any studies reporting an association between cancer and KIR gene content are not supported by the results of this analysis. It is still possible that combinations of KIRs and their cognate ligands are disease risk factors. As methods for predicting HLA alleles from NGS sequence data continue to make improvements in their

robustness and accuracy, KIR ligand typing results from sequencing repositories such as the TCGA and OKG databases can be combined with the KIR genotyping results from this analysis to study the relationships between receptor-ligand interactions and disease[60,61].

4.4 Methods

4.4.1 KIR gene content calling and sample demographic stratification

Whole exome BAM files from the blood-derived germline DNA of 5489 individuals spanning 22 disease groups and sequenced on the Illumina platform were downloaded from the TCGA CGHub repository and processed with the SeRRAMC algorithm. Seven samples produced an ambiguous KIR2DS4 presence/absence call and were excluded from the study. The SeRRAMC-typed OKG samples from the population genetics analysis were used as a control cohort of individuals not known to have cancer at the time of sequencing. However, the 26 groups comprising the worldwide OKG cohort exhibit a substantially wider range of frequencies for KIR genes compared to the respective KIR frequencies for the TCGA disease groups (Figure 22a). This is due to the fact that the 1000 Genomes Project deliberately sampled a broad range of the human population, while the TCGA project was concerned primarily with collecting a sufficient number of samples from cancer patients who gave informed consent to have their tumors profiled. Therefore, an attempt to compare whole cohorts from the two projects will produce statistically significant differences in KIR genotype and variant frequencies that result from disparities in genetic diversity and not from associations between cancer and KIR alleles. In order to reduce the confounding effect of disparate variation, the TCGA and OKG samples were stratified by race and ethnicity. The patient clinical data files for each disease group were downloaded from the TCGA open-access HTTP directory (https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/), and each

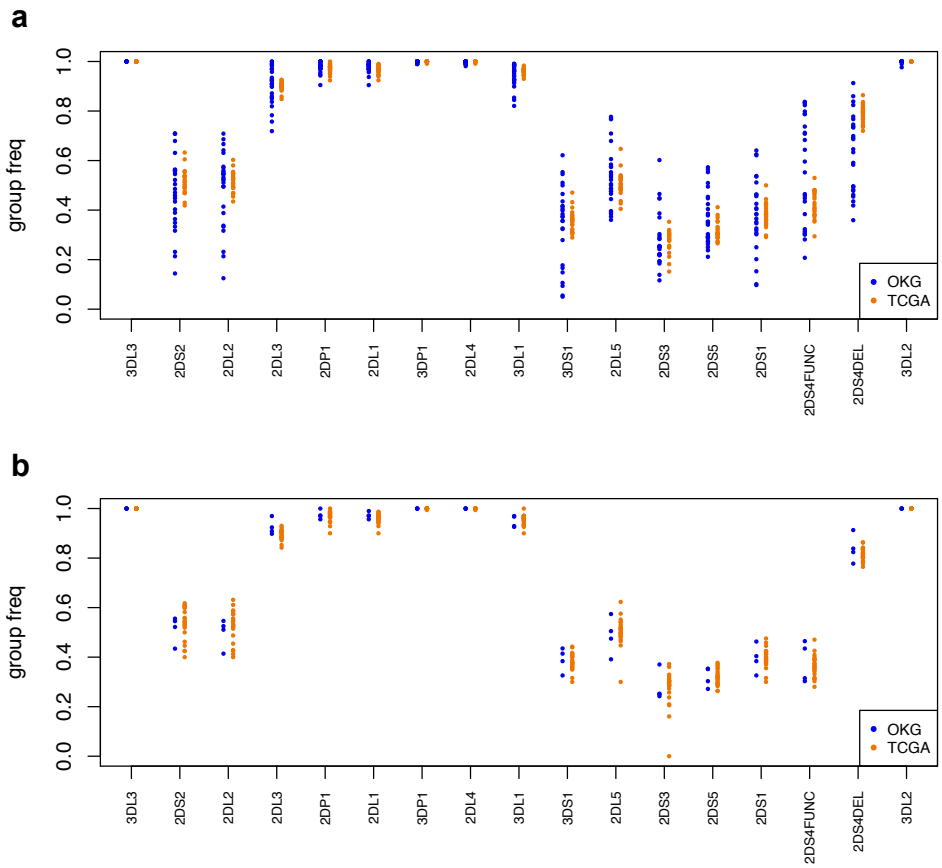


Figure 22 KIR frequency distributions of TCGA and OKG samples. (a) Whole cohorts, 22 cancer groups and 26 human populations. (b) Stratified cohorts, 22 cancer groups for nonhispanic Caucasians and four nonhispanic European populations.

KIR-typed sample was labeled with race and ethnicity information. Three cancer demographic groups were sufficiently large for a comparison to matched OKG populations (Figure 23). The largest cohort consisted of 3702 samples labeled as nonhispanic white, which were matched with the four nonhispanic European OKG groups (CEU, GBR, FIN, and TSI). A cohort of 373 TCGA samples labeled as nonhispanic black were matched with the two African OKG populations living outside of the African continent (ASW and ACB). The five OKG populations residing on the African continent (ESN, GWD, LWK, MSL, and YRI) were not included as matched controls because disparities in genetic admixture between those individuals

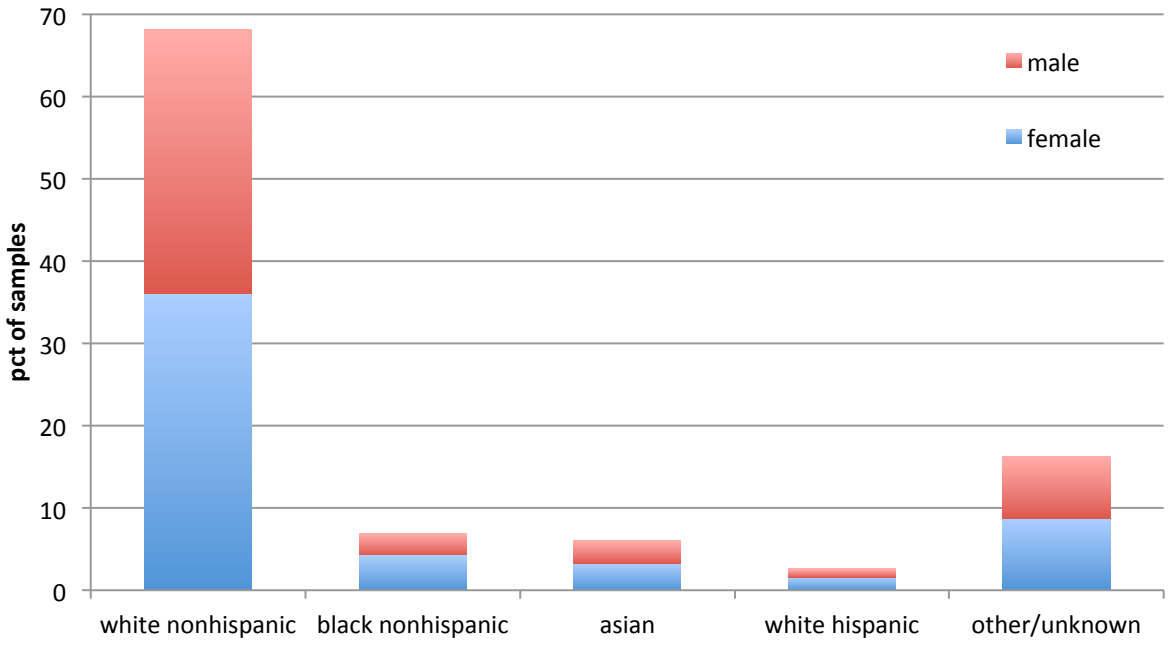


Figure 23 Distribution of TCGA samples by race and ethnicity.

and the TCGA participants would produce significant differences in KIR gene frequencies that have nothing to do with cancer. The 321 Asian TCGA samples were similarly matched with the admixed East Asian OKG groups (CDX and KHV), while the three Far Eastern OKG populations (CHB, CHS, and JPT) were excluded as controls. After stratification, the differences in KIR type and individual gene frequencies between TCGA and OKG samples were dramatically reduced, creating suitable comparisons for analyzing associations between KIR gene content and cancer or KIR allelic variation and cancer.

4.4.2 KIR type significance testing

For each unique KIR type, chi square testing compared each TCGA cancer group to its matched OKG controls in order to identify KIR genotypes significantly associated with cancer. As with the population genetics analysis, comparisons were restricted to the statistical tests with an expected frequency of five or greater in each chi square cell due to the large number of ultra-

rare KIR types. For the European cohort, 168 tests met this requirement, but only four had a P-value ≤ 0.05. None of these four tests were significant after a 10% FDR correction. One of seven tests for the African cohort and zero of 12 tests for the Asian cohort had a significant P-value. Chi square tests were oriented so that an odds ratio less than 1.0 indicates a genotype is associated with the non-cancer samples, while an odds ratio greater than 1.0 indicates an association between the KIR type and a specific disease.

4.4.3 KIR variant calling and testing

A VCF file for each KIR gene was generated from remapped BAM files for each of the three matched demographic cohorts using samtools 0.1.18 mpileup and bcftools 0.1.17. The same stringency requirements from the population genetics analysis were imposed for the cancer analysis (variant call quality score ≥ 13, genotype quality score ≥ 13, read depth ≥ 10). For each variant call that met these thresholds, chi square testing compared two genotypes for the cancer group versus the matched control group. Three sets of genotype tests (reference homozygous versus heterozygous, heterozygous versus alternative homozygous, and reference homozygous versus alternative homozygous) were conducted for each of the three targeted demographic cohorts. The three sets from the European cohort produced 874:70:14, 418:36:3, and 424:28:1 tests respectively (total tests:tests with P-value ≤ 0.05:significant tests after 10% FDR correction) (Tables A12a-c). The African test sets were 209:77:2, 43:0:0, and 40:1:0 respectively (Tables A12d-f). The Asian test sets were 108:5:0, 37:0:0, and 31:0:0 (Tables A12g-i). An odds ratio < 1.0 indicates a correlation between the first genotype and the specific cancer group, and an odds ratio > 1.0 indicates that the second genotype is associated with disease. These nine sets produced a combined 20 statistically significant tests for single base substitutions within 3DL3, 3DP1, and 2DP1.

Chapter 5: Discussion

5.1 Conclusion

SeRRAMC processing is a novel approach for recovering limited KIR genotyping information from short NGS reads. It has been validated by the current gold standard for KIR typing (SSO-PCR) as an accurate method for calling the presence or absence of KIR genes within individual genomes. The approach has been further validated at the cohort level, identifying linkage frequencies between pairs of KIR genes across the human population that share high concordance with the linkages reported in the world's largest repository of KIR genotyping data (http://www.allelefequencies.net). Multiple levels of validation provide proof of principle that KIR gene content can be called with a high degree of precision from short sequence reads. Furthermore, the elimination of read mismapping by the SeRRAMC remapping process enables high confidence short variant calling from NGS reads.

5.2 Advances to the immunogenetics field contributed by this research

The SeRRAMC method is the first approach that allows for KIR gene content calling from large cohorts of short read sequencing data. Prior to the development of this process, considerably smaller cohorts (consisting of dozens to hundreds of DNA samples) had been KIR-typed using SSO or SSP-PCR techniques with a high degree of overhead in terms of the aggregate amount of time and personnel required to obtain and type all samples. The SeRRAMC remapping algorithm called KIR gene content from the whole exome sequences of over 8000 samples on a typically configured desktop computer at an average rate of a few minutes per sample. Furthermore, over 5500 of these samples cannot be KIR-typed using any PCR-based approach because only the sequence data, and not cells or cell analytes, have been made available.

This is also the first approach to accurately call short variants across all KIR genes in the nonhomologous regions where each gene can be uniquely identified. Other methods for calling SNPs within KIRs have been limited approaches based on one or a few variant-specific PCR probes. The SNPs identified from the SeRRAMC-based analysis of over 8000 whole exome sequences within this research project could be used to develop oligonucleotide probes for the first multiplexed pan-KIR genotyping array. Current arrays, such as the Affymetrix SNP6 platform, do not have the specificity to call variants across all KIR genes.

The analyses made possible by these novel gene content and variant calling methods have revealed several previously unreported findings, including the first KIR genotyping results for the entire 1000 Genomes Project cohort. The population immunogenetics analysis identified a few common and many rare KIR gene content types across 26 human demographic groups. It showed that KIR framework and A content genes occur at very high frequencies around the world but that KIR B genes are found at their highest frequencies within and around the Indian subcontinent. The study further revealed that the most well-characterized KIR structural variant (a 22 base deletion in exon 5 of KIR2DS4) is commonly found within European and South Asian populations, while functional 2DS4 alleles exist at high frequencies in African and Far Eastern groups. Interestingly, single base substitutions within KIR2DL4 exhibit a similar axis between Africa/East Asia and Europe/South Asia. This is the first time anyone has reported that genetic variants that attenuated in frequency as humans moved from the African continent into Europe and Asia appear to have re-emerged once people reached the Far East. This finding may contribute significant evidence to the knowledge base used to develop models of human migration patterns. As expected, human populations that have low rates of genetic admixture due to cultural and/or geographic isolation (e.g. Chinese, Japanese, and Peruvian groups) have higher numbers of population-specific short KIR variants encoded within their genomes, while more admixed groups in the Americas feature fewer population-specific variants. In addition,

this is the first analysis to identify KIR gene content and short variant genotypes for Neandertals and the Denisovan, which may provide evidence to support hypotheses about human evolution and genetic code donation from ancient to modern humans (or vice-versa).

The SeRRAMC approach also enabled the first large-scale analysis of cancer exomes from the TCGA project. However, even though the initial patient cohort size was large, the wide range of KIR variation across human groups (as revealed by the population genetics study) necessitated the stratification of samples by race and ethnicity as a means to reduce the occurrence of significant results due to confounding factors and not due to disease. Further stratification by cancer type, coupled with multiple levels of stringency (e.g. minimum quality scores and read coverages), produced sample sizes that were insufficiently powered to identify significant associations between KIR variants and cancer within the African and Asian cohorts. Stringency in significance testing could have been relaxed, but it would have come at the expense of a higher risk of false positive discoveries. The European cohort contained a substantially higher number of samples but failed to find any significant associations between KIR gene content and cancer. The analysis did produce evidence of a significant KIR3DL3 single base substitution in melanoma and a polymorphism in the KIR3DP1 pseudogene relevant to prostate adenocarcinoma. It also revealed that calling short variants in highly homologous genomic regions from short sequence reads is sensitive to read length, and that batch effects from comparing samples with reads of disparate lengths can produce false positive variant calls. All of this information can be taken into consideration when designing future immunogenetic analyses of KIR variation in the context of disease to assist in determining sample sizes, stringency levels, sequence read lengths, and selection of samples suitable for comparison.

5.3 Limitations of the SeRRAMC approach

Since clusters of homologous genes only contain restricted regions of unique sequence, any analytical approach based on short reads will be limited in its ability to rescue genotyping function from sequence data. In the case of the KIR region, the utility of the SeRRAMC approach varies widely between individual genes. KIR2DL4 is the only gene in the group that contains enough islands of unique sequence across its exons to allow KIR-specific short reads to accurately cover at least 50% of the coding region. Four other KIRs (2DS2, 3DS1, 2DL2, and 2DS1) share so much common sequence with other members of the gene family that less than 10% of their respective coding regions can be covered by KIR-specific short reads. If nucleotide polymorphisms do not occur with a read length of these few nonhomologous areas, then the approach will be unable to call variants in these genes. This helps to explain why the population genetics analysis did not find significant variants within these particular genes. The genetic variation that discriminates the individual alleles of each one of these KIRs exists outside of the region covered by short KIR-specific reads.

The SeRRAMC method, as currently implemented, is also unable to accurately call variants for the genes within the MHC that encode KIR ligands. This is due to the fact that HLA genes exhibit polymorphism across hundreds of bases spanning exons 2 and 3 of their coding regions. As a result, the sequence oligomotifs that distinguish HLA loci from each other exceed the read length, and reads that originated from one HLA gene will mismap to another, leading to erroneous variant calling. For example, a variant called from reads mapped to the HLA-B locus may truly exist within an HLA-C allele.

The best solution to both of these issues is to use sequencing technologies that generate considerably longer reads - at least in complex regions with high degrees of homology, if not across the entire genome or exome. Platforms based on single molecule sequencing or synthetic

long-range linked reads can create reads thousands of bases in length, which can cover entire exons (and noncoding regions). This enables not only short variant calling across the entire length of a gene, but also phasing of the haplotypes and characterization of large structural variants, including *de novo* ones that do not exist within the human reference genome, such as complex segment rearrangements.

5.4 Translational applications for *in silico* KIR genotyping

Our lab has demonstrated the ability to generate unprecedented large-fold *ex vivo* expansions of allogeneic NK cells for adoptive transfer into patients with hematological (and possibly solid tumor) malignancies. These lymphocytes are grown in the presence of engineered K562 artificial antigen-presenting cells (aAPCs) that have been transfected with membrane-bound IL-21[62]. Currently, only a few basic selection criteria are used when choosing a donor for allotransplant of cytokine-expanded NK cells (Figure 24a). A fully HLA-matched or haploidentical donor is selected as a precautionary measure to reduce the risk of graft versus host disease (GVHD) caused by a small population of contaminating T cells within the therapeutic NK cell product[63]. An HLA haploidentical donor's NK cells may also be KIR-mismatched to the recipient, meaning that the donor genome encodes an HLA allele cognate to an inhibitory KIR, but the recipient genome does not. In this case, the NK cell is licensed by the donor HLA environment to recognize the absence of KIR ligand in the recipient as a missing-self condition. The absence of inhibitory ligand, along with the presence of activating ligands, results in alloreactive lymphocytes with robust antitumor responses[64-66].

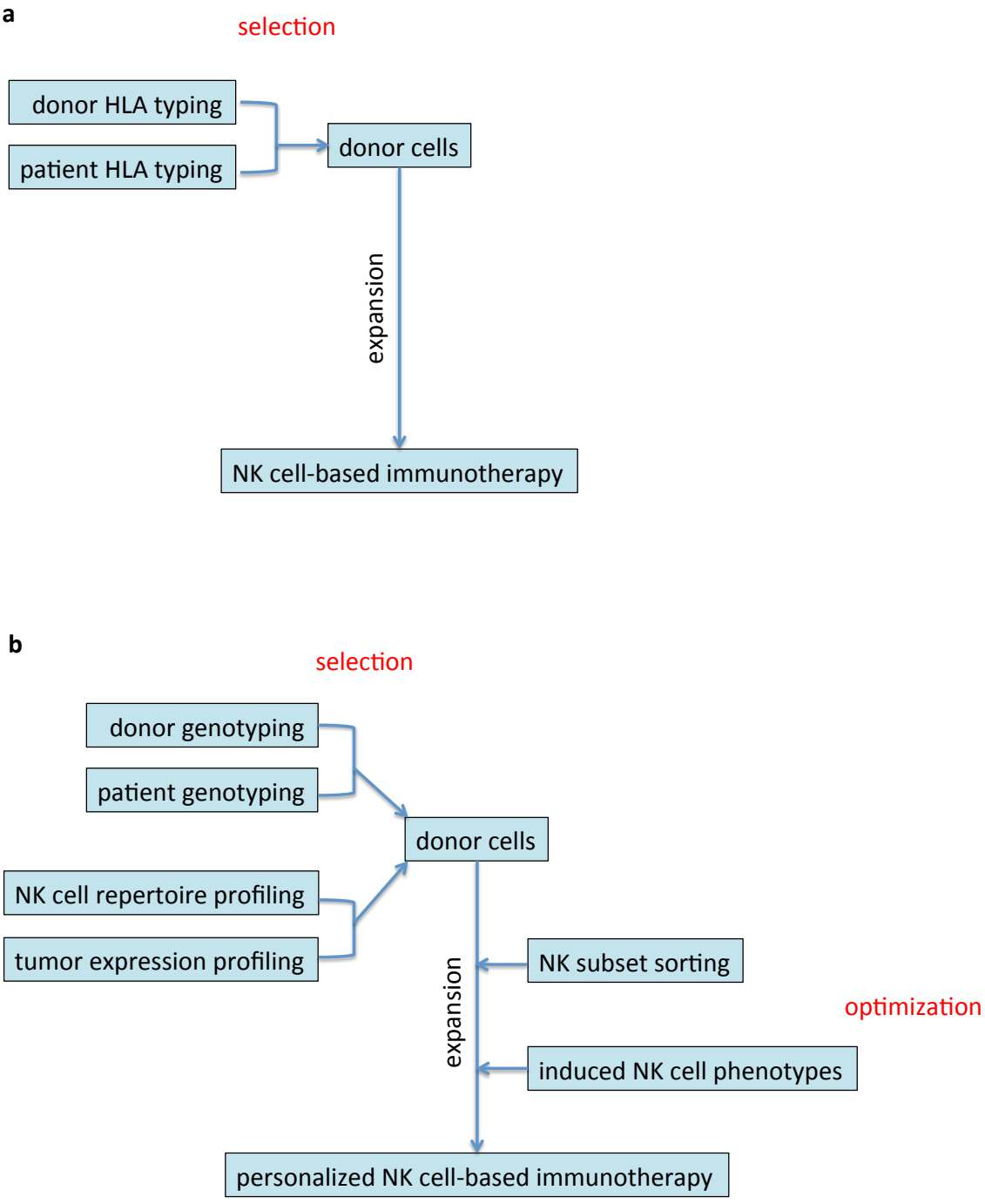


Figure 24 Approaches for the development of therapeutic NK cell products. (a) Current protocols use HLA typing to reduce the risk of GVHD and to achieve KIR mismatch when possible. (b) The SeRRAMC method enables analyses for identifying KIR variants and expression profiles associated with maximal NK cell cytotoxicity against tumors with specific molecular attributes to select optimal donors and NK cell subpopulations for personalized cancer immunotherapy.

However, low resolution KIR presence/absence typing methods do not enable studies investigating the role of specific KIR variants in the immunotherapeutic efficacy of allogeneic NK cells. High confidence variant calls from SeRRAMC genotyping can empower these types of inquiries. Furthermore, the combination of recent single-cell RNAseq methods[67,68] with the KIR-specific transcript measuring capabilities of SeRRAMC-mediated phenotyping permits the elucidation of lymphocyte gene expression profiles associated with strong therapeutic responses. This creates the possibility of preferentially expanding and sorting for subpopulations of NK cells predicted to exhibit maximal cytotoxicity against target tumor cells with particular molecular characteristics. Together, these approaches allow for considerably more informed and sophisticated selection criteria to identify optimal donors and optimal subsets of killers within heterogeneous NK cell repertoires for the development of personalized immuno-oncology therapies (Figure 24b).

5.5 Additional applications

The SeRRAMC approach can potentially be applied to any genomic region or gene family where a high degree of sequence similarity between loci causes the aligner software to mismap short sequence reads. Examples include the Sox family of transcription factors encoded across the genomes of several species or the large cluster of *n*-aliphatic olfactory receptor family genes and pseudogenes located on the p arm of human chromosome 11.

The method is also useful for quantifying the relative abundance of KIR-specific RNAseq transcripts for expression analysis. The same large cohort impracticality and cell analyte unavailability issues pertaining to DNA genotyping are relevant to RNA quantification as well. For instance, the TCGA data repository contains thousands of Illumina RNAseq data sets produced from molecular profiling of many different tumor types, but the mRNA isolated from those samples is not available for SSO-PCR typing of cDNA. The SeRRAMC approach

could be used to identify and quantify the presence of KIR transcripts from tumor-infiltrating lymphocytes. This would enable the first large-scale analysis to determine whether or not the infiltration of lymphocytes expressing specific KIR genes is a cancer prognostic factor.

In addition, components of the SeRRAMC process can be applied to KIR analysis of DNA samples measured with long-range sequence read technologies. After a *de novo* assembly of the KIR region is produced from a set of long reads, the SeRRAMC KIR-specific oligomotifs can be used to determine the order and placement of KIR exons within the gene cluster. Such an approach would enable direct counting of KIR copy numbers without requiring the imputation of copy number from read coverage or from array-hybridized DNA fragments. Furthermore, the placement of KIR-specific motifs within a long read assembly can assist in revealing complex structural rearrangements and gene fusion events.

Finally, SeRRAMC-mediated KIR analysis can be applied to the elucidation of rare genetic variants. This would be achieved by comparing individual remapped alignment files to the control cohort rather than comparing population or disease groups. Deviations from reference that may not occur at a high enough frequency to be called by the stringency thresholds of the variant calling software at the group level may be revealed when looking at individuals. However, for disease studies, rare variants by definition would translate to difficulty in finding the minimum number of people with the pathological condition of interest to perform an analysis sufficiently powered to identify high confidence correlations between genotype and disease.

Table A1 Raw counts of reads containing high frequency KIR-specific motifs for 2535 OKG and 5512 TCGA samples

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG00096.mapped.ILLUMINA.bwa.GBR.exome.20120522	122	141	136	0	0	0	136	152	174	0	0	0	0	0	56	87	102
HG00097.mapped.ILLUMINA.bwa.GBR.exome.20130415	64	0	1	26	37	47	55	42	46	0	0	0	0	0	25	0	64
HG00099.mapped.ILLUMINA.bwa.GBR.exome.20130415	76	0	2	38	58	68	68	48	34	11	10	0	37	47	0	28	79
HG00100.mapped.ILLUMINA.bwa.GBR.exome.20121211	155	0	0	74	139	147	120	90	80	19	54	0	62	91	0	52	135
HG00101.mapped.ILLUMINA.bwa.GBR.exome.20121211	111	0	0	94	137	145	148	187	190	0	0	0	0	0	58	100	112
HG00102.mapped.ILLUMINA.bwa.GBR.exome.20121211	82	0	0	90	120	111	125	122	119	0	0	0	0	0	0	97	86
HG00103.mapped.ILLUMINA.bwa.GBR.exome.20120522	105	0	0	85	121	107	124	97	112	0	0	0	0	0	0	106	91
HG00105.mapped.ILLUMINA.bwa.GBR.exome.20130415	59	23	0	16	43	53	63	30	29	8	6	0	26	25	0	32	55
HG00106.mapped.ILLUMINA.bwa.GBR.exome.20130415	76	0	0	32	37	60	59	38	79	0	0	0	0	0	0	46	72
HG00107.mapped.ILLUMINA.bwa.GBR.exome.20121211	94	93	102	41	103	95	134	157	167	0	0	0	0	0	0	172	95
HG00108.mapped.ILLUMINA.bwa.GBR.exome.20120522	71	81	75	46	126	89	95	77	51	28	88	67	60	68	0	64	90
HG00109.mapped.ILLUMINA.bwa.GBR.exome.20121211	80	79	70	51	79	65	106	72	96	0	0	0	0	0	38	67	89
HG00110.mapped.ILLUMINA.bwa.GBR.exome.20121211	71	83	81	38	140	100	95	85	58	33	76	67	66	77	0	61	83
HG00111.mapped.ILLUMINA.bwa.GBR.exome.20120522	81	82	83	39	77	60	93	89	86	0	0	0	0	0	0	113	92
HG00112.mapped.ILLUMINA.bwa.GBR.exome.20130415	55	0	0	27	32	42	63	43	0	13	20	0	40	48	0	0	68
HG00113.mapped.ILLUMINA.bwa.GBR.exome.20121211	73	0	1	76	91	106	98	76	93	0	0	0	0	0	0	127	86
HG00114.mapped.ILLUMINA.bwa.GBR.exome.20120522	122	0	0	76	180	156	175	166	183	0	0	0	0	0	63	94	145
HG00115.mapped.ILLUMINA.bwa.GBR.exome.20130415	63	0	0	32	42	50	66	31	26	7	10	0	22	34	0	21	63
HG00116.mapped.ILLUMINA.bwa.GBR.exome.20120522	150	91	101	53	170	136	131	125	97	16	107	92	87	94	0	90	184
HG00117.mapped.ILLUMINA.bwa.GBR.exome.20120522	123	63	66	35	70	69	86	85	99	0	0	0	0	0	0	83	116
HG00118.mapped.ILLUMINA.bwa.GBR.exome.20130415	59	0	0	40	31	61	69	36	67	0	0	0	0	0	0	37	81
HG00119.mapped.ILLUMINA.bwa.GBR.exome.20120522	111	0	0	65	104	114	107	98	127	0	0	0	0	0	23	55	122
HG00120.mapped.ILLUMINA.bwa.GBR.exome.20120522	114	64	70	40	137	106	97	87	103	0	36	73	0	0	0	98	116
HG00121.mapped.ILLUMINA.bwa.GBR.exome.20121211	70	75	77	44	112	106	92	91	85	0	43	60	0	0	45	58	84
HG00122.mapped.ILLUMINA.bwa.GBR.exome.20130415	66	28	30	16	29	54	66	59	31	13	25	34	17	24	0	20	54
HG00123.mapped.ILLUMINA.bwa.GBR.exome.20120522	132	0	0	76	135	100	103	106	81	14	53	0	66	89	0	51	112
HG00124.mapped.ILLUMINA.bwa.GBR.exome.20120522	119	0	1	93	132	141	107	109	107	0	0	0	0	1	0	121	139
HG00125.mapped.ILLUMINA.bwa.GBR.exome.20120522	68	80	124	41	72	71	100	101	98	1	0	0	1	0	0	122	89
HG00126.mapped.ILLUMINA.bwa.GBR.exome.20130415	54	26	29	22	28	33	60	35	53	0	0	0	0	0	11	39	65
HG00127.mapped.ILLUMINA.bwa.GBR.exome.20120522	70	0	0	56	89	83	94	92	97	0	1	0	0	0	33	46	83
HG00128.mapped.ILLUMINA.bwa.GBR.exome.20130415	79	0	1	37	92	83	111	95	86	16	21	41	1	1	18	35	92
HG00129.mapped.ILLUMINA.bwa.GBR.exome.20130415	60	26	33	16	53	60	56	28	64	0	11	33	1	0	9	18	76
HG00130.mapped.ILLUMINA.bwa.GBR.exome.20130415	63	0	0	20	39	54	54	37	65	0	0	0	0	0	0	51	63
HG00131.mapped.ILLUMINA.bwa.GBR.exome.20120522	181	0	1	88	177	148	137	120	176	0	0	0	0	2	61	0	179
HG00132.mapped.ILLUMINA.bwa.GBR.exome.20130415	61	0	0	27	39	67	75	51	63	0	0	0	0	0	0	69	73
HG00133.mapped.ILLUMINA.bwa.GBR.exome.20120522	155	77	74	44	166	132	102	113	80	18	87	80	78	82	0	70	138
HG00136.mapped.ILLUMINA.bwa.GBR.exome.20120522	97	96	83	58	156	117	118	97	101	0	74	82	0	1	45	89	105
HG00137.mapped.ILLUMINA.bwa.GBR.exome.20120522	77	71	59	33	69	54	91	77	89	0	0	0	0	0	28	55	95
HG00138.mapped.ILLUMINA.bwa.GBR.exome.20120522	69	113	108	0	1	0	85	100	94	0	0	0	0	0	53	64	93
HG00139.mapped.ILLUMINA.bwa.GBR.exome.20121211	97	0	4	97	121	99	105	110	90	0	0	0	0	0	0	164	99
HG00140.mapped.ILLUMINA.bwa.GBR.exome.20121211	74	76	73	36	128	100	88	75	41	32	78	68	62	64	0	61	80
HG00141.mapped.ILLUMINA.bwa.GBR.exome.20130415	71	39	35	20	27	42	78	58	60	0	0	0	0	4	14	41	77
HG00142.mapped.ILLUMINA.bwa.GBR.exome.20130415	74	0	0	37	59	52	43	28	36	0	0	0	0	35	19	1	61
HG00143.mapped.ILLUMINA.bwa.GBR.exome.20130415	66	39	32	21	33	51	65	45	73	0	0	0	0	0	12	29	68
HG00145.mapped.ILLUMINA.bwa.GBR.exome.20120522	156	86	95	54	101	87	119	136	137	0	0	0	0	0	40	83	168
HG00146.mapped.ILLUMINA.bwa.GBR.exome.20121211	136	3	2	78	120	104	94	113	67	19	50	0	65	84	0	72	116
HG00148.mapped.ILLUMINA.bwa.GBR.exome.20130415	72	30	32	19	25	41	63	38	61	0	0	0	1	0	0	72	86
HG00149.mapped.ILLUMINA.bwa.GBR.exome.20130415	73	2	0	28	40	47	51	31	81	0	0	0	0	0	7	37	97
HG00150.mapped.ILLUMINA.bwa.GBR.exome.20130415	68	33	34	24	39	67	65	66	32	9	39	61	0	37	0	29	82
HG00151.mapped.ILLUMINA.bwa.GBR.exome.20130415	47	0	0	23	30	45	56	24	57	0	0	1	0	0	0	41	60
HG00154.mapped.ILLUMINA.bwa.GBR.exome.20120522	84	0	0	66	121	159	111	95	96	0	0	0	0	0	55	74	111
HG00155.mapped.ILLUMINA.bwa.GBR.exome.20121211	131	1	1	59	106	98	102	140	122	0	0	1	0	3	29	79	136
HG00157.mapped.ILLUMINA.bwa.GBR.exome.20120522	130	77	74	49	74	67	106	93	126	0	0	0	0	0	28	64	127
HG00158.mapped.ILLUMINA.bwa.GBR.exome.20120522	152	0	0	71	125	123	103	85	93	20	37	0	67	85	21	0	137
HG00159.mapped.ILLUMINA.bwa.GBR.exome.20120522	120	0	0	60	169	138	102	114	74	20	66	62	62	71	0	66	126
HG00160.mapped.ILLUMINA.bwa.GBR.exome.20120522	101	54	63	38	77	69	74	91	90	0	1	0	0	0	15	46	120
HG00171.mapped.ILLUMINA.bwa.FIN.exome.20120522	72	0	1	73	114	110	105	80	96	0	0	0	0	0	38	77	90
HG00173.mapped.ILLUMINA.bwa.FIN.exome.20130415	61	0	0	43	63	75	87	47	40	9	34	0	36	47	11	1	63
HG00174.mapped.ILLUMINA.bwa.FIN.exome.20120522	81	0	0	82	117	114	96	72	101	0	0	0	0	0	0	130	85
HG00176.mapped.ILLUMINA.bwa.FIN.exome.20120522	115	1	2	81	112	97	101	97	88	0	0	0	0	1	0	106	119
HG00177.mapped.ILLUMINA.bwa.FIN.exome.20130415	86	0	2	29	49	63	70	52	69	0	0	0	0	2	16	25	73
HG00178.mapped.ILLUMINA.bwa.FIN.exome.20121211	131	0	0	104	182	159	176	156	114	8	81	1	95	111	42	0	135
HG00179.mapped.ILLUMINA.bwa.FIN.exome.20130415	66	0	0	31	50	44	46	28	35	0	0	0	0	39	0	42	49
HG00180.mapped.ILLUMINA.bwa.FIN.exome.20130415	65	0	0	37	30	60	70	29	53	0	0	0	0	0	7	21	73
HG00181.mapped.ILLUMINA.bwa.FIN.exome.20121211	125	0	0	96	178	172	230	243	185	9	0	0	0	1	73	109	144
HG00182.mapped.ILLUMINA.bwa.FIN.exome.20120522	98	0	0	66	132	143	128	139	108	15	86	1	90	108	0	91	115
HG00183.mapped.ILLUMINA.bwa.FIN.exome.20120522	119	139	139	57	226	178	178	185	136	13	166	106	116	135	56	0	146
HG00185.mapped.ILLUMINA.bwa.FIN.exome.20120522	115	103	109	44	206	146	173	238	176	10	82	106	0	0	57	90	113
HG00186.mapped.ILLUMINA.bwa.FIN.exome.20120522	93	0	1	74	124	120	137	166	92	10	80	0	87	96	0	83	108
HG00187.mapped.ILLUMINA.bwa.FIN.exome.20120522	110	0	0	63	151	158	153	159	175	0	0	0	0	0	63	109	134
HG00188.mapped.ILLUMINA.bwa.FIN.exome.20120522	106	0	0	95	125	122	152	118	137	0	0	0	0	0	73	1	96
HG00189.mapped.ILLUMINA.bwa.FIN.exome.20120522	98	0	0	53	115	81	87	73	0	7	71	0	70	119	0	0	82
HG00190.mapped.ILLUMINA.bwa.FIN.exome.20120522	125	98	101	50	98	91	134	119	166	0	0	0	0	0	78	0	97
HG00231.mapped.ILLUMINA.bwa.GBR.exome.20130415	73	0	1	32	59	62	74	40	58	0	0	0	0	0	0	49	81
HG00232.mapped.ILLUMINA.bwa.GBR.exome.20120522	83	96	78	38	85	73	103	94	99	0	0	0	1	0	51	76	96
HG00233.mapped.ILLUMINA.bwa.GBR.exome.20120522	95	135	138	0	108	106	148	163	108	10	108	138	0	112	0	90	115
HG00234.mapped.ILLUMINA.bwa.GBR.exome.20130415	50	0	2	18	46	52	64	46	51	0	0	0	0	1	0	64	64
HG00235.mapped.ILLUMINA.bwa.GBR.exome.20130415	45	0	0	30	33	43	56	34	48	0	0	0	0	0	0	47	60
HG00236.mapped.ILLUMINA.bwa.GBR.exome.20121211	91	118	105	1	85	69	101	97	60	27	86	66	73	71	38	0	95
HG00237.mapped.ILLUMINA.bwa.GBR.exome.20121211	72	0	2	62	110	101	101	70	98	0	0	0	0	0	36	67	94
HG00238.mapped.ILLUMINA.bwa.GBR.exome.20121211	89	0	0	60	137	115	130	130	170	0	0	0	0	0	0	164	111
HG00239.mapped.ILLUMINA.bwa.GBR.exome.20120522	142	78	84	51	96	89	112	100	98	16	53	0	69	97	0	72	158
HG00240.mapped.ILLUMINA.bwa.GBR.exome.20121211	130	1	1	103	186	147	174	158	197	0	1	0	0	0	0	172	131
HG00242.mapped.ILLUMINA.bwa.GBR.exome.20120522	165	0	1	94	147	162	116	151	137	0	0	0	0	0	32	91	143
HG00243.mapped.ILLUMINA.bwa.GBR.exome.20120522	152	121	124	0	0	0	117	143	151	0	0	0	0	0	36	88	140
HG00244.mapped.ILLUMINA.bwa.GBR.exome.20120522	146	0	1	77	139	131	111	109	145	0	0	0	0	0	0	107	131
HG00245.mapped.ILLUMINA.bwa.GBR.exome.20121211	108	78	85	46	84	79	86	99	82	19	51	0	65	77	0	63	112
HG00246.mapped.ILLUMINA.bwa.GBR.exome.20120522	77	80	81	38	80	75	93	85	99	0	0	0	0	0	43	53	82
HG00250.mapped.ILLUMINA.bwa.GBR.exome.20121211	67	0	0	75	101	79	87	91	84	0	0	0	0	0	36	61	87
HG00251.mapped.ILLUMINA.bwa.GBR.exome.20121211	78	89	69	47	132	103	93	107	60	25	91	53	65	69	0	50	86
HG00252.mapped.ILLUMINA.bwa.GBR.exome.20121211	87	1	0	70	125	122	126	107	120	0	0	0	0	0	0	137	115

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG00253.mapped.ILLUMINA.bwa.GBR.exome.20121211	67	64	66	46	116	94	98	83	60	34	88	58	60	60	0	67	91
HG00254.mapped.ILLUMINA.bwa.GBR.exome.20121211	87	87	77	44	86	60	106	88	63	33	58	0	83	72	0	66	93
HG00255.mapped.ILLUMINA.bwa.GBR.exome.20121211	129	77	84	41	85	65	107	107	70	19	43	0	68	90	0	62	128
HG00256.mapped.ILLUMINA.bwa.GBR.exome.20121211	72	0	0	57	104	89	60	34	0	31	48	52	1	69	25	0	65
HG00257.mapped.ILLUMINA.bwa.GBR.exome.20121211	101	0	1	66	143	115	103	101	109	0	0	1	0	1	48	91	97
HG00258.mapped.ILLUMINA.bwa.GBR.exome.20120522	102	74	76	51	141	113	96	113	127	0	65	83	0	1	0	113	117
HG00259.mapped.ILLUMINA.bwa.GBR.exome.20121211	97	0	0	68	130	111	114	122	138	0	0	1	0	1	63	99	108
HG00260.mapped.ILLUMINA.bwa.GBR.exome.20121211	76	78	77	47	76	59	93	79	90	0	0	1	0	0	39	74	90
HG00261.mapped.ILLUMINA.bwa.GBR.exome.20121211	75	99	93	1	1	1	93	86	90	0	0	0	0	1	47	61	90
HG00262.mapped.ILLUMINA.bwa.GBR.exome.20120522	149	82	88	59	183	143	128	134	1	29	107	133	86	136	0	0	150
HG00263.mapped.ILLUMINA.bwa.GBR.exome.20120522	90	0	0	78	112	110	98	97	100	0	0	0	0	0	0	133	88
HG00264.mapped.ILLUMINA.bwa.GBR.exome.20120522	148	78	93	52	160	135	113	120	84	15	84	141	0	90	0	66	157
HG00265.mapped.ILLUMINA.bwa.GBR.exome.20120522	147	96	109	0	85	70	102	93	127	0	59	70	0	0	20	60	129
HG00266.mapped.ILLUMINA.bwa.FIN.exome.20130415	53	0	0	28	35	51	51	40	0	8	32	0	30	49	0	0	55
HG00267.mapped.ILLUMINA.bwa.FIN.exome.20130415	73	42	37	20	34	48	71	64	72	0	0	0	0	1	0	79	76
HG00268.mapped.ILLUMINA.bwa.FIN.exome.20121211	99	0	0	65	110	114	108	95	112	1	0	0	0	0	41	76	86
HG00269.mapped.ILLUMINA.bwa.FIN.exome.20130415	76	0	0	40	61	72	112	95	72	7	0	0	0	0	19	42	88
HG00271.mapped.ILLUMINA.bwa.FIN.exome.20121211	96	0	0	61	125	120	95	89	101	1	0	0	0	0	69	0	95
HG00272.mapped.ILLUMINA.bwa.FIN.exome.20120522	87	56	54	34	57	62	77	61	73	0	0	0	0	0	31	0	95
HG00273.mapped.ILLUMINA.bwa.FIN.exome.20121211	96	84	56	54	98	55	104	105	116	0	0	0	0	0	0	119	87
HG00274.mapped.ILLUMINA.bwa.FIN.exome.20120522	84	103	83	50	140	116	147	145	114	34	56	74	0	0	46	79	115
HG00275.mapped.ILLUMINA.bwa.FIN.exome.20120522	81	0	0	80	114	104	104	62	41	30	49	0	62	70	0	58	85
HG00276.mapped.ILLUMINA.bwa.FIN.exome.20120522	94	85	85	50	161	129	111	85	102	0	38	69	0	0	72	0	96
HG00277.mapped.ILLUMINA.bwa.FIN.exome.20120522	76	0	0	71	123	138	110	81	97	0	0	0	0	0	0	130	104
HG00278.mapped.ILLUMINA.bwa.FIN.exome.20120522	100	94	86	57	81	77	113	85	109	0	0	0	0	0	73	0	114
HG00280.mapped.ILLUMINA.bwa.FIN.exome.20120522	93	0	0	72	129	83	119	90	59	38	40	0	81	77	0	73	105
HG00281.mapped.ILLUMINA.bwa.FIN.exome.20120522	73	84	75	53	67	68	98	100	101	0	0	0	0	0	43	66	104
HG00282.mapped.ILLUMINA.bwa.FIN.exome.20120522	87	77	81	44	72	68	102	84	98	0	0	0	0	0	44	61	94
HG00284.mapped.ILLUMINA.bwa.FIN.exome.20120522	83	0	0	101	117	125	106	88	92	0	0	0	0	0	23	65	118
HG00285.mapped.ILLUMINA.bwa.FIN.exome.20120522	87	90	84	39	149	113	96	78	70	29	75	63	75	81	28	0	103
HG00288.mapped.ILLUMINA.bwa.FIN.exome.20130415	91	1	1	122	160	179	193	158	158	0	0	0	1	0	72	0	114
HG00290.mapped.ILLUMINA.bwa.FIN.exome.20130415	92	1	1	77	162	152	221	227	186	22	0	0	0	1	56	104	116
HG00304.mapped.ILLUMINA.bwa.FIN.exome.20130415	40	2	0	21	76	68	80	64	107	0	0	1	0	0	0	63	68
HG00306.mapped.ILLUMINA.bwa.FIN.exome.20120522	99	0	0	46	79	77	65	76	70	9	18	0	40	72	0	46	101
HG00308.mapped.ILLUMINA.bwa.FIN.exome.20121211	113	73	75	50	84	75	100	117	126	1	0	0	1	1	35	83	127
HG00309.mapped.ILLUMINA.bwa.FIN.exome.20121211	73	71	61	31	101	79	92	78	80	0	35	59	0	0	37	51	77
HG00310.mapped.ILLUMINA.bwa.FIN.exome.20120522	109	0	0	97	127	134	128	98	128	0	0	0	0	0	0	164	100
HG00311.mapped.ILLUMINA.bwa.FIN.exome.20120522	86	0	1	56	101	87	90	79	52	10	26	0	36	56	0	51	102
HG00313.mapped.ILLUMINA.bwa.FIN.exome.20120522	70	70	61	32	111	91	98	78	51	24	82	58	58	62	0	61	86
HG00315.mapped.ILLUMINA.bwa.FIN.exome.20120522	93	0	0	64	132	112	107	94	56	29	59	0	78	89	0	75	97
HG00318.mapped.ILLUMINA.bwa.FIN.exome.20120522	86	0	0	96	110	102	97	94	82	0	0	0	1	0	0	139	94
HG00319.mapped.ILLUMINA.bwa.FIN.exome.20120522	86	137	113	0	87	65	116	84	64	33	104	58	66	77	40	1	113
HG00320.mapped.ILLUMINA.bwa.FIN.exome.20120522	84	0	0	84	132	138	111	95	92	0	1	0	0	1	0	127	121
HG00321.mapped.ILLUMINA.bwa.FIN.exome.20120522	80	99	67	32	141	101	102	96	47	27	95	97	0	71	0	74	90
HG00323.mapped.ILLUMINA.bwa.FIN.exome.20120522	81	79	73	46	150	102	114	78	94	0	54	55	0	1	0	146	81
HG00324.mapped.ILLUMINA.bwa.FIN.exome.20120522	87	80	77	39	126	110	86	61	83	0	43	48	0	0	0	92	102
HG00325.mapped.ILLUMINA.bwa.FIN.exome.20120522	80	76	76	40	125	99	128	103	86	29	37	71	0	0	48	61	88
HG00326.mapped.ILLUMINA.bwa.FIN.exome.20120522	86	86	83	48	157	127	99	75	97	0	52	72	0	1	0	129	109
HG00327.mapped.ILLUMINA.bwa.FIN.exome.20120522	72	83	55	37	61	69	86	75	46	29	37	0	65	71	0	71	82
HG00328.mapped.ILLUMINA.bwa.FIN.exome.20120522	72	72	62	33	102	93	80	60	42	27	68	78	0	61	0	64	83
HG00329.mapped.ILLUMINA.bwa.FIN.exome.20120522	88	0	0	46	108	64	51	39	0	28	52	0	60	112	0	1	59
HG00330.mapped.ILLUMINA.bwa.FIN.exome.20120522	86	0	0	90	124	115	105	89	95	0	1	0	0	0	49	76	98
HG00331.mapped.ILLUMINA.bwa.FIN.exome.20120522	86	1	2	78	109	109	98	85	99	0	0	0	0	0	35	71	98
HG00332.mapped.ILLUMINA.bwa.FIN.exome.20121211	95	0	1	88	107	106	96	91	92	0	0	0	0	0	41	68	99
HG00334.mapped.ILLUMINA.bwa.FIN.exome.20120522	89	75	65	41	140	74	56	36	36	0	40	66	0	63	0	57	62
HG00335.mapped.ILLUMINA.bwa.FIN.exome.20121211	76	94	68	44	68	64	104	88	104	0	0	1	0	0	46	81	106
HG00336.mapped.ILLUMINA.bwa.FIN.exome.20120522	81	1	0	57	112	102	103	73	60	31	46	62	0	79	31	0	90
HG00337.mapped.ILLUMINA.bwa.FIN.exome.20121211	87	0	0	56	90	100	124	91	46	42	44	0	79	61	36	0	86
HG00338.mapped.ILLUMINA.bwa.FIN.exome.20120522	79	0	0	73	101	73	89	86	44	28	35	0	54	61	0	54	82
HG00339.mapped.ILLUMINA.bwa.FIN.exome.20120522	63	0	0	79	97	100	83	73	42	31	41	0	54	69	0	58	84
HG00341.mapped.ILLUMINA.bwa.FIN.exome.20121211	78	81	72	43	65	0	64	60	51	0	0	0	0	80	0	77	74
HG00342.mapped.ILLUMINA.bwa.FIN.exome.20120522	88	66	95	42	69	65	103	123	50	34	81	0	93	76	0	58	90
HG00343.mapped.ILLUMINA.bwa.FIN.exome.20120522	73	1	0	81	102	93	101	65	76	0	0	0	0	1	0	107	83
HG00344.mapped.ILLUMINA.bwa.FIN.exome.20120522	77	0	0	64	114	102	79	68	51	27	47	0	66	75	0	69	81
HG00345.mapped.ILLUMINA.bwa.FIN.exome.20121211	91	0	0	86	102	105	90	77	80	1	0	0	0	0	0	113	86
HG00346.mapped.ILLUMINA.bwa.FIN.exome.20121211	105	0	0	55	115	115	104	85	50	34	48	0	79	75	0	87	97
HG00349.mapped.ILLUMINA.bwa.FIN.exome.20130415	55	0	0	29	44	53	63	44	59	0	0	0	0	0	14	20	53
HG00350.mapped.ILLUMINA.bwa.FIN.exome.20130415	60	0	0	29	50	68	68	49	33	9	14	38	0	36	0	25	72
HG00351.mapped.ILLUMINA.bwa.FIN.exome.20130415	62	39	19	15	25	30	51	35	64	0	0	0	0	0	14	29	70
HG00353.mapped.ILLUMINA.bwa.FIN.exome.20121211	82	84	74	34	64	63	109	79	64	33	46	0	73	73	47	0	103
HG00355.mapped.ILLUMINA.bwa.FIN.exome.20130415	52	30	18	16	21	29	55	29	38	0	0	0	0	0	13	0	56
HG00356.mapped.ILLUMINA.bwa.FIN.exome.20130415	48	26	19	11	20	19	52	39	48	0	0	0	0	0	0	48	56
HG00357.mapped.ILLUMINA.bwa.FIN.exome.20120522	103	60	64	36	111	96	79	74	95	0	35	70	0	0	0	87	102
HG00358.mapped.ILLUMINA.bwa.FIN.exome.20130415	52	1	1	33	31	54	57	31	53	0	0	0	0	0	9	32	53
HG00360.mapped.ILLUMINA.bwa.FIN.exome.20130415	51	0	0	36	29	56	48	33	26	8	12	0	16	23	12	0	58
HG00361.mapped.ILLUMINA.bwa.FIN.exome.20120522	110	11	7	69	100	107	108	123	117	0	1	1	2	3	0	120	127
HG00362.mapped.ILLUMINA.bwa.FIN.exome.20130415	58	42	45	1	17	24	67	42	54	0	9	29	0	0	26	1	69
HG00364.mapped.ILLUMINA.bwa.FIN.exome.20130415	60	37	42	21	40	60	81	65	62	0	0	0	0	0	0	70	83
HG00365.mapped.ILLUMINA.bwa.FIN.exome.20130415	78	0	0	39	42	77	64	73	46	9	19	0	38	33	21	0	94
HG00366.mapped.ILLUMINA.bwa.FIN.exome.20120522	93	83	91	2	98	92	81	78	74	0	48	91	0	2	0	59	110
HG00367.mapped.ILLUMINA.bwa.FIN.exome.20120522	97	1	0	54	108	102	86	68	61	11	39	0	54	77	0	53	120
HG00368.mapped.ILLUMINA.bwa.FIN.exome.20121211	88	2	1	59	85	96	77	69	101	0	1	0	0	0	0	74	100
HG00369.mapped.ILLUMINA.bwa.FIN.exome.20120522	109	59	72	39	129	98	95	72	86	0	27	71	0	1	0	78	115
HG00371.mapped.ILLUMINA.bwa.FIN.exome.20121211	101	62	1	38	120	91	78	83	114	0	25	67	0	1	0	71	113
HG00372.mapped.ILLUMINA.bwa.FIN.exome.20120522	97	0	2	80	117	101	88	70	123	0	0	0	0	0	0	84	110
HG00373.mapped.ILLUMINA.bwa.FIN.exome.20120522	105	58	57	40	120	106	84	75	74	19	58	92	0	82	0	53	118
HG00375.mapped.ILLUMINA.bwa.FIN.exome.20120522	103	0	0	97	135	130	118	103	95	0	0	0	0	0	0	170	119
HG00376.mapped.ILLUMINA.bwa.FIN.exome.20121211	66	82	73	42	56	56	85	82	92	0	0	0	0	0	44	64	84
HG00378.mapped.ILLUMINA.bwa.FIN.exome.20121211	106	0	0	94	125	104	111	95	85	31	39	0	73	75	0	71	92
HG00379.mapped.ILLUMINA.bwa.FIN.exome.20121211	89	51	50	34	114	85	83	60	51	14	41	46	43	52	0	39	105
HG00380.mapped.ILLUMINA.bwa.FIN.exome.20120522	90	44	51	35	87	83	67	72	104	0	30	57	0	0	8	33	98
HG00381.mapped.ILLUMINA.bwa.FIN.exome.20121211	79	0	0	84	102	90	81	72	93	0	0	0	0	0	0	90	79
HG00382.mapped.ILLUMINA.bwa.FIN.exome.20121211	80	0	0	73	105	98	92	88	49	26	30	0	69	65	0	49	83
HG00383.mapped.ILLUMINA.bwa.FIN.exome.20121211	70	1	1	78	104	93	93	81	79	0	0	0	1	0	41	53	82
HG00384.mapped.ILLUMINA.bwa.FIN.exome.20121211	109	71	71	44	83	82	102	95	107	0	0	0	0	0	24	59	114
HG00403.mapped.ILLUMINA.bwa.CHS.exome.20120522	89	0	1	59	89	97	87	88	114	0	0	0	1	1	16	45	99

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG00404.mapped.ILLUMINA.bwa.CHS.exome.20121211	115	0	2	65	105	82	102	94	105	0	0	0	0	1	24	48	116
HG00406.mapped.ILLUMINA.bwa.CHS.exome.20121211	98	0	0	84	125	104	113	97	68	31	48	84	0	81	44	0	95
HG00407.mapped.ILLUMINA.bwa.CHS.exome.20121211	69	0	0	77	88	83	81	65	72	0	0	0	0	0	55	0	71
HG00409.mapped.ILLUMINA.bwa.CHS.exome.20130415	89	0	0	60	91	102	75	77	67	15	43	4	46	68	0	59	127
HG00410.mapped.ILLUMINA.bwa.CHS.exome.20121211	87	0	2	50	86	86	90	67	101	0	0	0	0	0	37	0	111
HG00419.mapped.ILLUMINA.bwa.CHS.exome.20121211	77	0	0	53	81	99	82	75	44	25	33	46	0	60	34	0	82
HG00421.mapped.ILLUMINA.bwa.CHS.exome.20121211	67	0	0	59	92	92	90	80	83	0	0	0	0	0	37	47	85
HG00422.mapped.ILLUMINA.bwa.CHS.exome.20121211	82	0	0	77	97	91	101	57	70	0	0	0	0	0	48	64	79
HG00428.mapped.ILLUMINA.bwa.CHS.exome.20121211	76	0	0	72	138	99	84	76	95	0	0	0	0	0	0	116	90
HG00436.mapped.ILLUMINA.bwa.CHS.exome.20120522	92	1	0	87	127	126	114	104	127	0	0	0	0	1	40	81	105
HG00437.mapped.ILLUMINA.bwa.CHS.exome.20121211	71	0	0	64	113	101	109	76	108	0	0	0	0	0	54	0	91
HG00442.mapped.ILLUMINA.bwa.CHS.exome.20121211	70	0	0	53	106	92	101	74	83	0	0	0	0	1	66	0	90
HG00443.mapped.ILLUMINA.bwa.CHS.exome.20121211	95	0	0	73	97	101	82	61	52	28	44	0	48	60	0	51	77
HG00445.mapped.ILLUMINA.bwa.CHS.exome.20121211	80	0	1	51	98	97	83	71	44	30	39	58	0	59	43	0	86
HG00446.mapped.ILLUMINA.bwa.CHS.exome.20121211	72	0	0	59	91	100	85	85	83	0	0	0	0	0	38	61	79
HG00448.mapped.ILLUMINA.bwa.CHS.exome.20121211	72	0	1	53	94	92	88	68	85	1	0	0	0	0	57	0	74
HG00449.mapped.ILLUMINA.bwa.CHS.exome.20120522	89	0	0	62	119	106	131	93	103	0	0	0	0	0	62	1	96
HG00451.mapped.ILLUMINA.bwa.CHS.exome.20121211	71	81	56	36	129	91	105	104	52	35	77	49	62	77	31	0	82
HG00452.mapped.ILLUMINA.bwa.CHS.exome.20121211	102	0	0	70	126	112	106	93	71	34	75	0	100	102	0	99	139
HG00457.mapped.ILLUMINA.bwa.CHS.exome.20121211	110	0	1	63	76	88	97	97	84	0	0	0	0	0	72	1	84
HG00458.mapped.ILLUMINA.bwa.CHS.exome.20121211	70	0	0	55	103	89	94	62	78	0	0	0	0	0	69	1	88
HG00463.mapped.ILLUMINA.bwa.CHS.exome.20120522	68	0	0	65	97	106	98	71	88	0	0	0	1	0	64	0	106
HG00464.mapped.ILLUMINA.bwa.CHS.exome.20120522	82	82	73	41	68	72	98	66	2	41	86	0	97	113	0	0	89
HG00472.mapped.ILLUMINA.bwa.CHS.exome.20121211	88	0	0	72	97	87	92	80	86	0	0	0	0	0	40	64	85
HG00473.mapped.ILLUMINA.bwa.CHS.exome.20121211	110	0	1	55	119	112	117	104	78	32	65	81	0	90	46	0	99
HG00475.mapped.ILLUMINA.bwa.CHS.exome.20121211	98	0	0	46	74	78	79	96	67	0	1	0	0	0	70	0	68
HG00476.mapped.ILLUMINA.bwa.CHS.exome.20121211	85	0	1	65	108	103	96	100	61	36	53	0	77	75	45	1	93
HG00478.mapped.ILLUMINA.bwa.CHS.exome.20121211	83	91	76	46	81	68	104	78	54	31	48	69	0	81	0	73	91
HG00479.mapped.ILLUMINA.bwa.CHS.exome.20121211	92	0	0	54	111	103	93	72	97	0	0	0	0	0	58	0	65
HG00500.mapped.ILLUMINA.bwa.CHS.exome.20120522	64	1	3	73	106	102	98	71	93	0	0	0	0	0	0	91	91
HG00501.mapped.ILLUMINA.bwa.CHS.exome.20120522	91	0	0	83	112	99	105	67	75	0	0	0	0	0	0	95	94
HG00513.mapped.ILLUMINA.bwa.CHS.exome.20120522	80	0	0	57	101	98	131	90	86	0	0	0	0	0	39	67	88
HG00524.mapped.ILLUMINA.bwa.CHS.exome.20120522	104	1	1	107	137	108	107	97	108	0	0	0	0	0	0	168	114
HG00525.mapped.ILLUMINA.bwa.CHS.exome.20121211	79	0	1	59	107	109	95	100	116	0	0	0	0	2	46	82	98
HG00530.mapped.ILLUMINA.bwa.CHS.exome.20120522	66	0	0	52	97	89	89	75	68	0	0	0	0	0	37	46	84
HG00531.mapped.ILLUMINA.bwa.CHS.exome.20120522	78	0	0	70	112	104	111	94	66	30	47	68	0	81	0	70	94
HG00533.mapped.ILLUMINA.bwa.CHS.exome.20120522	87	84	83	46	74	68	104	77	45	37	38	0	70	68	0	64	121
HG00534.mapped.ILLUMINA.bwa.CHS.exome.20120522	103	102	85	45	86	81	114	94	100	0	0	0	0	0	42	73	112
HG00536.mapped.ILLUMINA.bwa.CHS.exome.20121211	101	0	0	61	108	106	103	94	59	33	42	0	74	74	49	0	105
HG00537.mapped.ILLUMINA.bwa.CHS.exome.20120522	78	0	0	100	119	105	110	108	59	35	62	0	78	73	47	2	86
HG00542.mapped.ILLUMINA.bwa.CHS.exome.20120522	80	0	0	82	106	97	96	68	44	33	38	0	56	74	0	68	110
HG00543.mapped.ILLUMINA.bwa.CHS.exome.20121211	83	0	0	89	115	96	96	81	63	26	62	0	67	74	0	82	98
HG00551.mapped.ILLUMINA.bwa.PUR.exome.20120522	148	71	90	44	87	77	98	140	126	0	0	0	0	1	38	74	123
HG00553.mapped.ILLUMINA.bwa.PUR.exome.20120522	147	0	1	111	222	200	210	184	177	0	0	0	0	0	69	112	152
HG00554.mapped.ILLUMINA.bwa.PUR.exome.20120522	122	0	0	72	205	178	189	147	205	0	0	0	0	1	61	109	147
HG00556.mapped.ILLUMINA.bwa.CHS.exome.20121211	120	0	0	63	130	137	134	129	119	0	0	0	1	0	88	0	112
HG00557.mapped.ILLUMINA.bwa.CHS.exome.20121211	116	0	0	53	89	93	48	70	0	0	0	0	1	0	42	0	44
HG00559.mapped.ILLUMINA.bwa.CHS.exome.20130415	65	0	0	38	59	76	74	63	73	0	0	0	0	2	16	42	83
HG00560.mapped.ILLUMINA.bwa.CHS.exome.20130415	86	36	35	18	65	67	73	57	73	0	25	44	1	0	6	38	80
HG00565.mapped.ILLUMINA.bwa.CHS.exome.20130415	56	29	22	16	23	29	62	37	46	0	0	0	0	0	14	0	55
HG00566.mapped.ILLUMINA.bwa.CHS.exome.20130415	51	0	1	20	31	54	53	19	26	0	0	0	0	0	17	0	48
HG00580.mapped.ILLUMINA.bwa.CHS.exome.20120522	80	87	74	40	69	49	56	30	67	0	59	53	0	72	41	0	104
HG00581.mapped.ILLUMINA.bwa.CHS.exome.20120522	82	85	75	45	147	119	125	109	92	39	43	70	0	0	47	66	100
HG00583.mapped.ILLUMINA.bwa.CHS.exome.20120522	69	0	1	70	88	86	81	59	49	25	29	0	57	72	31	0	79
HG00584.mapped.ILLUMINA.bwa.CHS.exome.20120522	89	91	73	45	74	76	122	74	107	1	0	0	0	0	36	64	120
HG00589.mapped.ILLUMINA.bwa.CHS.exome.20120522	69	79	57	39	123	98	83	60	38	27	74	91	0	62	0	66	77
HG00590.mapped.ILLUMINA.bwa.CHS.exome.20120522	70	0	0	58	102	104	95	77	91	0	0	0	0	0	39	53	90
HG00592.mapped.ILLUMINA.bwa.CHS.exome.20130415	54	0	0	27	45	63	51	36	45	0	0	0	0	0	22	1	67
HG00593.mapped.ILLUMINA.bwa.CHS.exome.20130415	53	0	0	27	36	58	67	53	57	0	0	0	0	1	13	19	67
HG00595.mapped.ILLUMINA.bwa.CHS.exome.20130415	62	1	0	28	28	65	69	41	25	5	8	0	17	35	0	19	64
HG00596.mapped.ILLUMINA.bwa.CHS.exome.20130415	64	24	32	18	23	47	64	41	45	0	0	0	2	1	17	33	68
HG00598.mapped.ILLUMINA.bwa.CHS.exome.20121211	108	66	65	55	124	101	97	125	75	24	78	64	60	80	34	1	112
HG00599.mapped.ILLUMINA.bwa.CHS.exome.20121211	123	0	0	76	86	87	79	87	67	13	36	0	58	75	31	0	107
HG00607.mapped.ILLUMINA.bwa.CHS.exome.20120522	68	0	0	65	109	95	95	85	53	31	41	74	1	68	39	0	91
HG00608.mapped.ILLUMINA.bwa.CHS.exome.20120522	86	0	0	67	116	106	92	80	49	31	48	0	67	74	34	0	93
HG00610.mapped.ILLUMINA.bwa.CHS.exome.20120522	105	83	88	0	68	67	100	88	76	15	52	75	49	75	13	1	114
HG00611.mapped.ILLUMINA.bwa.CHS.exome.20120522	99	50	61	38	103	80	78	67	63	16	39	76	0	65	14	0	97
HG00613.mapped.ILLUMINA.bwa.CHS.exome.20120522	73	0	0	63	124	99	87	78	51	32	39	64	0	71	43	0	99
HG00614.mapped.ILLUMINA.bwa.CHS.exome.20120522	81	0	1	59	93	104	86	66	49	33	42	1	68	74	29	0	90
HG00619.mapped.ILLUMINA.bwa.CHS.exome.20120522	87	0	0	73	127	109	110	91	51	30	46	66	0	89	50	0	95
HG00620.mapped.ILLUMINA.bwa.CHS.exome.20120522	75	0	0	68	125	107	99	86	67	32	47	0	67	77	50	0	105
HG00622.mapped.ILLUMINA.bwa.CHS.exome.20130415	88	0	0	93	93	103	88	76	93	0	1	0	0	1	42	1	104
HG00623.mapped.ILLUMINA.bwa.CHS.exome.20121211	95	63	53	49	60	59	86	78	72	17	37	0	44	64	0	54	111
HG00625.mapped.ILLUMINA.bwa.CHS.exome.20120522	94	0	1	52	84	97	74	72	81	0	0	0	0	2	30	0	96
HG00626.mapped.ILLUMINA.bwa.CHS.exome.20120522	117	1	1	74	103	89	84	83	78	17	30	0	45	71	21	0	97
HG00628.mapped.ILLUMINA.bwa.CHS.exome.20120522	117	0	1	51	93	87	73	74	96	0	0	0	0	1	29	0	92
HG00629.mapped.ILLUMINA.bwa.CHS.exome.20120522	105	0	0	57	112	97	93	71	102	0	0	0	0	0	36	0	130
HG00631.mapped.ILLUMINA.bwa.CHS.exome.20121211	104	60	63	45	118	90	100	108	105	15	41	62	2	0	39	0	121
HG00632.mapped.ILLUMINA.bwa.CHS.exome.20121211	91	0	0	53	92	86	82	102	101	0	0	3	1	0	29	73	95
HG00634.mapped.ILLUMINA.bwa.CHS.exome.20120522	100	0	0	74	102	95	83	73	53	17	28	0	48	67	0	49	104
HG00635.mapped.ILLUMINA.bwa.CHS.exome.20120522	92	44	57	39	112	82	88	96	77	14	30	53	0	0	27	0	93
HG00637.mapped.ILLUMINA.bwa.PUR.exome.20120522	126	0	1	91	159	175	182	192	194	0	0	0	1	0	0	204	154
HG00638.mapped.ILLUMINA.bwa.PUR.exome.20120522	166	0	0	75	194	181	185	170	190	0	0	0	0	0	0	162	185
HG00640.mapped.ILLUMINA.bwa.PUR.exome.20120522	130	104	105	57	117	100	144	157	115	9	85	0	97	125	75	4	134
HG00641.mapped.ILLUMINA.bwa.PUR.exome.20120522	192	89	96	63	138	122	143	179	163	0	1	1	0	2	36	99	204
HG00650.mapped.ILLUMINA.bwa.CHS.exome.20120522	85	0	0	64	139	107	109	87	111	0	0	0	0	0	50	79	114
HG00651.mapped.ILLUMINA.bwa.CHS.exome.20120522	78	0	1	80	142	130	111	70	111	0	0	0	0	0	43	78	123
HG00653.mapped.ILLUMINA.bwa.CHS.exome.20120522	94	144	130	0	0	1	112	80	100	0	0	0	0	0	71	1	119
HG00654.mapped.ILLUMINA.bwa.CHS.exome.20120522	88	1	0	77	137	81	117	70	94	0	0	0	0	1	80	0	113
HG00656.mapped.ILLUMINA.bwa.CHS.exome.20120522	105	0	0	81	161	120	112	95	109	0	0	0	0	0	46	65	112
HG00657.mapped.ILLUMINA.bwa.CHS.exome.20120522	82	93	78	44	76	72	67	50	1	0	0	0	0	0	0	0	57
HG00662.mapped.ILLUMINA.bwa.CHS.exome.20120522	89	0	1	63	134	113	116	68	102	0	0	0	0	0	35	75	112
HG00663.mapped.ILLUMINA.bwa.CHS.exome.20120522	77	0	0	59	127	107	110	69	61	37	46	63	0	73	41	0	100
HG00671.mapped.ILLUMINA.bwa.CHS.exome.20120522	66	74	76	38	62	43	80	71	1	35	76	0	102	82	0	0	97
HG00672.mapped.ILLUMINA.bwa.CHS.exome.20120522	77	0	0	76	98	95	80	74	77	0	0	0	0	0	0	101	83
HG00674.mapped.ILLUMINA.bwa.CHS.exome.20121211	90	76	58	46	66	75	86	104	80	16	46	0	53	78	33	0	112

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG00675.mapped.ILLUMINA.bwa.CHS.exome.20121211	95	2	0	59	97	90	81	76	95	0	1	1	0	0	44	0	105
HG00683.mapped.ILLUMINA.bwa.CHS.exome.20120522	85	0	0	51	103	103	101	85	62	29	48	65	0	66	0	63	87
HG00684.mapped.ILLUMINA.bwa.CHS.exome.20120522	84	0	0	64	120	110	100	97	59	27	49	0	67	72	43	1	87
HG00689.mapped.ILLUMINA.bwa.CHS.exome.20120522	79	0	2	76	113	102	92	78	84	0	0	0	0	0	34	53	93
HG00690.mapped.ILLUMINA.bwa.CHS.exome.20120522	79	0	1	51	90	79	88	79	62	26	50	66	0	66	37	1	88
HG00692.mapped.ILLUMINA.bwa.CHS.exome.20120522	104	0	0	100	130	128	118	91	119	0	0	0	0	0	80	0	117
HG00693.mapped.ILLUMINA.bwa.CHS.exome.20120522	81	93	87	54	93	74	72	44	64	0	33	72	0	74	36	0	111
HG00698.mapped.ILLUMINA.bwa.CHS.exome.20120522	87	0	0	72	120	133	109	76	107	0	0	0	0	0	37	85	112
HG00699.mapped.ILLUMINA.bwa.CHS.exome.20120522	112	0	0	80	147	125	130	86	112	0	0	0	0	0	72	0	115
HG00701.mapped.ILLUMINA.bwa.CHS.exome.20120522	86	1	0	73	116	120	84	69	102	0	0	0	0	0	60	0	114
HG00702.mapped.ILLUMINA.bwa.CHS.exome.20120522	96	97	70	47	71	73	107	77	119	0	0	0	0	1	0	122	112
HG00704.mapped.ILLUMINA.bwa.CHS.exome.20120522	113	0	1	71	154	143	112	86	59	40	41	69	0	81	32	0	112
HG00705.mapped.ILLUMINA.bwa.CHS.exome.20120522	93	0	0	77	145	121	122	70	125	0	0	1	0	0	70	0	103
HG00707.mapped.ILLUMINA.bwa.CHS.exome.20120522	95	109	86	45	104	95	115	90	109	0	0	0	0	0	27	84	125
HG00708.mapped.ILLUMINA.bwa.CHS.exome.20120522	109	0	0	121	142	126	134	100	67	39	39	1	85	81	34	0	121
HG00717.mapped.ILLUMINA.bwa.CHS.exome.20130415	64	5	4	41	111	114	127	96	122	0	0	0	1	0	0	105	95
HG00728.mapped.ILLUMINA.bwa.CHS.exome.20121211	98	0	1	60	91	95	89	89	118	0	4	0	0	3	31	63	115
HG00729.mapped.ILLUMINA.bwa.CHS.exome.20121211	127	2	0	61	100	88	85	97	80	19	47	1	51	79	31	0	121
HG00731.mapped.ILLUMINA.bwa.PUR.exome.20130422	270	160	175	1	160	151	247	295	216	31	99	167	4	8	58	147	261
HG00732.mapped.ILLUMINA.bwa.PUR.exome.20130422	271	4	4	5	1	11	150	135	9	32	121	0	126	173	0	3	182
HG00733.mapped.ILLUMINA.bwa.PUR.exome.20130422	112	91	76	65	138	108	113	140	113	22	64	80	4	5	33	75	147
HG00734.mapped.ILLUMINA.bwa.PUR.exome.20120522	189	0	1	2	1	3	103	119	4	0	0	0	0	0	0	0	126
HG00736.mapped.ILLUMINA.bwa.PUR.exome.20120522	134	69	68	41	87	83	90	94	74	15	47	0	60	78	0	87	123
HG00737.mapped.ILLUMINA.bwa.PUR.exome.20120522	185	88	96	61	108	107	95	112	3	18	85	0	97	106	39	0	122
HG00739.mapped.ILLUMINA.bwa.PUR.exome.20120522	165	77	80	53	97	1	91	88	107	0	0	0	0	96	33	0	118
HG00740.mapped.ILLUMINA.bwa.PUR.exome.20120522	126	80	85	45	150	120	110	93	157	0	44	96	0	0	0	115	139
HG00742.mapped.ILLUMINA.bwa.PUR.exome.20130415	45	89	79	5	64	55	97	101	70	11	53	84	0	52	41	3	73
HG00743.mapped.ILLUMINA.bwa.PUR.exome.20130415	35	52	43	11	55	52	95	86	65	9	36	5	43	58	0	46	63
HG00759.mapped.ILLUMINA.bwa.CDX.exome.20130415	169	215	164	84	158	171	233	219	148	55	138	0	180	177	68	6	154
HG00766.mapped.ILLUMINA.bwa.CDX.exome.20130415	99	0	0	118	162	155	182	158	117	29	110	0	124	120	0	121	113
HG00844.mapped.ILLUMINA.bwa.CDX.exome.20121211	68	0	0	50	93	101	83	72	91	0	0	0	0	0	58	1	96
HG00851.mapped.ILLUMINA.bwa.CDX.exome.20121211	75	81	69	45	126	88	97	86	64	32	85	61	67	52	34	0	93
HG00864.mapped.ILLUMINA.bwa.CDX.exome.20120522	82	0	0	69	112	98	89	70	89	0	0	0	0	0	0	101	87
HG00867.mapped.ILLUMINA.bwa.CDX.exome.20130415	89	1	3	69	183	166	185	218	146	26	122	0	136	122	56	3	125
HG00879.mapped.ILLUMINA.bwa.CDX.exome.20120522	74	0	0	59	99	84	104	71	78	0	0	0	0	0	53	0	79
HG00881.mapped.ILLUMINA.bwa.CDX.exome.20121211	90	0	0	60	106	102	91	66	56	34	43	65	0	76	47	0	94
HG00956.mapped.ILLUMINA.bwa.CDX.exome.20121211	60	56	51	34	87	75	72	52	38	22	68	45	42	49	0	53	61
HG00978.mapped.ILLUMINA.bwa.CDX.exome.20121211	93	88	73	41	68	67	93	75	86	0	0	0	0	0	60	0	85
HG00982.mapped.ILLUMINA.bwa.CDX.exome.20121211	78	1	0	82	108	96	92	86	61	27	50	0	65	60	30	0	81
HG01028.mapped.ILLUMINA.bwa.CDX.exome.20121211	102	0	0	97	126	120	112	91	68	36	60	0	86	77	0	86	97
HG01029.mapped.ILLUMINA.bwa.CDX.exome.20121211	96	0	0	77	108	109	95	87	71	32	59	68	0	72	0	91	91
HG01031.mapped.ILLUMINA.bwa.CDX.exome.20120522	72	1	0	74	99	84	89	69	41	24	51	0	47	68	0	67	75
HG01046.mapped.ILLUMINA.bwa.CDX.exome.20121211	81	0	0	53	92	90	79	71	48	27	46	0	70	60	34	0	53
HG01047.mapped.ILLUMINA.bwa.PUR.exome.20120522	122	95	97	0	0	0	91	115	123	0	0	0	0	0	0	140	134
HG01048.mapped.ILLUMINA.bwa.PUR.exome.20121211	215	0	0	122	208	175	167	189	200	0	0	0	0	1	41	106	234
HG01049.mapped.ILLUMINA.bwa.PUR.exome.20120522	179	86	96	67	193	174	137	201	97	18	100	177	1	120	0	107	196
HG01051.mapped.ILLUMINA.bwa.PUR.exome.20120522	84	0	0	59	108	94	87	82	107	0	0	0	0	0	0	111	91
HG01052.mapped.ILLUMINA.bwa.PUR.exome.20120522	94	0	71	46	140	106	97	99	109	0	63	0	62	0	36	72	99
HG01054.mapped.ILLUMINA.bwa.PUR.exome.20120522	249	0	1	139	222	221	187	177	226	0	0	0	0	1	0	184	244
HG01055.mapped.ILLUMINA.bwa.PUR.exome.20120522	185	0	0	131	180	189	147	171	189	0	0	0	0	1	61	0	197
HG01058.mapped.ILLUMINA.bwa.PUR.exome.20130415	31	2	8	33	91	81	88	73	117	1	1	0	0	1	0	71	80
HG01060.mapped.ILLUMINA.bwa.PUR.exome.20120522	112	152	144	0	0	0	119	74	129	0	0	0	0	0	62	0	124
HG01061.mapped.ILLUMINA.bwa.PUR.exome.20120522	90	86	81	41	160	134	115	62	98	0	44	66	0	0	0	94	118
HG01063.mapped.ILLUMINA.bwa.PUR.exome.20130415	53	47	42	18	50	52	83	84	88	0	2	2	0	2	21	40	69
HG01064.mapped.ILLUMINA.bwa.PUR.exome.20130415	48	1	0	23	82	79	94	79	100	0	2	0	0	0	32	54	62
HG01066.mapped.ILLUMINA.bwa.PUR.exome.20120522	224	0	1	101	196	198	172	175	187	0	0	1	0	0	0	169	212
HG01067.mapped.ILLUMINA.bwa.PUR.exome.20120522	165	92	92	60	190	146	122	130	145	0	49	86	0	1	0	134	196
HG01069.mapped.ILLUMINA.bwa.PUR.exome.20120522	84	0	0	62	101	105	104	96	90	1	0	0	0	0	0	137	96
HG01070.mapped.ILLUMINA.bwa.PUR.exome.20120522	83	0	0	76	95	94	91	75	90	0	0	0	0	0	43	64	82
HG01072.mapped.ILLUMINA.bwa.PUR.exome.20120522	78	0	0	51	99	95	80	99	97	0	0	0	0	0	0	123	81
HG01073.mapped.ILLUMINA.bwa.PUR.exome.20120522	67	95	94	1	0	0	48	43	1	26	77	54	55	92	0	0	87
HG01075.mapped.ILLUMINA.bwa.PUR.exome.20120522	121	80	84	43	94	81	107	102	118	0	0	0	0	0	0	110	123
HG01077.mapped.ILLUMINA.bwa.PUR.exome.20130415	38	5	5	30	85	88	89	60	92	1	0	2	2	0	46	1	70
HG01079.mapped.ILLUMINA.bwa.PUR.exome.20120522	129	0	1	89	125	127	109	116	135	0	0	0	0	0	0	133	129
HG01080.mapped.ILLUMINA.bwa.PUR.exome.20120522	150	0	0	55	141	117	108	138	80	13	55	0	68	94	0	63	121
HG01082.mapped.ILLUMINA.bwa.PUR.exome.20120522	97	94	86	46	80	76	106	104	124	0	0	0	0	0	0	116	92
HG01083.mapped.ILLUMINA.bwa.PUR.exome.20120522	81	82	75	41	121	99	98	80	47	29	74	59	65	63	0	63	97
HG01085.mapped.ILLUMINA.bwa.PUR.exome.20121211	85	86	79	50	88	84	111	89	95	0	0	0	0	0	0	139	104
HG01086.mapped.ILLUMINA.bwa.PUR.exome.20121211	75	0	0	86	105	95	92	69	84	0	0	0	0	1	0	114	101
HG01088.mapped.ILLUMINA.bwa.PUR.exome.20130415	40	2	3	19	76	73	90	80	98	0	0	0	0	0	0	79	67
HG01089.mapped.ILLUMINA.bwa.PUR.exome.20130415	47	77	81	1	50	55	101	108	106	8	37	44	1	1	30	40	66
HG01092.mapped.ILLUMINA.bwa.PUR.exome.20130415	39	51	71	1	29	48	77	65	81	0	44	0	42	0	49	1	72
HG01094.mapped.ILLUMINA.bwa.PUR.exome.20120522	151	82	83	59	94	96	118	128	142	0	0	0	0	0	62	0	141
HG01095.mapped.ILLUMINA.bwa.PUR.exome.20121211	120	0	1	67	143	112	111	94	125	0	58	72	0	1	0	67	81
HG01097.mapped.ILLUMINA.bwa.PUR.exome.20120522	100	0	0	59	136	112	128	124	148	0	0	0	0	0	0	126	106
HG01098.mapped.ILLUMINA.bwa.PUR.exome.20120522	124	96	125	49	213	166	184	159	192	0	82	121	0	0	49	80	144
HG01101.mapped.ILLUMINA.bwa.PUR.exome.20121211	113	0	1	88	113	104	87	125	92	1	1	1	0	1	0	136	120
HG01102.mapped.ILLUMINA.bwa.PUR.exome.20120522	136	102	115	0	0	1	107	110	59	18	68	0	71	87	0	73	139
HG01104.mapped.ILLUMINA.bwa.PUR.exome.20121211	68	1	0	58	104	92	118	81	58	30	67	0	76	75	42	0	91
HG01105.mapped.ILLUMINA.bwa.PUR.exome.20121211	64	73	69	43	62	54	92	54	36	28	35	48	0	68	27	0	74
HG01107.mapped.ILLUMINA.bwa.PUR.exome.20120522	82	93	82	53	151	114	109	90	93	1	46	62	0	0	33	63	106
HG01108.mapped.ILLUMINA.bwa.PUR.exome.20120522	110	3	4	91	149	109	100	85	119	0	2	2	1	2	0	117	87
HG01110.mapped.ILLUMINA.bwa.PUR.exome.20120522	160	80	92	54	189	142	139	151	148	0	72	96	0	1	30	75	166
HG01111.mapped.ILLUMINA.bwa.PUR.exome.20120522	180	83	109	62	111	112	128	174	145	0	0	0	0	0	40	95	184
HG01112.mapped.ILLUMINA.bwa.CLM.exome.20120522	134	0	0	86	207	204	189	162	199	0	0	0	0	0	0	159	156
HG01113.mapped.ILLUMINA.bwa.CLM.exome.20120522	117	0	0	102	152	141	158	123	106	14	78	0	95	113	0	70	116
HG01119.mapped.ILLUMINA.bwa.CLM.exome.20130415	86	0	2	118	176	170	216	231	194	0	0	0	0	0	0	256	122
HG01121.mapped.ILLUMINA.bwa.CLM.exome.20130415	90	18	129	56	157	171	224	192	126	39	165	7	156	117	0	6	91
HG01122.mapped.ILLUMINA.bwa.CLM.exome.20130415	82	156	152	2	124	109	191	214	193	4	106	114	17	11	54	105	108
HG01124.mapped.ILLUMINA.bwa.CLM.exome.20130415	73	0	0	20	56	32	40	31	0	7	29	0	27	68	0	0	87
HG01125.mapped.ILLUMINA.bwa.CLM.exome.20130415	52	0	0	26	44	43	52	51	64	0	0	0	0	1	9	33	62
HG01130.mapped.ILLUMINA.bwa.CLM.exome.20130415	88	146	142	68	141	130	191	265	243	0	0	0	0	0	58	123	135
HG01131.mapped.ILLUMINA.bwa.CLM.exome.20130415	89	0	2	61	172	143	160	203	167	1	1	0	1	2	57	112	116
HG01133.mapped.ILLUMINA.bwa.CLM.exome.20130415	71	0	1	30	35	51	59	40	57	0	1	0	0	1	0	53	72
HG01134.mapped.ILLUMINA.bwa.CLM.exome.20130415	61	0	0	27	45	65	60	40	29	5	16	0	28	39	13	1	56
HG01136.mapped.ILLUMINA.bwa.CLM.exome.20130415	53	1	0	31	44	56	66	40	58	0	0	0	0	0	22	0	65

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG01137.mapped.ILLUMINA.bwa.CLM.exome.20130415	69	3	1	26	53	64	71	44	37	4	34	0	31	30	9	1	76
HG01139.mapped.ILLUMINA.bwa.CLM.exome.20130415	69	0	0	27	32	61	76	39	48	0	0	0	0	0	0	64	68
HG01140.mapped.ILLUMINA.bwa.CLM.exome.20130415	66	0	0	26	29	63	71	56	42	3	8	23	1	0	0	51	54
HG01142.mapped.ILLUMINA.bwa.CLM.exome.20130415	93	0	2	78	157	152	195	207	131	24	122	0	127	112	58	2	110
HG01148.mapped.ILLUMINA.bwa.CLM.exome.20130415	62	0	0	25	48	63	52	51	58	0	0	0	0	0	17	0	68
HG01149.mapped.ILLUMINA.bwa.CLM.exome.20130415	76	34	36	16	24	36	93	89	35	16	20	0	39	41	0	31	73
HG01161.mapped.ILLUMINA.bwa.PUR.exome.20130415	35	0	1	20	65	61	74	63	49	13	24	0	37	48	0	39	53
HG01162.mapped.ILLUMINA.bwa.PUR.exome.20130415	27	2	1	22	63	58	62	60	53	12	29	0	39	45	0	38	64
HG01164.mapped.ILLUMINA.bwa.PUR.exome.20130415	47	89	92	0	95	83	101	75	100	0	73	92	1	0	0	76	83
HG01167.mapped.ILLUMINA.bwa.PUR.exome.20121211	126	90	95	1	3	2	94	124	91	20	55	0	70	93	31	2	120
HG01168.mapped.ILLUMINA.bwa.PUR.exome.20120522	211	94	99	67	117	109	139	190	111	24	74	123	0	121	36	0	226
HG01170.mapped.ILLUMINA.bwa.PUR.exome.20120522	92	4	1	84	112	98	92	103	101	0	1	3	0	0	39	71	85
HG01171.mapped.ILLUMINA.bwa.PUR.exome.20120522	71	0	0	45	81	78	76	41	75	0	0	0	0	0	27	48	73
HG01173.mapped.ILLUMINA.bwa.PUR.exome.20120522	95	134	114	0	0	0	113	70	60	32	49	57	0	75	47	0	109
HG01174.mapped.ILLUMINA.bwa.PUR.exome.20120522	70	0	0	51	98	89	80	75	75	0	0	0	0	0	0	84	87
HG01176.mapped.ILLUMINA.bwa.PUR.exome.20120522	127	82	73	46	147	116	101	113	68	17	93	111	0	86	0	67	115
HG01177.mapped.ILLUMINA.bwa.PUR.exome.20120522	122	0	0	61	111	102	87	108	116	0	0	0	0	1	46	0	128
HG01182.mapped.ILLUMINA.bwa.PUR.exome.20121211	103	71	77	45	140	105	120	105	109	0	46	80	0	0	32	50	109
HG01183.mapped.ILLUMINA.bwa.PUR.exome.20121211	104	74	75	58	97	77	100	127	89	20	43	1	87	88	36	1	133
HG01187.mapped.ILLUMINA.bwa.PUR.exome.20120522	142	0	0	76	171	127	114	107	88	17	53	0	71	89	31	0	157
HG01188.mapped.ILLUMINA.bwa.PUR.exome.20120522	146	0	0	68	128	135	108	110	132	0	0	0	0	0	0	121	138
HG01190.mapped.ILLUMINA.bwa.PUR.exome.20120522	95	0	0	81	98	99	85	85	102	0	0	0	0	0	0	98	120
HG01191.mapped.ILLUMINA.bwa.PUR.exome.20121211	113	88	95	1	89	76	121	163	130	20	43	80	1	3	30	61	110
HG01197.mapped.ILLUMINA.bwa.PUR.exome.20121211	118	76	78	48	140	93	94	92	103	0	49	70	0	2	0	102	125
HG01198.mapped.ILLUMINA.bwa.PUR.exome.20121211	94	78	71	49	88	78	87	92	92	1	0	0	1	2	0	90	119
HG01200.mapped.ILLUMINA.bwa.PUR.exome.20130415	47	2	1	25	75	71	81	77	55	13	41	1	45	44	0	32	63
HG01204.mapped.ILLUMINA.bwa.PUR.exome.20121211	124	84	70	52	150	105	88	121	116	0	53	80	3	0	28	79	143
HG01205.mapped.ILLUMINA.bwa.PUR.exome.20121211	137	97	116	1	79	95	71	63	101	0	92	112	0	82	0	76	124
HG01241.mapped.ILLUMINA.bwa.PUR.exome.20120522	117	98	80	0	0	1	1	0	0	0	89	1	95	136	0	0	132
HG01242.mapped.ILLUMINA.bwa.PUR.exome.20120522	121	77	121	0	0	75	77	48	91	0	46	0	60	85	27	0	147
HG01247.mapped.ILLUMINA.bwa.PUR.exome.20120522	121	0	1	83	128	138	110	95	115	0	0	0	0	0	0	94	143
HG01248.mapped.ILLUMINA.bwa.PUR.exome.20120522	131	1	1	96	126	144	109	119	122	0	0	0	0	1	0	113	146
HG01250.mapped.ILLUMINA.bwa.CLM.exome.20120522	128	0	0	129	190	161	159	145	155	0	0	0	0	0	0	162	138
HG01251.mapped.ILLUMINA.bwa.CLM.exome.20120522	99	89	96	51	84	93	139	147	149	0	0	0	0	0	33	68	144
HG01253.mapped.ILLUMINA.bwa.CLM.exome.20120522	126	102	115	57	112	114	170	162	194	0	0	0	0	0	0	84	142
HG01254.mapped.ILLUMINA.bwa.CLM.exome.20120522	157	0	0	105	235	217	240	168	249	0	0	1	0	1	116	0	194
HG01256.mapped.ILLUMINA.bwa.CLM.exome.20121211	80	48	51	30	63	65	64	75	52	15	26	0	45	62	0	28	103
HG01257.mapped.ILLUMINA.bwa.CLM.exome.20121211	111	57	61	41	66	65	85	68	2	24	43	0	62	106	0	0	110
HG01259.mapped.ILLUMINA.bwa.CLM.exome.20121211	90	67	65	2	70	69	59	42	71	0	32	0	47	80	0	43	107
HG01260.mapped.ILLUMINA.bwa.CLM.exome.20121211	116	66	77	49	78	74	98	87	79	15	32	0	62	79	0	67	133
HG01269.mapped.ILLUMINA.bwa.CLM.exome.20130415	112	6	7	92	228	200	218	184	228	1	0	0	0	0	82	0	143
HG01271.mapped.ILLUMINA.bwa.CLM.exome.20130415	63	20	24	22	38	60	58	54	60	0	16	38	0	0	8	26	66
HG01272.mapped.ILLUMINA.bwa.CLM.exome.20130415	64	0	0	19	31	61	64	38	24	7	14	0	16	23	15	0	74
HG01275.mapped.ILLUMINA.bwa.CLM.exome.20130415	64	0	2	31	51	79	69	59	45	10	37	0	21	40	0	33	72
HG01277.mapped.ILLUMINA.bwa.CLM.exome.20130415	73	0	0	34	37	63	73	54	43	11	13	0	33	37	0	42	63
HG01280.mapped.ILLUMINA.bwa.CLM.exome.20130415	79	157	153	1	4	3	176	195	150	0	0	0	0	0	61	100	123
HG01281.mapped.ILLUMINA.bwa.CLM.exome.20130415	97	139	138	52	228	175	230	267	221	33	117	141	1	4	0	247	137
HG01284.mapped.ILLUMINA.bwa.CLM.exome.20130415	94	158	150	64	140	121	204	225	133	30	114	0	125	124	0	120	140
HG01286.mapped.ILLUMINA.bwa.PUR.exome.20130415	29	64	64	2	3	8	79	55	49	10	27	32	0	48	0	38	54
HG01302.mapped.ILLUMINA.bwa.PUR.exome.20130415	28	53	37	11	52	47	52	40	44	1	35	0	48	53	0	40	56
HG01303.mapped.ILLUMINA.bwa.PUR.exome.20130415	43	57	44	17	46	51	51	53	62	0	34	2	39	53	0	45	64
HG01305.mapped.ILLUMINA.bwa.PUR.exome.20130415	41	41	48	15	54	57	77	74	5	14	62	2	82	75	0	0	65
HG01308.mapped.ILLUMINA.bwa.PUR.exome.20130415	43	3	4	29	58	71	99	65	88	0	0	1	1	2	50	2	63
HG01311.mapped.ILLUMINA.bwa.PUR.exome.20130415	59	53	53	16	58	67	94	94	119	0	0	1	2	1	0	108	72
HG01312.mapped.ILLUMINA.bwa.PUR.exome.20130415	35	59	48	15	48	47	75	74	59	6	37	48	0	51	36	0	62
HG01323.mapped.ILLUMINA.bwa.PUR.exome.20130415	37	2	4	29	66	75	73	80	107	0	0	1	0	0	32	42	58
HG01325.mapped.ILLUMINA.bwa.PUR.exome.20130415	34	1	4	16	66	82	81	78	53	8	35	2	50	60	0	40	70
HG01326.mapped.ILLUMINA.bwa.PUR.exome.20130415	46	53	56	18	47	56	80	76	63	12	46	4	55	50	0	49	65
HG01334.mapped.ILLUMINA.bwa.GBR.exome.20120522	78	0	0	50	98	102	99	88	101	0	0	0	0	0	40	65	88
HG01341.mapped.ILLUMINA.bwa.CLM.exome.20120522	99	1	2	71	101	102	93	82	101	0	0	0	0	1	0	96	123
HG01342.mapped.ILLUMINA.bwa.CLM.exome.20120522	86	90	91	0	111	91	93	64	62	17	85	89	50	59	0	48	119
HG01344.mapped.ILLUMINA.bwa.CLM.exome.20130415	61	0	1	22	39	57	58	38	64	0	0	0	1	0	0	50	67
HG01345.mapped.ILLUMINA.bwa.CLM.exome.20130415	77	37	34	20	42	55	60	48	0	17	47	41	16	60	0	0	69
HG01348.mapped.ILLUMINA.bwa.CLM.exome.20130415	57	27	22	21	33	51	46	47	29	4	26	19	15	22	0	21	68
HG01350.mapped.ILLUMINA.bwa.CLM.exome.20120522	75	75	72	43	127	106	98	73	84	0	56	63	0	0	39	61	82
HG01351.mapped.ILLUMINA.bwa.CLM.exome.20120522	68	0	0	95	104	95	90	80	97	0	0	0	0	0	0	132	95
HG01353.mapped.ILLUMINA.bwa.CLM.exome.20120522	86	165	127	0	84	96	103	78	113	0	44	60	0	0	42	95	101
HG01354.mapped.ILLUMINA.bwa.CLM.exome.20120522	106	0	1	94	135	86	1	0	1	0	0	0	0	76	0	0	82
HG01356.mapped.ILLUMINA.bwa.CLM.exome.20130415	53	0	0	21	26	54	49	40	43	0	0	3	0	0	10	28	51
HG01357.mapped.ILLUMINA.bwa.CLM.exome.20130415	65	35	34	13	25	35	28	26	1	6	38	0	44	64	0	0	95
HG01359.mapped.ILLUMINA.bwa.CLM.exome.20120522	77	0	1	54	80	84	62	58	81	0	0	0	1	0	0	67	98
HG01360.mapped.ILLUMINA.bwa.CLM.exome.20120522	97	129	123	0	96	90	120	120	0	8	177	92	112	132	0	0	110
HG01362.mapped.ILLUMINA.bwa.CLM.exome.20130415	100	167	176	0	1	0	176	211	243	0	1	4	0	0	68	110	128
HG01363.mapped.ILLUMINA.bwa.CLM.exome.20130415	110	230	224	0	150	160	256	287	257	0	130	163	1	0	0	276	167
HG01365.mapped.ILLUMINA.bwa.CLM.exome.20120522	69	77	71	39	71	65	95	67	52	29	48	0	64	63	0	75	76
HG01366.mapped.ILLUMINA.bwa.CLM.exome.20120522	69	81	81	39	72	64	91	75	96	0	0	0	0	0	41	69	86
HG01369.mapped.ILLUMINA.bwa.CLM.exome.20130415	80	116	120	52	200	151	167	205	194	0	94	113	0	0	49	111	114
HG01372.mapped.ILLUMINA.bwa.CLM.exome.20130415	98	124	138	58	120	122	170	148	121	23	103	0	132	113	0	107	129
HG01374.mapped.ILLUMINA.bwa.CLM.exome.20120522	66	0	0	52	92	84	84	66	76	0	0	0	0	0	58	0	67
HG01375.mapped.ILLUMINA.bwa.CLM.exome.20120522	69	0	0	58	108	92	96	98	58	29	50	0	72	75	46	0	89
HG01377.mapped.ILLUMINA.bwa.CLM.exome.20120522	131	1	0	64	125	111	95	92	108	0	0	0	0	3	40	2	121
HG01378.mapped.ILLUMINA.bwa.CLM.exome.20120522	87	2	1	49	102	96	79	71	99	0	0	0	0	0	0	72	117
HG01383.mapped.ILLUMINA.bwa.CLM.exome.20120522	103	49	53	28	67	54	83	81	66	9	38	0	50	61	14	1	90
HG01384.mapped.ILLUMINA.bwa.CLM.exome.20120522	92	51	51	36	99	91	80	73	56	7	52	59	51	66	0	37	101
HG01389.mapped.ILLUMINA.bwa.CLM.exome.20120522	100	95	1	46	140	120	101	82	70	34	63	0	84	81	0	75	85
HG01390.mapped.ILLUMINA.bwa.CLM.exome.20120522	81	70	67	37	71	60	58	46	53	0	57	57	0	66	0	53	88
HG01392.mapped.ILLUMINA.bwa.PUR.exome.20130415	90	116	124	56	209	153	161	148	167	0	116	109	0	0	76	0	117
HG01393.mapped.ILLUMINA.bwa.PUR.exome.20130415	88	122	115	53	208	140	153	178	172	0	95	104	0	0	49	91	108
HG01395.mapped.ILLUMINA.bwa.PUR.exome.20130415	89	1	1	112	152	165	189	212	198	0	0	0	0	4	0	212	116
HG01396.mapped.ILLUMINA.bwa.PUR.exome.20130415	86	131	114	64	116	128	117	118	131	1	109	0	115	122	58	1	113
HG01398.mapped.ILLUMINA.bwa.PUR.exome.20130415	46	57	52	20	50	53	82	76	83	0	0	0	1	2	30	42	66
HG01402.mapped.ILLUMINA.bwa.PUR.exome.20130415	103	0	2	119	181	164	187	167	6	41	170	0	176	176	0	0	125
HG01403.mapped.ILLUMINA.bwa.PUR.exome.20130415	86	0	0	104	217	148	170	189	157	0	0	0	1	1	60	103	118
HG01405.mapped.ILLUMINA.bwa.PUR.exome.20130415	106	188	163	1	125	121	187	218	213	0	114	144	0	0	0	238	132
HG01412.mapped.ILLUMINA.bwa.PUR.exome.20130415	102	2	2	111	174	163	193	157	171	0	5	1	0	0	0	177	140
HG01413.mapped.ILLUMINA.bwa.PUR.exome.20130415	81	125	124	61	110	113	179	210	130	29	113	119	2	119	0	104	137

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG01414.mapped.ILLUMINA.bwa.PUR.exome.20130415	90	118	108	61	97	104	147	186	111	23	98	0	112	110	0	97	95
HG01431.mapped.ILLUMINA.bwa.CLM.exome.20130415	91	140	123	59	132	129	191	159	123	22	128	0	134	122	0	124	130
HG01432.mapped.ILLUMINA.bwa.CLM.exome.20130415	87	133	133	58	121	120	168	165	153	0	2	0	0	2	0	150	123
HG01435.mapped.ILLUMINA.bwa.CLM.exome.20130415	70	0	1	99	145	139	159	176	177	0	0	1	0	0	0	202	109
HG01437.mapped.ILLUMINA.bwa.CLM.exome.20120522	112	93	93	1	78	64	100	97	101	0	37	51	1	0	22	52	113
HG01438.mapped.ILLUMINA.bwa.CLM.exome.20120522	97	54	60	41	62	58	85	65	95	0	1	0	0	0	0	112	117
HG01440.mapped.ILLUMINA.bwa.CLM.exome.20120522	88	55	62	49	65	56	86	61	0	18	64	0	70	99	0	0	109
HG01441.mapped.ILLUMINA.bwa.CLM.exome.20120522	98	48	57	41	57	55	99	99	84	0	0	0	0	0	22	52	112
HG01443.mapped.ILLUMINA.bwa.CLM.exome.20130415	95	119	127	53	122	112	184	209	125	28	115	0	122	133	58	1	111
HG01444.mapped.ILLUMINA.bwa.CLM.exome.20130415	104	124	123	61	117	126	170	244	192	0	0	1	0	0	50	100	107
HG01447.mapped.ILLUMINA.bwa.CLM.exome.20130415	103	2	2	64	175	168	170	229	238	0	0	1	0	0	66	111	127
HG01455.mapped.ILLUMINA.bwa.CLM.exome.20120522	144	0	0	87	190	170	174	191	235	0	0	0	0	0	0	166	147
HG01456.mapped.ILLUMINA.bwa.CLM.exome.20120522	100	167	1	0	143	165	164	140	173	0	0	0	0	0	0	124	125
HG01459.mapped.ILLUMINA.bwa.CLM.exome.20130415	70	1	0	59	135	126	135	153	166	0	0	0	0	0	47	82	97
HG01461.mapped.ILLUMINA.bwa.CLM.exome.20120522	107	63	97	0	102	97	84	87	105	0	67	60	55	0	16	56	117
HG01462.mapped.ILLUMINA.bwa.CLM.exome.20120522	92	59	58	51	68	61	90	80	85	0	0	1	0	0	0	102	127
HG01464.mapped.ILLUMINA.bwa.CLM.exome.20120522	101	70	92	1	124	103	86	90	124	0	73	60	51	2	32	57	121
HG01465.mapped.ILLUMINA.bwa.CLM.exome.20120522	112	58	0	47	115	103	99	69	83	0	0	1	0	0	19	53	107
HG01468.mapped.ILLUMINA.bwa.CLM.exome.20130415	58	86	92	1	61	66	101	96	71	14	76	58	57	68	45	1	75
HG01474.mapped.ILLUMINA.bwa.CLM.exome.20130415	42	66	61	19	102	89	101	88	76	11	70	61	60	72	0	46	75
HG01479.mapped.ILLUMINA.bwa.CLM.exome.20130415	48	64	49	16	61	62	93	89	68	11	42	1	47	55	30	2	65
HG01485.mapped.ILLUMINA.bwa.CLM.exome.20130415	93	0	1	82	165	157	187	157	200	0	0	0	0	0	82	0	112
HG01486.mapped.ILLUMINA.bwa.CLM.exome.20130415	107	0	1	82	186	182	242	163	226	0	0	1	0	1	78	0	120
HG01488.mapped.ILLUMINA.bwa.CLM.exome.20120522	96	1	0	69	101	93	90	79	57	13	37	0	51	63	0	43	108
HG01489.mapped.ILLUMINA.bwa.CLM.exome.20120522	98	0	0	75	111	100	84	82	102	0	0	0	0	0	18	0	69
HG01491.mapped.ILLUMINA.bwa.CLM.exome.20120522	93	0	1	81	112	100	88	77	116	0	0	0	0	1	0	92	121
HG01492.mapped.ILLUMINA.bwa.CLM.exome.20120522	106	72	71	46	76	64	89	87	68	14	55	0	65	67	21	0	127
HG01494.mapped.ILLUMINA.bwa.CLM.exome.20120522	103	118	122	0	90	102	120	133	93	7	99	126	0	99	0	83	109
HG01495.mapped.ILLUMINA.bwa.CLM.exome.20120522	106	95	93	49	164	115	110	111	136	0	76	86	0	0	72	0	98
HG01497.mapped.ILLUMINA.bwa.CLM.exome.20120522	88	93	90	42	168	124	133	147	166	0	74	91	0	1	0	158	96
HG01498.mapped.ILLUMINA.bwa.CLM.exome.20120522	91	0	1	56	120	126	133	129	105	13	93	0	87	98	0	78	95
HG01500.mapped.ILLUMINA.bwa.IBS.exome.20130415	54	37	34	24	53	63	64	65	39	10	19	59	0	40	0	8	77
HG01501.mapped.ILLUMINA.bwa.IBS.exome.20130415	58	32	16	15	15	21	54	47	0	11	39	0	42	51	0	1	58
HG01503.mapped.ILLUMINA.bwa.IBS.exome.20130415	47	20	12	9	43	33	49	44	44	0	8	19	0	2	0	20	59
HG01504.mapped.ILLUMINA.bwa.IBS.exome.20130415	45	0	0	30	38	39	46	40	44	0	0	0	0	0	0	43	65
HG01506.mapped.ILLUMINA.bwa.IBS.exome.20120522	71	0	0	80	102	101	95	93	88	0	0	0	0	0	0	109	91
HG01507.mapped.ILLUMINA.bwa.IBS.exome.20120522	85	0	1	78	107	101	97	90	86	0	0	0	0	0	0	119	90
HG01509.mapped.ILLUMINA.bwa.IBS.exome.20121211	83	0	0	65	117	105	89	110	98	0	0	0	0	0	0	137	91
HG01510.mapped.ILLUMINA.bwa.IBS.exome.20120522	92	96	72	42	83	57	98	74	0	42	100	0	108	110	0	0	87
HG01512.mapped.ILLUMINA.bwa.IBS.exome.20120522	71	0	0	51	138	94	93	82	38	34	36	0	52	52	0	75	91
HG01513.mapped.ILLUMINA.bwa.IBS.exome.20120522	93	0	0	71	116	100	109	98	104	1	1	0	0	0	0	139	106
HG01515.mapped.ILLUMINA.bwa.IBS.exome.20120522	119	118	134	0	105	104	138	154	85	6	142	94	101	85	0	93	106
HG01516.mapped.ILLUMINA.bwa.IBS.exome.20120522	114	144	144	0	0	0	139	149	175	0	0	0	0	0	0	133	117
HG01518.mapped.ILLUMINA.bwa.IBS.exome.20120522	144	99	99	50	105	115	165	171	166	0	0	0	0	2	0	160	131
HG01519.mapped.ILLUMINA.bwa.IBS.exome.20120522	138	0	0	100	183	162	165	170	151	0	0	0	0	0	60	118	126
HG01521.mapped.ILLUMINA.bwa.IBS.exome.20120522	169	148	171	0	195	190	174	233	135	14	301	195	127	135	102	0	143
HG01522.mapped.ILLUMINA.bwa.IBS.exome.20120522	144	0	0	75	176	218	177	231	191	10	92	0	110	0	0	176	127
HG01524.mapped.ILLUMINA.bwa.IBS.exome.20121211	94	91	83	43	152	126	116	112	123	0	66	75	0	1	0	172	102
HG01525.mapped.ILLUMINA.bwa.IBS.exome.20121211	83	92	86	42	77	61	67	46	56	0	52	67	0	62	0	77	89
HG01527.mapped.ILLUMINA.bwa.IBS.exome.20121211	85	1	0	63	101	95	93	85	80	0	0	1	0	0	42	70	83
HG01528.mapped.ILLUMINA.bwa.IBS.exome.20121211	85	0	0	98	125	103	103	111	92	0	0	0	0	0	0	172	97
HG01530.mapped.ILLUMINA.bwa.IBS.exome.20121211	76	2	1	75	114	110	111	89	106	0	0	0	0	0	43	85	104
HG01531.mapped.ILLUMINA.bwa.IBS.exome.20121211	101	95	101	51	174	127	124	108	112	0	59	83	0	0	45	97	108
HG01536.mapped.ILLUMINA.bwa.IBS.exome.20121211	96	82	80	45	78	82	92	106	62	33	58	0	91	77	0	89	104
HG01537.mapped.ILLUMINA.bwa.IBS.exome.20121211	86	96	76	49	83	74	104	110	119	0	0	0	0	0	0	149	103
HG01550.mapped.ILLUMINA.bwa.CLM.exome.20120522	115	179	178	0	105	117	160	169	113	14	142	152	0	123	61	0	130
HG01551.mapped.ILLUMINA.bwa.CLM.exome.20120522	127	0	0	110	206	227	235	189	242	0	0	0	0	1	0	177	209
HG01556.mapped.ILLUMINA.bwa.CLM.exome.20130415	98	136	131	49	133	115	178	223	232	0	0	0	0	0	62	116	124
HG01565.mapped.ILLUMINA.bwa.PEL.exome.20130415	80	33	39	22	66	74	69	48	73	0	30	0	39	2	26	1	82
HG01566.mapped.ILLUMINA.bwa.PEL.exome.20130415	57	41	35	19	32	26	63	41	76	0	0	2	0	0	21	0	82
HG01571.mapped.ILLUMINA.bwa.PEL.exome.20130415	51	0	0	22	29	49	44	37	45	0	0	0	0	0	16	0	66
HG01572.mapped.ILLUMINA.bwa.PEL.exome.20130415	59	0	0	30	45	45	59	43	66	0	1	0	0	0	20	1	70
HG01577.mapped.ILLUMINA.bwa.PEL.exome.20120522	85	0	0	72	124	117	109	92	110	0	0	0	0	1	64	0	95
HG01578.mapped.ILLUMINA.bwa.PEL.exome.20120522	92	100	85	43	84	76	104	92	74	39	95	76	74	74	45	0	101
HG01583.mapped.ILLUMINA.bwa.PJL.exome.20130415	41	83	71	0	48	46	84	69	90	0	36	46	1	1	0	79	64
HG01586.mapped.ILLUMINA.bwa.PJL.exome.20130415	39	1	1	21	83	55	76	56	54	9	29	2	36	38	33	2	59
HG01589.mapped.ILLUMINA.bwa.PJL.exome.20130415	46	51	31	12	85	67	81	67	57	9	45	63	2	37	0	31	61
HG01593.mapped.ILLUMINA.bwa.PJL.exome.20130415	38	53	49	16	46	44	84	76	98	0	0	1	2	0	0	73	59
HG01595.mapped.ILLUMINA.bwa.KHV.exome.20120522	115	0	1	73	129	113	109	107	94	0	0	0	0	0	58	73	99
HG01596.mapped.ILLUMINA.bwa.KHV.exome.20120522	87	0	0	67	119	95	100	75	92	0	0	0	0	0	60	0	89
HG01597.mapped.ILLUMINA.bwa.KHV.exome.20120522	76	0	0	84	111	94	91	99	83	0	0	0	0	0	39	79	100
HG01598.mapped.ILLUMINA.bwa.KHV.exome.20120522	64	1	0	77	95	95	84	75	91	0	0	0	1	0	59	1	79
HG01599.mapped.ILLUMINA.bwa.KHV.exome.20120522	79	0	0	51	104	97	93	73	92	0	0	0	0	1	51	0	85
HG01600.mapped.ILLUMINA.bwa.KHV.exome.20120522	72	0	0	55	103	94	91	68	84	0	0	0	0	0	53	0	80
HG01602.mapped.ILLUMINA.bwa.IBS.exome.20130415	61	59	49	0	43	54	74	50	67	6	28	62	0	1	12	22	60
HG01603.mapped.ILLUMINA.bwa.IBS.exome.20130415	50	1	0	27	35	58	66	52	58	0	0	0	0	0	0	35	71
HG01605.mapped.ILLUMINA.bwa.IBS.exome.20130415	64	0	0	31	41	46	64	27	31	7	13	0	22	29	0	22	81
HG01606.mapped.ILLUMINA.bwa.IBS.exome.20130415	55	0	0	24	35	52	57	35	56	0	0	0	0	0	0	57	63
HG01607.mapped.ILLUMINA.bwa.IBS.exome.20130415	48	1	0	28	46	56	48	41	34	2	7	0	17	29	0	12	67
HG01608.mapped.ILLUMINA.bwa.IBS.exome.20130415	65	22	28	14	22	28	49	31	53	0	0	0	0	0	17	0	70
HG01610.mapped.ILLUMINA.bwa.IBS.exome.20130415	67	1	0	30	40	49	67	29	35	7	14	0	26	26	0	26	63
HG01612.mapped.ILLUMINA.bwa.IBS.exome.20130415	53	20	29	13	40	36	56	33	0	11	32	45	11	49	0	0	55
HG01613.mapped.ILLUMINA.bwa.IBS.exome.20130415	82	1	1	47	53	60	77	61	47	9	25	0	33	32	0	36	87
HG01615.mapped.ILLUMINA.bwa.IBS.exome.20130415	56	0	1	24	28	40	50	26	47	0	0	0	0	0	0	35	57
HG01617.mapped.ILLUMINA.bwa.IBS.exome.20130415	62	0	0	34	36	45	51	43	48	0	0	0	0	1	0	48	62
HG01618.mapped.ILLUMINA.bwa.IBS.exome.20130415	67	44	36	15	44	64	68	53	63	0	15	40	0	0	0	65	82
HG01619.mapped.ILLUMINA.bwa.IBS.exome.20130415	77	32	35	15	25	44	60	68	36	10	16	0	23	35	0	37	85
HG01620.mapped.ILLUMINA.bwa.IBS.exome.20130415	61	2	1	41	43	53	66	35	31	9	11	0	21	36	0	32	69
HG01623.mapped.ILLUMINA.bwa.IBS.exome.20130415	78	0	0	40	54	67	69	38	52	2	0	0	0	1	12	40	81
HG01624.mapped.ILLUMINA.bwa.IBS.exome.20130415	79	35	38	10	23	49	77	39	36	7	16	1	28	42	0	23	72
HG01625.mapped.ILLUMINA.bwa.IBS.exome.20130415	61	13	22	14	14	32	58	43	43	0	1	0	0	0	0	57	63
HG01626.mapped.ILLUMINA.bwa.IBS.exome.20130415	70	0	0	26	21	73	76	47	56	0	0	0	0	0	6	48	74
HG01628.mapped.ILLUMINA.bwa.IBS.exome.20130415	89	39	23	15	18	39	63	40	59	0	0	0	0	0	17	26	80
HG01630.mapped.ILLUMINA.bwa.IBS.exome.20130415	71	64	57	0	0	1	63	54	55	0	0	0	2	2	0	69	67
HG01631.mapped.ILLUMINA.bwa.IBS.exome.20121211	95	0	0	75	107	97	92	96	68	26	42	0	60	68	0	67	86
HG01632.mapped.ILLUMINA.bwa.IBS.exome.20121211	94	105	89	51	146	120	115	103	0	40	142	74	125	133	0	0	109

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG01668.mapped.ILLUMINA.bwa.IBS.exome.20130415	59	1	0	30	45	78	59	48	67	0	0	0	0	0	0	41	84
HG01669.mapped.ILLUMINA.bwa.IBS.exome.20130415	47	0	0	23	27	46	64	29	34	6	11	0	22	17	0	21	69
HG01670.mapped.ILLUMINA.bwa.IBS.exome.20130415	46	0	0	22	25	40	48	27	50	0	0	0	0	0	14	0	47
HG01672.mapped.ILLUMINA.bwa.IBS.exome.20130415	75	2	1	37	44	60	77	27	39	6	9	1	23	25	0	21	82
HG01673.mapped.ILLUMINA.bwa.IBS.exome.20120522	82	0	0	96	109	93	88	101	107	0	0	0	0	0	43	69	81
HG01675.mapped.ILLUMINA.bwa.IBS.exome.20120522	70	0	0	86	109	93	98	86	96	0	0	0	0	0	38	70	86
HG01676.mapped.ILLUMINA.bwa.IBS.exome.20120522	91	0	1	89	100	91	99	84	97	0	0	0	0	0	56	0	85
HG01678.mapped.ILLUMINA.bwa.IBS.exome.20120522	91	89	78	42	77	79	72	54	64	0	54	0	80	85	0	82	95
HG01679.mapped.ILLUMINA.bwa.IBS.exome.20120522	105	0	1	61	107	98	90	95	67	33	53	0	73	80	0	66	108
HG01680.mapped.ILLUMINA.bwa.IBS.exome.20120522	94	0	0	104	103	111	105	110	117	1	0	0	0	0	0	150	93
HG01682.mapped.ILLUMINA.bwa.IBS.exome.20120522	76	0	0	89	129	118	95	113	100	0	0	0	0	0	41	78	96
HG01684.mapped.ILLUMINA.bwa.IBS.exome.20120522	75	0	0	60	106	103	99	91	100	0	0	0	1	0	0	138	102
HG01685.mapped.ILLUMINA.bwa.IBS.exome.20120522	75	0	0	94	123	108	105	71	101	0	0	0	0	0	0	118	93
HG01686.mapped.ILLUMINA.bwa.IBS.exome.20120522	99	91	80	45	84	77	68	60	73	0	48	78	0	89	0	82	100
HG01694.mapped.ILLUMINA.bwa.IBS.exome.20120522	71	85	68	44	138	113	105	80	66	26	92	96	1	68	0	72	78
HG01695.mapped.ILLUMINA.bwa.IBS.exome.20120522	92	92	80	44	77	85	114	105	107	0	0	1	0	0	47	69	98
HG01697.mapped.ILLUMINA.bwa.IBS.exome.20120522	324	112	136	104	134	125	276	327	215	0	1	3	3	9	0	232	386
HG01699.mapped.ILLUMINA.bwa.IBS.exome.20120522	125	82	86	52	91	82	94	99	80	16	52	1	64	94	0	73	133
HG01700.mapped.ILLUMINA.bwa.IBS.exome.20121211	95	0	0	95	104	121	108	126	118	0	0	0	0	0	0	156	92
HG01702.mapped.ILLUMINA.bwa.IBS.exome.20121211	90	89	69	49	74	61	110	95	90	0	0	0	0	0	39	70	98
HG01704.mapped.ILLUMINA.bwa.IBS.exome.20120522	140	0	2	86	141	130	123	146	92	17	64	0	86	96	0	87	167
HG01705.mapped.ILLUMINA.bwa.IBS.exome.20120522	144	96	87	60	160	125	126	143	162	0	62	79	0	1	0	107	165
HG01707.mapped.ILLUMINA.bwa.IBS.exome.20120522	164	1	2	117	122	129	116	136	137	0	0	0	0	1	39	85	172
HG01708.mapped.ILLUMINA.bwa.IBS.exome.20120522	160	1	1	74	201	140	114	141	142	0	1	1	0	4	42	84	152
HG01709.mapped.ILLUMINA.bwa.IBS.exome.20120522	162	133	115	0	130	136	160	194	148	18	101	124	0	1	50	1	169
HG01710.mapped.ILLUMINA.bwa.IBS.exome.20120522	148	82	87	61	111	91	123	161	141	0	1	0	1	0	0	171	157
HG01746.mapped.ILLUMINA.bwa.IBS.exome.20120522	143	81	82	59	161	132	119	134	94	21	94	96	78	106	0	81	167
HG01747.mapped.ILLUMINA.bwa.IBS.exome.20120522	146	1	1	89	128	123	126	147	170	0	0	0	0	2	0	169	178
HG01756.mapped.ILLUMINA.bwa.IBS.exome.20120522	173	234	262	0	171	176	287	318	186	24	240	153	171	166	92	2	204
HG01757.mapped.ILLUMINA.bwa.IBS.exome.20120522	113	0	1	95	137	135	152	137	212	0	0	0	0	0	0	138	103
HG01761.mapped.ILLUMINA.bwa.IBS.exome.20120522	116	0	3	69	165	149	151	163	0	18	130	0	147	160	0	0	136
HG01762.mapped.ILLUMINA.bwa.IBS.exome.20120522	100	114	107	55	196	129	157	189	126	16	146	139	0	116	0	111	122
HG01765.mapped.ILLUMINA.bwa.IBS.exome.20130415	70	12	7	73	133	132	140	176	188	0	0	1	0	0	0	194	101
HG01766.mapped.ILLUMINA.bwa.IBS.exome.20130415	69	115	96	42	180	129	142	117	130	0	87	102	0	1	62	0	91
HG01767.mapped.ILLUMINA.bwa.IBS.exome.20130415	92	0	1	93	163	139	161	139	158	0	3	0	0	2	0	138	100
HG01768.mapped.ILLUMINA.bwa.IBS.exome.20130415	70	0	0	61	149	128	139	177	116	25	96	0	102	110	0	104	99
HG01770.mapped.ILLUMINA.bwa.IBS.exome.20130415	66	34	35	27	24	39	70	39	69	1	0	0	0	1	0	57	67
HG01771.mapped.ILLUMINA.bwa.IBS.exome.20130415	53	27	25	14	36	47	58	31	1	9	36	33	14	45	0	0	55
HG01773.mapped.ILLUMINA.bwa.IBS.exome.20130415	77	44	41	22	57	75	80	62	39	10	42	40	27	44	0	24	73
HG01775.mapped.ILLUMINA.bwa.IBS.exome.20130415	52	1	0	35	29	41	53	50	0	10	17	0	39	57	0	0	56
HG01776.mapped.ILLUMINA.bwa.IBS.exome.20130415	60	20	18	21	23	25	49	34	63	0	0	0	0	1	8	16	50
HG01777.mapped.ILLUMINA.bwa.IBS.exome.20130415	56	33	28	21	19	36	51	37	57	0	0	0	0	0	6	31	64
HG01779.mapped.ILLUMINA.bwa.IBS.exome.20130415	64	34	32	25	44	54	61	54	39	7	32	32	35	25	0	29	73
HG01781.mapped.ILLUMINA.bwa.IBS.exome.20130415	63	36	28	20	22	28	64	36	57	0	0	0	1	0	11	29	72
HG01783.mapped.ILLUMINA.bwa.IBS.exome.20130415	52	30	26	8	17	25	53	36	57	0	0	0	0	0	12	20	57
HG01784.mapped.ILLUMINA.bwa.IBS.exome.20130415	58	25	24	14	36	54	53	37	65	0	9	29	0	0	14	20	62
HG01785.mapped.ILLUMINA.bwa.IBS.exome.20130415	44	58	55	11	102	77	91	76	110	0	38	60	0	0	31	53	70
HG01786.mapped.ILLUMINA.bwa.IBS.exome.20130415	47	3	2	32	84	74	100	77	106	0	0	0	0	2	0	68	85
HG01789.mapped.ILLUMINA.bwa.GBR.exome.20130415	67	33	34	13	63	72	71	48	50	4	31	39	36	34	0	35	68
HG01790.mapped.ILLUMINA.bwa.GBR.exome.20130415	43	26	18	18	18	29	61	25	30	5	7	0	21	22	0	17	57
HG01791.mapped.ILLUMINA.bwa.GBR.exome.20120522	91	92	79	54	84	80	94	112	106	0	0	0	0	0	44	87	97
HG01794.mapped.ILLUMINA.bwa.CDX.exome.20120522	75	111	108	0	77	72	106	87	0	40	103	69	104	104	0	0	97
HG01795.mapped.ILLUMINA.bwa.CDX.exome.20120522	70	92	87	50	140	106	115	111	104	33	53	70	1	0	60	0	84
HG01796.mapped.ILLUMINA.bwa.CDX.exome.20120522	93	0	1	69	118	106	105	86	103	0	0	0	0	0	60	0	92
HG01797.mapped.ILLUMINA.bwa.CDX.exome.20120522	87	0	0	65	104	93	90	92	60	32	55	0	75	66	44	0	89
HG01798.mapped.ILLUMINA.bwa.CDX.exome.20120522	82	0	1	86	109	102	92	83	110	0	0	0	0	0	45	72	91
HG01799.mapped.ILLUMINA.bwa.CDX.exome.20120522	79	82	77	45	78	81	92	84	110	0	0	0	0	0	0	105	96
HG01800.mapped.ILLUMINA.bwa.CDX.exome.20120522	83	0	0	60	103	96	102	75	59	30	50	68	0	86	0	79	84
HG01801.mapped.ILLUMINA.bwa.CDX.exome.20120522	91	0	0	63	118	113	109	90	71	33	57	0	73	77	0	86	100
HG01802.mapped.ILLUMINA.bwa.CDX.exome.20120522	75	0	1	68	111	105	109	76	91	0	0	0	0	0	60	0	81
HG01804.mapped.ILLUMINA.bwa.CDX.exome.20120522	86	0	1	100	109	115	108	112	108	0	0	0	0	0	45	88	108
HG01805.mapped.ILLUMINA.bwa.CDX.exome.20120522	74	1	0	85	107	100	95	94	2	37	81	0	98	102	0	0	90
HG01806.mapped.ILLUMINA.bwa.CDX.exome.20120522	86	79	77	50	76	71	99	93	75	34	59	0	76	79	40	0	96
HG01807.mapped.ILLUMINA.bwa.CDX.exome.20120522	95	0	0	108	105	101	100	85	78	33	57	0	74	78	0	73	88
HG01808.mapped.ILLUMINA.bwa.CDX.exome.20120522	84	0	0	62	115	99	94	74	99	0	0	0	0	0	59	1	96
HG01809.mapped.ILLUMINA.bwa.CDX.exome.20120522	82	90	81	54	83	76	103	86	1	40	113	73	62	109	0	0	86
HG01810.mapped.ILLUMINA.bwa.CDX.exome.20120522	86	79	74	47	135	99	90	90	59	36	106	71	80	79	0	79	102
HG01811.mapped.ILLUMINA.bwa.CDX.exome.20120522	85	83	75	49	73	65	62	48	60	0	55	0	81	76	42	0	80
HG01812.mapped.ILLUMINA.bwa.CDX.exome.20120522	72	0	0	58	98	91	95	99	104	0	0	0	0	0	38	69	89
HG01813.mapped.ILLUMINA.bwa.CDX.exome.20120522	91	95	80	52	144	107	102	89	70	36	87	70	74	76	41	0	90
HG01815.mapped.ILLUMINA.bwa.CDX.exome.20120522	113	95	83	52	76	82	100	103	72	32	52	0	87	89	48	0	96
HG01816.mapped.ILLUMINA.bwa.CDX.exome.20120522	89	132	120	0	85	75	108	112	127	0	59	90	0	0	47	82	92
HG01817.mapped.ILLUMINA.bwa.CDX.exome.20120522	106	1	1	90	119	102	106	75	88	0	0	0	0	0	0	111	91
HG01840.mapped.ILLUMINA.bwa.KHV.exome.20120522	84	86	77	46	144	106	127	114	91	35	63	69	0	0	63	0	95
HG01841.mapped.ILLUMINA.bwa.KHV.exome.20120522	79	1	2	62	103	99	85	76	49	32	49	63	0	67	0	70	84
HG01842.mapped.ILLUMINA.bwa.KHV.exome.20120522	89	85	74	42	82	72	109	95	57	33	52	0	68	85	48	0	85
HG01843.mapped.ILLUMINA.bwa.KHV.exome.20120522	76	1	1	72	115	115	94	86	101	1	0	0	0	0	42	89	100
HG01844.mapped.ILLUMINA.bwa.KHV.exome.20120522	81	0	0	60	115	107	112	105	76	39	55	69	0	79	51	0	89
HG01845.mapped.ILLUMINA.bwa.KHV.exome.20120522	85	0	0	64	104	109	88	118	126	0	1	0	0	0	45	80	92
HG01846.mapped.ILLUMINA.bwa.KHV.exome.20120522	104	93	79	55	88	86	79	60	67	0	59	72	0	91	0	81	95
HG01847.mapped.ILLUMINA.bwa.KHV.exome.20120522	83	1	0	83	97	89	101	74	97	0	0	0	0	0	35	74	89
HG01848.mapped.ILLUMINA.bwa.KHV.exome.20120522	94	0	1	71	110	108	104	95	91	0	0	0	1	0	0	106	95
HG01849.mapped.ILLUMINA.bwa.KHV.exome.20120522	79	0	0	61	117	101	100	94	95	0	0	0	0	0	48	68	87
HG01850.mapped.ILLUMINA.bwa.KHV.exome.20120522	83	0	2	65	97	103	95	89	105	0	0	0	0	0	62	0	93
HG01851.mapped.ILLUMINA.bwa.KHV.exome.20120522	80	0	0	86	103	106	98	78	86	0	0	0	0	0	38	72	89
HG01852.mapped.ILLUMINA.bwa.KHV.exome.20120522	90	93	86	51	85	66	110	91	2	36	64	0	72	77	0	72	99
HG01853.mapped.ILLUMINA.bwa.KHV.exome.20120522	77	1	0	66	97	109	102	94	121	0	0	0	0	0	50	71	109
HG01855.mapped.ILLUMINA.bwa.KHV.exome.20120522	84	0	0	65	108	113	98	100	60	32	65	71	0	77	0	72	91
HG01857.mapped.ILLUMINA.bwa.KHV.exome.20120522	86	0	0	63	118	134	110	96	98	1	0	0	0	0	0	143	98
HG01858.mapped.ILLUMINA.bwa.KHV.exome.20120522	91	0	0	100	110	127	93	79	71	33	52	74	0	0	0	81	88
HG01859.mapped.ILLUMINA.bwa.KHV.exome.20120522	97	0	2	58	118	113	96	79	103	0	0	0	0	0	63	1	83
HG01860.mapped.ILLUMINA.bwa.KHV.exome.20121211	69	1	1	51	89	85	90	71	82	0	0	0	0	0	56	0	81
HG01861.mapped.ILLUMINA.bwa.KHV.exome.20121211	104	0	0	88	102	107	95	76	88	0	0	0	0	0	59	0	100
HG01862.mapped.ILLUMINA.bwa.KHV.exome.20120522	132	85	84	63	86	94	74	83	79	0	65	0	74	89	0	70	158
HG01863.mapped.ILLUMINA.bwa.KHV.exome.20120522	186	78	101	62	92	97	119	154	146	0	0	0	0	1	36	84	158
HG01864.mapped.ILLUMINA.bwa.KHV.exome.20120522	156	1	0	89	127	125	123	139	140	0	1	1	2	0	35	76	156

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG01865.mapped.ILLUMINA.bwa.KHV.exome.20120522	146	1	2	121	151	136	120	119	160	0	1	1	1	1	0	112	186
HG01866.mapped.ILLUMINA.bwa.KHV.exome.20120522	127	1	3	86	132	108	106	116	128	0	0	2	0	1	0	144	163
HG01867.mapped.ILLUMINA.bwa.KHV.exome.20120522	138	0	2	94	119	124	106	115	135	0	0	0	0	0	45	1	140
HG01868.mapped.ILLUMINA.bwa.KHV.exome.20120522	145	1	2	77	130	111	118	130	90	13	61	2	75	88	33	1	186
HG01869.mapped.ILLUMINA.bwa.KHV.exome.20120522	171	86	87	63	100	87	120	128	138	0	0	0	0	0	0	157	155
HG01870.mapped.ILLUMINA.bwa.KHV.exome.20120522	148	0	0	56	142	129	130	181	126	16	93	115	0	109	68	0	105
HG01871.mapped.ILLUMINA.bwa.KHV.exome.20120522	130	0	1	88	189	175	173	203	181	0	0	0	1	0	81	105	159
HG01872.mapped.ILLUMINA.bwa.KHV.exome.20120522	100	0	0	108	137	146	160	145	0	18	129	0	129	167	0	0	106
HG01873.mapped.ILLUMINA.bwa.KHV.exome.20120522	119	0	0	63	140	130	135	177	176	0	0	0	0	3	63	107	127
HG01874.mapped.ILLUMINA.bwa.KHV.exome.20120522	145	0	0	113	180	162	198	207	238	0	0	0	0	1	69	128	159
HG01878.mapped.ILLUMINA.bwa.KHV.exome.20120522	160	120	115	55	119	125	129	123	128	0	111	121	0	122	65	0	142
HG01879.mapped.ILLUMINA.bwa.ACB.exome.20120522	70	81	68	45	91	65	70	47	1	30	99	0	103	99	0	1	88
HG01880.mapped.ILLUMINA.bwa.ACB.exome.20120522	90	82	76	44	83	72	54	50	63	0	58	0	79	78	0	76	91
HG01882.mapped.ILLUMINA.bwa.ACB.exome.20121211	77	85	68	46	129	108	96	71	105	0	56	73	0	2	62	0	96
HG01883.mapped.ILLUMINA.bwa.ACB.exome.20121211	86	0	0	82	115	109	105	99	62	37	50	69	0	86	0	0	74
HG01885.mapped.ILLUMINA.bwa.ACB.exome.20120522	139	2	0	93	133	143	128	131	132	0	0	1	1	1	50	0	160
HG01886.mapped.ILLUMINA.bwa.ACB.exome.20120522	130	0	0	79	163	169	164	201	199	0	0	0	0	1	0	234	152
HG01889.mapped.ILLUMINA.bwa.ACB.exome.20130415	71	27	29	24	42	60	57	35	62	0	9	0	27	0	16	21	77
HG01890.mapped.ILLUMINA.bwa.ACB.exome.20130415	54	0	0	25	52	50	65	29	53	0	0	0	0	0	10	0	35
HG01892.mapped.ILLUMINA.bwa.PEL.exome.20120522	69	0	0	61	109	98	103	86	91	0	0	0	0	1	0	107	96
HG01893.mapped.ILLUMINA.bwa.PEL.exome.20120522	98	0	0	69	114	110	90	91	105	0	0	0	0	0	72	0	85
HG01894.mapped.ILLUMINA.bwa.ACB.exome.20130415	50	0	0	25	38	48	63	40	59	0	0	0	0	0	0	36	68
HG01896.mapped.ILLUMINA.bwa.ACB.exome.20120522	84	0	0	99	137	108	106	103	118	0	0	0	0	0	48	75	100
HG01912.mapped.ILLUMINA.bwa.ACB.exome.20130415	57	45	42	17	54	57	75	38	71	1	21	31	0	1	0	22	57
HG01914.mapped.ILLUMINA.bwa.ACB.exome.20120522	80	0	1	94	113	101	104	96	98	0	0	0	0	0	44	88	85
HG01915.mapped.ILLUMINA.bwa.ACB.exome.20120522	88	104	85	50	84	71	108	108	109	0	0	0	0	0	49	0	78
HG01917.mapped.ILLUMINA.bwa.PEL.exome.20120522	88	0	1	74	123	108	110	102	63	36	71	0	66	81	0	3	98
HG01918.mapped.ILLUMINA.bwa.PEL.exome.20120522	85	0	0	62	114	101	101	77	88	1	0	0	1	2	43	75	102
HG01920.mapped.ILLUMINA.bwa.PEL.exome.20120522	82	102	82	50	89	92	104	106	73	34	62	0	80	86	51	1	100
HG01921.mapped.ILLUMINA.bwa.PEL.exome.20120522	83	0	0	95	115	113	102	105	64	33	64	0	68	73	0	78	91
HG01923.mapped.ILLUMINA.bwa.PEL.exome.20121211	91	1	0	62	112	109	89	108	65	30	55	0	78	79	51	0	103
HG01924.mapped.ILLUMINA.bwa.PEL.exome.20121211	80	0	0	62	101	106	93	73	97	0	0	0	0	0	41	76	96
HG01926.mapped.ILLUMINA.bwa.PEL.exome.20120522	150	0	1	97	134	120	128	127	148	0	1	0	1	1	49	0	169
HG01927.mapped.ILLUMINA.bwa.PEL.exome.20120522	141	1	2	83	141	129	119	114	154	0	0	0	1	0	48	1	167
HG01932.mapped.ILLUMINA.bwa.PEL.exome.20120522	133	86	101	65	150	133	118	137	156	0	61	97	1	0	38	82	161
HG01933.mapped.ILLUMINA.bwa.PEL.exome.20120522	150	93	79	58	89	1	83	83	87	0	0	0	0	91	37	1	160
HG01935.mapped.ILLUMINA.bwa.PEL.exome.20120522	146	0	0	85	151	123	134	115	153	0	0	1	0	0	47	1	157
HG01936.mapped.ILLUMINA.bwa.PEL.exome.20120522	133	1	0	117	118	118	114	117	147	0	0	2	0	2	32	74	147
HG01938.mapped.ILLUMINA.bwa.PEL.exome.20120522	144	86	92	68	96	96	119	121	126	0	0	0	1	1	49	1	163
HG01939.mapped.ILLUMINA.bwa.PEL.exome.20120522	133	92	97	67	104	98	117	150	86	16	66	0	84	107	0	88	160
HG01941.mapped.ILLUMINA.bwa.PEL.exome.20120522	132	0	3	110	140	135	138	159	146	0	0	0	0	0	40	75	163
HG01942.mapped.ILLUMINA.bwa.PEL.exome.20120522	136	1	1	75	122	114	116	114	127	0	0	1	1	1	46	0	144
HG01944.mapped.ILLUMINA.bwa.PEL.exome.20120522	129	0	6	84	119	123	97	112	128	0	1	0	0	0	44	0	147
HG01945.mapped.ILLUMINA.bwa.PEL.exome.20120522	149	0	2	85	142	130	136	122	115	0	0	1	0	2	48	2	173
HG01947.mapped.ILLUMINA.bwa.PEL.exome.20120522	120	106	102	0	73	75	101	104	84	18	80	62	61	85	30	0	139
HG01948.mapped.ILLUMINA.bwa.PEL.exome.20120522	149	0	0	83	137	113	114	139	145	0	1	1	1	0	36	82	165
HG01950.mapped.ILLUMINA.bwa.PEL.exome.20120522	142	84	95	66	177	113	109	176	147	0	67	82	1	2	44	80	163
HG01951.mapped.ILLUMINA.bwa.PEL.exome.20120522	139	1	2	88	129	113	111	102	139	0	1	1	1	1	39	0	161
HG01953.mapped.ILLUMINA.bwa.PEL.exome.20120522	114	125	120	51	115	102	169	177	122	11	94	0	109	118	61	0	137
HG01954.mapped.ILLUMINA.bwa.PEL.exome.20120522	136	2	0	70	146	160	157	195	199	0	2	0	0	1	68	109	128
HG01956.mapped.ILLUMINA.bwa.ACB.exome.20120522	127	96	84	59	93	87	108	169	141	0	0	0	1	2	31	79	142
HG01958.mapped.ILLUMINA.bwa.ACB.exome.20120522	82	87	77	54	154	109	118	95	95	0	62	70	0	1	68	0	97
HG01961.mapped.ILLUMINA.bwa.PEL.exome.20130415	49	55	60	14	63	57	73	42	74	0	37	1	59	56	26	2	79
HG01965.mapped.ILLUMINA.bwa.PEL.exome.20130415	39	1	1	39	96	99	99	88	107	2	2	0	3	7	39	58	81
HG01967.mapped.ILLUMINA.bwa.PEL.exome.20120522	113	1	0	58	144	144	161	182	159	0	0	0	0	1	72	116	138
HG01968.mapped.ILLUMINA.bwa.PEL.exome.20120522	107	0	1	74	151	143	137	152	151	0	0	0	0	0	85	0	145
HG01970.mapped.ILLUMINA.bwa.PEL.exome.20120522	114	0	2	72	154	146	155	192	175	0	0	0	0	0	67	116	118
HG01971.mapped.ILLUMINA.bwa.PEL.exome.20120522	123	0	1	66	157	156	156	151	175	0	0	1	0	0	83	0	133
HG01973.mapped.ILLUMINA.bwa.PEL.exome.20120522	119	0	1	112	142	154	161	134	149	0	0	0	0	1	82	0	132
HG01974.mapped.ILLUMINA.bwa.PEL.exome.20120522	144	0	2	68	175	163	159	151	177	1	0	0	1	0	86	0	130
HG01976.mapped.ILLUMINA.bwa.PEL.exome.20120522	112	0	1	68	160	136	139	209	207	1	0	0	0	1	68	103	141
HG01977.mapped.ILLUMINA.bwa.PEL.exome.20120522	145	0	0	68	165	155	149	148	175	0	0	0	0	1	88	1	126
HG01979.mapped.ILLUMINA.bwa.PEL.exome.20130415	57	0	0	18	36	46	53	40	48	0	0	0	0	0	0	47	48
HG01980.mapped.ILLUMINA.bwa.PEL.exome.20130415	77	38	28	16	46	57	65	50	32	4	31	48	0	38	0	31	60
HG01982.mapped.ILLUMINA.bwa.PEL.exome.20120522	87	0	0	61	117	120	103	94	95	0	0	0	0	0	59	1	99
HG01983.mapped.ILLUMINA.bwa.PEL.exome.20120522	78	88	71	47	72	103	93	78	87	1	40	0	55	0	37	69	83
HG01985.mapped.ILLUMINA.bwa.ACB.exome.20120522	73	87	69	48	105	111	106	80	102	0	62	0	76	1	55	0	95
HG01986.mapped.ILLUMINA.bwa.ACB.exome.20120522	73	0	1	60	102	101	89	104	78	0	0	0	0	0	42	78	90
HG01988.mapped.ILLUMINA.bwa.ACB.exome.20121211	120	0	1	108	120	106	102	104	124	0	0	0	0	2	40	1	150
HG01989.mapped.ILLUMINA.bwa.ACB.exome.20121211	144	71	81	52	143	111	99	101	66	16	76	76	66	87	0	79	138
HG01990.mapped.ILLUMINA.bwa.ACB.exome.20121211	82	0	0	106	148	101	107	87	113	1	1	0	1	2	66	2	99
HG01991.mapped.ILLUMINA.bwa.PEL.exome.20130415	55	0	0	22	27	43	49	30	42	0	1	0	0	0	14	18	60
HG01992.mapped.ILLUMINA.bwa.PEL.exome.20130415	45	20	22	14	22	28	45	22	46	0	0	0	0	0	15	0	46
HG01997.mapped.ILLUMINA.bwa.PEL.exome.20130415	30	0	1	15	27	41	42	27	47	0	0	0	0	0	16	0	60
HG02002.mapped.ILLUMINA.bwa.PEL.exome.20130415	44	17	26	14	19	29	45	33	46	0	1	0	0	0	14	1	64
HG02003.mapped.ILLUMINA.bwa.PEL.exome.20130415	55	33	36	12	41	59	51	34	59	0	17	30	0	0	7	19	73
HG02006.mapped.ILLUMINA.bwa.PEL.exome.20130415	93	0	1	88	171	160	178	162	172	4	5	0	7	6	0	153	128
HG02008.mapped.ILLUMINA.bwa.PEL.exome.20130415	60	31	20	9	37	38	56	36	27	3	25	35	0	23	0	24	71
HG02009.mapped.ILLUMINA.bwa.ACB.exome.20130415	47	26	11	14	47	44	45	25	31	1	21	22	15	25	0	0	32
HG02010.mapped.ILLUMINA.bwa.ACB.exome.20130415	53	0	0	35	31	46	59	42	60	0	0	0	0	1	0	33	53
HG02012.mapped.ILLUMINA.bwa.ACB.exome.20121211	92	101	90	51	161	122	117	102	63	32	106	82	82	83	52	0	113
HG02013.mapped.ILLUMINA.bwa.ACB.exome.20120522	69	0	0	73	122	94	102	66	92	0	0	0	0	0	56	0	87
HG02014.mapped.ILLUMINA.bwa.ACB.exome.20120522	115	0	1	106	230	137	157	207	114	11	98	0	124	125	64	0	123
HG02016.mapped.ILLUMINA.bwa.KHV.exome.20130415	58	19	34	18	25	30	56	53	33	6	17	0	35	43	13	2	79
HG02017.mapped.ILLUMINA.bwa.KHV.exome.20130415	70	0	0	35	59	59	79	61	75	0	0	0	3	0	0	56	70
HG02019.mapped.ILLUMINA.bwa.KHV.exome.20130415	71	38	28	12	29	44	72	54	73	0	0	0	0	1	0	55	67
HG02020.mapped.ILLUMINA.bwa.KHV.exome.20130415	70	0	0	25	48	64	55	46	70	0	1	0	0	0	7	24	65
HG02023.mapped.ILLUMINA.bwa.KHV.exome.20120522	133	83	81	66	152	115	117	121	96	0	65	83	0	1	34	80	154
HG02024.mapped.ILLUMINA.bwa.KHV.exome.20130422	112	96	113	6	95	89	104	93	11	27	104	81	96	105	0	2	130
HG02025.mapped.ILLUMINA.bwa.KHV.exome.20130422	179	99	104	85	192	175	168	124	109	28	116	106	98	117	0	112	219
HG02026.mapped.ILLUMINA.bwa.KHV.exome.20130422	153	94	113	78	116	107	124	151	111	33	89	7	92	117	0	89	200
HG02028.mapped.ILLUMINA.bwa.KHV.exome.20120522	128	0	2	90	134	118	102	133	96	16	54	0	66	96	42	0	141
HG02029.mapped.ILLUMINA.bwa.KHV.exome.20120522	151	0	4	80	133	130	129	110	123	0	1	1	0	5	52	1	159
HG02031.mapped.ILLUMINA.bwa.KHV.exome.20121211	101	0	0	59	109	100	107	107	91	0	0	0	0	0	40	57	94
HG02032.mapped.ILLUMINA.bwa.KHV.exome.20121211	70	0	0	76	98	102	88	74	88	0	0	0	1	1	36	84	78
HG02035.mapped.ILLUMINA.bwa.KHV.exome.20130415	46	0	0	22	48	47	57	35	38	8	11	0	15	20	14	3	50

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02040.mapped.ILLUMINA.bwa.KHV.exome.20120522	128	0	0	78	118	113	118	113	130	0	0	0	1	1	30	79	149
HG02046.mapped.ILLUMINA.bwa.KHV.exome.20120522	157	65	76	51	126	105	121	141	145	16	47	79	0	0	31	67	144
HG02047.mapped.ILLUMINA.bwa.KHV.exome.20120522	112	0	1	70	106	97	119	95	88	13	55	81	0	83	0	68	135
HG02048.mapped.ILLUMINA.bwa.KHV.exome.20120522	120	0	1	70	156	160	167	199	231	0	0	0	1	0	74	107	132
HG02049.mapped.ILLUMINA.bwa.KHV.exome.20120522	122	0	0	71	169	140	153	159	183	0	0	0	0	1	96	0	137
HG02050.mapped.ILLUMINA.bwa.KHV.exome.20121211	93	0	1	92	122	103	90	90	104	0	0	0	0	0	45	75	94
HG02051.mapped.ILLUMINA.bwa.ACB.exome.20120522	79	0	71	46	133	94	96	109	94	0	50	0	66	0	42	68	96
HG02052.mapped.ILLUMINA.bwa.ACB.exome.20121211	130	0	1	71	102	104	103	107	124	0	1	1	0	1	35	61	127
HG02053.mapped.ILLUMINA.bwa.ACB.exome.20121211	85	109	79	48	124	131	116	130	78	37	119	85	79	94	0	76	110
HG02054.mapped.ILLUMINA.bwa.ACB.exome.20130415	68	0	2	29	46	57	73	42	63	0	0	0	0	1	17	0	66
HG02057.mapped.ILLUMINA.bwa.KHV.exome.20120522	155	0	4	100	205	180	180	245	200	0	0	1	0	1	78	127	152
HG02058.mapped.ILLUMINA.bwa.KHV.exome.20120522	142	119	106	55	211	156	151	201	135	10	175	106	113	121	69	2	142
HG02060.mapped.ILLUMINA.bwa.KHV.exome.20120522	88	85	82	47	82	73	103	101	113	0	0	0	1	0	46	76	98
HG02061.mapped.ILLUMINA.bwa.KHV.exome.20120522	86	97	85	87	114	121	123	92	62	37	67	0	66	82	0	79	106
HG02064.mapped.ILLUMINA.bwa.KHV.exome.20120522	79	86	78	39	132	105	96	82	2	38	131	53	113	114	0	0	104
HG02067.mapped.ILLUMINA.bwa.KHV.exome.20120522	81	82	81	46	135	106	127	120	99	35	50	69	0	1	60	0	100
HG02069.mapped.ILLUMINA.bwa.KHV.exome.20120522	171	144	150	60	149	142	211	250	161	11	133	0	148	151	77	1	189
HG02070.mapped.ILLUMINA.bwa.KHV.exome.20120522	200	130	142	55	134	149	193	215	0	20	194	2	167	186	0	1	168
HG02072.mapped.ILLUMINA.bwa.KHV.exome.20120522	119	114	108	47	113	101	160	167	214	0	0	1	0	0	0	224	137
HG02073.mapped.ILLUMINA.bwa.KHV.exome.20120522	154	0	2	85	207	189	198	214	216	0	2	2	2	0	81	122	173
HG02075.mapped.ILLUMINA.bwa.KHV.exome.20130415	66	30	27	18	32	35	62	48	59	0	0	0	0	0	16	20	65
HG02076.mapped.ILLUMINA.bwa.KHV.exome.20130415	57	0	1	36	39	48	57	37	64	0	1	1	0	2	14	15	66
HG02078.mapped.ILLUMINA.bwa.KHV.exome.20130415	57	32	30	13	24	36	64	37	37	9	8	0	30	39	0	23	61
HG02079.mapped.ILLUMINA.bwa.KHV.exome.20130415	69	0	0	23	47	69	64	43	56	0	0	0	0	0	28	0	62
HG02081.mapped.ILLUMINA.bwa.KHV.exome.20130415	50	0	2	33	45	49	50	28	54	0	2	0	0	0	14	1	60
HG02082.mapped.ILLUMINA.bwa.KHV.exome.20130415	54	31	35	12	25	28	51	39	66	0	0	0	2	0	11	31	67
HG02084.mapped.ILLUMINA.bwa.KHV.exome.20130415	58	0	0	35	40	57	62	34	1	5	31	0	28	53	0	0	63
HG02085.mapped.ILLUMINA.bwa.KHV.exome.20130415	69	0	0	34	54	72	73	40	79	0	0	0	0	0	29	0	86
HG02086.mapped.ILLUMINA.bwa.KHV.exome.20130415	32	0	0	18	19	32	37	35	17	5	10	0	16	24	0	9	47
HG02087.mapped.ILLUMINA.bwa.KHV.exome.20130415	74	0	1	38	43	58	51	47	42	6	13	0	27	24	0	18	72
HG02088.mapped.ILLUMINA.bwa.KHV.exome.20130415	56	0	0	21	41	50	50	42	58	0	1	0	0	0	32	0	61
HG02089.mapped.ILLUMINA.bwa.PEL.exome.20130415	72	31	35	20	26	28	59	42	32	8	14	0	29	31	12	0	70
HG02090.mapped.ILLUMINA.bwa.PEL.exome.20130415	50	0	0	30	32	54	46	42	48	0	0	0	0	0	0	50	60
HG02095.mapped.ILLUMINA.bwa.ACB.exome.20120522	116	0	0	78	112	108	72	68	82	0	55	0	63	89	31	1	131
HG02102.mapped.ILLUMINA.bwa.PEL.exome.20130415	86	134	123	55	122	130	175	201	123	25	117	0	124	124	56	7	122
HG02104.mapped.ILLUMINA.bwa.PEL.exome.20130415	59	27	26	17	25	34	52	43	34	6	23	0	30	40	0	38	70
HG02105.mapped.ILLUMINA.bwa.PEL.exome.20130415	46	1	0	18	20	33	41	26	62	0	0	0	0	0	4	26	51
HG02107.mapped.ILLUMINA.bwa.ACB.exome.20121211	151	1	0	89	105	93	91	95	87	12	51	0	64	81	0	72	135
HG02108.mapped.ILLUMINA.bwa.ACB.exome.20120522	105	75	2	54	80	81	68	71	88	0	58	0	71	76	33	1	126
HG02111.mapped.ILLUMINA.bwa.ACB.exome.20120522	126	66	76	55	95	75	94	111	115	1	0	0	0	1	31	67	134
HG02113.mapped.ILLUMINA.bwa.KHV.exome.20130415	83	1	0	28	50	56	69	55	38	8	17	43	0	52	0	33	76
HG02116.mapped.ILLUMINA.bwa.KHV.exome.20120522	129	0	1	76	115	114	110	130	112	0	0	0	0	3	33	60	140
HG02121.mapped.ILLUMINA.bwa.KHV.exome.20130415	77	0	0	39	55	63	62	71	64	0	0	0	0	0	16	35	67
HG02122.mapped.ILLUMINA.bwa.KHV.exome.20130415	50	22	26	14	17	21	50	25	47	0	0	0	0	0	18	0	53
HG02127.mapped.ILLUMINA.bwa.KHV.exome.20130415	63	38	31	21	49	58	66	45	35	8	31	28	28	42	11	0	74
HG02128.mapped.ILLUMINA.bwa.KHV.exome.20130415	67	0	0	29	54	65	68	57	37	12	21	2	32	35	13	0	68
HG02130.mapped.ILLUMINA.bwa.KHV.exome.20120522	82	76	68	45	78	64	98	93	90	0	0	0	0	1	36	57	93
HG02131.mapped.ILLUMINA.bwa.KHV.exome.20120522	90	102	79	47	91	68	113	106	63	37	66	76	0	76	0	83	124
HG02133.mapped.ILLUMINA.bwa.KHV.exome.20120522	88	0	0	98	119	113	108	113	98	0	0	0	0	0	45	80	97
HG02134.mapped.ILLUMINA.bwa.KHV.exome.20120522	96	0	0	76	125	131	106	95	74	36	55	0	91	86	49	1	105
HG02136.mapped.ILLUMINA.bwa.KHV.exome.20120522	80	0	1	83	100	97	103	81	91	0	0	0	0	0	40	74	92
HG02137.mapped.ILLUMINA.bwa.KHV.exome.20120522	93	0	0	60	114	107	100	88	96	0	0	0	0	0	73	0	101
HG02138.mapped.ILLUMINA.bwa.KHV.exome.20130415	52	0	0	22	59	56	75	50	41	6	7	24	0	35	0	28	70
HG02139.mapped.ILLUMINA.bwa.KHV.exome.20130415	64	0	0	27	45	61	65	50	67	0	0	0	0	0	8	23	68
HG02140.mapped.ILLUMINA.bwa.KHV.exome.20130415	56	21	29	19	29	36	59	34	74	0	1	0	0	0	16	32	69
HG02141.mapped.ILLUMINA.bwa.KHV.exome.20130415	45	0	0	17	43	46	54	38	54	0	0	0	0	0	12	25	59
HG02142.mapped.ILLUMINA.bwa.KHV.exome.20121211	110	2	1	101	119	114	112	97	110	0	0	0	0	2	0	133	98
HG02143.mapped.ILLUMINA.bwa.ACB.exome.20120522	117	0	2	65	133	101	103	122	92	16	58	0	80	87	26	0	140
HG02144.mapped.ILLUMINA.bwa.ACB.exome.20120522	118	76	79	52	139	113	101	99	117	0	92	77	67	1	37	1	136
HG02146.mapped.ILLUMINA.bwa.PEL.exome.20120522	95	0	0	100	126	106	112	105	107	0	0	0	0	0	42	89	100
HG02147.mapped.ILLUMINA.bwa.PEL.exome.20120522	73	0	0	107	124	111	93	78	80	0	0	0	0	0	60	0	95
HG02150.mapped.ILLUMINA.bwa.PEL.exome.20130415	82	3	1	73	151	155	206	183	5	42	160	0	163	167	0	2	118
HG02151.mapped.ILLUMINA.bwa.CDX.exome.20120522	94	2	0	66	123	114	103	107	71	34	68	0	82	75	51	0	103
HG02152.mapped.ILLUMINA.bwa.CDX.exome.20130415	68	1	0	28	45	70	85	74	63	7	0	0	0	0	27	0	70
HG02153.mapped.ILLUMINA.bwa.CDX.exome.20130415	49	0	0	22	22	42	37	22	39	0	0	0	0	0	0	27	53
HG02154.mapped.ILLUMINA.bwa.CDX.exome.20130415	71	0	0	29	47	67	65	45	37	3	21	42	0	50	0	29	75
HG02155.mapped.ILLUMINA.bwa.CDX.exome.20130415	59	44	56	1	21	36	51	49	27	5	29	39	0	39	0	20	63
HG02156.mapped.ILLUMINA.bwa.CDX.exome.20130415	53	0	0	22	37	40	42	42	61	0	0	0	0	0	6	13	54
HG02164.mapped.ILLUMINA.bwa.CDX.exome.20130415	61	0	0	18	34	56	69	32	46	0	0	0	0	0	10	26	71
HG02165.mapped.ILLUMINA.bwa.CDX.exome.20130415	38	0	0	21	27	39	37	22	40	0	0	0	1	0	8	10	52
HG02166.mapped.ILLUMINA.bwa.CDX.exome.20130415	72	1	0	31	55	64	65	38	67	0	0	2	0	0	25	0	74
HG02178.mapped.ILLUMINA.bwa.CDX.exome.20130415	57	0	0	23	48	47	56	33	63	0	0	0	0	0	30	0	68
HG02179.mapped.ILLUMINA.bwa.CDX.exome.20130415	88	70	60	2	39	48	93	80	82	10	25	39	0	0	30	0	90
HG02180.mapped.ILLUMINA.bwa.CDX.exome.20130415	50	0	1	29	43	37	44	35	33	4	13	0	24	24	9	0	56
HG02181.mapped.ILLUMINA.bwa.CDX.exome.20130415	53	0	0	28	41	43	56	27	49	0	0	0	0	0	17	1	54
HG02182.mapped.ILLUMINA.bwa.CDX.exome.20130415	63	0	0	31	52	69	71	40	59	0	0	0	0	0	18	0	70
HG02184.mapped.ILLUMINA.bwa.CDX.exome.20130415	40	0	0	28	46	37	49	35	26	5	4	0	13	27	9	1	56
HG02185.mapped.ILLUMINA.bwa.CDX.exome.20130415	39	0	0	22	26	41	37	35	36	0	0	0	0	0	0	28	55
HG02186.mapped.ILLUMINA.bwa.CDX.exome.20130415	49	0	0	25	25	57	59	33	29	6	13	0	31	24	0	34	69
HG02187.mapped.ILLUMINA.bwa.CDX.exome.20130415	36	16	19	12	25	17	47	28	36	0	0	0	0	0	4	20	40
HG02188.mapped.ILLUMINA.bwa.CDX.exome.20130415	51	0	0	34	53	57	58	27	34	5	18	0	32	38	0	17	59
HG02190.mapped.ILLUMINA.bwa.CDX.exome.20130415	67	28	36	17	19	24	67	35	0	17	26	0	46	60	0	0	66
HG02215.mapped.ILLUMINA.bwa.GBR.exome.20120522	79	96	90	46	80	76	107	109	125	1	0	0	0	1	0	151	80
HG02219.mapped.ILLUMINA.bwa.IBS.exome.20130415	50	1	1	30	84	87	106	74	100	0	0	1	0	0	0	65	76
HG02220.mapped.ILLUMINA.bwa.IBS.exome.20130415	67	22	27	13	16	25	67	27	51	0	0	0	0	0	9	24	61
HG02221.mapped.ILLUMINA.bwa.IBS.exome.20130415	53	35	32	12	22	33	55	32	56	0	0	0	0	0	17	40	63
HG02223.mapped.ILLUMINA.bwa.IBS.exome.20120522	116	74	80	50	82	85	105	90	93	15	42	0	75	87	0	71	112
HG02224.mapped.ILLUMINA.bwa.IBS.exome.20120522	130	75	83	58	89	80	111	103	2	24	88	75	72	111	0	0	159
HG02230.mapped.ILLUMINA.bwa.IBS.exome.20120522	126	0	0	72	117	95	93	94	132	0	0	0	0	3	0	88	129
HG02231.mapped.ILLUMINA.bwa.IBS.exome.20120522	135	80	99	57	96	84	98	104	129	0	0	0	0	1	32	71	141
HG02232.mapped.ILLUMINA.bwa.IBS.exome.20120522	92	100	71	49	128	109	111	88	72	35	96	76	82	81	0	73	96
HG02233.mapped.ILLUMINA.bwa.IBS.exome.20120522	85	0	0	73	108	113	106	95	103	1	0	0	0	0	41	72	91
HG02235.mapped.ILLUMINA.bwa.IBS.exome.20130415	61	0	2	34	44	50	55	31	42	9	18	0	26	29	0	20	64
HG02236.mapped.ILLUMINA.bwa.IBS.exome.20130415	69	0	0	29	35	71	72	63	66	0	0	0	0	0	9	27	76
HG02238.mapped.ILLUMINA.bwa.IBS.exome.20120522	75	0	0	62	97	96	107	93	63	27	58	0	80	75	0	85	93
HG02239.mapped.ILLUMINA.bwa.IBS.exome.20120522	82	0	0	78	109	108	97	89	99	0	0	0	0	0	0	124	92

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02250.mapped.ILLUMINA.bwa.CDX.exome.20120522	83	88	82	50	78	62	94	75	0	41	83	71	69	109	0	0	105
HG02252.mapped.ILLUMINA.bwa.PEL.exome.20130415	107	0	2	130	177	194	200	240	260	1	0	0	1	0	71	120	135
HG02253.mapped.ILLUMINA.bwa.PEL.exome.20130415	90	0	0	67	166	152	174	164	148	24	111	0	114	131	0	107	126
HG02255.mapped.ILLUMINA.bwa.ACB.exome.20130415	51	0	24	10	41	49	58	49	46	0	11	26	1	0	0	46	75
HG02256.mapped.ILLUMINA.bwa.ACB.exome.20130415	49	21	22	15	47	64	68	28	67	0	11	25	0	0	13	28	68
HG02259.mapped.ILLUMINA.bwa.PEL.exome.20121211	90	87	76	47	78	75	103	91	64	35	55	1	69	79	41	1	105
HG02260.mapped.ILLUMINA.bwa.PEL.exome.20121211	81	0	0	63	112	101	93	81	109	1	0	1	0	0	39	78	103
HG02262.mapped.ILLUMINA.bwa.PEL.exome.20130415	90	117	124	53	101	112	140	143	151	3	0	0	0	1	75	1	94
HG02265.mapped.ILLUMINA.bwa.PEL.exome.20130422	132	64	71	60	147	131	113	116	140	1	40	70	0	3	36	75	158
HG02266.mapped.ILLUMINA.bwa.PEL.exome.20130422	150	2	1	116	122	116	117	114	142	0	3	0	3	2	32	72	160
HG02271.mapped.ILLUMINA.bwa.PEL.exome.20121211	83	0	1	61	130	124	111	112	125	0	2	0	2	1	55	78	106
HG02272.mapped.ILLUMINA.bwa.PEL.exome.20130415	53	0	0	16	28	53	69	39	63	0	0	0	0	0	18	1	65
HG02274.mapped.ILLUMINA.bwa.PEL.exome.20130422	145	0	0	80	139	142	124	100	133	0	0	0	0	1	44	3	159
HG02275.mapped.ILLUMINA.bwa.PEL.exome.20130422	159	57	7	49	130	124	112	118	91	20	45	3	48	101	30	3	155
HG02277.mapped.ILLUMINA.bwa.PEL.exome.20130415	64	2	0	29	45	54	74	68	31	7	17	0	18	37	15	0	73
HG02278.mapped.ILLUMINA.bwa.PEL.exome.20130415	57	0	0	24	38	51	49	39	47	0	0	1	0	0	11	0	53
HG02281.mapped.ILLUMINA.bwa.ACB.exome.20130415	67	38	16	14	26	31	56	50	65	0	1	0	2	0	10	24	83
HG02282.mapped.ILLUMINA.bwa.ACB.exome.20130415	44	0	0	17	30	55	38	30	39	0	1	0	0	0	8	17	53
HG02283.mapped.ILLUMINA.bwa.ACB.exome.20120522	124	69	1	48	83	72	71	69	78	0	54	0	72	79	34	2	140
HG02284.mapped.ILLUMINA.bwa.ACB.exome.20121211	126	66	85	62	123	112	106	106	125	0	66	0	76	2	0	104	131
HG02285.mapped.ILLUMINA.bwa.PEL.exome.20130415	61	33	39	16	15	35	66	42	63	0	0	0	0	0	9	33	75
HG02286.mapped.ILLUMINA.bwa.PEL.exome.20130415	67	0	0	28	45	66	64	45	67	0	0	0	1	0	26	0	74
HG02291.mapped.ILLUMINA.bwa.PEL.exome.20120522	125	0	0	73	175	169	162	135	210	0	0	1	0	1	45	93	149
HG02292.mapped.ILLUMINA.bwa.PEL.exome.20120522	159	0	1	102	254	243	250	151	153	9	83	132	0	163	53	0	206
HG02298.mapped.ILLUMINA.bwa.PEL.exome.20120522	121	0	0	65	162	154	151	135	162	0	0	0	0	0	86	2	136
HG02299.mapped.ILLUMINA.bwa.PEL.exome.20120522	190	148	165	68	175	150	260	202	184	13	95	0	133	173	49	0	220
HG02301.mapped.ILLUMINA.bwa.PEL.exome.20130415	48	0	1	28	53	54	48	31	48	0	1	0	0	0	15	0	58
HG02304.mapped.ILLUMINA.bwa.PEL.exome.20130415	114	135	136	68	137	138	204	228	130	38	131	0	150	134	0	115	131
HG02307.mapped.ILLUMINA.bwa.ACB.exome.20120522	118	2	86	52	111	116	103	126	118	0	51	1	73	0	33	83	139
HG02308.mapped.ILLUMINA.bwa.ACB.exome.20120522	116	2	2	98	121	108	105	146	126	0	0	0	0	0	38	69	147
HG02309.mapped.ILLUMINA.bwa.ACB.exome.20120522	117	69	1	50	91	77	69	72	87	0	49	0	62	78	0	77	133
HG02312.mapped.ILLUMINA.bwa.PEL.exome.20130415	55	0	0	53	140	97	101	118	82	18	71	0	72	84	31	0	64
HG02314.mapped.ILLUMINA.bwa.ACB.exome.20120522	120	68	83	60	88	80	102	147	136	0	0	1	0	0	35	81	126
HG02315.mapped.ILLUMINA.bwa.ACB.exome.20120522	123	0	0	90	111	101	102	117	110	0	0	1	2	2	31	63	125
HG02317.mapped.ILLUMINA.bwa.ACB.exome.20130415	58	24	31	12	19	30	46	25	48	0	0	0	0	0	12	24	61
HG02318.mapped.ILLUMINA.bwa.ACB.exome.20130415	40	37	26	0	0	2	27	18	27	0	14	0	17	21	0	12	51
HG02322.mapped.ILLUMINA.bwa.ACB.exome.20120522	120	0	3	77	110	102	102	100	112	0	0	0	0	2	42	0	131
HG02323.mapped.ILLUMINA.bwa.ACB.exome.20120522	121	2	1	92	129	115	101	147	118	0	1	1	0	0	30	1	104
HG02325.mapped.ILLUMINA.bwa.ACB.exome.20120522	160	76	81	46	88	115	107	145	136	0	1	0	0	5	29	72	149
HG02330.mapped.ILLUMINA.bwa.ACB.exome.20120522	109	0	1	99	98	106	110	125	136	0	1	0	0	1	0	137	132
HG02332.mapped.ILLUMINA.bwa.ACB.exome.20120522	127	1	2	99	127	118	134	114	132	20	0	0	0	0	0	116	127
HG02334.mapped.ILLUMINA.bwa.ACB.exome.20120522	114	87	85	53	79	77	111	136	124	0	0	1	0	3	0	148	138
HG02337.mapped.ILLUMINA.bwa.ACB.exome.20120522	120	1	2	69	114	113	102	132	99	0	2	0	0	0	0	69	136
HG02339.mapped.ILLUMINA.bwa.ACB.exome.20120522	124	0	1	82	138	114	99	128	115	0	1	1	1	1	29	87	129
HG02343.mapped.ILLUMINA.bwa.ACB.exome.20120522	116	88	75	52	121	114	100	89	127	1	54	79	0	1	43	1	140
HG02345.mapped.ILLUMINA.bwa.PEL.exome.20130415	46	0	1	23	91	90	81	61	103	1	1	0	0	0	43	2	76
HG02348.mapped.ILLUMINA.bwa.PEL.exome.20130415	72	99	97	47	89	91	146	137	105	20	87	0	92	86	44	0	104
HG02351.mapped.ILLUMINA.bwa.CDX.exome.20120522	96	0	0	119	154	137	121	117	77	34	39	73	0	97	0	84	98
HG02353.mapped.ILLUMINA.bwa.CDX.exome.20120522	82	0	1	76	127	114	108	99	103	0	0	0	0	0	72	0	104
HG02355.mapped.ILLUMINA.bwa.CDX.exome.20120522	82	92	86	56	91	73	113	116	104	0	0	0	0	0	45	88	104
HG02356.mapped.ILLUMINA.bwa.CDX.exome.20120522	91	0	0	60	115	115	112	72	100	0	0	0	0	0	0	119	96
HG02360.mapped.ILLUMINA.bwa.CDX.exome.20120522	77	0	0	64	115	114	95	89	56	31	53	0	66	76	39	0	91
HG02363.mapped.ILLUMINA.bwa.CDX.exome.20120522	88	108	89	55	91	92	127	95	0	49	110	0	127	125	0	0	112
HG02364.mapped.ILLUMINA.bwa.CDX.exome.20120522	91	1	0	74	106	108	100	87	109	2	0	0	1	3	69	0	97
HG02367.mapped.ILLUMINA.bwa.CDX.exome.20120522	74	82	78	48	74	68	96	80	98	0	0	0	0	0	0	124	87
HG02371.mapped.ILLUMINA.bwa.CDX.exome.20120522	97	132	128	1	1	1	111	92	0	44	108	90	84	109	0	0	93
HG02372.mapped.ILLUMINA.bwa.CDX.exome.20120522	76	134	111	1	0	0	100	88	57	33	55	69	0	73	0	88	90
HG02373.mapped.ILLUMINA.bwa.CDX.exome.20120522	108	2	4	69	136	119	117	88	118	0	1	0	0	4	75	2	98
HG02374.mapped.ILLUMINA.bwa.CDX.exome.20120522	87	1	1	73	110	101	144	135	66	46	70	1	87	87	53	0	97
HG02375.mapped.ILLUMINA.bwa.CDX.exome.20120522	88	98	86	55	81	75	127	114	73	33	65	0	81	85	41	0	97
HG02377.mapped.ILLUMINA.bwa.CDX.exome.20120522	76	0	0	64	104	104	100	102	113	0	0	0	0	1	53	74	93
HG02379.mapped.ILLUMINA.bwa.CDX.exome.20120522	83	0	0	59	114	113	94	110	98	0	0	0	0	0	58	73	93
HG02380.mapped.ILLUMINA.bwa.CDX.exome.20120522	77	2	1	55	98	108	89	78	91	0	1	1	0	0	69	0	93
HG02381.mapped.ILLUMINA.bwa.CDX.exome.20120522	95	85	80	46	89	79	110	84	63	30	58	75	0	79	0	83	93
HG02382.mapped.ILLUMINA.bwa.CDX.exome.20120522	81	0	0	65	107	71	98	98	66	31	67	0	79	81	44	0	91
HG02383.mapped.ILLUMINA.bwa.CDX.exome.20120522	90	97	81	54	78	75	73	53	64	0	60	71	0	77	51	0	100
HG02384.mapped.ILLUMINA.bwa.CDX.exome.20120522	88	1	0	72	119	108	104	93	98	0	0	0	0	0	72	0	97
HG02385.mapped.ILLUMINA.bwa.CDX.exome.20120522	68	0	0	61	113	102	95	88	101	0	0	0	0	0	69	0	89
HG02386.mapped.ILLUMINA.bwa.CDX.exome.20120522	76	82	77	44	147	108	104	79	109	0	58	65	0	1	0	132	92
HG02387.mapped.ILLUMINA.bwa.CDX.exome.20120522	84	0	0	74	123	111	121	95	64	35	61	64	0	70	0	91	99
HG02388.mapped.ILLUMINA.bwa.CDX.exome.20120522	77	0	3	64	116	106	103	84	64	37	47	0	71	71	37	0	96
HG02389.mapped.ILLUMINA.bwa.CDX.exome.20120522	84	85	74	48	143	105	76	98	63	33	77	65	55	78	41	0	98
HG02390.mapped.ILLUMINA.bwa.CDX.exome.20120522	88	0	0	92	122	117	96	82	1	34	77	0	110	124	0	1	110
HG02391.mapped.ILLUMINA.bwa.CDX.exome.20120522	83	123	114	1	0	0	105	97	106	3	0	0	1	3	0	123	109
HG02392.mapped.ILLUMINA.bwa.CDX.exome.20120522	79	0	0	70	99	105	104	93	76	37	55	68	0	81	43	1	94
HG02394.mapped.ILLUMINA.bwa.CDX.exome.20120522	83	0	1	66	109	113	97	92	110	0	0	0	0	0	32	72	89
HG02395.mapped.ILLUMINA.bwa.CDX.exome.20120522	81	0	0	72	118	105	97	80	101	0	0	0	0	0	39	58	100
HG02396.mapped.ILLUMINA.bwa.CDX.exome.20120522	86	0	1	80	119	109	97	81	105	0	0	0	0	0	63	0	99
HG02397.mapped.ILLUMINA.bwa.CDX.exome.20120522	77	98	81	50	83	78	98	88	51	33	51	0	78	85	0	79	97
HG02398.mapped.ILLUMINA.bwa.CDX.exome.20120522	79	0	1	68	118	116	103	77	88	0	0	0	0	0	54	1	92
HG02399.mapped.ILLUMINA.bwa.CDX.exome.20120522	78	93	78	42	90	91	115	99	119	0	0	0	0	0	0	160	100
HG02401.mapped.ILLUMINA.bwa.CDX.exome.20120522	82	0	0	61	108	109	101	81	63	34	50	0	70	79	0	72	96
HG02402.mapped.ILLUMINA.bwa.CDX.exome.20120522	89	0	0	89	113	114	113	98	68	35	67	0	87	67	0	75	91
HG02406.mapped.ILLUMINA.bwa.CDX.exome.20120522	115	0	0	100	122	129	130	112	0	47	91	0	130	125	0	0	101
HG02407.mapped.ILLUMINA.bwa.CDX.exome.20120522	87	96	76	49	91	81	116	115	68	36	58	0	73	88	57	0	104
HG02408.mapped.ILLUMINA.bwa.CDX.exome.20130422	83	4	6	49	91	82	71	90	87	1	5	0	3	8	26	53	87
HG02409.mapped.ILLUMINA.bwa.CDX.exome.20120522	77	0	1	96	121	105	97	96	0	42	107	65	75	117	0	0	105
HG02410.mapped.ILLUMINA.bwa.CDX.exome.20130422	105	2	0	79	91	71	70	73	99	0	4	4	0	5	22	49	91
HG02419.mapped.ILLUMINA.bwa.ACB.exome.20120522	127	76	92	1	110	113	97	97	115	0	80	68	67	2	35	0	119
HG02420.mapped.ILLUMINA.bwa.CDX.exome.20120522	129	0	84	53	136	110	97	117	102	14	79	0	92	82	36	2	131
HG02425.mapped.ILLUMINA.bwa.PEL.exome.20130422	121	62	64	58	85	68	110	111	83	17	27	0	53	73	0	79	153
HG02427.mapped.ILLUMINA.bwa.ACB.exome.20121211	103	0	0	65	91	84	83	103	103	0	0	0	0	1	26	58	105
HG02429.mapped.ILLUMINA.bwa.ACB.exome.20121211	94	0	0	82	84	85	84	101	86	0	0	0	0	2	27	61	109
HG02433.mapped.ILLUMINA.bwa.ACB.exome.20121211	125	0	1	100	116	102	101	119	82	16	54	1	64	87	0	75	127
HG02439.mapped.ILLUMINA.bwa.ACB.exome.20130415	73	0	115	54	158	143	151	193	155	0	113	0	119	0	48	2	82
HG02442.mapped.ILLUMINA.bwa.ACB.exome.20121211	116	0	3	75	115	105	97	98	126	0	0	0	0	2	43	0	132

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02445.mapped.ILLUMINA.bwa.ACB.exome.20121211	121	1	1	75	113	109	108	124	124	0	1	1	0	1	32	70	129
HG02449.mapped.ILLUMINA.bwa.ACB.exome.20120522	135	0	0	104	208	180	159	189	195	0	0	0	0	1	150	0	131
HG02450.mapped.ILLUMINA.bwa.ACB.exome.20120522	143	131	130	56	246	169	187	212	208	0	120	0	132	0	0	134	104
HG02455.mapped.ILLUMINA.bwa.ACB.exome.20130415	85	0	2	83	154	155	151	138	177	0	8	0	6	0	0	158	118
HG02461.mapped.ILLUMINA.bwa.GWD.exome.20130415	95	0	67	46	123	101	83	96	101	0	73	66	48	0	27	66	111
HG02462.mapped.ILLUMINA.bwa.GWD.exome.20130415	107	0	1	111	125	101	101	89	104	1	0	2	1	1	43	2	125
HG02464.mapped.ILLUMINA.bwa.GWD.exome.20130415	96	0	0	96	103	97	86	85	105	0	0	0	0	1	0	79	98
HG02465.mapped.ILLUMINA.bwa.GWD.exome.20130415	83	0	0	62	93	85	88	77	109	0	0	0	0	0	30	56	104
HG02470.mapped.ILLUMINA.bwa.ACB.exome.20120522	171	169	1	63	168	177	164	116	182	0	131	1	168	166	85	0	204
HG02471.mapped.ILLUMINA.bwa.ACB.exome.20120522	164	126	142	52	252	198	181	201	241	0	97	134	1	0	79	123	156
HG02476.mapped.ILLUMINA.bwa.ACB.exome.20130415	52	60	61	20	121	107	107	112	137	0	58	1	62	1	40	63	79
HG02477.mapped.ILLUMINA.bwa.ACB.exome.20130415	35	80	82	1	41	53	77	79	60	8	55	79	0	37	28	0	74
HG02479.mapped.ILLUMINA.bwa.ACB.exome.20130415	49	0	0	28	34	41	45	30	40	1	0	0	0	0	11	19	57
HG02481.mapped.ILLUMINA.bwa.ACB.exome.20130415	49	51	45	9	102	82	90	91	68	7	77	61	47	63	30	3	70
HG02484.mapped.ILLUMINA.bwa.ACB.exome.20130415	66	40	25	16	23	53	62	46	58	0	9	0	13	0	9	20	72
HG02485.mapped.ILLUMINA.bwa.ACB.exome.20130415	49	28	26	9	66	54	67	52	36	9	31	51	15	30	0	19	69
HG02489.mapped.ILLUMINA.bwa.ACB.exome.20120522	157	144	153	56	303	250	210	266	283	0	127	164	1	0	0	249	175
HG02490.mapped.ILLUMINA.bwa.PJL.exome.20121211	72	53	44	37	70	65	51	45	52	0	36	0	47	72	0	43	106
HG02491.mapped.ILLUMINA.bwa.PJL.exome.20130415	96	65	69	47	113	89	79	73	1	23	81	67	73	92	0	1	115
HG02493.mapped.ILLUMINA.bwa.PJL.exome.20130415	85	113	121	50	178	140	151	148	2	25	208	100	133	140	0	0	122
HG02494.mapped.ILLUMINA.bwa.PJL.exome.20130415	94	0	1	100	183	173	188	219	130	22	117	0	143	126	0	112	110
HG02496.mapped.ILLUMINA.bwa.ACB.exome.20130415	77	2	0	36	73	82	77	56	83	0	0	0	0	0	13	41	95
HG02497.mapped.ILLUMINA.bwa.ACB.exome.20130415	53	0	1	33	37	62	53	40	62	0	0	0	0	0	7	30	69
HG02501.mapped.ILLUMINA.bwa.ACB.exome.20130415	53	1	58	22	116	90	94	76	97	0	45	0	56	1	34	49	77
HG02502.mapped.ILLUMINA.bwa.ACB.exome.20130415	42	2	3	33	72	70	85	73	95	0	1	2	1	1	31	47	59
HG02505.mapped.ILLUMINA.bwa.ACB.exome.20130415	49	40	38	14	90	64	77	75	116	1	35	39	2	0	0	76	56
HG02508.mapped.ILLUMINA.bwa.ACB.exome.20130415	54	27	20	18	20	25	50	38	45	0	0	0	0	0	11	0	34
HG02511.mapped.ILLUMINA.bwa.ACB.exome.20130415	60	24	0	16	24	64	22	23	21	0	19	0	24	35	14	0	70
HG02512.mapped.ILLUMINA.bwa.KHV.exome.20120522	123	0	1	74	107	102	129	122	118	0	1	0	1	0	29	83	127
HG02513.mapped.ILLUMINA.bwa.KHV.exome.20120522	153	1	4	98	107	93	108	105	77	24	47	75	0	96	0	76	129
HG02521.mapped.ILLUMINA.bwa.KHV.exome.20120522	164	0	1	73	113	114	105	139	140	0	0	0	2	1	33	78	133
HG02522.mapped.ILLUMINA.bwa.KHV.exome.20120522	123	71	83	54	151	111	101	92	96	21	97	70	64	93	0	67	134
HG02536.mapped.ILLUMINA.bwa.ACB.exome.20130415	33	0	1	18	59	70	67	50	81	0	0	0	0	0	0	62	59
HG02537.mapped.ILLUMINA.bwa.ACB.exome.20130415	141	0	1	97	193	178	216	187	217	0	1	0	2	5	87	5	176
HG02541.mapped.ILLUMINA.bwa.ACB.exome.20130415	91	161	175	2	1	0	184	202	195	0	0	0	0	0	64	98	129
HG02545.mapped.ILLUMINA.bwa.ACB.exome.20130415	32	0	36	5	65	73	73	49	73	1	32	0	41	2	32	1	50
HG02546.mapped.ILLUMINA.bwa.ACB.exome.20130415	28	0	0	14	61	55	83	73	69	6	0	0	0	2	20	27	53
HG02549.mapped.ILLUMINA.bwa.ACB.exome.20130415	87	133	127	57	214	157	185	157	166	0	94	117	0	2	88	1	122
HG02554.mapped.ILLUMINA.bwa.ACB.exome.20130415	81	0	0	105	200	155	187	186	115	36	107	0	110	127	0	95	114
HG02555.mapped.ILLUMINA.bwa.ACB.exome.20130415	83	128	109	56	176	137	151	150	122	19	177	107	122	118	0	106	115
HG02557.mapped.ILLUMINA.bwa.ACB.exome.20130415	28	0	2	26	69	75	64	55	78	0	0	0	0	0	44	1	64
HG02558.mapped.ILLUMINA.bwa.ACB.exome.20130415	48	0	0	23	79	78	87	59	110	0	0	0	0	0	44	1	69
HG02561.mapped.ILLUMINA.bwa.GWD.exome.20121211	101	0	74	53	88	79	93	79	112	0	45	62	0	1	35	68	129
HG02562.mapped.ILLUMINA.bwa.GWD.exome.20130415	101	0	2	80	118	81	88	86	109	0	1	0	3	5	34	6	108
HG02568.mapped.ILLUMINA.bwa.GWD.exome.20130415	93	1	4	123	185	227	188	161	168	3	1	2	1	3	78	1	126
HG02570.mapped.ILLUMINA.bwa.GWD.exome.20130415	107	1	3	106	138	117	93	117	110	0	54	93	2	1	27	82	122
HG02571.mapped.ILLUMINA.bwa.GWD.exome.20121211	107	0	65	50	146	105	95	80	105	0	42	0	52	1	41	0	143
HG02573.mapped.ILLUMINA.bwa.GWD.exome.20130415	100	58	62	55	79	80	134	70	103	0	0	0	0	0	31	0	114
HG02574.mapped.ILLUMINA.bwa.GWD.exome.20121211	90	0	1	66	83	79	70	89	98	0	0	0	1	1	21	56	106
HG02577.mapped.ILLUMINA.bwa.ACB.exome.20130415	39	1	56	18	81	71	82	75	86	0	36	0	46	1	45	0	64
HG02580.mapped.ILLUMINA.bwa.ACB.exome.20130415	88	1	1	81	164	162	177	160	181	0	0	0	1	1	80	1	127
HG02582.mapped.ILLUMINA.bwa.GWD.exome.20130415	103	0	3	54	95	92	96	87	113	0	3	0	0	0	0	83	114
HG02583.mapped.ILLUMINA.bwa.GWD.exome.20130415	88	86	84	5	78	76	87	81	93	1	52	69	3	4	38	0	124
HG02585.mapped.ILLUMINA.bwa.GWD.exome.20121211	107	66	61	49	116	93	99	77	98	0	45	67	0	0	34	1	134
HG02586.mapped.ILLUMINA.bwa.GWD.exome.20121211	109	0	1	109	119	105	98	109	114	0	0	1	0	1	0	124	142
HG02588.mapped.ILLUMINA.bwa.GWD.exome.20130415	110	1	1	90	107	100	95	102	124	0	0	0	0	0	30	72	136
HG02589.mapped.ILLUMINA.bwa.GWD.exome.20130415	233	2	8	140	229	166	191	170	178	0	2	2	2	5	74	2	294
HG02594.mapped.ILLUMINA.bwa.GWD.exome.20121211	106	63	63	59	119	97	102	89	119	0	48	71	0	6	0	139	127
HG02595.mapped.ILLUMINA.bwa.GWD.exome.20130415	110	0	61	52	147	104	93	119	125	0	62	0	63	0	35	68	148
HG02597.mapped.ILLUMINA.bwa.PJL.exome.20130415	42	47	44	10	74	73	75	71	78	0	24	41	0	0	0	57	66
HG02600.mapped.ILLUMINA.bwa.PJL.exome.20130415	87	0	0	57	93	92	80	72	0	21	68	0	70	97	0	0	96
HG02601.mapped.ILLUMINA.bwa.PJL.exome.20121211	77	68	83	2	63	62	77	55	88	0	28	61	0	1	0	70	102
HG02603.mapped.ILLUMINA.bwa.PJL.exome.20130415	90	0	0	86	95	92	81	76	88	0	0	0	0	2	0	73	113
HG02604.mapped.ILLUMINA.bwa.PJL.exome.20121211	94	2	1	80	93	88	86	90	72	18	46	0	49	74	27	0	98
HG02610.mapped.ILLUMINA.bwa.GWD.exome.20121211	98	69	70	53	139	112	99	111	127	0	44	0	67	1	35	73	130
HG02611.mapped.ILLUMINA.bwa.GWD.exome.20130415	85	80	84	1	97	86	88	92	96	0	75	86	0	1	32	52	104
HG02613.mapped.ILLUMINA.bwa.GWD.exome.20130415	92	1	60	47	65	83	81	102	76	19	41	0	54	74	33	0	119
HG02614.mapped.ILLUMINA.bwa.GWD.exome.20121211	85	0	0	78	88	88	80	66	82	0	0	0	0	1	32	0	111
HG02620.mapped.ILLUMINA.bwa.GWD.exome.20130415	96	0	1	84	97	87	113	113	119	16	1	0	1	1	30	58	119
HG02621.mapped.ILLUMINA.bwa.GWD.exome.20130415	82	63	1	44	67	65	62	43	76	0	43	0	53	75	23	2	103
HG02623.mapped.ILLUMINA.bwa.GWD.exome.20121211	115	0	3	100	107	115	99	104	118	0	0	0	0	0	28	67	121
HG02624.mapped.ILLUMINA.bwa.GWD.exome.20130415	107	1	66	55	157	115	97	118	114	0	55	0	63	1	32	79	145
HG02628.mapped.ILLUMINA.bwa.GWD.exome.20121211	95	0	0	68	113	85	93	97	75	23	35	0	47	68	32	1	96
HG02629.mapped.ILLUMINA.bwa.GWD.exome.20130415	94	68	62	51	100	92	91	90	94	0	47	61	0	1	48	1	104
HG02634.mapped.ILLUMINA.bwa.GWD.exome.20121211	102	0	2	73	111	115	94	99	114	0	0	0	1	1	0	122	135
HG02635.mapped.ILLUMINA.bwa.GWD.exome.20121211	88	1	0	93	111	84	86	83	99	0	1	2	0	0	29	68	101
HG02642.mapped.ILLUMINA.bwa.GWD.exome.20130415	90	62	63	50	80	74	77	112	111	0	0	0	1	4	34	63	124
HG02643.mapped.ILLUMINA.bwa.GWD.exome.20130415	71	0	1	49	91	70	65	48	69	0	23	35	0	0	29	0	94
HG02645.mapped.ILLUMINA.bwa.GWD.exome.20121211	90	0	1	63	123	91	79	70	94	0	40	62	0	0	41	0	100
HG02646.mapped.ILLUMINA.bwa.GWD.exome.20130415	74	53	45	45	100	79	75	109	105	0	33	55	0	0	20	50	89
HG02648.mapped.ILLUMINA.bwa.PJL.exome.20130415	86	0	0	107	170	161	169	212	207	0	1	0	1	0	0	209	129
HG02649.mapped.ILLUMINA.bwa.PJL.exome.20130415	99	1	0	89	166	164	164	188	130	24	119	0	117	122	0	109	136
HG02651.mapped.ILLUMINA.bwa.PJL.exome.20130415	107	151	135	59	137	133	131	125	131	0	129	0	129	130	58	2	133
HG02652.mapped.ILLUMINA.bwa.PJL.exome.20130415	96	247	137	1	139	124	143	118	120	0	214	128	146	131	0	119	159
HG02654.mapped.ILLUMINA.bwa.PJL.exome.20121211	98	0	2	67	88	85	85	76	2	21	56	0	72	101	0	1	114
HG02655.mapped.ILLUMINA.bwa.PJL.exome.20121211	80	53	1	42	74	70	62	56	0	15	60	1	62	90	0	1	89
HG02657.mapped.ILLUMINA.bwa.PJL.exome.20121211	84	51	52	40	102	70	76	79	82	0	31	56	2	0	21	55	90
HG02658.mapped.ILLUMINA.bwa.PJL.exome.20130415	112	53	54	43	65	71	80	78	57	14	37	0	48	74	0	52	104
HG02660.mapped.ILLUMINA.bwa.PJL.exome.20121211	81	70	72	0	76	70	70	82	73	18	76	70	41	64	20	0	92
HG02661.mapped.ILLUMINA.bwa.PJL.exome.20130415	101	0	1	88	97	83	86	70	95	0	2	0	0	0	0	86	108
HG02666.mapped.ILLUMINA.bwa.GWD.exome.20130415	93	0	56	43	112	109	66	74	88	0	32	0	43	1	34	1	111
HG02667.mapped.ILLUMINA.bwa.GWD.exome.20121211	95	1	0	54	103	93	88	87	90	0	0	2	0	1	38	0	103
HG02675.mapped.ILLUMINA.bwa.GWD.exome.20130415	93	56	63	41	113	85	86	90	110	0	45	66	1	2	31	62	111
HG02676.mapped.ILLUMINA.bwa.GWD.exome.20130415	92	0	1	56	105	87	81	78	91	0	0	0	1	2	37	1	107
HG02678.mapped.ILLUMINA.bwa.GWD.exome.20130415	102	1	1	76	90	86	75	77	88	0	0	2	2	0	37	0	112
HG02679.mapped.ILLUMINA.bwa.GWD.exome.20130415	100	54	55	49	69	84	82	105	107	0	0	0	0	1	31	55	127

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02681.mapped.ILLUMINA.bwa.PJL.exome.20130415	76	1	1	72	158	144	160	168	114	26	91	0	111	109	0	92	104
HG02682.mapped.ILLUMINA.bwa.PJL.exome.20130415	71	119	115	51	108	108	110	98	114	0	101	0	117	115	54	3	100
HG02684.mapped.ILLUMINA.bwa.PJL.exome.20121211	90	87	82	1	76	67	63	51	73	0	62	55	48	72	0	62	105
HG02685.mapped.ILLUMINA.bwa.PJL.exome.20121211	92	2	0	62	84	84	85	75	5	24	64	0	79	89	0	0	99
HG02687.mapped.ILLUMINA.bwa.PJL.exome.20121211	102	72	85	0	72	69	66	57	2	15	68	0	68	93	0	2	106
HG02688.mapped.ILLUMINA.bwa.PJL.exome.20130415	96	46	62	48	63	75	69	85	108	0	0	0	0	0	0	127	118
HG02690.mapped.ILLUMINA.bwa.PJL.exome.20130415	101	0	4	54	154	133	146	151	188	0	0	0	0	1	72	0	109
HG02691.mapped.ILLUMINA.bwa.PJL.exome.20130415	88	124	120	51	203	158	194	199	122	34	168	119	116	100	52	0	101
HG02694.mapped.ILLUMINA.bwa.PJL.exome.20130415	28	45	39	10	67	58	60	54	73	0	29	40	0	2	0	58	50
HG02696.mapped.ILLUMINA.bwa.PJL.exome.20121211	96	57	58	47	132	78	76	66	64	15	47	52	46	64	0	62	104
HG02697.mapped.ILLUMINA.bwa.PJL.exome.20121211	90	81	81	3	83	72	77	72	102	0	39	58	1	1	0	74	119
HG02699.mapped.ILLUMINA.bwa.PJL.exome.20130415	84	0	1	65	154	131	144	163	146	0	1	0	0	1	0	201	109
HG02700.mapped.ILLUMINA.bwa.PJL.exome.20130415	80	160	151	0	1	1	148	204	154	0	0	0	0	0	0	137	104
HG02702.mapped.ILLUMINA.bwa.GWD.exome.20130415	84	0	1	51	74	82	62	53	83	0	0	1	0	2	35	1	97
HG02703.mapped.ILLUMINA.bwa.GWD.exome.20130415	87	0	2	47	67	85	85	68	97	0	1	1	0	0	39	0	107
HG02715.mapped.ILLUMINA.bwa.GWD.exome.20121211	107	68	70	55	142	122	97	96	112	0	59	85	1	2	43	0	124
HG02716.mapped.ILLUMINA.bwa.GWD.exome.20130415	93	0	67	48	85	72	113	104	121	15	0	0	0	0	24	71	122
HG02721.mapped.ILLUMINA.bwa.GWD.exome.20121211	97	58	65	3	76	91	83	71	72	19	67	58	46	74	28	0	107
HG02722.mapped.ILLUMINA.bwa.GWD.exome.20121211	75	43	47	38	61	66	66	71	94	1	0	0	0	1	17	49	103
HG02724.mapped.ILLUMINA.bwa.PJL.exome.20121211	94	85	84	0	105	84	84	88	2	21	91	84	77	127	0	3	119
HG02725.mapped.ILLUMINA.bwa.PJL.exome.20121211	102	0	0	55	91	83	84	80	93	0	1	2	0	0	37	0	103
HG02727.mapped.ILLUMINA.bwa.PJL.exome.20130415	91	83	78	0	80	68	79	84	62	16	70	70	46	78	0	60	95
HG02728.mapped.ILLUMINA.bwa.PJL.exome.20121211	98	79	85	1	107	88	86	101	71	15	72	77	51	75	28	0	105
HG02731.mapped.ILLUMINA.bwa.PJL.exome.20130415	52	77	56	0	83	80	81	68	62	12	59	50	47	45	0	48	66
HG02733.mapped.ILLUMINA.bwa.PJL.exome.20130415	83	96	90	0	86	84	81	80	66	15	80	82	55	75	0	69	107
HG02734.mapped.ILLUMINA.bwa.PJL.exome.20121211	95	63	71	50	75	70	62	59	1	13	64	1	81	95	0	0	112
HG02736.mapped.ILLUMINA.bwa.PJL.exome.20130415	93	116	127	52	124	114	140	208	206	0	1	1	0	1	55	111	120
HG02737.mapped.ILLUMINA.bwa.PJL.exome.20130415	100	148	141	56	250	195	215	189	145	32	215	133	138	142	0	122	138
HG02756.mapped.ILLUMINA.bwa.GWD.exome.20130415	103	1	1	98	113	101	101	85	96	0	0	0	0	0	40	0	122
HG02757.mapped.ILLUMINA.bwa.GWD.exome.20121211	105	0	1	91	99	95	102	85	124	0	0	0	0	1	0	126	149
HG02759.mapped.ILLUMINA.bwa.GWD.exome.20130415	76	124	167	0	160	157	150	186	166	0	172	120	123	0	61	102	107
HG02760.mapped.ILLUMINA.bwa.GWD.exome.20130415	71	1	173	0	111	100	126	104	119	0	142	0	152	115	50	0	109
HG02763.mapped.ILLUMINA.bwa.GWD.exome.20130415	47	79	66	20	90	105	110	110	106	0	55	59	0	3	39	1	57
HG02768.mapped.ILLUMINA.bwa.GWD.exome.20121211	105	0	1	100	156	108	125	121	79	21	83	1	74	90	38	4	130
HG02769.mapped.ILLUMINA.bwa.GWD.exome.20121211	116	72	64	51	76	67	98	126	123	0	0	1	0	2	32	71	124
HG02771.mapped.ILLUMINA.bwa.GWD.exome.20130415	124	0	1	70	118	105	87	88	108	0	1	0	0	0	41	0	126
HG02772.mapped.ILLUMINA.bwa.GWD.exome.20121211	95	54	60	51	78	71	99	69	111	0	2	0	0	0	43	1	123
HG02774.mapped.ILLUMINA.bwa.PJL.exome.20130415	90	120	109	49	122	104	156	188	121	22	111	0	129	109	50	0	118
HG02775.mapped.ILLUMINA.bwa.PJL.exome.20130415	99	169	174	0	166	164	180	155	6	49	287	159	169	171	0	0	112
HG02778.mapped.ILLUMINA.bwa.PJL.exome.20130415	34	2	0	25	67	81	71	84	82	0	1	1	1	3	24	42	61
HG02780.mapped.ILLUMINA.bwa.PJL.exome.20130415	36	38	2	11	67	63	62	56	46	9	29	0	41	47	0	36	54
HG02783.mapped.ILLUMINA.bwa.PJL.exome.20121211	100	74	69	55	117	101	85	94	72	19	69	68	60	74	0	72	112
HG02784.mapped.ILLUMINA.bwa.PJL.exome.20121211	78	69	64	0	53	45	68	52	92	0	34	43	0	1	0	72	88
HG02786.mapped.ILLUMINA.bwa.PJL.exome.20130415	89	58	63	51	113	87	81	85	90	0	45	63	1	1	30	74	112
HG02787.mapped.ILLUMINA.bwa.PJL.exome.20121211	100	56	63	52	153	121	111	115	73	30	88	97	52	75	27	1	109
HG02789.mapped.ILLUMINA.bwa.PJL.exome.20121211	90	56	50	39	89	90	71	72	106	0	33	63	0	1	39	0	90
HG02790.mapped.ILLUMINA.bwa.PJL.exome.20121211	94	74	88	2	104	90	83	70	4	22	90	81	69	91	0	0	109
HG02792.mapped.ILLUMINA.bwa.PJL.exome.20130415	98	135	141	52	118	120	162	170	121	27	133	3	109	115	0	118	114
HG02793.mapped.ILLUMINA.bwa.PJL.exome.20130415	79	136	139	48	215	174	182	200	175	0	111	118	4	0	55	116	114
HG02798.mapped.ILLUMINA.bwa.GWD.exome.20130415	119	2	0	80	143	99	92	102	114	0	49	72	0	2	45	0	141
HG02799.mapped.ILLUMINA.bwa.GWD.exome.20130415	80	1	0	52	109	89	71	88	94	0	0	1	0	1	26	61	114
HG02804.mapped.ILLUMINA.bwa.GWD.exome.20130415	97	74	77	57	110	110	96	87	111	1	53	1	63	0	0	150	142
HG02805.mapped.ILLUMINA.bwa.GWD.exome.20130415	83	1	49	40	54	58	69	59	88	0	0	1	0	0	27	0	101
HG02807.mapped.ILLUMINA.bwa.GWD.exome.20121211	101	1	0	107	132	91	108	97	103	0	0	1	0	1	25	69	145
HG02808.mapped.ILLUMINA.bwa.GWD.exome.20130415	109	87	93	1	131	100	95	78	115	0	71	72	58	2	45	0	136
HG02810.mapped.ILLUMINA.bwa.GWD.exome.20130415	122	0	1	75	116	102	89	125	129	0	0	1	0	1	34	82	141
HG02811.mapped.ILLUMINA.bwa.GWD.exome.20121211	121	59	60	46	119	102	88	100	119	0	45	1	51	1	28	1	95
HG02813.mapped.ILLUMINA.bwa.GWD.exome.20130415	102	145	145	119	207	288	196	165	191	0	0	0	0	0	93	0	152
HG02814.mapped.ILLUMINA.bwa.GWD.exome.20130415	92	1	111	58	214	171	185	228	236	0	116	0	131	0	51	130	131
HG02816.mapped.ILLUMINA.bwa.GWD.exome.20130415	90	1	1	69	151	129	134	127	157	0	0	0	0	0	69	0	128
HG02817.mapped.ILLUMINA.bwa.GWD.exome.20130415	103	0	1	123	223	187	187	228	244	0	0	0	0	0	0	232	129
HG02819.mapped.ILLUMINA.bwa.GWD.exome.20130415	89	3	61	42	68	61	76	79	73	0	4	2	5	7	34	0	92
HG02820.mapped.ILLUMINA.bwa.GWD.exome.20130415	84	0	2	66	91	72	69	57	81	0	0	0	0	0	0	83	93
HG02836.mapped.ILLUMINA.bwa.GWD.exome.20130415	77	0	1	109	201	170	184	143	178	0	1	0	1	0	0	163	124
HG02837.mapped.ILLUMINA.bwa.GWD.exome.20130415	67	0	88	0	90	135	156	132	159	0	94	0	101	0	61	0	106
HG02839.mapped.ILLUMINA.bwa.GWD.exome.20130415	78	124	121	47	125	108	177	133	0	26	108	1	115	127	0	0	80
HG02840.mapped.ILLUMINA.bwa.GWD.exome.20130415	99	149	139	66	138	136	194	236	241	0	3	0	2	4	0	261	144
HG02851.mapped.ILLUMINA.bwa.GWD.exome.20130415	111	3	156	63	139	144	236	274	264	0	0	4	0	0	60	148	150
HG02852.mapped.ILLUMINA.bwa.GWD.exome.20130415	118	146	149	70	271	227	225	261	262	0	132	147	0	1	0	249	146
HG02854.mapped.ILLUMINA.bwa.GWD.exome.20130415	71	67	74	2	57	55	67	90	84	0	34	59	1	1	26	51	85
HG02855.mapped.ILLUMINA.bwa.GWD.exome.20130415	83	52	56	36	92	73	82	99	101	0	43	59	0	5	0	102	85
HG02860.mapped.ILLUMINA.bwa.GWD.exome.20130415	78	0	0	99	167	165	172	188	154	0	0	0	0	0	52	102	115
HG02861.mapped.ILLUMINA.bwa.GWD.exome.20130415	97	3	0	114	204	259	192	166	188	0	2	0	3	2	73	0	115
HG02870.mapped.ILLUMINA.bwa.GWD.exome.20130415	56	2	59	26	68	64	97	85	116	0	53	52	1	2	61	4	91
HG02878.mapped.ILLUMINA.bwa.GWD.exome.20130415	80	0	1	85	174	160	179	168	200	0	0	0	2	0	78	0	120
HG02879.mapped.ILLUMINA.bwa.GWD.exome.20130415	90	0	4	75	198	187	215	162	197	0	0	0	0	0	76	0	135
HG02881.mapped.ILLUMINA.bwa.GWD.exome.20130415	87	144	135	53	250	177	169	163	208	0	109	142	2	0	75	0	131
HG02882.mapped.ILLUMINA.bwa.GWD.exome.20130415	84	131	128	56	133	126	180	198	205	0	0	0	0	0	0	113	94
HG02884.mapped.ILLUMINA.bwa.GWD.exome.20130415	84	0	0	52	76	70	77	81	58	8	54	54	45	60	21	0	77
HG02885.mapped.ILLUMINA.bwa.GWD.exome.20130415	79	1	0	57	82	72	79	100	78	14	0	0	0	0	33	1	78
HG02887.mapped.ILLUMINA.bwa.GWD.exome.20130415	108	0	0	90	206	181	192	175	184	0	0	0	0	0	71	0	155
HG02888.mapped.ILLUMINA.bwa.GWD.exome.20130415	104	0	2	94	220	192	230	200	212	0	0	1	0	1	86	0	140
HG02890.mapped.ILLUMINA.bwa.GWD.exome.20130415	76	44	54	42	69	51	70	91	61	13	35	1	46	60	24	0	93
HG02891.mapped.ILLUMINA.bwa.GWD.exome.20130415	79	2	55	44	78	68	71	85	75	0	37	0	50	2	31	43	93
HG02895.mapped.ILLUMINA.bwa.GWD.exome.20130415	108	141	138	66	279	190	214	222	254	0	127	144	0	0	57	131	143
HG02896.mapped.ILLUMINA.bwa.GWD.exome.20130415	99	5	5	129	238	181	211	168	239	0	0	2	0	0	86	3	127
HG02922.mapped.ILLUMINA.bwa.ESN.exome.20121211	87	4	2	91	89	88	94	92	99	0	0	0	0	1	36	62	115
HG02923.mapped.ILLUMINA.bwa.ESN.exome.20121211	105	1	0	78	106	101	101	78	117	0	0	0	0	1	42	0	129
HG02938.mapped.ILLUMINA.bwa.ESN.exome.20130415	91	191	172	2	173	178	181	186	204	0	168	186	3	0	61	107	120
HG02941.mapped.ILLUMINA.bwa.ESN.exome.20130415	101	123	146	53	242	184	171	201	148	35	187	113	130	140	0	116	129
HG02943.mapped.ILLUMINA.bwa.ESN.exome.20130415	101	3	3	89	121	95	95	110	109	1	2	0	4	6	0	133	110
HG02944.mapped.ILLUMINA.bwa.ESN.exome.20121211	100	64	70	55	139	105	97	93	107	0	37	73	0	0	32	60	144
HG02946.mapped.ILLUMINA.bwa.ESN.exome.20130415	92	0	3	105	214	185	220	204	220	0	0	0	0	1	60	130	130
HG02947.mapped.ILLUMINA.bwa.ESN.exome.20130415	97	0	0	111	198	262	205	189	199	0	0	0	1	0	85	2	138
HG02952.mapped.ILLUMINA.bwa.ESN.exome.20130415	87	1	1	90	211	176	211	222	242	0	0	0	0	0	0	242	137
HG02953.mapped.ILLUMINA.bwa.ESN.exome.20130415	96	0	3	139	256	322	222	186	213	0	0	0	0	0	81	3	157

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02968.mapped.ILLUMINA.bwa.ESN.exome.20130415	89	149	130	51	131	214	162	199	195	0	1	0	0	1	54	100	117
HG02970.mapped.ILLUMINA.bwa.ESN.exome.20130415	95	1	2	83	185	168	192	175	195	0	0	1	0	0	68	0	136
HG02971.mapped.ILLUMINA.bwa.ESN.exome.20130415	88	266	141	1	129	195	187	222	185	1	113	119	0	0	59	112	117
HG02973.mapped.ILLUMINA.bwa.ESN.exome.20121211	118	1	1	68	112	114	92	84	110	0	1	0	0	0	38	0	140
HG02974.mapped.ILLUMINA.bwa.ESN.exome.20121211	93	0	1	70	136	97	86	84	105	0	0	0	0	1	36	1	111
HG02976.mapped.ILLUMINA.bwa.ESN.exome.20130415	104	0	141	65	139	148	204	170	180	0	0	0	1	0	79	0	153
HG02977.mapped.ILLUMINA.bwa.ESN.exome.20130415	106	0	130	65	198	182	198	215	195	0	125	1	135	1	62	121	150
HG02979.mapped.ILLUMINA.bwa.ESN.exome.20130415	99	0	1	78	171	165	177	159	163	0	0	0	1	0	72	4	110
HG02981.mapped.ILLUMINA.bwa.ESN.exome.20130415	88	0	0	102	210	162	173	158	211	0	0	0	0	0	0	161	123
HG02982.mapped.ILLUMINA.bwa.GWD.exome.20130415	96	3	132	62	218	171	159	180	165	0	111	0	117	0	61	106	112
HG02983.mapped.ILLUMINA.bwa.GWD.exome.20130415	95	173	183	2	138	111	182	196	197	0	125	132	2	0	60	112	133
HG03006.mapped.ILLUMINA.bwa.BEB.exome.20130415	86	66	65	49	72	70	91	86	79	18	54	4	65	71	0	61	113
HG03007.mapped.ILLUMINA.bwa.BEB.exome.20130415	79	62	73	41	106	82	91	95	130	12	33	62	3	1	0	73	96
HG03009.mapped.ILLUMINA.bwa.BEB.exome.20130422	75	0	0	67	67	82	80	78	66	24	40	50	0	59	0	53	91
HG03012.mapped.ILLUMINA.bwa.BEB.exome.20130422	80	49	49	38	59	54	76	76	55	13	34	5	49	61	0	50	84
HG03015.mapped.ILLUMINA.bwa.PJL.exome.20130415	81	164	158	0	0	1	118	107	119	0	106	0	120	115	0	90	116
HG03016.mapped.ILLUMINA.bwa.PJL.exome.20130415	96	137	136	58	130	139	185	200	171	0	0	0	0	1	60	112	123
HG03018.mapped.ILLUMINA.bwa.PJL.exome.20130415	41	43	46	16	44	44	84	56	86	0	0	0	0	3	0	62	65
HG03019.mapped.ILLUMINA.bwa.PJL.exome.20130415	37	77	76	1	36	48	80	72	93	0	29	45	0	1	30	33	67
HG03021.mapped.ILLUMINA.bwa.PJL.exome.20130415	33	0	1	22	68	77	80	67	58	4	35	0	46	52	31	1	71
HG03022.mapped.ILLUMINA.bwa.PJL.exome.20130415	28	55	41	0	51	49	80	67	53	16	30	0	42	61	0	46	65
HG03024.mapped.ILLUMINA.bwa.GWD.exome.20130415	79	59	59	35	106	92	73	84	70	13	46	47	43	55	23	1	90
HG03025.mapped.ILLUMINA.bwa.GWD.exome.20130415	83	49	72	2	96	71	72	68	54	16	66	51	61	60	0	1	76
HG03027.mapped.ILLUMINA.bwa.GWD.exome.20130415	107	72	70	54	81	83	118	122	123	0	0	1	0	1	31	74	126
HG03028.mapped.ILLUMINA.bwa.GWD.exome.20130415	103	0	71	62	119	107	87	87	96	0	40	0	52	1	39	0	123
HG03039.mapped.ILLUMINA.bwa.GWD.exome.20130415	84	0	56	49	106	84	84	67	95	0	42	0	40	0	36	0	110
HG03040.mapped.ILLUMINA.bwa.GWD.exome.20130415	104	83	75	62	87	87	97	113	111	0	2	0	0	2	0	138	130
HG03045.mapped.ILLUMINA.bwa.GWD.exome.20130415	98	1	75	2	82	99	80	94	106	0	63	0	55	0	24	59	120
HG03046.mapped.ILLUMINA.bwa.GWD.exome.20121211	102	64	76	49	133	96	90	102	121	0	54	74	1	2	30	63	133
HG03048.mapped.ILLUMINA.bwa.GWD.exome.20121211	85	46	64	39	95	86	77	70	89	0	37	56	0	0	36	0	116
HG03049.mapped.ILLUMINA.bwa.GWD.exome.20130415	100	57	70	48	114	83	89	78	95	0	44	1	47	0	38	2	108
HG03052.mapped.ILLUMINA.bwa.MSL.exome.20121211	106	59	56	53	128	104	98	96	77	21	54	63	46	74	25	1	125
HG03054.mapped.ILLUMINA.bwa.MSL.exome.20130415	86	115	122	118	265	151	176	144	157	0	109	125	1	1	89	0	113
HG03055.mapped.ILLUMINA.bwa.MSL.exome.20130415	114	0	2	92	189	183	219	190	201	0	1	0	1	1	0	190	138
HG03057.mapped.ILLUMINA.bwa.MSL.exome.20121211	119	64	79	54	140	100	101	89	113	0	55	83	0	2	36	0	121
HG03058.mapped.ILLUMINA.bwa.MSL.exome.20121211	81	0	0	56	82	87	81	88	100	0	0	1	0	0	22	49	101
HG03060.mapped.ILLUMINA.bwa.MSL.exome.20130415	97	1	0	86	251	175	176	212	198	0	125	134	0	0	65	111	129
HG03061.mapped.ILLUMINA.bwa.MSL.exome.20130415	89	130	123	55	162	135	157	151	153	0	109	1	121	2	0	124	90
HG03063.mapped.ILLUMINA.bwa.MSL.exome.20130415	76	10	6	94	169	151	159	147	157	0	3	0	1	0	0	144	112
HG03064.mapped.ILLUMINA.bwa.MSL.exome.20130415	88	118	114	45	142	105	167	209	191	0	0	0	0	0	72	3	109
HG03066.mapped.ILLUMINA.bwa.MSL.exome.20130415	75	69	80	3	72	61	82	96	103	0	35	61	2	3	32	61	87
HG03069.mapped.ILLUMINA.bwa.MSL.exome.20130415	84	0	1	72	103	79	82	76	92	1	0	2	3	2	37	0	98
HG03072.mapped.ILLUMINA.bwa.MSL.exome.20130415	79	1	56	40	59	60	67	62	66	0	34	0	51	63	28	1	95
HG03073.mapped.ILLUMINA.bwa.MSL.exome.20130415	106	0	4	78	159	163	250	163	173	0	0	0	0	0	76	2	127
HG03074.mapped.ILLUMINA.bwa.MSL.exome.20130415	95	0	2	107	227	167	178	201	181	0	0	0	0	0	0	120	109
HG03077.mapped.ILLUMINA.bwa.MSL.exome.20130415	97	1	0	76	175	171	193	197	176	1	0	0	0	0	61	108	119
HG03078.mapped.ILLUMINA.bwa.MSL.exome.20121211	110	0	1	74	119	121	91	95	111	0	0	0	0	3	38	79	120
HG03079.mapped.ILLUMINA.bwa.MSL.exome.20130415	78	124	108	54	129	107	160	144	157	0	0	1	0	0	0	1	1
HG03081.mapped.ILLUMINA.bwa.MSL.exome.20130415	86	123	132	52	239	167	249	184	202	29	113	1	148	2	0	102	87
HG03082.mapped.ILLUMINA.bwa.MSL.exome.20130415	97	134	131	67	273	170	188	169	205	0	142	0	132	1	62	117	124
HG03084.mapped.ILLUMINA.bwa.MSL.exome.20121211	113	1	94	0	107	100	108	86	101	0	75	0	78	0	42	1	138
HG03085.mapped.ILLUMINA.bwa.MSL.exome.20121211	105	57	73	47	78	83	67	60	66	0	50	1	52	80	0	64	135
HG03086.mapped.ILLUMINA.bwa.MSL.exome.20130415	43	116	133	0	109	108	125	103	113	0	81	105	1	0	37	74	82
HG03088.mapped.ILLUMINA.bwa.MSL.exome.20130415	88	0	0	77	187	147	187	219	207	0	1	0	0	0	53	117	114
HG03091.mapped.ILLUMINA.bwa.MSL.exome.20130415	80	0	0	78	158	121	143	126	136	0	0	0	0	0	52	106	102
HG03095.mapped.ILLUMINA.bwa.MSL.exome.20130415	90	0	3	90	166	159	160	192	166	0	0	1	0	0	57	106	113
HG03096.mapped.ILLUMINA.bwa.MSL.exome.20121211	102	97	97	3	92	85	76	72	4	20	96	76	85	113	0	0	133
HG03097.mapped.ILLUMINA.bwa.MSL.exome.20121211	118	0	1	70	118	108	96	114	105	0	0	0	0	3	32	2	111
HG03099.mapped.ILLUMINA.bwa.ESN.exome.20121211	109	64	85	1	86	82	108	102	124	0	51	1	62	0	0	100	131
HG03100.mapped.ILLUMINA.bwa.ESN.exome.20121211	99	58	54	55	116	99	96	69	103	0	36	62	0	1	38	0	118
HG03103.mapped.ILLUMINA.bwa.ESN.exome.20130415	102	0	129	0	146	186	188	114	1	0	127	0	137	1	68	0	80
HG03105.mapped.ILLUMINA.bwa.ESN.exome.20130415	100	0	12	74	157	172	198	148	201	0	4	2	7	0	83	0	125
HG03108.mapped.ILLUMINA.bwa.ESN.exome.20121211	103	0	0	82	99	147	91	78	97	0	0	0	0	0	37	0	112
HG03109.mapped.ILLUMINA.bwa.ESN.exome.20121211	98	1	1	106	143	109	84	108	114	0	0	0	1	3	33	72	129
HG03111.mapped.ILLUMINA.bwa.ESN.exome.20130415	112	194	199	1	140	131	199	191	217	0	115	135	0	0	0	223	122
HG03112.mapped.ILLUMINA.bwa.ESN.exome.20130415	110	0	5	125	223	184	202	165	213	0	0	0	0	1	94	1	137
HG03114.mapped.ILLUMINA.bwa.ESN.exome.20121211	113	0	1	69	109	117	99	83	119	0	0	0	0	0	44	1	126
HG03115.mapped.ILLUMINA.bwa.ESN.exome.20121211	107	79	64	55	87	79	79	69	85	0	48	1	60	94	34	0	129
HG03117.mapped.ILLUMINA.bwa.ESN.exome.20130415	81	55	60	35	61	67	76	74	89	0	0	1	1	1	0	96	94
HG03118.mapped.ILLUMINA.bwa.ESN.exome.20130415	84	1	2	64	78	76	77	94	94	0	0	0	1	4	28	53	88
HG03120.mapped.ILLUMINA.bwa.ESN.exome.20121211	98	2	0	67	115	101	89	86	113	0	0	0	0	0	37	0	123
HG03121.mapped.ILLUMINA.bwa.ESN.exome.20121211	106	0	65	54	107	107	99	120	106	0	47	0	63	2	35	0	105
HG03123.mapped.ILLUMINA.bwa.ESN.exome.20121211	87	1	1	77	88	83	88	90	81	0	0	0	0	2	20	1	80
HG03124.mapped.ILLUMINA.bwa.ESN.exome.20121211	80	64	57	42	123	85	83	80	95	0	32	62	3	0	27	64	120
HG03126.mapped.ILLUMINA.bwa.ESN.exome.20130415	116	244	196	1	235	202	206	195	194	0	176	211	0	1	86	0	165
HG03127.mapped.ILLUMINA.bwa.ESN.exome.20130415	110	5	5	144	218	206	245	236	220	0	5	1	0	1	0	139	108
HG03129.mapped.ILLUMINA.bwa.ESN.exome.20130415	82	0	0	59	100	75	68	73	79	0	0	0	0	0	35	0	96
HG03130.mapped.ILLUMINA.bwa.ESN.exome.20130415	80	2	53	32	99	84	74	72	82	0	38	1	45	0	32	0	97
HG03132.mapped.ILLUMINA.bwa.ESN.exome.20130415	95	0	0	79	119	97	85	89	102	0	0	0	0	2	31	59	111
HG03133.mapped.ILLUMINA.bwa.ESN.exome.20121211	112	1	4	88	111	115	105	120	115	0	0	1	1	0	32	0	100
HG03135.mapped.ILLUMINA.bwa.ESN.exome.20121211	89	0	0	78	93	87	84	84	77	15	38	0	40	69	27	0	109
HG03136.mapped.ILLUMINA.bwa.ESN.exome.20130415	92	1	58	47	107	84	76	72	79	0	49	0	51	1	37	2	104
HG03139.mapped.ILLUMINA.bwa.ESN.exome.20130415	105	1	2	127	221	184	230	190	196	0	0	1	2	1	88	0	142
HG03157.mapped.ILLUMINA.bwa.ESN.exome.20130415	104	154	147	72	262	203	217	212	204	0	138	0	139	0	0	130	93
HG03159.mapped.ILLUMINA.bwa.ESN.exome.20130415	79	1	3	64	93	73	66	72	74	0	1	2	1	0	35	0	88
HG03160.mapped.ILLUMINA.bwa.ESN.exome.20130422	88	57	55	1	58	76	76	87	83	0	41	2	48	2	27	50	92
HG03162.mapped.ILLUMINA.bwa.ESN.exome.20130415	86	62	66	41	70	63	71	76	79	0	1	0	5	3	0	98	79
HG03163.mapped.ILLUMINA.bwa.ESN.exome.20130415	83	1	2	51	81	76	66	69	79	0	1	2	0	0	37	2	80
HG03166.mapped.ILLUMINA.bwa.ESN.exome.20130415	103	1	2	139	256	182	200	218	208	0	2	0	1	1	60	128	135
HG03168.mapped.ILLUMINA.bwa.ESN.exome.20130415	73	4	6	50	79	77	77	71	112	0	3	5	0	0	0	62	86
HG03169.mapped.ILLUMINA.bwa.ESN.exome.20130415	81	49	2	30	63	60	51	53	62	0	44	2	51	65	22	2	84
HG03172.mapped.ILLUMINA.bwa.ESN.exome.20130415	80	2	7	50	88	79	72	92	75	0	1	2	1	3	22	46	89
HG03175.mapped.ILLUMINA.bwa.ESN.exome.20130415	101	0	140	68	268	193	206	185	151	0	131	0	140	1	84	0	155
HG03189.mapped.ILLUMINA.bwa.ESN.exome.20130415	106	0	156	67	248	205	231	179	239	0	142	0	161	2	89	0	150
HG03190.mapped.ILLUMINA.bwa.ESN.exome.20130415	107	0	4	131	234	201	212	212	234	0	1	0	0	1	88	0	164
HG03193.mapped.ILLUMINA.bwa.ESN.exome.20130415	102	2	1	135	236	195	216	178	226	0	1	1	1	2	91	2	137

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG03195.mapped.ILLUMINA.bwa.ESN.exome.20130415	87	0	0	46	84	76	77	78	74	1	1	2	0	3	30	3	85
HG03196.mapped.ILLUMINA.bwa.ESN.exome.20130415	79	2	0	49	87	87	76	92	98	0	0	0	0	0	0	101	93
HG03198.mapped.ILLUMINA.bwa.ESN.exome.20130415	78	77	69	2	2	3	70	85	73	0	0	0	0	1	0	97	93
HG03199.mapped.ILLUMINA.bwa.ESN.exome.20130415	79	53	53	40	104	19	59	68	0	0	44	56	0	0	27	0	68
HG03202.mapped.ILLUMINA.bwa.ESN.exome.20130415	78	128	130	57	128	134	185	200	195	0	0	0	0	1	58	109	125
HG03209.mapped.ILLUMINA.bwa.MSL.exome.20130415	93	131	131	69	173	151	189	151	181	0	162	169	0	1	72	0	116
HG03212.mapped.ILLUMINA.bwa.MSL.exome.20130415	92	0	1	114	237	178	189	221	209	0	1	0	0	0	0	238	136
HG03224.mapped.ILLUMINA.bwa.MSL.exome.20130415	113	140	134	58	241	185	190	165	231	0	117	135	1	1	68	0	137
HG03225.mapped.ILLUMINA.bwa.MSL.exome.20130415	108	0	1	93	202	205	194	179	238	1	0	1	0	0	77	0	148
HG03228.mapped.ILLUMINA.bwa.PJL.exome.20130415	77	1	1	117	165	164	189	157	2	32	157	0	177	165	0	0	132
HG03229.mapped.ILLUMINA.bwa.PJL.exome.20130415	109	126	134	54	118	128	188	217	230	0	1	0	2	2	48	122	135
HG03234.mapped.ILLUMINA.bwa.PJL.exome.20130415	101	192	182	1	206	186	201	178	141	24	220	252	3	141	0	126	128
HG03235.mapped.ILLUMINA.bwa.PJL.exome.20130415	109	1	0	79	177	175	198	167	137	29	131	1	135	127	0	127	121
HG03237.mapped.ILLUMINA.bwa.PJL.exome.20130415	104	216	190	0	4	5	156	123	161	0	132	2	153	149	0	119	148
HG03238.mapped.ILLUMINA.bwa.PJL.exome.20130415	102	257	188	0	136	125	233	197	212	35	118	142	3	0	0	176	125
HG03240.mapped.ILLUMINA.bwa.GWD.exome.20130415	78	1	2	61	85	90	75	67	80	0	0	3	0	1	31	0	96
HG03241.mapped.ILLUMINA.bwa.GWD.exome.20130415	79	0	0	73	109	76	80	93	73	0	0	0	0	0	22	46	85
HG03246.mapped.ILLUMINA.bwa.GWD.exome.20130415	72	0	1	58	95	76	69	90	82	0	0	0	0	0	25	2	72
HG03247.mapped.ILLUMINA.bwa.GWD.exome.20130415	79	50	56	34	101	72	73	78	107	0	39	1	50	1	0	40	72
HG03258.mapped.ILLUMINA.bwa.GWD.exome.20130415	113	0	69	60	98	75	98	109	126	0	0	0	0	1	25	74	149
HG03259.mapped.ILLUMINA.bwa.GWD.exome.20130415	102	54	63	53	135	96	98	67	103	0	44	71	0	1	37	1	127
HG03265.mapped.ILLUMINA.bwa.ESN.exome.20130415	90	146	154	67	235	192	206	260	227	0	118	139	2	2	54	122	142
HG03267.mapped.ILLUMINA.bwa.ESN.exome.20130415	99	0	3	122	171	262	182	163	194	0	0	0	0	0	74	1	133
HG03268.mapped.ILLUMINA.bwa.ESN.exome.20130415	100	2	1	125	179	196	187	242	201	0	0	0	1	1	62	0	95
HG03270.mapped.ILLUMINA.bwa.ESN.exome.20130415	92	190	118	7	156	141	134	118	17	30	265	137	157	204	0	0	122
HG03271.mapped.ILLUMINA.bwa.ESN.exome.20130415	100	143	129	67	237	223	191	213	145	22	193	122	150	137	55	2	125
HG03279.mapped.ILLUMINA.bwa.ESN.exome.20130415	91	1	2	86	185	158	184	167	182	0	1	0	0	0	73	1	137
HG03280.mapped.ILLUMINA.bwa.ESN.exome.20130415	89	1	3	103	177	166	172	201	201	0	0	1	0	1	59	108	121
HG03291.mapped.ILLUMINA.bwa.ESN.exome.20130415	71	122	117	57	117	120	163	142	205	0	0	0	0	2	0	158	109
HG03294.mapped.ILLUMINA.bwa.ESN.exome.20130415	82	0	122	47	126	123	123	113	123	0	125	0	115	133	0	117	118
HG03295.mapped.ILLUMINA.bwa.ESN.exome.20130415	93	4	135	58	242	258	207	177	171	0	140	0	124	6	80	3	137
HG03297.mapped.ILLUMINA.bwa.ESN.exome.20130415	109	1	2	96	208	206	243	182	242	0	0	1	0	1	84	0	166
HG03298.mapped.ILLUMINA.bwa.ESN.exome.20130415	106	1	2	101	232	211	238	253	306	0	1	0	0	1	70	152	154
HG03300.mapped.ILLUMINA.bwa.ESN.exome.20130415	102	177	179	0	1	2	129	123	129	0	138	0	132	132	0	124	129
HG03301.mapped.ILLUMINA.bwa.ESN.exome.20130415	87	141	111	60	111	102	165	190	195	0	1	3	0	0	0	216	111
HG03303.mapped.ILLUMINA.bwa.ESN.exome.20130415	97	1	136	63	138	132	219	250	235	0	3	1	0	1	62	117	148
HG03304.mapped.ILLUMINA.bwa.ESN.exome.20130415	93	0	0	72	229	153	185	143	215	0	0	0	0	0	83	4	114
HG03311.mapped.ILLUMINA.bwa.ESN.exome.20130415	40	60	39	16	58	67	98	89	108	0	0	0	1	1	0	95	70
HG03313.mapped.ILLUMINA.bwa.ESN.exome.20130415	54	3	2	26	118	106	106	90	122	0	0	2	1	0	0	93	83
HG03342.mapped.ILLUMINA.bwa.ESN.exome.20130415	84	0	1	52	106	74	75	76	92	0	0	0	0	1	33	2	86
HG03343.mapped.ILLUMINA.bwa.ESN.exome.20130415	75	53	66	43	123	82	82	91	110	0	45	4	50	2	25	61	92
HG03351.mapped.ILLUMINA.bwa.ESN.exome.20130415	57	73	67	25	74	79	109	90	119	0	0	0	0	1	54	2	94
HG03352.mapped.ILLUMINA.bwa.ESN.exome.20130415	53	71	67	16	121	131	106	95	137	0	54	0	63	3	28	59	93
HG03354.mapped.ILLUMINA.bwa.ESN.exome.20130415	76	1	1	75	162	147	174	159	226	0	0	0	0	0	0	170	112
HG03363.mapped.ILLUMINA.bwa.ESN.exome.20130415	43	47	48	16	54	50	88	85	109	0	0	1	0	1	30	48	62
HG03366.mapped.ILLUMINA.bwa.ESN.exome.20130415	92	120	118	59	183	169	170	200	166	0	102	102	0	0	0	233	124
HG03367.mapped.ILLUMINA.bwa.ESN.exome.20130415	88	180	138	1	113	130	146	130	152	0	182	3	193	125	0	119	147
HG03369.mapped.ILLUMINA.bwa.ESN.exome.20130415	45	42	51	13	85	103	86	71	92	0	23	50	1	0	44	1	55
HG03370.mapped.ILLUMINA.bwa.ESN.exome.20130415	40	1	2	28	92	94	97	75	120	0	2	0	0	3	48	4	70
HG03372.mapped.ILLUMINA.bwa.ESN.exome.20130415	45	2	1	21	74	104	68	66	90	0	0	1	0	0	44	2	58
HG03376.mapped.ILLUMINA.bwa.MSL.exome.20130415	96	140	1	62	140	128	153	138	139	0	118	1	141	117	62	0	129
HG03378.mapped.ILLUMINA.bwa.MSL.exome.20130415	113	1	5	96	211	195	195	208	231	0	1	0	0	0	96	0	144
HG03380.mapped.ILLUMINA.bwa.MSL.exome.20130415	99	202	190	0	185	189	176	163	209	0	187	188	0	0	83	2	152
HG03382.mapped.ILLUMINA.bwa.MSL.exome.20130415	108	0	0	133	241	191	214	188	231	0	0	0	0	0	90	0	149
HG03385.mapped.ILLUMINA.bwa.MSL.exome.20130415	84	7	3	100	210	170	182	208	224	0	106	107	0	0	57	117	126
HG03388.mapped.ILLUMINA.bwa.MSL.exome.20130415	101	143	135	52	238	174	228	158	215	0	113	124	2	2	76	2	130
HG03391.mapped.ILLUMINA.bwa.MSL.exome.20130415	78	65	72	2	62	61	66	87	82	1	36	4	41	0	33	2	79
HG03394.mapped.ILLUMINA.bwa.MSL.exome.20130415	43	2	1	23	73	74	86	65	109	0	1	0	1	0	48	1	74
HG03397.mapped.ILLUMINA.bwa.MSL.exome.20121211	93	1	3	70	91	99	100	114	123	0	1	2	2	1	30	68	133
HG03401.mapped.ILLUMINA.bwa.MSL.exome.20130415	76	0	0	96	200	141	156	179	190	0	0	0	0	0	76	97	102
HG03410.mapped.ILLUMINA.bwa.MSL.exome.20130415	97	0	2	139	192	194	193	194	223	0	0	2	0	1	92	0	126
HG03419.mapped.ILLUMINA.bwa.MSL.exome.20130415	84	142	122	58	243	188	221	238	180	34	118	1	126	2	59	106	132
HG03428.mapped.ILLUMINA.bwa.MSL.exome.20130415	99	147	135	69	200	221	183	187	156	28	206	151	126	125	0	126	121
HG03432.mapped.ILLUMINA.bwa.MSL.exome.20130415	44	78	67	0	71	77	87	69	100	0	68	51	43	1	0	0	1
HG03433.mapped.ILLUMINA.bwa.MSL.exome.20130415	91	0	0	81	200	152	167	204	187	0	0	0	0	0	74	122	130
HG03436.mapped.ILLUMINA.bwa.MSL.exome.20130415	83	53	56	41	105	80	73	88	85	0	39	59	0	0	27	50	90
HG03437.mapped.ILLUMINA.bwa.MSL.exome.20130415	87	1	61	32	85	76	71	60	77	0	40	3	41	0	35	0	94
HG03439.mapped.ILLUMINA.bwa.MSL.exome.20130415	75	1	0	117	170	156	162	197	166	0	1	1	0	1	56	97	120
HG03442.mapped.ILLUMINA.bwa.MSL.exome.20130415	86	189	159	1	0	0	125	121	143	0	115	0	119	127	62	0	104
HG03445.mapped.ILLUMINA.bwa.MSL.exome.20130415	110	172	181	2	123	129	183	226	256	0	126	0	130	4	67	124	134
HG03446.mapped.ILLUMINA.bwa.MSL.exome.20130415	99	143	126	62	146	128	193	223	234	0	0	0	0	0	0	251	132
HG03449.mapped.ILLUMINA.bwa.MSL.exome.20130415	95	5	5	81	223	168	190	178	225	0	120	133	0	2	74	4	127
HG03451.mapped.ILLUMINA.bwa.MSL.exome.20121211	103	59	67	54	126	105	87	92	112	0	42	63	0	1	32	57	121
HG03452.mapped.ILLUMINA.bwa.MSL.exome.20130415	94	2	57	40	110	118	75	80	96	0	31	0	42	0	36	1	107
HG03455.mapped.ILLUMINA.bwa.MSL.exome.20130415	82	0	4	63	77	71	72	82	86	0	1	0	1	7	27	46	86
HG03457.mapped.ILLUMINA.bwa.MSL.exome.20130415	62	102	109	1	80	60	73	60	80	0	84	69	78	72	0	44	86
HG03458.mapped.ILLUMINA.bwa.MSL.exome.20130415	86	48	55	38	62	55	64	51	63	0	38	0	49	56	21	1	100
HG03460.mapped.ILLUMINA.bwa.MSL.exome.20130415	115	139	130	61	173	167	205	167	213	0	209	135	124	3	77	2	139
HG03461.mapped.ILLUMINA.bwa.MSL.exome.20130415	100	2	148	69	130	124	153	112	147	0	126	1	142	131	0	132	122
HG03464.mapped.ILLUMINA.bwa.MSL.exome.20121211	107	0	2	96	111	119	113	127	125	16	0	1	1	3	33	65	137
HG03469.mapped.ILLUMINA.bwa.MSL.exome.20121211	129	63	63	51	118	114	101	80	116	0	53	68	1	3	37	1	132
HG03470.mapped.ILLUMINA.bwa.MSL.exome.20130415	98	124	139	53	124	125	160	209	188	0	0	0	0	1	60	0	84
HG03472.mapped.ILLUMINA.bwa.MSL.exome.20121211	94	53	55	46	68	59	83	100	107	0	0	0	0	1	28	60	106
HG03473.mapped.ILLUMINA.bwa.MSL.exome.20130415	95	5	0	82	171	145	186	156	181	1	0	0	0	0	75	1	122
HG03476.mapped.ILLUMINA.bwa.MSL.exome.20130415	79	0	0	53	83	85	75	65	85	0	0	0	1	0	33	1	89
HG03478.mapped.ILLUMINA.bwa.MSL.exome.20130415	102	0	6	88	171	184	207	221	196	0	0	1	3	1	63	1	101
HG03479.mapped.ILLUMINA.bwa.MSL.exome.20130415	90	155	176	1	127	121	130	111	127	0	188	126	124	116	58	0	112
HG03484.mapped.ILLUMINA.bwa.MSL.exome.20130415	88	3	9	44	80	80	75	92	85	0	1	3	0	1	31	5	89
HG03485.mapped.ILLUMINA.bwa.MSL.exome.20130415	80	45	61	38	94	76	77	88	92	0	43	1	49	3	30	1	65
HG03488.mapped.ILLUMINA.bwa.PJL.exome.20130422	140	105	109	1	10	5	122	100	95	17	47	0	52	86	0	80	150
HG03490.mapped.ILLUMINA.bwa.PJL.exome.20130415	52	0	0	34	85	87	96	83	100	0	0	0	1	0	0	81	68
HG03491.mapped.ILLUMINA.bwa.PJL.exome.20130415	44	1	0	27	72	91	92	80	97	1	1	0	2	1	0	75	72
HG03499.mapped.ILLUMINA.bwa.ESN.exome.20130415	48	49	55	22	97	85	102	94	100	1	30	53	1	1	30	47	71
HG03511.mapped.ILLUMINA.bwa.ESN.exome.20130415	56	0	2	28	96	95	100	117	94	0	0	0	0	0	31	2	55
HG03514.mapped.ILLUMINA.bwa.ESN.exome.20130415	95	136	203	3	242	159	182	205	178	1	204	129	135	1	60	113	133
HG03515.mapped.ILLUMINA.bwa.ESN.exome.20130415	84	0	0	102	187	190	180	187	186	0	0	3	1	0	0	180	129

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG03517.mapped.ILLUMINA.bwa.ESN.exome.20130415	51	165	120	3	65	75	105	116	77	15	87	70	67	84	0	47	82
HG03518.mapped.ILLUMINA.bwa.ESN.exome.20130415	50	0	2	25	78	81	94	70	90	0	0	0	0	1	0	79	63
HG03520.mapped.ILLUMINA.bwa.ESN.exome.20130415	82	8	5	64	92	80	80	73	84	0	0	1	0	0	32	7	96
HG03521.mapped.ILLUMINA.bwa.ESN.exome.20130415	77	0	66	39	79	90	74	67	84	0	38	0	53	0	35	0	105
HG03538.mapped.ILLUMINA.bwa.GWD.exome.20130415	84	45	58	40	102	78	74	73	77	0	41	49	1	1	37	0	93
HG03539.mapped.ILLUMINA.bwa.GWD.exome.20130415	79	55	64	42	61	54	101	69	97	0	0	0	0	0	0	62	80
HG03547.mapped.ILLUMINA.bwa.MSL.exome.20130415	85	58	58	42	94	84	88	74	74	0	41	51	0	0	32	0	95
HG03548.mapped.ILLUMINA.bwa.MSL.exome.20130415	84	5	3	47	84	76	89	72	87	0	2	0	3	2	34	2	89
HG03556.mapped.ILLUMINA.bwa.MSL.exome.20130415	88	2	0	57	85	82	80	101	84	0	0	0	0	0	31	70	103
HG03557.mapped.ILLUMINA.bwa.MSL.exome.20130415	89	4	77	0	59	57	76	83	84	0	47	1	46	0	26	57	91
HG03558.mapped.ILLUMINA.bwa.MSL.exome.20130415	54	4	2	27	80	70	85	99	104	8	0	0	0	0	28	35	71
HG03559.mapped.ILLUMINA.bwa.MSL.exome.20130415	40	59	48	17	83	73	77	76	88	0	31	44	2	1	28	42	68
HG03563.mapped.ILLUMINA.bwa.MSL.exome.20130422	70	60	63	42	117	74	71	89	87	0	41	0	59	0	33	3	86
HG03565.mapped.ILLUMINA.bwa.MSL.exome.20130415	50	1	0	27	89	76	95	89	106	0	0	0	0	1	30	43	65
HG03567.mapped.ILLUMINA.bwa.MSL.exome.20130415	36	1	2	20	81	77	80	86	61	12	35	1	39	53	28	1	68
HG03571.mapped.ILLUMINA.bwa.MSL.exome.20130415	83	4	3	78	169	159	171	159	165	0	0	1	0	1	72	1	123
HG03572.mapped.ILLUMINA.bwa.MSL.exome.20130415	82	1	56	36	63	56	54	42	60	0	34	3	46	55	0	4	68
HG03575.mapped.ILLUMINA.bwa.MSL.exome.20130415	84	59	56	35	98	78	72	76	78	1	36	3	52	0	26	59	91
HG03577.mapped.ILLUMINA.bwa.MSL.exome.20130415	89	2	2	87	91	88	85	115	99	0	50	65	0	0	30	67	93
HG03578.mapped.ILLUMINA.bwa.MSL.exome.20130415	82	52	58	30	102	77	79	80	88	0	32	51	0	0	26	57	85
HG03583.mapped.ILLUMINA.bwa.MSL.exome.20130415	69	0	53	36	89	78	71	63	77	0	27	1	46	2	37	1	80
HG03585.mapped.ILLUMINA.bwa.BEB.exome.20130422	77	41	54	27	53	54	70	70	80	0	0	0	0	0	28	50	86
HG03589.mapped.ILLUMINA.bwa.BEB.exome.20130422	68	46	50	37	61	59	75	73	64	16	47	0	44	61	0	43	84
HG03593.mapped.ILLUMINA.bwa.BEB.exome.20130422	108	60	55	48	105	84	82	87	54	22	82	57	45	63	0	44	85
HG03594.mapped.ILLUMINA.bwa.BEB.exome.20130415	89	186	174	0	128	132	173	159	122	24	157	180	0	126	0	118	132
HG03595.mapped.ILLUMINA.bwa.BEB.exome.20130415	118	196	196	1	141	147	160	143	145	0	229	160	143	135	63	0	137
HG03598.mapped.ILLUMINA.bwa.BEB.exome.20130415	43	67	40	0	68	81	99	72	54	12	40	37	35	41	0	35	57
HG03600.mapped.ILLUMINA.bwa.BEB.exome.20130415	65	109	100	45	187	128	128	140	198	1	93	110	3	0	0	129	112
HG03603.mapped.ILLUMINA.bwa.BEB.exome.20130415	105	192	189	2	210	185	207	229	203	0	179	199	0	1	66	129	150
HG03604.mapped.ILLUMINA.bwa.BEB.exome.20130415	92	10	13	88	194	178	167	220	151	23	129	12	134	129	56	1	117
HG03607.mapped.ILLUMINA.bwa.BEB.exome.20130415	95	133	125	64	214	169	175	194	166	0	113	118	2	4	58	111	112
HG03611.mapped.ILLUMINA.bwa.BEB.exome.20130415	94	1	3	88	164	170	156	207	184	0	1	0	1	2	64	115	121
HG03615.mapped.ILLUMINA.bwa.BEB.exome.20130415	87	62	62	44	64	66	65	63	68	1	46	0	57	73	33	1	100
HG03616.mapped.ILLUMINA.bwa.BEB.exome.20130415	98	65	54	47	73	66	80	83	96	0	0	0	0	0	0	115	101
HG03619.mapped.ILLUMINA.bwa.PJL.exome.20130415	132	264	265	0	0	1	181	153	180	0	148	0	195	154	0	156	172
HG03624.mapped.ILLUMINA.bwa.PJL.exome.20130415	57	2	2	29	87	100	100	91	82	13	46	1	66	64	0	61	77
HG03625.mapped.ILLUMINA.bwa.PJL.exome.20130415	45	2	1	21	86	85	79	72	107	1	3	0	5	2	0	64	68
HG03629.mapped.ILLUMINA.bwa.PJL.exome.20130415	64	98	1	19	122	69	73	59	69	0	51	67	1	75	0	58	84
HG03631.mapped.ILLUMINA.bwa.PJL.exome.20130415	43	66	54	15	103	85	80	78	63	12	70	80	0	59	0	48	62
HG03634.mapped.ILLUMINA.bwa.PJL.exome.20130415	91	2	4	139	209	199	226	179	221	0	3	1	0	2	0	192	166
HG03636.mapped.ILLUMINA.bwa.PJL.exome.20130415	49	60	40	10	59	59	84	69	96	0	0	0	1	3	53	1	66
HG03640.mapped.ILLUMINA.bwa.PJL.exome.20130415	47	49	2	26	74	69	93	73	62	10	40	3	41	50	0	38	56
HG03642.mapped.ILLUMINA.bwa.STU.exome.20130415	83	55	67	42	97	76	73	75	62	11	65	54	54	63	0	65	94
HG03643.mapped.ILLUMINA.bwa.STU.exome.20130415	94	2	3	54	91	79	81	96	93	1	5	1	3	3	0	81	93
HG03644.mapped.ILLUMINA.bwa.STU.exome.20130415	90	63	65	42	122	96	91	88	108	22	67	77	0	0	0	85	154
HG03645.mapped.ILLUMINA.bwa.STU.exome.20130415	81	169	153	1	157	151	158	137	4	36	251	166	154	165	0	0	108
HG03646.mapped.ILLUMINA.bwa.STU.exome.20130415	98	152	121	57	254	175	199	162	145	35	167	179	1	130	0	130	116
HG03649.mapped.ILLUMINA.bwa.PJL.exome.20130415	43	74	74	0	76	84	85	87	91	0	53	75	0	2	27	35	65
HG03652.mapped.ILLUMINA.bwa.PJL.exome.20130415	39	87	82	0	4	4	67	43	68	0	35	45	0	49	33	1	76
HG03653.mapped.ILLUMINA.bwa.PJL.exome.20130415	34	3	0	22	75	77	73	55	91	0	2	1	0	0	25	40	62
HG03660.mapped.ILLUMINA.bwa.PJL.exome.20130422	131	67	78	63	91	84	81	69	93	0	52	2	56	81	0	73	156
HG03663.mapped.ILLUMINA.bwa.PJL.exome.20130422	141	105	113	2	97	83	82	71	99	0	93	82	72	97	0	73	154
HG03667.mapped.ILLUMINA.bwa.PJL.exome.20130415	104	215	206	1	226	199	212	233	153	36	258	222	145	143	78	0	140
HG03668.mapped.ILLUMINA.bwa.PJL.exome.20130415	108	169	153	77	273	211	215	208	236	0	119	141	0	0	80	2	128
HG03672.mapped.ILLUMINA.bwa.STU.exome.20130415	104	151	132	56	134	149	186	178	198	0	0	1	0	2	0	184	125
HG03673.mapped.ILLUMINA.bwa.STU.exome.20130422	86	52	62	43	101	73	85	80	56	18	57	55	48	64	0	63	96
HG03679.mapped.ILLUMINA.bwa.STU.exome.20130422	105	3	2	57	81	94	87	123	108	0	0	0	2	2	22	60	103
HG03680.mapped.ILLUMINA.bwa.STU.exome.20130415	85	6	3	59	84	83	79	100	100	0	1	1	0	2	28	61	103
HG03681.mapped.ILLUMINA.bwa.STU.exome.20130415	114	67	62	42	114	83	76	74	88	2	29	55	1	4	0	78	105
HG03684.mapped.ILLUMINA.bwa.STU.exome.20130415	88	47	63	33	66	57	61	51	3	15	58	0	67	82	0	1	98
HG03685.mapped.ILLUMINA.bwa.STU.exome.20130415	93	64	67	37	64	61	85	95	77	14	53	0	66	73	0	51	95
HG03686.mapped.ILLUMINA.bwa.STU.exome.20130415	121	2	0	116	197	174	219	238	188	1	2	3	1	3	62	135	128
HG03687.mapped.ILLUMINA.bwa.STU.exome.20130415	101	206	185	0	161	132	207	161	2	47	255	138	198	205	0	0	132
HG03689.mapped.ILLUMINA.bwa.STU.exome.20130415	108	197	186	0	128	133	207	217	134	27	209	149	130	131	65	0	141
HG03690.mapped.ILLUMINA.bwa.STU.exome.20130415	111	156	156	73	278	200	206	244	223	0	140	144	0	0	72	115	149
HG03691.mapped.ILLUMINA.bwa.STU.exome.20130415	102	148	123	63	131	115	198	220	184	1	0	0	2	0	0	253	127
HG03692.mapped.ILLUMINA.bwa.STU.exome.20130422	94	58	68	41	70	65	76	85	101	0	0	0	4	3	22	57	95
HG03693.mapped.ILLUMINA.bwa.STU.exome.20130415	96	0	0	75	78	82	83	89	98	0	3	0	2	3	0	76	103
HG03694.mapped.ILLUMINA.bwa.STU.exome.20130415	102	161	150	68	150	142	233	204	2	45	231	152	152	205	0	0	156
HG03695.mapped.ILLUMINA.bwa.STU.exome.20130415	105	2	1	74	166	164	171	227	215	0	0	0	1	0	0	221	105
HG03696.mapped.ILLUMINA.bwa.STU.exome.20130415	95	0	0	75	171	170	162	149	191	0	0	0	0	2	0	148	124
HG03697.mapped.ILLUMINA.bwa.STU.exome.20130415	84	191	184	1	124	126	187	190	132	26	181	138	150	141	0	101	134
HG03698.mapped.ILLUMINA.bwa.STU.exome.20130415	84	9	11	91	187	176	189	192	218	3	13	8	5	10	55	104	134
HG03702.mapped.ILLUMINA.bwa.PJL.exome.20130415	67	0	0	65	156	136	145	137	99	24	93	0	110	100	0	81	107
HG03703.mapped.ILLUMINA.bwa.PJL.exome.20130415	75	170	118	46	112	106	165	172	157	0	2	0	0	2	54	99	115
HG03705.mapped.ILLUMINA.bwa.PJL.exome.20130415	43	60	54	19	94	89	84	86	68	5	60	42	39	48	24	4	63
HG03706.mapped.ILLUMINA.bwa.PJL.exome.20130415	39	61	1	23	111	85	83	80	73	9	43	0	53	68	0	49	83
HG03708.mapped.ILLUMINA.bwa.PJL.exome.20130415	97	125	131	55	250	180	206	171	157	27	193	136	131	131	56	1	114
HG03709.mapped.ILLUMINA.bwa.PJL.exome.20130415	93	3	1	73	196	188	180	221	128	27	123	2	153	129	53	2	136
HG03711.mapped.ILLUMINA.bwa.STU.exome.20130415	115	219	245	3	244	203	247	196	159	33	249	280	1	156	0	137	157
HG03713.mapped.ILLUMINA.bwa.ITU.exome.20130415	96	2	8	57	99	94	88	103	105	0	0	1	0	4	0	87	121
HG03714.mapped.ILLUMINA.bwa.ITU.exome.20130415	87	0	4	79	88	73	75	77	71	15	38	1	54	57	0	64	104
HG03715.mapped.ILLUMINA.bwa.ITU.exome.20130415	84	1	1	69	86	91	81	90	62	20	43	3	52	67	0	58	96
HG03716.mapped.ILLUMINA.bwa.ITU.exome.20130415	94	81	89	3	60	68	63	54	8	15	76	77	55	92	0	4	95
HG03717.mapped.ILLUMINA.bwa.ITU.exome.20130422	83	65	56	46	56	71	79	115	100	0	0	1	1	0	0	103	90
HG03718.mapped.ILLUMINA.bwa.ITU.exome.20130415	43	84	73	0	3	6	55	39	62	0	33	0	44	57	0	51	61
HG03720.mapped.ILLUMINA.bwa.ITU.exome.20130415	128	63	73	50	123	108	115	113	122	0	40	73	1	1	24	54	152
HG03722.mapped.ILLUMINA.bwa.ITU.exome.20130415	87	0	0	52	84	81	81	83	89	0	0	0	0	1	34	6	107
HG03727.mapped.ILLUMINA.bwa.ITU.exome.20130415	90	57	64	47	63	71	57	51	3	14	63	0	78	78	0	1	94
HG03729.mapped.ILLUMINA.bwa.ITU.exome.20130415	101	6	3	76	89	78	91	94	103	0	4	7	0	6	0	114	101
HG03730.mapped.ILLUMINA.bwa.ITU.exome.20130415	80	0	1	47	82	89	69	69	86	0	0	0	0	0	0	75	93
HG03731.mapped.ILLUMINA.bwa.ITU.exome.20130415	77	55	52	37	64	56	74	84	63	12	38	0	51	65	21	0	93
HG03733.mapped.ILLUMINA.bwa.STU.exome.20130415	125	3	2	100	225	223	244	275	252	0	2	2	0	1	69	143	154
HG03736.mapped.ILLUMINA.bwa.STU.exome.20130415	119	0	1	118	229	238	258	256	223	0	0	1	0	0	0	207	157
HG03738.mapped.ILLUMINA.bwa.STU.exome.20130415	99	149	154	61	145	119	204	202	149	31	114	0	142	135	0	116	147
HG03740.mapped.ILLUMINA.bwa.STU.exome.20130415	81	53	58	40	62	60	79	72	63	17	33	0	48	63	0	58	87

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG03741.mapped.ILLUMINA.bwa.STU.exome.20130422	87	63	66	25	108	76	80	97	98	1	34	72	0	3	29	62	100
HG03742.mapped.ILLUMINA.bwa.ITU.exome.20130415	76	118	111	57	105	114	108	91	122	0	87	1	116	120	50	1	106
HG03743.mapped.ILLUMINA.bwa.STU.exome.20130415	90	0	2	47	86	80	93	89	0	21	55	82	6	91	0	1	95
HG03744.mapped.ILLUMINA.bwa.STU.exome.20130415	76	186	115	0	172	167	188	163	173	0	101	116	0	0	47	102	104
HG03745.mapped.ILLUMINA.bwa.STU.exome.20130415	96	141	130	73	259	205	209	218	141	31	166	198	0	132	0	116	138
HG03746.mapped.ILLUMINA.bwa.STU.exome.20130415	89	53	65	44	61	59	59	41	74	0	33	0	54	68	0	48	101
HG03750.mapped.ILLUMINA.bwa.STU.exome.20130415	91	51	64	38	102	77	80	88	90	0	35	55	1	3	0	95	97
HG03752.mapped.ILLUMINA.bwa.STU.exome.20130415	102	216	214	0	151	151	236	226	173	32	232	162	158	140	0	147	150
HG03753.mapped.ILLUMINA.bwa.STU.exome.20130415	113	227	218	1	257	224	241	268	181	33	293	233	170	161	69	4	166
HG03754.mapped.ILLUMINA.bwa.STU.exome.20130415	84	3	4	74	76	76	71	79	89	0	0	0	0	0	0	94	99
HG03755.mapped.ILLUMINA.bwa.STU.exome.20130415	135	114	106	0	88	83	73	67	6	20	94	130	94	125	0	3	154
HG03756.mapped.ILLUMINA.bwa.STU.exome.20130415	129	85	86	3	102	92	88	116	88	17	89	85	61	69	31	0	115
HG03757.mapped.ILLUMINA.bwa.STU.exome.20130422	91	69	65	47	119	88	73	85	96	1	50	63	0	0	37	9	107
HG03760.mapped.ILLUMINA.bwa.STU.exome.20130415	102	208	187	3	229	230	223	214	134	32	187	255	1	0	0	117	99
HG03762.mapped.ILLUMINA.bwa.PJL.exome.20130415	32	2	0	19	82	78	74	65	111	0	1	1	2	0	0	73	73
HG03765.mapped.ILLUMINA.bwa.PJL.exome.20130415	45	55	57	13	83	73	52	75	1	21	80	48	73	92	0	4	62
HG03767.mapped.ILLUMINA.bwa.PJL.exome.20130415	45	2	2	31	80	90	91	78	3	17	79	0	76	99	0	5	80
HG03770.mapped.ILLUMINA.bwa.ITU.exome.20130415	94	65	62	52	66	62	90	86	86	14	0	0	0	0	0	81	95
HG03771.mapped.ILLUMINA.bwa.ITU.exome.20130415	96	5	0	77	81	83	75	72	88	0	1	3	0	1	24	59	103
HG03772.mapped.ILLUMINA.bwa.ITU.exome.20130415	85	65	60	46	107	81	85	70	74	19	70	63	59	67	0	51	98
HG03773.mapped.ILLUMINA.bwa.ITU.exome.20130415	90	52	57	44	65	60	74	115	95	0	0	0	0	0	28	63	100
HG03774.mapped.ILLUMINA.bwa.ITU.exome.20130415	31	48	46	10	82	72	73	60	83	1	18	52	1	3	0	57	61
HG03775.mapped.ILLUMINA.bwa.ITU.exome.20130415	86	86	83	5	61	65	77	91	86	0	46	63	4	3	25	70	93
HG03777.mapped.ILLUMINA.bwa.ITU.exome.20130415	101	7	5	79	174	164	191	197	148	28	126	3	133	132	0	112	138
HG03778.mapped.ILLUMINA.bwa.ITU.exome.20130415	88	127	119	61	243	187	193	200	133	28	178	175	14	128	0	114	137
HG03779.mapped.ILLUMINA.bwa.ITU.exome.20130415	81	174	152	1	112	119	164	179	121	32	179	107	125	116	0	100	114
HG03780.mapped.ILLUMINA.bwa.ITU.exome.20130415	64	1	2	25	83	80	84	110	55	12	47	1	59	62	0	51	75
HG03781.mapped.ILLUMINA.bwa.ITU.exome.20130415	84	0	0	58	92	79	79	92	73	14	33	59	1	62	26	2	90
HG03782.mapped.ILLUMINA.bwa.ITU.exome.20130415	93	21	14	112	186	158	185	154	137	25	123	19	117	129	0	102	131
HG03784.mapped.ILLUMINA.bwa.ITU.exome.20130415	88	6	1	59	89	82	79	88	73	17	39	3	53	66	29	4	88
HG03785.mapped.ILLUMINA.bwa.ITU.exome.20130415	92	176	193	0	196	163	255	209	142	55	236	192	148	132	0	108	132
HG03786.mapped.ILLUMINA.bwa.ITU.exome.20130415	101	57	45	35	59	60	82	83	92	0	0	0	5	0	0	98	90
HG03787.mapped.ILLUMINA.bwa.ITU.exome.20130415	89	62	62	42	63	57	65	64	76	1	35	1	53	64	31	2	106
HG03788.mapped.ILLUMINA.bwa.ITU.exome.20130415	79	0	0	52	87	84	69	79	65	17	38	0	53	65	0	55	105
HG03789.mapped.ILLUMINA.bwa.ITU.exome.20130415	104	57	57	47	106	71	75	83	70	18	65	75	0	64	0	47	91
HG03790.mapped.ILLUMINA.bwa.ITU.exome.20130415	94	139	143	61	334	227	243	268	202	31	242	196	5	0	66	119	138
HG03792.mapped.ILLUMINA.bwa.ITU.exome.20130415	111	1	2	84	155	152	179	191	174	0	1	0	1	1	57	108	121
HG03793.mapped.ILLUMINA.bwa.BEB.exome.20130415	109	70	65	45	74	69	85	69	83	19	47	2	57	70	0	57	90
HG03796.mapped.ILLUMINA.bwa.BEB.exome.20130415	88	1	3	54	97	87	80	76	95	2	0	0	0	2	25	58	107
HG03800.mapped.ILLUMINA.bwa.BEB.exome.20130415	135	57	69	46	128	97	92	120	93	1	54	70	0	5	31	66	115
HG03802.mapped.ILLUMINA.bwa.BEB.exome.20130415	88	91	95	1	66	62	77	85	73	13	66	77	0	64	0	58	94
HG03803.mapped.ILLUMINA.bwa.BEB.exome.20130415	82	62	0	39	105	83	78	76	70	17	39	0	45	70	0	61	92
HG03805.mapped.ILLUMINA.bwa.BEB.exome.20130415	86	129	118	56	135	112	162	161	2	41	156	0	170	163	0	1	124
HG03808.mapped.ILLUMINA.bwa.BEB.exome.20130415	98	136	139	55	241	176	189	173	189	0	132	139	0	1	0	181	139
HG03809.mapped.ILLUMINA.bwa.BEB.exome.20130415	111	196	174	2	136	133	176	210	142	33	191	121	136	132	62	0	107
HG03812.mapped.ILLUMINA.bwa.BEB.exome.20130422	80	1	2	68	76	71	71	68	78	1	2	2	2	2	0	71	87
HG03814.mapped.ILLUMINA.bwa.BEB.exome.20130415	98	1	1	91	137	146	157	163	145	0	4	2	1	1	47	99	114
HG03815.mapped.ILLUMINA.bwa.BEB.exome.20130415	127	0	3	84	78	77	78	76	3	21	70	0	80	77	0	0	99
HG03817.mapped.ILLUMINA.bwa.BEB.exome.20130422	104	0	0	59	74	71	75	94	94	0	2	0	1	2	21	52	90
HG03821.mapped.ILLUMINA.bwa.BEB.exome.20130415	51	58	67	21	57	61	104	95	108	0	5	0	1	2	0	85	79
HG03823.mapped.ILLUMINA.bwa.BEB.exome.20130415	80	122	127	51	188	131	153	139	105	24	156	103	112	114	0	100	102
HG03824.mapped.ILLUMINA.bwa.BEB.exome.20130415	84	126	118	49	114	104	114	103	1	23	142	0	145	133	0	2	96
HG03826.mapped.ILLUMINA.bwa.BEB.exome.20130415	92	125	113	53	208	143	152	154	1	32	171	186	0	142	0	0	103
HG03829.mapped.ILLUMINA.bwa.BEB.exome.20130415	77	151	128	0	117	108	115	107	108	1	164	118	111	119	57	0	97
HG03830.mapped.ILLUMINA.bwa.BEB.exome.20130415	89	134	113	63	232	169	161	160	172	0	106	121	2	1	0	147	106
HG03832.mapped.ILLUMINA.bwa.BEB.exome.20130415	89	5	0	55	160	139	157	151	136	1	1	3	2	2	69	0	110
HG03833.mapped.ILLUMINA.bwa.BEB.exome.20130415	116	147	149	61	228	176	198	191	2	39	240	147	190	194	0	1	130
HG03836.mapped.ILLUMINA.bwa.STU.exome.20130415	98	1	1	101	138	151	165	193	146	1	0	0	0	0	52	104	112
HG03837.mapped.ILLUMINA.bwa.STU.exome.20130415	91	119	116	49	117	113	151	131	4	35	164	116	112	142	0	0	107
HG03838.mapped.ILLUMINA.bwa.STU.exome.20130415	113	96	92	2	106	102	107	97	125	0	72	89	0	1	0	91	127
HG03844.mapped.ILLUMINA.bwa.STU.exome.20130415	81	63	60	37	103	84	71	74	5	23	75	58	73	84	0	0	95
HG03846.mapped.ILLUMINA.bwa.STU.exome.20130415	134	0	0	106	128	123	127	115	138	0	0	0	1	2	32	64	155
HG03848.mapped.ILLUMINA.bwa.STU.exome.20130415	149	102	108	2	8	2	117	130	103	0	5	6	5	13	0	131	157
HG03849.mapped.ILLUMINA.bwa.STU.exome.20130415	107	51	54	44	67	55	72	86	93	0	2	0	0	0	0	78	101
HG03850.mapped.ILLUMINA.bwa.STU.exome.20130415	46	75	72	1	70	70	80	74	4	17	87	41	67	81	0	3	63
HG03851.mapped.ILLUMINA.bwa.STU.exome.20130415	152	103	110	2	134	115	120	104	97	24	99	110	52	89	0	91	147
HG03854.mapped.ILLUMINA.bwa.STU.exome.20130415	82	122	126	55	113	117	160	139	146	23	111	0	135	114	0	127	116
HG03856.mapped.ILLUMINA.bwa.STU.exome.20130415	138	70	73	64	149	107	104	126	94	15	73	67	57	91	32	0	178
HG03857.mapped.ILLUMINA.bwa.STU.exome.20130415	91	0	2	77	168	168	180	151	131	23	116	0	125	133	0	122	124
HG03858.mapped.ILLUMINA.bwa.STU.exome.20130415	89	7	5	56	91	84	72	74	75	16	40	4	57	66	0	44	102
HG03861.mapped.ILLUMINA.bwa.ITU.exome.20130415	83	1	2	69	146	133	149	153	150	1	2	0	0	1	0	190	106
HG03862.mapped.ILLUMINA.bwa.ITU.exome.20130415	90	56	70	40	107	80	82	70	89	0	35	60	0	1	0	76	94
HG03863.mapped.ILLUMINA.bwa.ITU.exome.20130415	83	122	105	57	121	113	153	177	117	24	122	2	133	119	0	101	113
HG03864.mapped.ILLUMINA.bwa.ITU.exome.20130415	109	0	1	53	93	83	79	85	73	14	46	0	51	71	0	2	77
HG03866.mapped.ILLUMINA.bwa.ITU.exome.20130415	35	2	1	29	72	76	93	79	58	17	25	0	45	48	31	0	69
HG03867.mapped.ILLUMINA.bwa.ITU.exome.20130415	130	0	3	87	125	121	103	96	94	24	50	0	54	94	0	66	154
HG03868.mapped.ILLUMINA.bwa.ITU.exome.20130415	46	1	6	32	78	78	93	70	92	0	2	1	2	3	0	63	62
HG03869.mapped.ILLUMINA.bwa.ITU.exome.20130415	84	54	72	37	105	82	89	93	70	18	60	55	62	63	0	55	97
HG03870.mapped.ILLUMINA.bwa.ITU.exome.20130415	144	1	3	79	141	143	134	119	102	18	52	1	68	84	0	64	164
HG03871.mapped.ILLUMINA.bwa.ITU.exome.20130415	39	83	83	2	3	5	6	6	4	1	59	1	75	86	0	0	64
HG03872.mapped.ILLUMINA.bwa.ITU.exome.20130415	136	1	2	86	122	130	121	111	87	12	46	1	56	88	0	57	164
HG03873.mapped.ILLUMINA.bwa.ITU.exome.20130415	80	132	111	50	180	164	165	171	102	20	147	134	0	98	50	1	101
HG03874.mapped.ILLUMINA.bwa.ITU.exome.20130415	90	58	62	41	66	57	65	53	6	12	68	0	70	90	0	0	97
HG03875.mapped.ILLUMINA.bwa.ITU.exome.20130415	98	2	1	77	167	163	173	208	141	34	120	0	132	131	0	109	121
HG03882.mapped.ILLUMINA.bwa.ITU.exome.20130415	92	4	2	90	86	87	88	93	87	2	6	4	3	2	25	56	102
HG03884.mapped.ILLUMINA.bwa.STU.exome.20130415	95	80	64	48	110	89	86	87	71	14	63	68	60	71	0	66	103
HG03885.mapped.ILLUMINA.bwa.STU.exome.20130415	103	75	81	52	81	76	77	75	4	17	81	79	60	105	0	0	115
HG03886.mapped.ILLUMINA.bwa.STU.exome.20130415	96	0	1	64	97	78	83	81	5	27	64	0	76	86	0	2	101
HG03887.mapped.ILLUMINA.bwa.STU.exome.20130415	92	59	67	49	62	63	95	99	68	17	38	0	60	74	27	0	92
HG03888.mapped.ILLUMINA.bwa.STU.exome.20130415	87	81	87	1	88	79	81	72	59	12	79	87	53	67	0	63	94
HG03890.mapped.ILLUMINA.bwa.STU.exome.20130415	134	1	0	83	121	120	118	102	103	21	46	0	71	91	0	69	170
HG03894.mapped.ILLUMINA.bwa.STU.exome.20130415	54	3	8	34	96	91	106	96	76	8	43	0	58	62	34	5	65
HG03895.mapped.ILLUMINA.bwa.STU.exome.20130415	131	63	75	54	75	93	82	55	91	2	39	0	64	91	0	49	157
HG03896.mapped.ILLUMINA.bwa.STU.exome.20130422	81	2	4	74	84	84	72	75	96	0	4	3	0	2	0	80	106
HG03897.mapped.ILLUMINA.bwa.STU.exome.20130415	125	105	116	0	83	94	126	116	98	23	97	74	71	86	0	71	161
HG03898.mapped.ILLUMINA.bwa.STU.exome.20130415	96	61	64	46	113	93	87	100	74	12	63	63	58	71	27	0	101

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG03899.mapped.ILLUMINA.bwa.STU.exome.20130415	103	0	1	91	197	210	203	236	215	2	0	0	2	4	66	134	148
HG03900.mapped.ILLUMINA.bwa.STU.exome.20130415	96	0	1	71	94	95	99	114	76	15	46	0	54	75	30	4	108
HG03902.mapped.ILLUMINA.bwa.BEB.exome.20130422	89	43	53	35	54	57	69	73	73	0	4	0	1	3	0	72	81
HG03905.mapped.ILLUMINA.bwa.BEB.exome.20130422	77	67	75	1	57	61	70	82	61	12	49	49	45	61	24	3	92
HG03907.mapped.ILLUMINA.bwa.BEB.exome.20130415	86	185	122	54	260	145	210	199	180	1	119	124	2	10	58	112	109
HG03908.mapped.ILLUMINA.bwa.BEB.exome.20130415	100	135	119	52	209	156	169	155	1	35	207	112	180	233	0	0	130
HG03910.mapped.ILLUMINA.bwa.BEB.exome.20130422	112	51	61	32	68	53	71	99	65	15	36	0	47	67	0	46	91
HG03911.mapped.ILLUMINA.bwa.BEB.exome.20130422	90	0	1	75	87	85	80	73	61	16	38	1	63	69	0	74	100
HG03913.mapped.ILLUMINA.bwa.BEB.exome.20130415	117	137	137	54	246	171	206	197	143	25	211	136	135	122	0	121	147
HG03914.mapped.ILLUMINA.bwa.BEB.exome.20130415	84	131	128	54	221	148	190	186	188	0	111	134	3	1	0	153	138
HG03916.mapped.ILLUMINA.bwa.BEB.exome.20130422	77	53	61	36	62	63	72	82	76	1	1	0	0	0	29	59	98
HG03917.mapped.ILLUMINA.bwa.BEB.exome.20130415	120	149	135	67	128	120	173	237	153	33	127	0	152	122	0	116	138
HG03919.mapped.ILLUMINA.bwa.BEB.exome.20130422	77	69	79	3	77	68	72	79	80	0	46	70	0	0	21	56	79
HG03920.mapped.ILLUMINA.bwa.BEB.exome.20130415	107	0	3	131	202	180	230	212	213	0	3	0	1	0	0	255	157
HG03922.mapped.ILLUMINA.bwa.BEB.exome.20130415	94	10	8	81	186	162	189	208	258	0	5	7	1	1	0	160	125
HG03925.mapped.ILLUMINA.bwa.BEB.exome.20130415	90	146	137	64	139	125	184	215	247	0	0	0	1	0	61	122	125
HG03926.mapped.ILLUMINA.bwa.BEB.exome.20130415	81	0	0	64	157	142	161	178	114	23	110	0	120	110	0	102	117
HG03928.mapped.ILLUMINA.bwa.BEB.exome.20130422	73	2	2	65	92	80	76	83	80	0	0	3	2	2	29	43	85
HG03931.mapped.ILLUMINA.bwa.BEB.exome.20130422	76	39	56	34	74	54	76	63	58	15	36	0	56	61	0	50	85
HG03934.mapped.ILLUMINA.bwa.BEB.exome.20130422	106	52	57	34	61	61	47	49	62	0	36	0	46	62	0	49	79
HG03937.mapped.ILLUMINA.bwa.BEB.exome.20130422	86	48	55	38	98	80	78	74	78	1	40	63	2	1	30	1	86
HG03940.mapped.ILLUMINA.bwa.BEB.exome.20130415	97	0	0	113	154	154	159	193	166	0	0	0	0	2	58	119	113
HG03941.mapped.ILLUMINA.bwa.BEB.exome.20130415	72	2	0	54	145	145	146	146	112	21	100	1	118	103	0	93	122
HG03943.mapped.ILLUMINA.bwa.STU.exome.20130415	91	81	76	1	0	2	8	1	4	1	65	0	83	97	0	4	102
HG03944.mapped.ILLUMINA.bwa.STU.exome.20130415	41	64	51	12	52	60	90	81	86	0	1	1	3	6	0	68	75
HG03945.mapped.ILLUMINA.bwa.STU.exome.20130415	87	2	3	84	336	197	247	245	218	32	109	129	0	1	0	161	132
HG03947.mapped.ILLUMINA.bwa.STU.exome.20130415	133	68	68	52	140	125	123	110	69	15	65	71	55	89	0	74	159
HG03948.mapped.ILLUMINA.bwa.STU.exome.20130422	87	47	64	43	116	87	79	76	65	18	60	57	43	75	0	53	104
HG03949.mapped.ILLUMINA.bwa.STU.exome.20130415	136	56	66	56	184	140	132	134	122	8	77	103	0	1	29	67	138
HG03950.mapped.ILLUMINA.bwa.STU.exome.20130415	102	65	69	50	119	99	89	80	75	20	64	95	0	76	0	64	126
HG03951.mapped.ILLUMINA.bwa.STU.exome.20130415	93	145	134	64	235	178	160	214	133	24	184	123	140	123	0	116	125
HG03953.mapped.ILLUMINA.bwa.STU.exome.20130415	124	71	76	55	97	82	108	102	90	21	47	0	44	105	0	72	168
HG03955.mapped.ILLUMINA.bwa.STU.exome.20130415	112	199	217	0	2	1	195	195	157	33	141	1	142	140	0	129	141
HG03960.mapped.ILLUMINA.bwa.ITU.exome.20130415	139	6	8	99	123	113	107	89	0	31	75	6	73	110	0	3	145
HG03963.mapped.ILLUMINA.bwa.ITU.exome.20130415	105	86	66	55	144	116	112	125	90	21	73	63	58	85	0	66	143
HG03965.mapped.ILLUMINA.bwa.ITU.exome.20130415	134	2	4	88	228	185	210	176	268	27	121	0	148	139	0	203	151
HG03967.mapped.ILLUMINA.bwa.ITU.exome.20130415	111	157	164	73	156	154	167	148	6	35	224	0	240	232	0	0	156
HG03968.mapped.ILLUMINA.bwa.ITU.exome.20130415	140	68	84	66	137	115	115	93	180	0	50	70	0	0	0	105	155
HG03969.mapped.ILLUMINA.bwa.ITU.exome.20130415	31	1	5	19	69	71	76	60	75	0	0	0	2	0	0	69	59
HG03971.mapped.ILLUMINA.bwa.ITU.exome.20130415	98	131	129	49	221	164	210	303	226	30	114	114	19	13	0	231	127
HG03973.mapped.ILLUMINA.bwa.ITU.exome.20130415	99	130	127	58	118	112	166	199	170	1	0	0	1	0	63	99	113
HG03974.mapped.ILLUMINA.bwa.ITU.exome.20130415	85	130	124	48	210	152	151	134	121	23	177	105	113	133	0	110	123
HG03976.mapped.ILLUMINA.bwa.ITU.exome.20130415	77	126	120	52	121	101	123	113	113	0	110	1	122	115	52	2	107
HG03977.mapped.ILLUMINA.bwa.ITU.exome.20130415	40	75	72	0	86	84	101	99	51	14	88	87	41	51	25	3	63
HG03978.mapped.ILLUMINA.bwa.ITU.exome.20130415	111	1	2	57	84	87	76	96	61	15	39	0	53	65	0	53	97
HG03985.mapped.ILLUMINA.bwa.STU.exome.20130415	32	53	47	12	51	43	91	71	77	0	0	0	0	3	21	38	70
HG03986.mapped.ILLUMINA.bwa.STU.exome.20130415	87	65	59	44	106	88	76	95	65	12	65	70	0	66	0	50	91
HG03989.mapped.ILLUMINA.bwa.STU.exome.20130415	42	59	52	15	87	80	83	71	69	7	73	52	48	57	0	50	65
HG03990.mapped.ILLUMINA.bwa.STU.exome.20130415	37	65	34	9	82	84	87	90	111	1	43	50	1	1	27	36	68
HG03991.mapped.ILLUMINA.bwa.STU.exome.20130415	41	0	1	23	83	95	78	82	8	18	77	1	76	87	0	3	78
HG03995.mapped.ILLUMINA.bwa.STU.exome.20130415	109	0	1	119	203	205	198	173	201	1	1	1	1	1	0	171	130
HG03998.mapped.ILLUMINA.bwa.STU.exome.20130415	39	51	48	11	103	86	81	68	5	12	62	85	0	64	0	1	57
HG03999.mapped.ILLUMINA.bwa.STU.exome.20130415	76	115	117	44	190	138	140	141	115	28	140	102	104	113	0	107	107
HG04001.mapped.ILLUMINA.bwa.ITU.exome.20130415	41	46	38	10	54	56	73	72	80	1	0	4	3	2	0	74	71
HG04002.mapped.ILLUMINA.bwa.ITU.exome.20130415	82	121	121	52	201	139	146	151	171	0	105	116	0	0	0	137	100
HG04003.mapped.ILLUMINA.bwa.STU.exome.20130415	41	3	3	13	110	86	93	82	5	15	70	61	40	68	0	1	54
HG04006.mapped.ILLUMINA.bwa.STU.exome.20130422	119	55	68	39	96	80	83	77	10	21	80	80	45	92	0	1	95
HG04014.mapped.ILLUMINA.bwa.ITU.exome.20130415	151	63	63	47	146	109	108	124	137	0	32	66	0	1	36	66	159
HG04015.mapped.ILLUMINA.bwa.ITU.exome.20130415	150	115	131	0	135	116	119	111	94	24	86	125	65	106	0	86	165
HG04017.mapped.ILLUMINA.bwa.ITU.exome.20130415	92	2	2	77	178	140	160	182	178	0	0	0	0	0	0	205	127
HG04018.mapped.ILLUMINA.bwa.ITU.exome.20130415	88	0	3	100	170	152	165	192	129	24	97	114	0	117	0	106	122
HG04019.mapped.ILLUMINA.bwa.ITU.exome.20130415	134	8	4	93	144	114	112	88	113	0	1	6	1	0	0	115	149
HG04020.mapped.ILLUMINA.bwa.ITU.exome.20130415	172	5	3	81	144	145	125	116	109	17	47	1	66	97	0	83	171
HG04022.mapped.ILLUMINA.bwa.ITU.exome.20130415	134	0	0	102	135	112	132	119	150	0	0	0	0	1	0	116	148
HG04023.mapped.ILLUMINA.bwa.ITU.exome.20130415	41	42	46	8	90	79	84	70	62	9	58	48	52	47	0	35	60
HG04025.mapped.ILLUMINA.bwa.ITU.exome.20130415	145	105	110	0	7	3	73	69	3	16	72	2	107	140	0	3	172
HG04026.mapped.ILLUMINA.bwa.ITU.exome.20130415	92	124	118	49	185	132	140	126	142	1	83	103	0	1	0	136	108
HG04029.mapped.ILLUMINA.bwa.STU.exome.20130415	129	101	115	2	78	78	124	92	81	24	67	80	54	91	0	75	159
HG04033.mapped.ILLUMINA.bwa.STU.exome.20130415	148	75	68	56	150	128	135	127	90	32	74	81	54	93	34	5	136
HG04035.mapped.ILLUMINA.bwa.STU.exome.20130415	146	108	119	3	89	90	85	69	6	22	113	124	52	136	0	7	164
HG04038.mapped.ILLUMINA.bwa.STU.exome.20130415	31	1	1	21	70	74	74	54	1	13	62	45	43	74	0	4	61
HG04039.mapped.ILLUMINA.bwa.STU.exome.20130415	34	0	0	22	67	71	69	69	59	6	34	0	38	41	0	36	51
HG04042.mapped.ILLUMINA.bwa.STU.exome.20130415	133	107	114	3	99	89	135	103	94	21	83	77	57	96	0	58	151
HG04047.mapped.ILLUMINA.bwa.STU.exome.20130415	42	60	50	18	56	58	54	51	75	0	32	0	50	59	32	1	65
HG04054.mapped.ILLUMINA.bwa.ITU.exome.20130415	42	4	5	27	83	92	91	82	102	1	1	2	0	0	48	3	78
HG04056.mapped.ILLUMINA.bwa.ITU.exome.20130415	43	1	4	28	63	80	89	80	56	11	29	1	38	42	0	39	69
HG04059.mapped.ILLUMINA.bwa.ITU.exome.20130415	44	85	77	1	86	84	92	80	74	9	74	88	0	48	0	47	71
HG04060.mapped.ILLUMINA.bwa.ITU.exome.20130415	48	72	66	22	60	70	71	47	71	1	38	59	1	64	0	47	84
HG04061.mapped.ILLUMINA.bwa.ITU.exome.20130415	50	94	82	0	64	60	99	89	110	0	32	59	1	2	33	58	83
HG04062.mapped.ILLUMINA.bwa.ITU.exome.20130415	52	0	2	38	85	94	98	99	64	11	43	0	48	57	0	52	67
HG04063.mapped.ILLUMINA.bwa.ITU.exome.20130415	157	56	76	53	77	96	90	77	91	0	41	0	62	94	34	0	166
HG04070.mapped.ILLUMINA.bwa.ITU.exome.20130415	92	202	135	57	247	163	201	166	2	44	266	118	184	177	0	2	126
HG04075.mapped.ILLUMINA.bwa.STU.exome.20130415	106	139	130	59	251	178	192	216	255	0	110	131	1	1	0	240	119
HG04076.mapped.ILLUMINA.bwa.ITU.exome.20130415	44	69	51	18	52	61	56	38	52	0	35	0	44	52	0	44	84
HG04080.mapped.ILLUMINA.bwa.ITU.exome.20130415	42	46	57	10	79	72	85	71	89	0	28	45	0	2	30	36	73
HG04090.mapped.ILLUMINA.bwa.ITU.exome.20130415	41	60	54	17	48	41	56	38	65	0	31	2	29	48	0	36	64
HG04093.mapped.ILLUMINA.bwa.ITU.exome.20130415	111	110	111	0	74	84	121	101	82	16	78	81	56	97	0	75	145
HG04094.mapped.ILLUMINA.bwa.ITU.exome.20130415	28	55	48	12	73	60	89	78	97	0	22	39	0	1	0	56	62
HG04096.mapped.ILLUMINA.bwa.ITU.exome.20130415	104	142	135	54	154	148	205	179	3	55	202	0	214	182	0	0	152
HG04098.mapped.ILLUMINA.bwa.ITU.exome.20130415	80	154	141	65	138	125	205	196	211	0	0	1	3	0	0	171	143
HG04099.mapped.ILLUMINA.bwa.STU.exome.20130415	115	111	111	7	142	125	115	101	70	13	96	116	52	92	0	57	151
HG04100.mapped.ILLUMINA.bwa.STU.exome.20130415	89	111	109	50	171	123	133	153	107	20	154	1	106	96	49	1	104
HG04106.mapped.ILLUMINA.bwa.STU.exome.20130415	173	5	8	93	122	117	117	108	81	16	35	79	1	92	0	79	150
HG04107.mapped.ILLUMINA.bwa.STU.exome.20130415	136	106	102	5	93	127	104	103	90	20	79	113	0	79	0	63	152
HG04118.mapped.ILLUMINA.bwa.ITU.exome.20130415	46	88	74	1	55	44	92	77	63	16	50	52	37	54	0	48	69
HG04131.mapped.ILLUMINA.bwa.BEB.exome.20130415	37	43	49	20	57	52	49	43	7	7	61	0	71	82	0	5	65

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG04134.mapped.ILLUMINA.bwa.BEB.exome.20130415	42	2	4	30	95	77	94	69	111	0	3	4	3	4	47	0	73
HG04140.mapped.ILLUMINA.bwa.BEB.exome.20130415	41	1	2	26	89	96	100	105	118	1	0	0	1	0	41	67	78
HG04141.mapped.ILLUMINA.bwa.BEB.exome.20130415	37	0	5	39	92	92	89	90	98	1	3	2	1	1	41	46	65
HG04144.mapped.ILLUMINA.bwa.BEB.exome.20130415	88	2	5	123	190	177	211	172	130	49	113	1	122	123	0	117	139
HG04146.mapped.ILLUMINA.bwa.BEB.exome.20130422	82	0	0	69	80	80	81	69	64	16	42	0	53	66	0	52	92
HG04152.mapped.ILLUMINA.bwa.BEB.exome.20130415	105	269	253	2	169	147	246	199	178	56	216	153	171	156	0	146	174
HG04153.mapped.ILLUMINA.bwa.BEB.exome.20130415	129	203	197	87	172	196	278	297	315	2	2	1	3	5	85	168	223
HG04155.mapped.ILLUMINA.bwa.BEB.exome.20130415	108	159	147	74	251	188	217	229	232	0	143	138	0	2	58	124	150
HG04156.mapped.ILLUMINA.bwa.BEB.exome.20130415	53	81	1	31	136	88	116	86	58	18	69	0	66	67	0	60	80
HG04158.mapped.ILLUMINA.bwa.BEB.exome.20130415	54	58	66	25	115	94	110	91	106	0	44	50	0	0	55	2	80
HG04159.mapped.ILLUMINA.bwa.BEB.exome.20130422	78	50	51	38	91	73	63	73	59	13	45	55	37	57	0	53	82
HG04161.mapped.ILLUMINA.bwa.BEB.exome.20130415	120	1	0	123	277	253	270	285	181	59	154	2	180	174	74	0	192
HG04162.mapped.ILLUMINA.bwa.BEB.exome.20130415	99	8	7	85	187	183	184	170	174	1	5	2	0	4	75	4	125
HG04164.mapped.ILLUMINA.bwa.BEB.exome.20130415	98	204	185	1	189	125	167	178	139	27	257	178	150	126	0	132	114
HG04171.mapped.ILLUMINA.bwa.BEB.exome.20130415	88	0	2	122	275	217	277	261	196	40	121	129	0	2	0	239	134
HG04173.mapped.ILLUMINA.bwa.BEB.exome.20130415	56	3	2	20	91	91	92	107	108	1	0	1	2	1	0	79	80
HG04176.mapped.ILLUMINA.bwa.BEB.exome.20130415	105	123	136	59	132	124	176	175	211	1	0	0	0	3	0	241	127
HG04177.mapped.ILLUMINA.bwa.BEB.exome.20130415	97	150	141	1	136	132	136	126	134	1	169	124	127	117	0	134	151
HG04180.mapped.ILLUMINA.bwa.BEB.exome.20130415	73	164	139	0	156	140	150	133	110	22	185	137	116	108	0	99	95
HG04182.mapped.ILLUMINA.bwa.BEB.exome.20130415	51	61	40	17	101	75	82	83	98	0	45	53	0	1	53	1	74
HG04183.mapped.ILLUMINA.bwa.BEB.exome.20130415	52	72	60	17	91	86	86	84	98	0	40	50	0	0	39	27	75
HG04185.mapped.ILLUMINA.bwa.BEB.exome.20130415	54	76	68	16	119	105	103	109	119	1	49	68	1	5	40	54	83
HG04186.mapped.ILLUMINA.bwa.BEB.exome.20130415	40	51	37	19	50	2	54	33	59	0	2	3	3	0	0	35	67
HG04188.mapped.ILLUMINA.bwa.BEB.exome.20130415	87	137	134	67	224	163	181	151	186	0	130	130	4	3	0	149	124
HG04189.mapped.ILLUMINA.bwa.BEB.exome.20130415	89	2	4	80	158	156	172	135	128	25	129	3	119	137	0	108	117
HG04194.mapped.ILLUMINA.bwa.BEB.exome.20130415	100	199	206	1	137	118	198	209	144	27	197	131	131	125	0	127	134
HG04195.mapped.ILLUMINA.bwa.BEB.exome.20130415	78	1	4	81	180	173	162	183	180	0	1	0	0	2	0	170	128
HG04198.mapped.ILLUMINA.bwa.ITU.exome.20130415	84	136	122	61	224	167	180	192	224	0	113	125	0	0	53	121	124
HG04200.mapped.ILLUMINA.bwa.ITU.exome.20130415	96	187	187	0	136	132	183	230	139	37	206	130	133	127	62	2	146
HG04202.mapped.ILLUMINA.bwa.ITU.exome.20130415	98	138	126	61	229	157	188	199	172	0	110	123	0	1	0	223	124
HG04206.mapped.ILLUMINA.bwa.ITU.exome.20130415	94	3	5	96	214	184	184	192	215	2	5	4	4	5	0	114	121
HG04209.mapped.ILLUMINA.bwa.ITU.exome.20130415	105	133	127	59	236	200	193	209	146	33	217	128	144	124	52	3	144
HG04210.mapped.ILLUMINA.bwa.STU.exome.20130415	107	0	1	103	238	236	248	266	258	0	0	0	0	0	89	3	149
HG04211.mapped.ILLUMINA.bwa.ITU.exome.20130415	125	150	156	62	140	156	245	201	283	1	6	7	0	3	0	229	171
HG04212.mapped.ILLUMINA.bwa.ITU.exome.20130415	96	1	2	84	191	154	181	173	134	29	117	0	130	121	61	0	128
HG04214.mapped.ILLUMINA.bwa.ITU.exome.20130415	84	112	113	57	120	149	163	155	128	21	104	0	128	107	0	105	118
HG04216.mapped.ILLUMINA.bwa.ITU.exome.20130415	109	212	206	1	321	261	291	338	175	46	332	379	6	160	70	2	150
HG04219.mapped.ILLUMINA.bwa.ITU.exome.20130415	71	120	103	41	86	90	133	129	0	32	143	0	136	134	0	0	97
HG04222.mapped.ILLUMINA.bwa.ITU.exome.20130415	86	0	1	63	142	129	133	124	103	19	2	6	112	100	0	94	97
HG04225.mapped.ILLUMINA.bwa.ITU.exome.20130415	102	122	125	62	218	164	157	167	135	26	177	117	121	129	0	131	126
HG04227.mapped.ILLUMINA.bwa.STU.exome.20130415	93	8	4	71	171	158	177	158	187	0	4	1	0	2	59	113	126
HG04229.mapped.ILLUMINA.bwa.STU.exome.20130415	93	153	118	2	139	153	150	142	155	0	93	115	0	0	0	143	104
HG04235.mapped.ILLUMINA.bwa.ITU.exome.20130415	95	131	126	49	126	113	179	229	206	0	0	0	0	1	54	122	136
HG04238.mapped.ILLUMINA.bwa.ITU.exome.20130415	100	1	1	113	175	152	180	207	169	0	0	0	0	0	62	111	107
HG04239.mapped.ILLUMINA.bwa.ITU.exome.20130415	71	132	107	49	200	147	158	130	110	21	169	102	125	112	0	103	99
NA06984.mapped.ILLUMINA.bwa.CEU.exome.20120522	84	64	62	37	114	101	88	75	63	14	76	55	40	67	0	54	114
NA06985.mapped.ILLUMINA.bwa.CEU.exome.20130415	59	27	25	11	25	30	68	39	50	1	0	0	0	0	9	25	70
NA06986.mapped.ILLUMINA.bwa.CEU.exome.20121211	203	126	154	0	0	0	147	187	185	0	0	0	0	1	0	218	209
NA06989.mapped.ILLUMINA.bwa.CEU.exome.20120522	135	80	90	56	98	85	123	101	75	13	54	0	77	86	0	80	125
NA06994.mapped.ILLUMINA.bwa.CEU.exome.20120522	87	0	0	56	140	127	165	159	122	0	0	0	0	0	0	165	89
NA07000.mapped.ILLUMINA.bwa.CEU.exome.20130415	61	30	0	1	47	62	52	41	35	7	18	0	22	38	0	30	69
NA07037.mapped.ILLUMINA.bwa.CEU.exome.20121211	89	0	0	66	109	108	106	91	99	0	0	0	0	0	0	123	101
NA07048.mapped.ILLUMINA.bwa.CEU.exome.20120522	149	83	83	43	97	92	120	151	160	0	0	0	0	0	31	69	173
NA07051.mapped.ILLUMINA.bwa.CEU.exome.20120522	131	88	78	53	166	135	125	100	97	13	69	122	0	81	0	67	153
NA07056.mapped.ILLUMINA.bwa.CEU.exome.20130415	38	20	16	9	23	32	47	25	45	0	0	0	0	0	0	42	58
NA07347.mapped.ILLUMINA.bwa.CEU.exome.20121211	146	0	0	89	147	153	126	109	132	0	0	0	0	1	0	133	129
NA07357.mapped.ILLUMINA.bwa.CEU.exome.20130415	58	1	0	22	41	50	58	34	50	0	0	0	0	0	0	57	59
NA10847.mapped.ILLUMINA.bwa.CEU.exome.20121211	118	107	0	40	184	142	138	121	0	16	131	89	92	134	0	0	119
NA10851.mapped.ILLUMINA.bwa.CEU.exome.20130415	58	0	0	30	51	60	68	55	58	0	0	0	0	0	0	64	69
NA11829.mapped.ILLUMINA.bwa.CEU.exome.20130415	60	24	35	22	25	31	58	42	45	0	0	0	1	0	21	0	77
NA11830.mapped.ILLUMINA.bwa.CEU.exome.20130415	54	44	43	1	0	0	50	23	45	0	0	0	0	0	16	0	63
NA11831.mapped.ILLUMINA.bwa.CEU.exome.20130415	67	23	31	16	18	36	47	47	54	0	0	0	0	0	10	20	77
NA11832.mapped.ILLUMINA.bwa.CEU.exome.20130415	66	31	30	20	52	50	66	35	59	0	17	38	1	1	0	43	78
NA11840.mapped.ILLUMINA.bwa.CEU.exome.20120522	91	0	0	96	144	126	136	118	107	4	77	0	95	104	0	92	99
NA11843.mapped.ILLUMINA.bwa.CEU.exome.20120522	94	0	2	80	97	96	96	81	105	0	1	1	0	0	0	78	103
NA11881.mapped.ILLUMINA.bwa.CEU.exome.20130415	64	31	38	23	29	28	64	49	56	0	0	1	1	0	26	0	70
NA11892.mapped.ILLUMINA.bwa.CEU.exome.20121211	84	100	97	0	102	96	83	83	105	0	72	88	0	0	34	63	90
NA11893.mapped.ILLUMINA.bwa.CEU.exome.20121211	85	0	0	83	119	98	97	77	99	0	0	0	0	0	0	139	96
NA11894.mapped.ILLUMINA.bwa.CEU.exome.20121211	81	92	82	41	73	66	94	69	111	0	0	0	0	0	0	104	93
NA11918.mapped.ILLUMINA.bwa.CEU.exome.20121211	197	1	1	109	167	186	137	198	162	0	0	0	1	0	28	97	190
NA11919.mapped.ILLUMINA.bwa.CEU.exome.20121211	96	1	2	49	88	83	88	88	109	0	0	0	0	0	0	98	102
NA11920.mapped.ILLUMINA.bwa.CEU.exome.20121211	201	100	105	55	113	114	145	174	190	0	0	0	0	0	32	88	207
NA11930.mapped.ILLUMINA.bwa.CEU.exome.20121211	85	92	88	0	63	69	91	83	57	14	73	55	48	60	0	52	108
NA11931.mapped.ILLUMINA.bwa.CEU.exome.20121211	77	84	80	46	119	102	101	77	46	30	76	96	0	65	0	63	86
NA11932.mapped.ILLUMINA.bwa.CEU.exome.20121211	86	86	70	45	131	93	101	99	52	30	87	66	76	73	0	70	93
NA11933.mapped.ILLUMINA.bwa.CEU.exome.20121211	71	0	0	94	119	118	95	106	97	0	0	0	0	0	0	149	89
NA11992.mapped.ILLUMINA.bwa.CEU.exome.20130415	56	39	39	19	27	36	67	47	28	3	18	0	22	44	0	29	64
NA11994.mapped.ILLUMINA.bwa.CEU.exome.20130415	73	0	1	31	48	51	71	37	2	11	32	0	49	62	0	0	68
NA11995.mapped.ILLUMINA.bwa.CEU.exome.20130415	49	0	1	13	23	44	35	24	13	3	10	1	7	25	0	15	54
NA12003.mapped.ILLUMINA.bwa.CEU.exome.20130415	42	17	14	4	8	21	34	13	33	0	0	0	0	2	0	19	48
NA12004.mapped.ILLUMINA.bwa.CEU.exome.20130415	52	30	26	16	23	23	40	42	52	0	0	0	0	2	0	36	58
NA12005.mapped.ILLUMINA.bwa.CEU.exome.20130415	48	39	38	14	26	27	61	60	39	7	12	0	29	32	0	29	87
NA12006.mapped.ILLUMINA.bwa.CEU.exome.20130415	74	55	58	1	20	36	72	36	70	0	15	30	0	1	0	56	80
NA12043.mapped.ILLUMINA.bwa.CEU.exome.20130415	57	30	37	12	40	59	67	45	48	8	25	35	25	42	0	27	85
NA12044.mapped.ILLUMINA.bwa.CEU.exome.20130415	62	29	30	19	20	23	57	43	28	12	18	0	21	41	12	0	65
NA12045.mapped.ILLUMINA.bwa.CEU.exome.20121211	141	73	82	53	98	99	122	99	153	0	0	0	0	1	31	60	167
NA12046.mapped.ILLUMINA.bwa.CEU.exome.20130415	55	18	26	14	48	51	58	36	44	0	13	26	0	0	0	46	62
NA12058.mapped.ILLUMINA.bwa.CEU.exome.20120522	116	0	0	80	113	100	89	112	79	13	51	2	65	81	0	63	109
NA12144.mapped.ILLUMINA.bwa.CEU.exome.20130415	60	0	0	41	43	58	63	42	56	0	2	0	0	1	0	50	60
NA12154.mapped.ILLUMINA.bwa.CEU.exome.20130415	74	0	0	31	52	63	65	52	30	7	17	0	28	32	0	26	63
NA12155.mapped.ILLUMINA.bwa.CEU.exome.20130415	65	29	38	19	29	35	61	41	50	0	0	0	0	0	11	25	72
NA12156.mapped.ILLUMINA.bwa.CEU.exome.20130415	49	0	0	18	28	50	37	26	24	4	15	0	24	20	0	23	53
NA12234.mapped.ILLUMINA.bwa.CEU.exome.20130415	60	0	0	45	56	44	70	34	43	8	13	0	30	43	0	24	64
NA12249.mapped.ILLUMINA.bwa.CEU.exome.20120522	115	0	0	96	141	151	144	150	91	8	76	0	76	116	0	85	131
NA12272.mapped.ILLUMINA.bwa.CEU.exome.20120522	103	0	0	76	136	127	119	126	108	11	82	1	80	103	0	94	100
NA12273.mapped.ILLUMINA.bwa.CEU.exome.20120522	72	0	0	52	115	111	104	108	144	0	0	0	0	1	0	104	96

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA12275.mapped.ILLUMINA.bwa.CEU.exome.20120522	84	117	115	0	115	113	132	138	72	12	127	115	84	87	0	78	91
NA12282.mapped.ILLUMINA.bwa.CEU.exome.20121211	109	0	0	51	139	145	114	136	212	0	0	0	0	0	0	138	100
NA12283.mapped.ILLUMINA.bwa.CEU.exome.20121211	99	103	102	41	95	90	128	134	163	0	0	0	0	0	0	132	117
NA12286.mapped.ILLUMINA.bwa.CEU.exome.20121211	92	0	0	89	129	123	125	150	160	0	0	0	0	0	61	100	94
NA12287.mapped.ILLUMINA.bwa.CEU.exome.20121211	82	0	1	87	104	89	95	64	52	30	45	0	68	82	0	60	75
NA12340.mapped.ILLUMINA.bwa.CEU.exome.20120522	98	1	1	90	116	92	82	89	64	11	37	0	64	64	18	0	128
NA12341.mapped.ILLUMINA.bwa.CEU.exome.20120522	89	0	0	65	101	93	80	74	88	0	0	0	1	0	15	47	124
NA12342.mapped.ILLUMINA.bwa.CEU.exome.20120522	87	0	2	82	107	79	78	92	85	0	0	0	0	0	17	65	95
NA12347.mapped.ILLUMINA.bwa.CEU.exome.20121211	81	82	74	48	86	71	100	99	91	1	0	0	0	0	40	65	83
NA12348.mapped.ILLUMINA.bwa.CEU.exome.20121211	96	1	0	59	114	93	101	90	0	37	87	72	79	103	0	0	82
NA12383.mapped.ILLUMINA.bwa.CEU.exome.20121211	80	81	72	39	121	104	91	67	0	36	108	69	96	92	0	0	90
NA12399.mapped.ILLUMINA.bwa.CEU.exome.20120522	137	74	86	54	90	82	119	116	152	0	0	0	0	1	0	127	140
NA12400.mapped.ILLUMINA.bwa.CEU.exome.20121211	110	0	2	71	110	107	103	93	115	0	0	0	1	0	43	3	127
NA12413.mapped.ILLUMINA.bwa.CEU.exome.20121211	85	0	0	70	109	103	105	86	64	30	51	71	0	76	0	76	107
NA12414.mapped.ILLUMINA.bwa.CEU.exome.20130415	70	0	0	40	58	57	69	40	78	0	0	0	0	0	9	33	72
NA12489.mapped.ILLUMINA.bwa.CEU.exome.20130415	59	0	0	26	50	62	66	51	69	0	0	0	0	0	16	37	71
NA12546.mapped.ILLUMINA.bwa.CEU.exome.20121211	83	0	0	87	116	97	102	98	64	33	47	58	0	71	48	0	92
NA12716.mapped.ILLUMINA.bwa.CEU.exome.20121211	89	1	0	81	130	132	140	119	91	5	77	0	82	107	0	106	94
NA12717.mapped.ILLUMINA.bwa.CEU.exome.20121211	88	0	0	73	122	109	110	124	111	0	0	0	0	0	0	106	96
NA12718.mapped.ILLUMINA.bwa.CEU.exome.20120522	92	95	101	44	167	128	118	119	140	0	82	88	0	0	0	132	98
NA12748.mapped.ILLUMINA.bwa.CEU.exome.20121211	90	54	62	48	73	67	86	62	99	0	0	0	0	0	0	87	105
NA12749.mapped.ILLUMINA.bwa.CEU.exome.20121211	79	0	0	91	114	100	91	83	102	0	0	1	0	0	0	132	79
NA12750.mapped.ILLUMINA.bwa.CEU.exome.20130415	96	120	109	52	119	105	166	173	196	0	1	3	2	2	54	88	128
NA12751.mapped.ILLUMINA.bwa.CEU.exome.20121211	104	0	0	68	147	138	153	124	188	0	0	1	0	0	0	141	114
NA12760.mapped.ILLUMINA.bwa.CEU.exome.20120522	93	99	86	42	102	95	132	122	187	0	0	0	0	0	0	129	99
NA12761.mapped.ILLUMINA.bwa.CEU.exome.20121211	86	120	119	1	0	2	109	103	0	13	108	0	106	128	0	0	91
NA12762.mapped.ILLUMINA.bwa.CEU.exome.20130415	59	37	27	12	24	30	46	31	57	0	0	0	0	1	0	41	74
NA12763.mapped.ILLUMINA.bwa.CEU.exome.20121211	84	94	89	44	158	134	109	113	148	0	72	82	0	0	51	71	99
NA12775.mapped.ILLUMINA.bwa.CEU.exome.20121211	85	124	114	0	64	69	127	97	48	44	65	73	64	80	35	1	84
NA12776.mapped.ILLUMINA.bwa.CEU.exome.20121211	103	98	87	47	75	71	111	88	120	1	0	0	0	0	42	87	111
NA12777.mapped.ILLUMINA.bwa.CEU.exome.20121211	93	0	0	45	133	121	108	107	123	0	0	0	0	1	41	74	113
NA12778.mapped.ILLUMINA.bwa.CEU.exome.20121211	86	0	0	96	133	110	122	88	66	30	44	0	88	73	34	1	101
NA12812.mapped.ILLUMINA.bwa.CEU.exome.20130415	54	28	33	16	43	51	50	31	57	0	18	37	0	0	0	43	73
NA12813.mapped.ILLUMINA.bwa.CEU.exome.20130415	79	77	69	0	44	62	92	65	56	3	53	82	0	63	0	57	71
NA12814.mapped.ILLUMINA.bwa.CEU.exome.20130415	65	0	0	22	46	56	55	36	42	11	23	0	25	24	0	34	58
NA12815.mapped.ILLUMINA.bwa.CEU.exome.20130415	68	28	20	21	44	65	61	35	36	6	33	29	17	28	0	23	70
NA12827.mapped.ILLUMINA.bwa.CEU.exome.20121211	102	101	78	51	92	79	73	54	0	34	45	0	67	85	0	0	68
NA12828.mapped.ILLUMINA.bwa.CEU.exome.20121211	87	0	0	95	125	121	106	92	75	39	57	0	59	84	0	83	92
NA12829.mapped.ILLUMINA.bwa.CEU.exome.20121211	103	72	72	44	127	95	89	94	0	23	93	72	84	98	0	0	106
NA12830.mapped.ILLUMINA.bwa.CEU.exome.20121211	107	0	1	81	96	104	94	87	97	0	1	0	0	0	21	54	109
NA12842.mapped.ILLUMINA.bwa.CEU.exome.20121211	203	103	119	63	136	126	146	181	149	0	0	1	0	2	0	228	218
NA12843.mapped.ILLUMINA.bwa.CEU.exome.20121211	111	0	2	69	107	88	91	79	101	0	0	1	0	1	0	106	102
NA12872.mapped.ILLUMINA.bwa.CEU.exome.20130415	35	26	11	11	15	38	50	33	31	5	15	0	14	23	0	17	53
NA12873.mapped.ILLUMINA.bwa.CEU.exome.20130415	56	0	2	34	35	49	55	39	56	0	0	0	0	0	12	24	66
NA12874.mapped.ILLUMINA.bwa.CEU.exome.20130415	52	0	0	25	33	52	43	35	48	0	0	0	0	0	0	35	63
NA12878.mapped.ILLUMINA.bwa.CEU.exome.20121211	129	71	80	49	156	109	94	87	85	22	80	76	74	83	0	66	135
NA12889.mapped.ILLUMINA.bwa.CEU.exome.20121211	213	95	94	67	131	133	145	170	179	0	0	0	1	0	0	154	170
NA12890.mapped.ILLUMINA.bwa.CEU.exome.20121211	258	134	157	83	127	136	221	220	249	0	0	0	0	0	57	116	307
NA18486.mapped.ILLUMINA.bwa.YRI.exome.20120522	168	92	0	59	115	89	87	81	94	0	76	0	93	111	0	84	191
NA18488.mapped.ILLUMINA.bwa.YRI.exome.20120522	124	0	0	52	86	112	92	91	114	0	0	0	0	2	29	73	135
NA18489.mapped.ILLUMINA.bwa.YRI.exome.20121211	152	0	84	52	164	148	120	113	149	0	57	0	67	0	54	0	145
NA18498.mapped.ILLUMINA.bwa.YRI.exome.20120522	87	49	46	30	53	54	78	55	83	0	0	1	0	0	0	91	106
NA18499.mapped.ILLUMINA.bwa.YRI.exome.20121211	128	85	88	46	92	77	105	159	147	0	0	0	0	0	0	140	158
NA18501.mapped.ILLUMINA.bwa.YRI.exome.20121211	135	1	1	86	134	119	118	112	127	0	0	0	0	0	47	0	130
NA18502.mapped.ILLUMINA.bwa.YRI.exome.20130415	66	53	41	16	39	49	80	73	66	0	0	3	0	1	23	53	77
NA18504.mapped.ILLUMINA.bwa.YRI.exome.20120522	135	0	0	95	139	131	110	98	117	0	0	0	0	1	47	1	133
NA18505.mapped.ILLUMINA.bwa.YRI.exome.20130415	84	3	58	18	81	101	91	85	75	0	33	0	45	1	24	50	81
NA18507.mapped.ILLUMINA.bwa.YRI.exome.20130415	65	1	2	21	54	70	69	34	38	8	26	0	30	35	14	0	68
NA18508.mapped.ILLUMINA.bwa.YRI.exome.20130415	81	60	56	22	83	95	80	110	97	1	21	53	2	2	26	55	92
NA18510.mapped.ILLUMINA.bwa.YRI.exome.20121211	165	0	1	124	185	170	144	140	184	0	0	0	1	1	34	78	189
NA18511.mapped.ILLUMINA.bwa.YRI.exome.20121211	81	79	76	37	120	85	105	81	83	0	52	51	0	0	40	0	59
NA18516.mapped.ILLUMINA.bwa.YRI.exome.20120522	138	157	83	64	154	128	116	112	132	0	54	80	0	0	43	0	134
NA18517.mapped.ILLUMINA.bwa.YRI.exome.20121211	64	73	71	36	69	53	87	86	92	0	0	0	0	0	29	67	70
NA18519.mapped.ILLUMINA.bwa.YRI.exome.20121211	94	0	0	62	108	103	103	71	105	0	1	0	0	0	31	0	117
NA18520.mapped.ILLUMINA.bwa.YRI.exome.20120522	162	0	1	100	146	156	125	127	141	0	0	0	0	1	55	0	163
NA18522.mapped.ILLUMINA.bwa.YRI.exome.20120522	225	93	99	61	126	122	105	112	118	0	57	0	93	123	58	0	226
NA18523.mapped.ILLUMINA.bwa.YRI.exome.20121211	74	110	105	0	100	92	94	96	93	0	77	90	0	0	0	123	90
NA18525.mapped.ILLUMINA.bwa.CHB.exome.20130415	61	0	0	27	51	61	58	32	48	0	0	0	0	2	13	15	63
NA18526.mapped.ILLUMINA.bwa.CHB.exome.20121211	92	0	0	93	121	105	96	74	88	0	0	0	0	0	42	51	105
NA18528.mapped.ILLUMINA.bwa.CHB.exome.20130415	65	0	0	32	56	57	57	41	62	0	0	0	1	0	0	63	74
NA18530.mapped.ILLUMINA.bwa.CHB.exome.20120522	69	0	0	62	102	96	95	82	85	0	0	0	0	0	60	0	88
NA18531.mapped.ILLUMINA.bwa.CHB.exome.20130415	58	0	0	22	49	60	52	38	29	10	18	0	18	39	6	2	75
NA18532.mapped.ILLUMINA.bwa.CHB.exome.20121211	98	0	0	90	169	125	128	86	120	0	0	0	0	1	73	0	134
NA18533.mapped.ILLUMINA.bwa.CHB.exome.20121211	119	0	2	57	101	106	99	102	111	0	0	1	1	2	44	0	118
NA18534.mapped.ILLUMINA.bwa.CHB.exome.20120522	82	0	0	56	93	87	79	66	80	0	0	0	0	0	54	0	72
NA18535.mapped.ILLUMINA.bwa.CHB.exome.20120522	220	0	0	113	181	190	143	178	1	32	110	192	0	187	0	0	206
NA18536.mapped.ILLUMINA.bwa.CHB.exome.20121211	82	0	0	58	108	84	104	95	67	33	50	69	0	74	38	0	87
NA18537.mapped.ILLUMINA.bwa.CHB.exome.20120522	82	90	96	52	85	66	59	35	42	0	37	0	63	61	32	0	106
NA18538.mapped.ILLUMINA.bwa.CHB.exome.20120522	134	85	87	53	95	96	104	139	103	18	56	77	1	89	30	1	154
NA18539.mapped.ILLUMINA.bwa.CHB.exome.20121211	111	1	0	63	124	112	89	111	83	20	46	0	77	90	0	79	141
NA18541.mapped.ILLUMINA.bwa.CHB.exome.20121211	102	1	1	84	100	97	91	113	77	18	36	0	76	73	36	0	116
NA18542.mapped.ILLUMINA.bwa.CHB.exome.20121211	104	78	73	58	182	113	144	145	69	52	121	77	95	82	50	1	100
NA18543.mapped.ILLUMINA.bwa.CHB.exome.20121211	98	0	0	94	108	105	104	100	106	1	0	0	0	0	42	62	83
NA18544.mapped.ILLUMINA.bwa.CHB.exome.20121211	80	0	0	62	101	126	111	94	54	36	68	94	0	65	31	0	77
NA18545.mapped.ILLUMINA.bwa.CHB.exome.20121211	87	0	0	88	109	112	111	91	99	0	2	0	1	0	44	64	109
NA18546.mapped.ILLUMINA.bwa.CHB.exome.20121211	76	0	0	56	95	108	91	80	57	30	49	0	63	61	0	72	89
NA18547.mapped.ILLUMINA.bwa.CHB.exome.20121211	65	0	0	61	127	107	97	54	45	31	40	0	67	73	42	0	104
NA18548.mapped.ILLUMINA.bwa.CHB.exome.20121211	71	0	0	55	115	95	92	92	108	0	0	0	0	0	43	67	85
NA18549.mapped.ILLUMINA.bwa.CHB.exome.20121211	74	77	76	40	71	67	82	78	82	0	0	0	0	0	33	66	93
NA18550.mapped.ILLUMINA.bwa.CHB.exome.20121211	80	0	1	76	118	99	104	81	96	0	0	0	0	0	35	40	98
NA18552.mapped.ILLUMINA.bwa.CHB.exome.20121211	88	0	0	68	127	113	124	100	60	30	38	59	0	75	0	42	108
NA18553.mapped.ILLUMINA.bwa.CHB.exome.20120522	120	0	0	64	122	85	94	89	111	0	0	0	0	1	46	0	118
NA18555.mapped.ILLUMINA.bwa.CHB.exome.20121211	82	0	0	59	124	116	108	103	111	0	0	0	0	0	43	76	97
NA18557.mapped.ILLUMINA.bwa.CHB.exome.20121211	74	0	0	63	109	108	93	99	106	0	0	0	0	0	49	74	92
NA18558.mapped.ILLUMINA.bwa.CHB.exome.20121211	81	0	0	70	104	99	99	56	91	0	0	0	0	0	58	0	100
NA18559.mapped.ILLUMINA.bwa.CHB.exome.20121211	98	93	78	55	88	72	99	89	61	29	55	0	78	78	46	0	97

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA18560.mapped.ILLUMINA.bwa.CHB.exome.20120522	155	0	0	69	161	128	116	106	157	0	0	0	0	0	32	0	168
NA18561.mapped.ILLUMINA.bwa.CHB.exome.20121211	95	0	0	64	104	111	118	93	0	43	81	0	111	116	0	0	102
NA18562.mapped.ILLUMINA.bwa.CHB.exome.20121211	83	0	0	60	127	117	103	82	102	0	2	0	0	2	65	0	95
NA18563.mapped.ILLUMINA.bwa.CHB.exome.20121211	91	0	0	69	107	109	101	89	61	28	42	72	0	77	39	0	88
NA18564.mapped.ILLUMINA.bwa.CHB.exome.20121211	80	0	0	66	113	104	90	73	56	31	35	59	0	69	0	47	87
NA18565.mapped.ILLUMINA.bwa.CHB.exome.20120522	108	62	57	31	72	65	86	89	58	10	39	0	53	70	0	51	128
NA18566.mapped.ILLUMINA.bwa.CHB.exome.20121211	70	0	0	90	107	89	93	47	81	0	0	0	0	0	54	0	82
NA18567.mapped.ILLUMINA.bwa.CHB.exome.20120522	136	85	96	55	94	86	105	122	138	0	0	0	0	0	33	83	145
NA18570.mapped.ILLUMINA.bwa.CHB.exome.20121211	72	0	0	89	106	106	83	57	87	0	0	0	0	1	56	0	85
NA18571.mapped.ILLUMINA.bwa.CHB.exome.20121211	76	0	0	64	108	100	103	68	93	0	0	0	0	0	63	0	87
NA18572.mapped.ILLUMINA.bwa.CHB.exome.20120522	78	0	0	72	107	106	92	68	52	25	36	0	73	67	43	0	86
NA18573.mapped.ILLUMINA.bwa.CHB.exome.20121211	70	0	0	66	110	71	60	54	49	0	0	0	0	71	0	68	95
NA18574.mapped.ILLUMINA.bwa.CHB.exome.20120522	113	0	0	64	115	117	97	95	123	0	0	0	0	0	40	0	109
NA18577.mapped.ILLUMINA.bwa.CHB.exome.20121211	113	0	0	69	131	123	111	94	117	0	0	0	0	0	67	0	109
NA18579.mapped.ILLUMINA.bwa.CHB.exome.20121211	116	1	0	71	126	129	128	95	115	0	0	0	0	0	79	0	121
NA18582.mapped.ILLUMINA.bwa.CHB.exome.20121211	141	125	125	64	209	161	154	129	149	0	88	106	0	0	62	0	100
NA18591.mapped.ILLUMINA.bwa.CHB.exome.20130415	44	59	68	30	125	81	108	115	66	19	58	83	2	72	33	0	75
NA18592.mapped.ILLUMINA.bwa.CHB.exome.20121211	70	77	60	37	61	64	52	28	41	0	32	51	0	54	29	0	98
NA18593.mapped.ILLUMINA.bwa.CHB.exome.20121211	85	0	0	62	152	105	107	74	94	0	0	0	0	0	60	1	87
NA18595.mapped.ILLUMINA.bwa.CHB.exome.20121211	67	0	0	59	107	87	79	73	77	0	0	0	0	0	52	0	83
NA18596.mapped.ILLUMINA.bwa.CHB.exome.20121211	79	0	0	90	103	97	112	119	62	45	49	0	66	65	42	0	84
NA18597.mapped.ILLUMINA.bwa.CHB.exome.20121211	87	0	0	61	109	111	98	91	100	0	0	0	0	2	63	0	88
NA18599.mapped.ILLUMINA.bwa.CHB.exome.20121211	68	0	0	53	96	80	103	70	86	0	0	0	0	1	61	0	88
NA18602.mapped.ILLUMINA.bwa.CHB.exome.20120522	86	0	0	62	109	106	104	58	92	0	0	0	0	0	66	0	88
NA18603.mapped.ILLUMINA.bwa.CHB.exome.20121211	92	82	82	50	87	68	103	106	63	32	46	0	66	87	40	0	97
NA18605.mapped.ILLUMINA.bwa.CHB.exome.20121211	76	85	76	37	71	64	95	74	50	28	35	0	63	69	43	0	85
NA18606.mapped.ILLUMINA.bwa.CHB.exome.20121211	78	0	0	60	111	109	102	80	57	29	58	0	68	73	46	0	102
NA18608.mapped.ILLUMINA.bwa.CHB.exome.20121211	66	0	0	58	112	109	99	95	64	33	49	0	74	73	40	0	95
NA18609.mapped.ILLUMINA.bwa.CHB.exome.20120522	82	87	78	47	74	68	75	41	54	0	50	0	75	75	0	80	101
NA18610.mapped.ILLUMINA.bwa.CHB.exome.20121211	77	90	78	44	138	103	89	71	90	1	39	64	0	0	0	127	93
NA18611.mapped.ILLUMINA.bwa.CHB.exome.20120522	83	0	0	65	100	101	90	55	73	1	0	0	1	1	51	73	92
NA18612.mapped.ILLUMINA.bwa.CHB.exome.20121211	74	1	0	92	119	109	96	100	54	31	57	0	75	76	49	0	90
NA18613.mapped.ILLUMINA.bwa.CHB.exome.20120522	71	80	71	43	72	77	73	46	45	0	47	55	1	75	0	76	98
NA18614.mapped.ILLUMINA.bwa.CHB.exome.20130415	72	1	0	33	58	70	73	43	42	6	20	0	26	51	14	0	77
NA18615.mapped.ILLUMINA.bwa.CHB.exome.20130415	71	0	0	32	32	56	66	36	48	0	0	0	0	0	27	0	76
NA18616.mapped.ILLUMINA.bwa.CHB.exome.20120522	153	1	1	90	165	142	127	135	164	0	0	0	0	0	35	76	165
NA18617.mapped.ILLUMINA.bwa.CHB.exome.20130415	94	0	0	41	78	98	121	85	87	0	0	0	0	0	0	87	91
NA18618.mapped.ILLUMINA.bwa.CHB.exome.20130415	58	0	1	27	30	61	59	46	22	10	12	0	27	40	0	34	70
NA18619.mapped.ILLUMINA.bwa.CHB.exome.20130415	70	1	0	26	22	80	46	36	41	0	0	0	0	0	10	34	73
NA18620.mapped.ILLUMINA.bwa.CHB.exome.20121211	77	0	0	67	113	101	104	69	55	30	38	0	67	82	39	1	95
NA18621.mapped.ILLUMINA.bwa.CHB.exome.20121211	76	0	0	62	135	101	102	83	90	0	0	0	0	0	42	66	88
NA18622.mapped.ILLUMINA.bwa.CHB.exome.20121211	83	0	0	69	111	104	111	87	116	0	2	0	0	0	44	74	94
NA18623.mapped.ILLUMINA.bwa.CHB.exome.20121211	100	1	1	77	134	137	123	89	115	0	0	0	0	2	90	0	113
NA18624.mapped.ILLUMINA.bwa.CHB.exome.20121211	74	0	0	54	104	87	89	73	75	0	0	1	0	0	44	62	90
NA18625.mapped.ILLUMINA.bwa.CHB.exome.20130415	51	0	0	23	32	45	52	36	30	8	16	0	18	26	12	0	54
NA18626.mapped.ILLUMINA.bwa.CHB.exome.20130415	76	0	2	39	55	74	67	55	50	8	17	0	42	43	15	0	73
NA18627.mapped.ILLUMINA.bwa.CHB.exome.20130415	57	28	37	17	25	38	75	51	63	1	1	2	1	3	17	32	75
NA18628.mapped.ILLUMINA.bwa.CHB.exome.20130415	60	0	1	34	45	59	57	43	56	0	0	0	0	1	20	0	82
NA18629.mapped.ILLUMINA.bwa.CHB.exome.20130415	49	0	0	35	82	119	86	88	70	10	38	1	60	49	32	1	63
NA18630.mapped.ILLUMINA.bwa.CHB.exome.20130415	79	0	0	21	36	60	51	32	70	0	0	0	0	0	9	21	55
NA18631.mapped.ILLUMINA.bwa.CHB.exome.20120522	155	100	97	62	103	102	133	129	106	27	47	95	0	117	37	1	183
NA18632.mapped.ILLUMINA.bwa.CHB.exome.20121211	74	78	70	44	129	106	84	88	61	30	84	97	0	80	0	60	90
NA18633.mapped.ILLUMINA.bwa.CHB.exome.20121211	80	0	0	71	108	106	94	77	84	0	0	0	0	0	74	0	89
NA18634.mapped.ILLUMINA.bwa.CHB.exome.20120522	139	0	0	98	152	131	139	130	99	31	65	0	75	107	34	0	161
NA18635.mapped.ILLUMINA.bwa.CHB.exome.20121211	75	0	0	59	104	85	99	76	82	0	0	0	0	0	40	46	90
NA18636.mapped.ILLUMINA.bwa.CHB.exome.20121211	91	97	75	53	78	70	108	91	97	0	0	1	0	0	42	85	99
NA18637.mapped.ILLUMINA.bwa.CHB.exome.20121211	82	1	0	60	109	85	93	68	43	35	34	62	0	63	34	0	104
NA18638.mapped.ILLUMINA.bwa.CHB.exome.20121211	147	88	93	46	83	85	107	107	87	13	45	84	0	85	24	1	145
NA18639.mapped.ILLUMINA.bwa.CHB.exome.20130415	71	0	0	25	35	64	59	36	48	0	0	0	0	0	0	4	71
NA18640.mapped.ILLUMINA.bwa.CHB.exome.20130415	48	0	0	25	39	41	45	30	51	0	0	0	0	0	16	0	65
NA18641.mapped.ILLUMINA.bwa.CHB.exome.20130415	64	28	33	14	22	46	67	46	34	5	13	0	24	39	16	0	81
NA18642.mapped.ILLUMINA.bwa.CHB.exome.20130415	67	0	1	32	31	62	58	50	29	6	8	22	0	35	14	1	71
NA18643.mapped.ILLUMINA.bwa.CHB.exome.20130415	54	25	24	22	13	32	27	22	33	0	10	0	20	30	14	0	58
NA18644.mapped.ILLUMINA.bwa.CHB.exome.20130415	43	2	0	31	83	78	93	84	82	0	0	1	2	1	47	2	71
NA18645.mapped.ILLUMINA.bwa.CHB.exome.20130415	63	0	0	14	35	64	47	37	51	0	0	0	0	1	24	0	54
NA18646.mapped.ILLUMINA.bwa.CHB.exome.20130415	52	1	1	34	89	93	100	83	71	16	46	1	56	62	0	55	80
NA18647.mapped.ILLUMINA.bwa.CHB.exome.20130415	38	2	0	24	28	29	44	30	27	5	9	0	14	16	10	2	44
NA18648.mapped.ILLUMINA.bwa.CHB.exome.20130415	37	1	1	28	94	79	89	67	88	0	0	2	0	1	52	4	69
NA18740.mapped.ILLUMINA.bwa.CHB.exome.20130415	45	0	0	30	45	52	58	37	27	3	11	0	18	27	13	0	58
NA18745.mapped.ILLUMINA.bwa.CHB.exome.20130415	59	0	0	29	38	44	54	22	47	0	0	0	0	1	22	0	58
NA18747.mapped.ILLUMINA.bwa.CHB.exome.20130415	64	0	0	36	59	69	76	55	67	0	0	0	0	1	9	31	80
NA18748.mapped.ILLUMINA.bwa.CHB.exome.20130415	56	0	0	25	37	58	64	34	24	2	13	35	0	34	9	1	83
NA18749.mapped.ILLUMINA.bwa.CHB.exome.20130415	67	0	0	27	44	67	70	46	73	0	0	0	1	0	0	62	82
NA18757.mapped.ILLUMINA.bwa.CHB.exome.20130415	55	1	2	29	47	58	52	24	51	0	0	0	0	0	15	0	65
NA18853.mapped.ILLUMINA.bwa.YRI.exome.20120522	163	0	94	49	188	132	118	122	139	0	71	89	0	2	59	0	157
NA18856.mapped.ILLUMINA.bwa.YRI.exome.20120522	129	78	103	0	93	82	71	58	89	0	87	0	97	95	0	64	121
NA18858.mapped.ILLUMINA.bwa.YRI.exome.20121211	79	83	79	50	86	75	99	97	104	0	0	0	0	0	0	149	100
NA18861.mapped.ILLUMINA.bwa.YRI.exome.20121211	94	0	0	55	150	100	100	78	94	0	0	0	0	0	43	79	94
NA18864.mapped.ILLUMINA.bwa.YRI.exome.20130415	103	135	131	55	220	165	171	172	175	1	120	122	1	1	81	3	120
NA18865.mapped.ILLUMINA.bwa.YRI.exome.20130415	83	2	1	113	223	137	175	159	195	0	0	0	0	0	67	0	112
NA18867.mapped.ILLUMINA.bwa.YRI.exome.20120522	245	0	1	104	207	199	165	225	202	0	0	0	1	3	0	252	216
NA18868.mapped.ILLUMINA.bwa.YRI.exome.20120522	139	0	91	48	162	115	103	112	112	0	70	0	73	0	50	0	139
NA18870.mapped.ILLUMINA.bwa.YRI.exome.20121211	164	0	0	71	170	149	150	153	159	0	0	1	0	1	44	0	130
NA18871.mapped.ILLUMINA.bwa.YRI.exome.20120522	96	67	83	48	117	90	90	93	120	0	55	0	64	1	24	0	83
NA18873.mapped.ILLUMINA.bwa.YRI.exome.20120522	174	70	90	52	171	138	164	159	148	0	50	107	0	1	0	67	128
NA18874.mapped.ILLUMINA.bwa.YRI.exome.20120522	88	0	0	71	96	140	87	57	88	0	1	0	0	2	25	0	103
NA18876.mapped.ILLUMINA.bwa.YRI.exome.20130415	86	136	130	66	234	175	194	245	194	0	110	128	0	0	64	113	130
NA18877.mapped.ILLUMINA.bwa.YRI.exome.20130415	92	0	2	123	204	176	214	198	220	0	0	1	0	1	82	0	164
NA18878.mapped.ILLUMINA.bwa.YRI.exome.20130415	100	1	2	90	203	195	250	199	211	0	0	0	1	0	101	0	153
NA18879.mapped.ILLUMINA.bwa.YRI.exome.20130415	123	160	149	68	238	206	255	272	161	33	235	141	158	146	64	1	176
NA18881.mapped.ILLUMINA.bwa.YRI.exome.20130415	82	168	156	7	135	113	161	204	213	8	107	129	0	9	0	119	116
NA18907.mapped.ILLUMINA.bwa.YRI.exome.20121211	85	0	0	64	156	104	98	96	98	0	0	0	0	0	0	159	92
NA18908.mapped.ILLUMINA.bwa.YRI.exome.20120522	126	83	88	52	94	94	108	140	145	0	0	0	0	2	0	179	148
NA18909.mapped.ILLUMINA.bwa.YRI.exome.20121211	84	90	70	52	141	116	99	99	108	0	57	73	0	0	45	60	89
NA18910.mapped.ILLUMINA.bwa.YRI.exome.20120522	143	77	114	0	97	96	84	82	95	0	97	0	106	92	35	1	138
NA18912.mapped.ILLUMINA.bwa.YRI.exome.20120522	203	107	106	79	129	117	120	119	124	0	66	0	86	141	45	0	217

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA18915.mapped.ILLUMINA.bwa.YRI.exome.20130415	89	0	2	107	170	156	169	141	186	0	0	2	0	1	78	3	128
NA18916.mapped.ILLUMINA.bwa.YRI.exome.20121211	89	1	0	2	0	0	67	62	1	0	0	0	0	0	22	0	40
NA18917.mapped.ILLUMINA.bwa.YRI.exome.20120522	94	0	146	0	91	98	123	126	142	0	65	0	78	0	77	0	100
NA18923.mapped.ILLUMINA.bwa.YRI.exome.20120522	86	0	0	53	123	120	120	128	124	0	0	0	0	0	85	0	90
NA18924.mapped.ILLUMINA.bwa.YRI.exome.20120522	109	0	0	94	165	137	137	128	153	0	0	0	0	0	95	0	96
NA18933.mapped.ILLUMINA.bwa.YRI.exome.20120522	112	97	109	46	107	159	120	166	185	0	0	0	0	0	38	0	74
NA18934.mapped.ILLUMINA.bwa.YRI.exome.20120522	92	96	96	48	156	139	132	122	161	0	72	80	0	1	73	0	129
NA18939.mapped.ILLUMINA.bwa.JPT.exome.20130415	69	0	0	30	37	61	58	44	29	4	12	0	20	38	10	3	67
NA18940.mapped.ILLUMINA.bwa.JPT.exome.20121211	76	0	0	87	100	96	81	77	100	0	0	0	0	0	40	60	86
NA18941.mapped.ILLUMINA.bwa.JPT.exome.20130415	59	0	0	35	48	52	63	29	50	0	0	1	0	0	18	0	74
NA18942.mapped.ILLUMINA.bwa.JPT.exome.20121211	77	0	0	56	100	103	91	78	92	0	0	0	0	0	63	0	92
NA18943.mapped.ILLUMINA.bwa.JPT.exome.20121211	91	0	0	88	116	112	110	93	64	33	51	76	1	83	0	71	100
NA18944.mapped.ILLUMINA.bwa.JPT.exome.20121211	89	0	1	62	120	103	99	73	68	30	51	67	0	80	38	0	97
NA18945.mapped.ILLUMINA.bwa.JPT.exome.20121211	83	0	0	65	126	118	113	91	111	0	0	0	0	0	45	67	91
NA18946.mapped.ILLUMINA.bwa.JPT.exome.20130415	72	1	0	29	57	54	69	37	69	0	2	0	0	0	24	0	79
NA18947.mapped.ILLUMINA.bwa.JPT.exome.20121211	77	1	0	63	114	106	102	79	94	0	0	0	0	0	37	71	96
NA18948.mapped.ILLUMINA.bwa.JPT.exome.20121211	72	89	68	44	68	61	99	81	49	33	79	0	114	92	0	63	90
NA18949.mapped.ILLUMINA.bwa.JPT.exome.20121211	71	0	0	57	106	114	108	93	66	36	78	0	102	69	33	0	92
NA18950.mapped.ILLUMINA.bwa.JPT.exome.20120522	114	0	1	44	91	84	79	75	103	0	0	0	0	0	0	85	87
NA18951.mapped.ILLUMINA.bwa.JPT.exome.20121211	90	0	1	101	132	116	106	46	0	0	0	0	1	1	0	1	66
NA18952.mapped.ILLUMINA.bwa.JPT.exome.20121211	78	88	1	53	139	102	103	87	66	35	89	74	71	81	42	0	101
NA18953.mapped.ILLUMINA.bwa.JPT.exome.20120522	233	0	0	94	211	196	178	213	132	28	77	0	99	131	39	0	145
NA18954.mapped.ILLUMINA.bwa.JPT.exome.20130415	68	0	1	17	42	64	68	41	34	5	14	38	0	44	14	1	72
NA18956.mapped.ILLUMINA.bwa.JPT.exome.20130415	89	0	0	49	54	71	80	60	42	10	20	0	28	42	0	45	81
NA18957.mapped.ILLUMINA.bwa.JPT.exome.20130415	51	0	0	17	41	44	52	45	48	0	0	0	1	3	7	22	52
NA18959.mapped.ILLUMINA.bwa.JPT.exome.20121211	202	0	0	112	186	157	131	142	161	0	0	1	0	0	65	0	186
NA18960.mapped.ILLUMINA.bwa.JPT.exome.20120522	243	1	0	129	214	198	163	203	225	0	0	0	0	0	45	109	226
NA18961.mapped.ILLUMINA.bwa.JPT.exome.20120522	151	0	1	69	152	119	119	150	90	23	62	93	0	90	41	0	144
NA18962.mapped.ILLUMINA.bwa.JPT.exome.20130415	50	0	0	26	33	55	46	39	50	0	0	0	0	1	26	0	65
NA18963.mapped.ILLUMINA.bwa.JPT.exome.20130415	68	0	1	37	55	81	75	53	74	0	0	0	0	0	20	47	81
NA18964.mapped.ILLUMINA.bwa.JPT.exome.20120522	205	0	1	94	148	162	142	154	175	0	0	0	0	0	69	0	180
NA18965.mapped.ILLUMINA.bwa.JPT.exome.20130415	73	0	0	35	55	54	57	51	66	0	0	0	0	0	27	0	76
NA18966.mapped.ILLUMINA.bwa.JPT.exome.20121211	99	0	0	79	142	125	128	130	160	0	0	0	0	0	0	155	102
NA18967.mapped.ILLUMINA.bwa.JPT.exome.20121211	113	88	96	52	90	92	113	122	157	0	0	0	0	0	69	1	96
NA18968.mapped.ILLUMINA.bwa.JPT.exome.20120522	92	1	1	57	128	116	117	132	194	0	0	0	0	0	52	82	80
NA18969.mapped.ILLUMINA.bwa.JPT.exome.20120522	97	0	0	58	177	118	129	144	173	0	0	0	0	0	50	78	99
NA18970.mapped.ILLUMINA.bwa.JPT.exome.20120522	91	2	1	60	118	111	121	108	163	0	0	0	0	0	69	0	101
NA18971.mapped.ILLUMINA.bwa.JPT.exome.20120522	110	0	0	111	178	168	151	131	167	0	0	0	0	1	0	133	121
NA18972.mapped.ILLUMINA.bwa.JPT.exome.20121211	136	0	0	113	158	157	162	132	174	0	0	0	0	0	37	74	113
NA18973.mapped.ILLUMINA.bwa.JPT.exome.20121211	94	0	0	61	130	131	130	145	109	8	69	94	2	108	55	0	107
NA18974.mapped.ILLUMINA.bwa.JPT.exome.20120522	83	0	0	58	137	119	115	129	169	0	0	0	0	1	79	0	97
NA18975.mapped.ILLUMINA.bwa.JPT.exome.20120522	81	0	0	60	129	115	115	145	108	8	72	0	75	106	53	0	126
NA18976.mapped.ILLUMINA.bwa.JPT.exome.20120522	92	0	1	55	119	118	107	113	87	7	83	0	91	101	0	84	97
NA18977.mapped.ILLUMINA.bwa.JPT.exome.20130415	78	2	1	38	72	88	76	67	89	0	4	1	0	0	32	0	78
NA18978.mapped.ILLUMINA.bwa.JPT.exome.20130415	62	0	0	29	40	72	79	34	62	0	0	0	0	0	27	0	73
NA18979.mapped.ILLUMINA.bwa.JPT.exome.20130415	46	0	0	22	31	45	36	48	23	7	14	0	19	19	0	13	68
NA18980.mapped.ILLUMINA.bwa.JPT.exome.20130415	86	0	0	35	69	84	97	71	57	10	30	58	0	71	16	1	87
NA18981.mapped.ILLUMINA.bwa.JPT.exome.20120522	117	0	1	92	160	138	145	143	149	0	0	0	0	0	68	70	124
NA18982.mapped.ILLUMINA.bwa.JPT.exome.20120522	185	0	0	81	171	157	145	159	162	0	0	0	0	1	71	0	189
NA18983.mapped.ILLUMINA.bwa.JPT.exome.20120522	164	0	0	88	138	123	107	132	109	20	77	101	0	101	0	78	149
NA18984.mapped.ILLUMINA.bwa.JPT.exome.20121211	120	2	1	63	104	97	97	122	97	18	55	81	0	85	34	0	117
NA18985.mapped.ILLUMINA.bwa.JPT.exome.20120522	92	0	0	70	105	88	78	75	93	0	0	0	0	3	33	1	112
NA18986.mapped.ILLUMINA.bwa.JPT.exome.20120522	141	0	1	97	147	143	113	131	99	18	56	0	74	94	37	1	140
NA18987.mapped.ILLUMINA.bwa.JPT.exome.20120522	112	0	1	92	183	155	169	148	155	0	0	0	0	1	57	80	135
NA18988.mapped.ILLUMINA.bwa.JPT.exome.20120522	105	0	0	70	115	96	95	104	111	0	0	0	0	0	25	78	118
NA18989.mapped.ILLUMINA.bwa.JPT.exome.20120522	160	81	94	62	115	106	143	162	138	0	0	0	0	1	59	0	178
NA18990.mapped.ILLUMINA.bwa.JPT.exome.20120522	104	0	1	67	160	141	140	125	0	13	147	85	85	154	0	1	107
NA18991.mapped.ILLUMINA.bwa.JPT.exome.20120522	94	0	0	64	133	128	128	102	87	7	72	0	90	94	0	74	111
NA18992.mapped.ILLUMINA.bwa.JPT.exome.20130415	55	25	29	18	15	28	48	36	56	0	0	0	0	0	8	40	64
NA18993.mapped.ILLUMINA.bwa.JPT.exome.20130415	53	0	0	33	34	37	47	49	44	0	0	0	0	0	0	39	58
NA18994.mapped.ILLUMINA.bwa.JPT.exome.20130415	59	0	1	24	40	57	58	37	46	0	0	0	0	1	22	1	62
NA18995.mapped.ILLUMINA.bwa.JPT.exome.20130415	32	0	0	24	33	51	37	33	0	7	22	0	24	36	0	1	47
NA18997.mapped.ILLUMINA.bwa.JPT.exome.20130415	49	20	20	15	18	27	50	30	44	0	0	0	1	0	4	16	48
NA18998.mapped.ILLUMINA.bwa.JPT.exome.20130415	66	0	0	28	52	71	75	52	70	0	0	0	0	1	13	32	70
NA18999.mapped.ILLUMINA.bwa.JPT.exome.20120522	182	0	1	81	158	166	124	163	160	0	0	0	1	1	57	0	194
NA19000.mapped.ILLUMINA.bwa.JPT.exome.20120522	210	0	1	103	217	190	162	206	118	22	79	119	0	122	49	1	226
NA19001.mapped.ILLUMINA.bwa.JPT.exome.20130415	52	0	0	19	37	44	56	22	24	4	12	25	0	33	7	0	52
NA19002.mapped.ILLUMINA.bwa.JPT.exome.20130415	87	0	3	27	64	95	90	55	69	0	0	0	0	0	39	0	85
NA19003.mapped.ILLUMINA.bwa.JPT.exome.20120522	124	75	0	50	149	113	103	104	1	23	87	112	0	101	0	0	136
NA19004.mapped.ILLUMINA.bwa.JPT.exome.20120522	152	0	0	79	132	120	116	169	150	0	0	0	0	1	43	95	153
NA19005.mapped.ILLUMINA.bwa.JPT.exome.20130415	67	0	1	27	42	62	64	46	50	0	0	1	0	0	28	0	80
NA19006.mapped.ILLUMINA.bwa.JPT.exome.20130415	139	1	1	142	264	247	300	278	328	0	2	1	2	1	72	152	201
NA19007.mapped.ILLUMINA.bwa.JPT.exome.20120522	227	115	117	62	242	215	172	180	228	0	75	154	0	1	54	58	238
NA19009.mapped.ILLUMINA.bwa.JPT.exome.20130415	47	0	1	24	38	55	47	23	52	0	0	0	0	1	12	18	66
NA19010.mapped.ILLUMINA.bwa.JPT.exome.20130415	80	0	0	34	65	80	92	59	76	0	0	0	0	0	43	2	83
NA19011.mapped.ILLUMINA.bwa.JPT.exome.20130415	137	6	1	100	305	238	254	214	247	0	0	1	2	0	113	0	176
NA19012.mapped.ILLUMINA.bwa.JPT.exome.20120522	197	94	95	58	205	166	129	150	113	19	98	113	87	112	36	0	182
NA19017.mapped.ILLUMINA.bwa.LWK.exome.20121211	93	1	1	57	88	94	95	72	70	14	43	0	53	71	0	59	125
NA19019.mapped.ILLUMINA.bwa.LWK.exome.20121211	75	0	1	79	88	83	70	78	93	16	1	0	1	1	25	61	88
NA19020.mapped.ILLUMINA.bwa.LWK.exome.20130422	69	25	0	17	26	40	34	25	0	5	49	0	45	68	0	1	68
NA19023.mapped.ILLUMINA.bwa.LWK.exome.20121211	89	0	3	50	77	70	89	102	95	0	0	3	0	2	30	0	82
NA19024.mapped.ILLUMINA.bwa.LWK.exome.20121211	87	64	63	43	123	88	79	100	101	1	41	58	0	3	27	60	103
NA19025.mapped.ILLUMINA.bwa.LWK.exome.20130415	97	141	156	61	133	120	163	105	137	0	139	0	150	150	57	0	151
NA19026.mapped.ILLUMINA.bwa.LWK.exome.20121211	95	61	55	45	73	75	83	78	89	0	0	1	1	0	39	1	116
NA19027.mapped.ILLUMINA.bwa.LWK.exome.20130415	44	26	0	16	37	49	40	38	17	3	15	27	19	23	4	0	62
NA19028.mapped.ILLUMINA.bwa.LWK.exome.20130422	62	34	0	11	18	30	31	22	22	0	12	0	25	26	0	34	58
NA19030.mapped.ILLUMINA.bwa.LWK.exome.20121211	82	0	1	80	95	92	93	79	78	15	31	1	43	76	0	0	89
NA19031.mapped.ILLUMINA.bwa.LWK.exome.20130422	58	23	33	7	44	56	57	39	30	7	31	0	40	36	0	20	55
NA19035.mapped.ILLUMINA.bwa.LWK.exome.20130422	47	0	0	44	40	55	67	44	56	0	0	0	0	0	0	18	45
NA19036.mapped.ILLUMINA.bwa.LWK.exome.20130422	66	1	0	28	42	61	54	34	57	0	9	0	30	0	26	0	51
NA19037.mapped.ILLUMINA.bwa.LWK.exome.20130415	106	151	155	52	144	142	204	174	200	0	2	1	0	0	67	125	148
NA19038.mapped.ILLUMINA.bwa.LWK.exome.20130415	54	22	24	15	28	23	60	33	50	0	0	0	0	0	0	44	66
NA19041.mapped.ILLUMINA.bwa.LWK.exome.20130415	56	65	27	0	0	0	34	20	1	6	35	0	45	60	0	0	66
NA19042.mapped.ILLUMINA.bwa.LWK.exome.20130415	87	150	132	56	120	131	151	118	137	0	129	1	133	138	0	115	144
NA19043.mapped.ILLUMINA.bwa.LWK.exome.20121211	93	60	3	46	73	92	75	67	92	0	0	0	0	3	39	1	109
NA19054.mapped.ILLUMINA.bwa.JPT.exome.20120522	104	0	0	75	120	110	93	89	115	0	0	0	0	0	44	0	113

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA19055.mapped.ILLUMINA.bwa.JPT.exome.20120522	121	0	1	70	124	112	94	116	133	0	0	0	0	0	28	77	123
NA19056.mapped.ILLUMINA.bwa.JPT.exome.20120522	182	0	1	74	137	137	136	155	189	0	0	1	0	0	56	88	158
NA19057.mapped.ILLUMINA.bwa.JPT.exome.20120522	100	0	1	64	112	118	96	98	87	10	49	0	63	90	26	0	113
NA19058.mapped.ILLUMINA.bwa.JPT.exome.20120522	135	0	1	73	141	116	110	139	103	24	72	0	81	97	38	0	142
NA19059.mapped.ILLUMINA.bwa.JPT.exome.20120522	110	0	0	63	122	103	109	106	108	0	0	0	0	1	45	0	125
NA19060.mapped.ILLUMINA.bwa.JPT.exome.20120522	247	0	1	120	241	246	174	215	131	23	89	119	0	140	52	0	261
NA19062.mapped.ILLUMINA.bwa.JPT.exome.20120522	110	0	0	65	106	111	85	94	2	19	46	0	61	76	21	0	75
NA19063.mapped.ILLUMINA.bwa.JPT.exome.20120522	194	0	1	136	183	223	152	151	106	26	82	0	86	123	0	106	204
NA19064.mapped.ILLUMINA.bwa.JPT.exome.20120522	142	0	0	88	162	159	144	129	118	24	50	94	0	107	40	0	182
NA19065.mapped.ILLUMINA.bwa.JPT.exome.20120522	207	0	38	117	187	185	199	181	193	0	0	0	0	0	0	80	216
NA19066.mapped.ILLUMINA.bwa.JPT.exome.20120522	170	90	0	60	183	155	141	165	169	0	69	106	0	1	39	1	114
NA19067.mapped.ILLUMINA.bwa.JPT.exome.20120522	124	0	0	64	140	138	116	113	136	0	0	1	0	2	38	77	138
NA19068.mapped.ILLUMINA.bwa.JPT.exome.20120522	167	0	0	82	159	134	124	132	132	0	0	0	0	2	58	1	159
NA19070.mapped.ILLUMINA.bwa.JPT.exome.20120522	199	0	0	92	160	141	122	129	164	0	0	0	0	0	40	84	178
NA19072.mapped.ILLUMINA.bwa.JPT.exome.20120522	106	0	2	63	149	146	134	146	154	0	0	0	0	0	46	88	105
NA19074.mapped.ILLUMINA.bwa.JPT.exome.20120522	80	86	94	39	94	86	81	76	83	0	60	78	0	107	0	77	93
NA19075.mapped.ILLUMINA.bwa.JPT.exome.20120522	74	0	0	51	112	104	104	114	139	0	0	0	0	0	74	0	83
NA19076.mapped.ILLUMINA.bwa.JPT.exome.20120522	103	0	0	82	158	140	150	144	157	0	0	0	0	0	60	82	114
NA19077.mapped.ILLUMINA.bwa.JPT.exome.20120522	84	0	0	57	109	119	112	120	158	0	0	0	0	1	54	79	93
NA19078.mapped.ILLUMINA.bwa.JPT.exome.20130415	94	2	0	71	156	126	143	121	148	1	1	1	1	1	65	0	125
NA19079.mapped.ILLUMINA.bwa.JPT.exome.20120522	112	105	102	44	113	109	152	152	115	11	82	93	0	108	65	0	118
NA19080.mapped.ILLUMINA.bwa.JPT.exome.20120522	90	0	0	46	116	117	119	153	105	9	79	0	84	98	53	0	91
NA19081.mapped.ILLUMINA.bwa.JPT.exome.20120522	83	94	86	39	79	96	115	135	151	0	0	0	0	0	51	69	99
NA19082.mapped.ILLUMINA.bwa.JPT.exome.20120522	96	0	0	54	130	118	125	153	167	0	0	0	0	0	0	173	106
NA19083.mapped.ILLUMINA.bwa.JPT.exome.20120522	110	0	0	85	121	117	118	141	140	0	0	0	1	0	47	66	98
NA19084.mapped.ILLUMINA.bwa.JPT.exome.20120522	90	0	0	54	149	136	129	126	89	6	88	80	0	105	0	78	104
NA19085.mapped.ILLUMINA.bwa.JPT.exome.20120522	115	90	86	41	89	85	122	125	106	7	82	0	78	100	0	64	83
NA19086.mapped.ILLUMINA.bwa.JPT.exome.20130422	52	0	0	27	33	53	58	50	62	0	0	0	0	1	7	36	55
NA19087.mapped.ILLUMINA.bwa.JPT.exome.20120522	92	0	0	102	126	126	119	100	64	38	56	0	79	102	37	0	111
NA19088.mapped.ILLUMINA.bwa.JPT.exome.20120522	100	101	71	60	92	79	108	75	106	0	0	0	0	0	70	0	113
NA19089.mapped.ILLUMINA.bwa.JPT.exome.20130415	134	0	2	122	302	238	263	223	263	0	0	0	0	1	102	0	198
NA19090.mapped.ILLUMINA.bwa.JPT.exome.20130415	112	0	1	119	227	208	254	199	233	0	0	1	0	2	0	209	185
NA19091.mapped.ILLUMINA.bwa.JPT.exome.20130415	128	0	0	162	225	203	246	234	143	47	143	1	177	155	0	139	171
NA19092.mapped.ILLUMINA.bwa.YRI.exome.20120522	154	0	2	66	146	113	119	115	149	0	0	0	0	0	38	0	143
NA19093.mapped.ILLUMINA.bwa.YRI.exome.20121211	141	0	0	60	120	118	106	118	120	0	0	1	0	0	50	0	144
NA19095.mapped.ILLUMINA.bwa.YRI.exome.20130415	84	0	0	37	50	99	68	50	59	2	2	0	0	0	22	1	87
NA19096.mapped.ILLUMINA.bwa.YRI.exome.20130422	46	0	0	27	23	29	53	18	42	0	0	0	0	0	7	0	33
NA19098.mapped.ILLUMINA.bwa.YRI.exome.20121211	102	113	101	47	205	174	155	143	181	0	82	89	1	0	61	83	129
NA19099.mapped.ILLUMINA.bwa.YRI.exome.20130422	77	0	0	37	81	91	98	85	86	0	1	0	0	2	45	1	58
NA19102.mapped.ILLUMINA.bwa.YRI.exome.20121211	172	0	1	112	202	150	129	183	161	0	0	0	0	2	52	87	162
NA19107.mapped.ILLUMINA.bwa.YRI.exome.20121211	82	91	76	40	78	70	109	85	60	37	48	0	65	72	51	0	88
NA19108.mapped.ILLUMINA.bwa.YRI.exome.20121211	88	85	87	38	143	97	91	92	108	1	51	0	75	1	0	111	100
NA19113.mapped.ILLUMINA.bwa.YRI.exome.20130415	51	0	0	32	25	46	44	34	45	0	0	0	0	0	20	0	59
NA19114.mapped.ILLUMINA.bwa.YRI.exome.20121211	74	0	0	52	102	79	96	91	57	28	39	0	74	76	39	0	87
NA19116.mapped.ILLUMINA.bwa.YRI.exome.20120522	175	91	85	68	124	113	151	158	176	0	67	100	0	3	45	91	202
NA19117.mapped.ILLUMINA.bwa.YRI.exome.20130415	75	39	25	10	25	36	60	39	56	1	0	0	0	1	15	38	62
NA19118.mapped.ILLUMINA.bwa.YRI.exome.20130415	74	0	69	2	20	45	76	53	78	0	21	0	28	0	20	32	69
NA19119.mapped.ILLUMINA.bwa.YRI.exome.20120522	86	97	95	48	106	96	86	87	111	0	86	0	93	106	0	84	101
NA19121.mapped.ILLUMINA.bwa.YRI.exome.20130415	49	0	0	33	41	56	74	47	42	0	0	1	0	0	0	12	44
NA19129.mapped.ILLUMINA.bwa.YRI.exome.20121211	84	0	74	51	112	92	92	88	86	0	49	0	81	0	34	67	79
NA19130.mapped.ILLUMINA.bwa.YRI.exome.20120522	197	95	105	85	174	181	208	253	241	0	0	0	1	2	69	107	226
NA19131.mapped.ILLUMINA.bwa.YRI.exome.20120522	114	97	104	40	124	157	143	135	175	0	0	0	0	0	91	0	120
NA19137.mapped.ILLUMINA.bwa.YRI.exome.20130415	107	161	155	4	12	4	16	6	6	2	135	0	137	147	0	4	133
NA19138.mapped.ILLUMINA.bwa.YRI.exome.20121211	91	0	0	67	129	116	118	105	129	0	0	0	0	0	74	0	95
NA19141.mapped.ILLUMINA.bwa.YRI.exome.20120522	93	128	88	0	100	97	85	64	99	0	145	93	84	85	0	89	99
NA19143.mapped.ILLUMINA.bwa.YRI.exome.20120522	82	96	98	45	88	77	89	84	103	0	65	0	83	97	49	0	92
NA19144.mapped.ILLUMINA.bwa.YRI.exome.20121211	100	142	134	1	152	156	137	131	100	12	169	97	128	112	0	89	118
NA19146.mapped.ILLUMINA.bwa.YRI.exome.20130422	76	25	33	12	28	45	38	26	43	0	16	0	24	33	17	0	76
NA19147.mapped.ILLUMINA.bwa.YRI.exome.20121211	80	93	2	47	82	86	66	51	71	0	59	0	77	70	45	0	85
NA19149.mapped.ILLUMINA.bwa.YRI.exome.20130415	71	0	34	16	44	57	67	46	54	0	15	0	20	0	18	24	71
NA19152.mapped.ILLUMINA.bwa.YRI.exome.20120522	90	0	0	55	173	130	112	154	158	0	80	90	0	1	0	176	94
NA19153.mapped.ILLUMINA.bwa.YRI.exome.20121211	118	0	0	92	138	137	129	159	156	0	1	0	0	0	53	90	122
NA19159.mapped.ILLUMINA.bwa.YRI.exome.20121211	112	0	0	55	152	122	127	169	144	0	0	0	0	0	64	66	102
NA19160.mapped.ILLUMINA.bwa.YRI.exome.20120522	96	0	0	91	185	124	123	119	161	0	0	0	0	0	87	0	114
NA19171.mapped.ILLUMINA.bwa.YRI.exome.20120522	114	102	109	50	113	98	135	147	160	0	0	0	0	0	57	85	115
NA19172.mapped.ILLUMINA.bwa.YRI.exome.20120522	187	91	100	60	192	156	142	130	168	0	53	108	0	0	58	0	184
NA19175.mapped.ILLUMINA.bwa.YRI.exome.20130422	39	1	1	21	36	48	44	32	51	0	0	0	0	0	15	0	49
NA19184.mapped.ILLUMINA.bwa.YRI.exome.20130415	54	0	27	12	10	29	33	18	30	0	11	0	14	23	12	0	62
NA19185.mapped.ILLUMINA.bwa.YRI.exome.20130415	51	0	0	31	31	82	46	34	49	0	0	0	0	0	10	26	65
NA19189.mapped.ILLUMINA.bwa.YRI.exome.20120522	89	0	0	104	147	102	98	94	109	0	0	0	0	0	76	0	100
NA19190.mapped.ILLUMINA.bwa.YRI.exome.20121211	85	0	0	94	103	142	97	86	89	0	0	0	0	0	59	0	82
NA19197.mapped.ILLUMINA.bwa.YRI.exome.20120522	102	121	119	0	83	89	112	129	175	0	80	78	0	0	0	162	96
NA19198.mapped.ILLUMINA.bwa.YRI.exome.20120522	126	0	0	120	197	195	184	193	201	0	0	0	0	0	0	196	147
NA19200.mapped.ILLUMINA.bwa.YRI.exome.20120522	125	129	117	61	203	161	158	179	188	0	88	105	1	0	61	100	139
NA19201.mapped.ILLUMINA.bwa.YRI.exome.20121211	92	0	0	56	133	126	131	145	149	0	0	0	0	0	65	105	86
NA19204.mapped.ILLUMINA.bwa.YRI.exome.20120522	100	98	0	47	102	91	95	82	99	0	62	0	83	98	0	95	88
NA19206.mapped.ILLUMINA.bwa.YRI.exome.20121211	114	0	0	113	195	137	155	155	148	0	0	0	0	0	76	95	139
NA19207.mapped.ILLUMINA.bwa.YRI.exome.20121211	122	126	105	49	195	151	153	147	176	0	81	99	0	0	61	86	122
NA19209.mapped.ILLUMINA.bwa.YRI.exome.20121211	110	0	0	94	199	135	136	170	141	0	0	0	0	0	64	105	119
NA19210.mapped.ILLUMINA.bwa.YRI.exome.20121211	97	0	0	95	131	122	112	151	193	0	70	99	1	0	54	93	100
NA19213.mapped.ILLUMINA.bwa.YRI.exome.20120522	139	0	3	90	139	195	115	96	141	0	0	0	0	1	51	0	141
NA19214.mapped.ILLUMINA.bwa.YRI.exome.20130422	73	0	0	35	38	59	62	48	52	0	0	0	0	0	12	0	53
NA19222.mapped.ILLUMINA.bwa.YRI.exome.20130422	36	16	23	15	30	36	37	25	38	0	11	19	0	1	15	1	52
NA19223.mapped.ILLUMINA.bwa.YRI.exome.20120522	100	0	0	95	149	128	119	131	129	0	0	0	1	0	60	88	108
NA19225.mapped.ILLUMINA.bwa.YRI.exome.20121211	77	2	0	94	123	105	112	72	99	0	0	0	0	0	63	0	99
NA19235.mapped.ILLUMINA.bwa.YRI.exome.20120522	250	0	1	126	265	219	177	211	224	0	0	0	0	0	48	111	256
NA19236.mapped.ILLUMINA.bwa.YRI.exome.20120522	136	81	89	56	90	103	79	76	86	0	69	1	72	87	39	1	136
NA19238.mapped.ILLUMINA.bwa.YRI.exome.20130415	107	116	1	51	115	116	122	115	138	0	116	1	109	122	90	2	135
NA19239.mapped.ILLUMINA.bwa.YRI.exome.20130415	45	3	8	24	80	81	81	74	116	0	1	1	1	1	44	46	67
NA19240.mapped.ILLUMINA.bwa.YRI.exome.20130415	35	52	3	19	48	56	45	32	61	0	30	1	37	55	48	1	58
NA19247.mapped.ILLUMINA.bwa.YRI.exome.20120522	172	0	0	87	157	151	128	181	156	0	0	1	0	2	37	108	189
NA19248.mapped.ILLUMINA.bwa.YRI.exome.20120522	105	0	68	42	78	68	63	35	58	0	52	0	56	76	0	52	120
NA19256.mapped.ILLUMINA.bwa.YRI.exome.20121211	85	0	76	54	117	113	108	106	99	0	53	0	80	0	39	78	102
NA19257.mapped.ILLUMINA.bwa.YRI.exome.20121211	79	117	105	0	104	104	103	74	104	1	87	96	0	0	0	107	94
NA19307.mapped.ILLUMINA.bwa.LWK.exome.20130415	58	29	36	21	31	33	39	20	33	0	14	0	28	32	11	0	81
NA19308.mapped.ILLUMINA.bwa.LWK.exome.20130422	73	88	71	0	25	40	0	0	2	0	34	0	88	67	0	0	74

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA19309.mapped.ILLUMINA.bwa.LWK.exome.20130415	59	25	29	13	17	31	25	18	20	0	14	0	19	22	9	0	61
NA19310.mapped.ILLUMINA.bwa.LWK.exome.20130422	47	21	0	10	27	23	20	15	25	0	12	0	22	22	7	0	58
NA19311.mapped.ILLUMINA.bwa.LWK.exome.20120522	103	120	100	55	117	116	117	101	122	0	76	0	101	113	55	0	130
NA19312.mapped.ILLUMINA.bwa.LWK.exome.20130422	70	33	44	28	29	31	26	32	37	0	22	0	24	32	0	39	83
NA19313.mapped.ILLUMINA.bwa.LWK.exome.20120522	95	99	98	49	106	112	122	131	141	0	0	0	0	1	79	0	113
NA19314.mapped.ILLUMINA.bwa.LWK.exome.20130422	48	29	18	19	30	40	54	39	51	0	10	1	20	0	0	0	0
NA19315.mapped.ILLUMINA.bwa.LWK.exome.20120522	91	0	0	55	127	126	117	151	132	0	0	0	0	0	61	81	107
NA19316.mapped.ILLUMINA.bwa.LWK.exome.20120522	126	236	150	0	172	168	169	166	178	0	135	160	0	0	103	0	131
NA19317.mapped.ILLUMINA.bwa.LWK.exome.20120522	117	0	0	87	202	176	200	159	163	0	0	0	0	0	0	105	141
NA19318.mapped.ILLUMINA.bwa.LWK.exome.20120522	76	0	0	39	104	88	91	103	107	0	58	62	0	0	37	65	81
NA19319.mapped.ILLUMINA.bwa.LWK.exome.20120522	87	0	125	0	96	93	96	80	102	0	118	0	129	109	0	68	100
NA19320.mapped.ILLUMINA.bwa.LWK.exome.20130415	121	1	1	131	236	226	273	252	234	0	0	1	2	0	115	2	190
NA19321.mapped.ILLUMINA.bwa.LWK.exome.20120522	107	0	0	100	188	158	132	143	195	0	0	0	0	0	0	163	123
NA19323.mapped.ILLUMINA.bwa.LWK.exome.20130415	90	4	2	72	107	78	85	77	81	14	38	5	51	74	32	0	100
NA19324.mapped.ILLUMINA.bwa.LWK.exome.20120522	84	0	1	99	178	140	134	170	167	0	0	0	0	0	0	196	113
NA19327.mapped.ILLUMINA.bwa.LWK.exome.20120522	105	0	0	89	175	118	115	145	140	0	0	0	0	0	43	0	75
NA19328.mapped.ILLUMINA.bwa.LWK.exome.20120522	129	0	114	59	227	154	168	178	202	0	76	0	101	1	0	108	112
NA19331.mapped.ILLUMINA.bwa.LWK.exome.20120522	212	332	280	0	1	0	279	240	332	0	0	0	0	0	134	0	253
NA19332.mapped.ILLUMINA.bwa.LWK.exome.20120522	118	75	76	54	137	112	63	74	106	0	83	0	98	78	34	1	114
NA19334.mapped.ILLUMINA.bwa.LWK.exome.20120522	153	122	117	1	95	99	130	122	144	0	64	88	0	2	55	0	158
NA19338.mapped.ILLUMINA.bwa.LWK.exome.20120522	116	69	80	48	147	106	92	98	101	0	47	76	0	2	48	0	133
NA19346.mapped.ILLUMINA.bwa.LWK.exome.20120522	159	0	0	103	132	125	121	146	131	0	0	0	0	0	54	0	132
NA19347.mapped.ILLUMINA.bwa.LWK.exome.20120522	284	162	198	0	144	146	208	223	217	0	78	0	106	0	54	0	167
NA19350.mapped.ILLUMINA.bwa.LWK.exome.20120522	128	0	0	93	146	136	116	111	129	0	0	0	0	1	0	89	92
NA19351.mapped.ILLUMINA.bwa.LWK.exome.20130415	63	0	1	23	28	67	73	41	68	0	0	0	0	0	12	28	81
NA19355.mapped.ILLUMINA.bwa.LWK.exome.20130415	56	52	58	1	22	32	59	43	54	0	11	30	0	0	0	18	40
NA19360.mapped.ILLUMINA.bwa.LWK.exome.20130415	53	35	44	0	37	68	52	42	62	0	30	32	33	0	11	23	67
NA19372.mapped.ILLUMINA.bwa.LWK.exome.20130422	55	25	1	17	22	44	28	25	44	0	18	0	22	38	0	40	63
NA19374.mapped.ILLUMINA.bwa.LWK.exome.20130415	51	0	0	24	54	64	72	47	43	9	9	0	22	0	0	32	69
NA19375.mapped.ILLUMINA.bwa.LWK.exome.20130422	66	0	0	36	61	69	65	56	79	0	0	0	0	0	13	0	43
NA19376.mapped.ILLUMINA.bwa.LWK.exome.20130415	53	34	14	19	35	55	47	42	47	0	7	1	31	0	0	27	29
NA19377.mapped.ILLUMINA.bwa.LWK.exome.20130422	55	41	34	20	22	46	66	44	69	0	0	0	0	0	28	0	76
NA19378.mapped.ILLUMINA.bwa.LWK.exome.20130415	80	52	69	45	111	88	89	74	97	0	51	67	0	1	28	65	105
NA19379.mapped.ILLUMINA.bwa.LWK.exome.20130415	58	39	27	17	43	58	42	41	48	0	13	21	0	0	13	33	71
NA19380.mapped.ILLUMINA.bwa.LWK.exome.20120522	125	0	0	71	162	146	185	160	177	0	0	0	0	1	86	0	122
NA19383.mapped.ILLUMINA.bwa.LWK.exome.20130422	58	0	0	29	44	51	55	37	47	0	1	0	0	0	18	1	71
NA19384.mapped.ILLUMINA.bwa.LWK.exome.20130422	68	37	38	17	31	47	68	56	62	0	0	1	1	1	0	51	84
NA19385.mapped.ILLUMINA.bwa.LWK.exome.20120522	93	96	89	48	95	108	86	78	104	0	80	0	86	101	51	0	84
NA19390.mapped.ILLUMINA.bwa.LWK.exome.20130415	59	26	24	14	25	29	36	16	32	0	10	0	23	29	0	24	51
NA19391.mapped.ILLUMINA.bwa.LWK.exome.20130415	42	0	18	18	20	25	35	21	41	0	8	0	10	0	0	30	54
NA19393.mapped.ILLUMINA.bwa.LWK.exome.20130422	76	0	0	35	34	51	61	38	51	0	13	1	16	1	14	14	57
NA19394.mapped.ILLUMINA.bwa.LWK.exome.20130422	55	0	0	29	49	60	80	39	74	0	0	0	0	0	20	22	65
NA19395.mapped.ILLUMINA.bwa.LWK.exome.20130422	50	0	0	27	39	47	41	30	60	0	0	0	0	0	20	0	60
NA19397.mapped.ILLUMINA.bwa.LWK.exome.20130422	66	31	38	16	50	59	57	38	34	4	18	29	12	36	0	0	39
NA19399.mapped.ILLUMINA.bwa.LWK.exome.20130422	69	1	24	16	55	59	76	52	69	0	19	0	29	0	31	1	67
NA19401.mapped.ILLUMINA.bwa.LWK.exome.20130415	54	0	48	0	41	48	57	33	46	0	29	0	37	0	0	12	45
NA19403.mapped.ILLUMINA.bwa.LWK.exome.20130415	58	0	0	21	27	41	46	49	45	0	0	0	0	0	0	35	58
NA19404.mapped.ILLUMINA.bwa.LWK.exome.20130422	54	0	0	33	19	20	25	24	27	0	6	0	22	35	0	28	55
NA19428.mapped.ILLUMINA.bwa.LWK.exome.20130422	65	0	21	15	43	61	73	49	46	0	15	0	31	0	16	29	58
NA19429.mapped.ILLUMINA.bwa.LWK.exome.20130422	55	26	21	14	38	57	63	45	69	0	10	0	13	0	11	0	43
NA19430.mapped.ILLUMINA.bwa.LWK.exome.20130415	41	0	0	23	37	44	43	39	43	0	0	0	0	1	24	0	55
NA19431.mapped.ILLUMINA.bwa.LWK.exome.20130422	60	0	0	22	37	59	52	36	54	0	0	0	0	0	7	21	58
NA19434.mapped.ILLUMINA.bwa.LWK.exome.20130422	58	0	0	23	37	48	75	43	61	3	0	0	0	0	0	50	79
NA19435.mapped.ILLUMINA.bwa.LWK.exome.20130415	49	0	0	39	43	51	57	40	58	0	0	0	0	0	15	0	63
NA19436.mapped.ILLUMINA.bwa.LWK.exome.20130415	35	0	0	18	24	28	34	28	39	0	0	0	0	0	4	10	41
NA19437.mapped.ILLUMINA.bwa.LWK.exome.20130415	76	0	0	37	51	78	70	43	40	11	16	0	22	44	0	0	45
NA19438.mapped.ILLUMINA.bwa.LWK.exome.20130415	45	1	0	19	36	35	47	32	44	0	0	0	0	0	20	1	48
NA19439.mapped.ILLUMINA.bwa.LWK.exome.20130422	55	32	35	11	49	58	62	46	54	0	15	0	18	1	0	39	66
NA19440.mapped.ILLUMINA.bwa.LWK.exome.20130422	42	0	0	32	18	38	37	21	45	0	0	0	1	0	9	18	43
NA19443.mapped.ILLUMINA.bwa.LWK.exome.20130422	68	38	35	21	35	28	57	31	36	11	15	0	21	37	0	32	74
NA19445.mapped.ILLUMINA.bwa.LWK.exome.20130415	59	0	1	35	23	47	57	42	62	0	0	0	1	0	9	21	59
NA19446.mapped.ILLUMINA.bwa.LWK.exome.20130415	51	0	0	20	32	49	49	29	52	0	0	0	0	0	14	0	47
NA19448.mapped.ILLUMINA.bwa.LWK.exome.20130415	44	0	0	33	54	53	50	44	55	0	0	0	0	0	10	21	61
NA19449.mapped.ILLUMINA.bwa.LWK.exome.20130422	61	36	30	24	24	36	46	35	41	0	16	0	23	25	17	0	88
NA19451.mapped.ILLUMINA.bwa.LWK.exome.20130422	52	0	0	30	30	44	55	28	46	0	0	0	0	0	16	0	53
NA19452.mapped.ILLUMINA.bwa.LWK.exome.20130422	58	0	0	26	38	49	63	41	32	7	15	0	18	25	13	0	65
NA19454.mapped.ILLUMINA.bwa.LWK.exome.20130415	89	2	0	55	96	88	75	74	2	27	67	0	85	93	0	1	101
NA19455.mapped.ILLUMINA.bwa.LWK.exome.20130422	72	0	1	31	54	54	62	63	65	0	11	0	29	1	12	1	55
NA19456.mapped.ILLUMINA.bwa.LWK.exome.20130422	41	40	42	1	18	28	49	37	54	0	8	0	25	0	14	0	37
NA19457.mapped.ILLUMINA.bwa.LWK.exome.20120522	130	0	0	88	156	162	159	136	187	0	0	0	0	0	79	0	130
NA19461.mapped.ILLUMINA.bwa.LWK.exome.20130422	54	0	3	32	46	69	56	44	62	0	0	0	0	1	22	0	63
NA19462.mapped.ILLUMINA.bwa.LWK.exome.20130422	63	24	16	18	17	12	23	17	30	0	4	0	14	23	8	0	47
NA19463.mapped.ILLUMINA.bwa.LWK.exome.20130422	64	37	30	22	32	35	60	41	65	0	0	0	0	0	10	28	87
NA19466.mapped.ILLUMINA.bwa.LWK.exome.20130422	53	30	16	21	24	30	60	37	59	0	0	0	0	0	0	64	74
NA19467.mapped.ILLUMINA.bwa.LWK.exome.20130415	52	0	31	15	45	56	53	37	55	0	3	23	0	0	9	25	55
NA19468.mapped.ILLUMINA.bwa.LWK.exome.20130422	67	61	41	0	66	80	68	55	71	0	23	0	57	0	0	24	49
NA19471.mapped.ILLUMINA.bwa.LWK.exome.20120522	153	0	102	53	202	163	89	194	149	0	68	0	82	1	67	0	176
NA19472.mapped.ILLUMINA.bwa.LWK.exome.20120522	123	0	84	55	122	120	99	102	120	0	53	0	62	0	28	75	113
NA19473.mapped.ILLUMINA.bwa.LWK.exome.20120522	81	80	73	0	0	0	56	37	51	0	26	0	55	55	19	0	86
NA19474.mapped.ILLUMINA.bwa.LWK.exome.20120522	164	94	99	56	120	107	119	151	142	0	0	0	0	0	38	84	154
NA19475.mapped.ILLUMINA.bwa.LWK.exome.20130415	151	215	196	96	182	197	218	167	191	0	176	0	196	195	0	172	230
NA19625.mapped.ILLUMINA.bwa.ASW.exome.20120522	147	95	87	53	156	148	112	110	143	0	48	88	0	1	25	57	154
NA19648.mapped.ILLUMINA.bwa.MXL.exome.20120522	190	143	104	0	208	195	151	147	4	29	175	0	123	223	0	0	223
NA19649.mapped.ILLUMINA.bwa.MXL.exome.20120522	96	0	1	59	121	116	92	93	104	0	0	0	0	0	23	47	118
NA19651.mapped.ILLUMINA.bwa.MXL.exome.20120522	101	62	60	37	121	97	92	91	105	0	45	76	0	0	21	62	128
NA19652.mapped.ILLUMINA.bwa.MXL.exome.20120522	96	73	57	49	55	59	92	71	94	0	0	1	0	0	0	112	114
NA19654.mapped.ILLUMINA.bwa.MXL.exome.20120522	109	62	58	45	118	103	93	76	98	0	44	62	0	0	28	0	111
NA19655.mapped.ILLUMINA.bwa.MXL.exome.20120522	93	0	0	59	94	101	86	74	103	0	0	0	0	0	18	59	107
NA19657.mapped.ILLUMINA.bwa.MXL.exome.20120522	102	0	0	64	102	84	89	71	102	0	1	0	0	0	0	78	100
NA19658.mapped.ILLUMINA.bwa.MXL.exome.20120522	92	60	56	37	58	61	66	75	85	0	0	0	0	0	18	55	95
NA19660.mapped.ILLUMINA.bwa.MXL.exome.20120522	87	56	67	40	52	60	96	91	65	12	39	61	0	58	14	0	118
NA19661.mapped.ILLUMINA.bwa.MXL.exome.20120522	93	0	0	76	98	98	81	77	67	13	40	0	57	67	0	52	112
NA19663.mapped.ILLUMINA.bwa.MXL.exome.20120522	101	68	53	37	145	133	96	78	93	0	68	0	83	1	0	89	121
NA19664.mapped.ILLUMINA.bwa.MXL.exome.20120522	101	50	55	47	120	89	90	69	1	21	97	83	43	95	0	0	113
NA19669.mapped.ILLUMINA.bwa.MXL.exome.20120522	84	55	0	45	106	82	79	71	47	16	34	1	43	61	0	49	110
NA19670.mapped.ILLUMINA.bwa.MXL.exome.20120522	87	0	1	73	103	91	89	63	55	9	44	0	54	59	0	45	115

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA19675.mapped.ILLUMINA.bwa.MXL.exome.20120522	90	0	2	68	111	96	87	87	101	0	0	0	0	0	19	56	99
NA19676.mapped.ILLUMINA.bwa.MXL.exome.20120522	97	50	49	44	104	86	76	63	62	12	74	61	47	54	0	49	114
NA19678.mapped.ILLUMINA.bwa.MXL.exome.20120522	89	0	0	84	111	92	93	72	98	0	0	0	0	1	17	46	113
NA19679.mapped.ILLUMINA.bwa.MXL.exome.20120522	108	62	55	34	125	93	91	66	95	0	39	67	0	0	0	88	112
NA19681.mapped.ILLUMINA.bwa.MXL.exome.20120522	110	0	1	70	109	89	97	75	101	0	0	0	0	0	13	61	98
NA19682.mapped.ILLUMINA.bwa.MXL.exome.20120522	135	0	0	60	133	99	100	77	118	0	1	1	0	0	29	63	114
NA19684.mapped.ILLUMINA.bwa.MXL.exome.20120522	99	58	55	48	67	50	87	74	65	16	40	0	45	71	0	41	90
NA19685.mapped.ILLUMINA.bwa.MXL.exome.20120522	74	2	0	80	99	101	90	79	108	0	0	0	0	2	23	47	108
NA19700.mapped.ILLUMINA.bwa.ASW.exome.20120522	119	53	65	36	61	63	89	77	97	0	0	0	0	2	0	77	98
NA19701.mapped.ILLUMINA.bwa.ASW.exome.20120522	116	68	63	50	58	62	84	91	106	0	0	2	1	1	0	93	100
NA19703.mapped.ILLUMINA.bwa.ASW.exome.20120522	103	56	64	52	69	65	88	79	107	0	0	0	0	0	0	99	119
NA19704.mapped.ILLUMINA.bwa.ASW.exome.20120522	106	0	0	75	111	85	77	87	107	0	0	0	0	3	0	105	107
NA19707.mapped.ILLUMINA.bwa.ASW.exome.20120522	116	0	0	78	109	90	81	75	90	0	0	0	0	0	14	53	111
NA19711.mapped.ILLUMINA.bwa.ASW.exome.20120522	84	50	59	29	122	78	84	70	89	0	45	43	0	1	19	39	115
NA19712.mapped.ILLUMINA.bwa.ASW.exome.20120522	100	95	64	0	0	0	46	36	65	0	35	0	48	67	0	51	107
NA19713.mapped.ILLUMINA.bwa.ASW.exome.20120522	96	0	3	71	115	83	88	71	93	0	0	0	0	3	36	1	119
NA19716.mapped.ILLUMINA.bwa.MXL.exome.20120522	99	57	57	44	60	63	88	74	106	0	1	1	1	1	21	48	115
NA19717.mapped.ILLUMINA.bwa.MXL.exome.20120522	91	1	1	65	101	89	87	78	4	24	71	2	74	100	0	3	121
NA19719.mapped.ILLUMINA.bwa.MXL.exome.20120522	110	0	1	80	105	92	80	70	102	0	0	0	0	0	0	97	100
NA19720.mapped.ILLUMINA.bwa.MXL.exome.20120522	110	0	0	84	108	96	96	83	57	10	39	0	52	64	25	0	114
NA19722.mapped.ILLUMINA.bwa.MXL.exome.20120522	98	68	55	41	59	57	84	81	99	0	0	0	0	0	20	50	106
NA19723.mapped.ILLUMINA.bwa.MXL.exome.20120522	87	64	0	49	114	112	121	83	52	10	36	0	53	63	0	46	126
NA19725.mapped.ILLUMINA.bwa.MXL.exome.20120522	97	0	0	70	94	101	87	88	88	0	0	0	0	1	18	41	109
NA19726.mapped.ILLUMINA.bwa.MXL.exome.20120522	96	0	1	82	107	97	85	79	120	0	0	0	0	1	0	87	121
NA19728.mapped.ILLUMINA.bwa.MXL.exome.20120522	132	111	117	50	202	156	184	225	120	15	138	103	100	107	59	0	143
NA19729.mapped.ILLUMINA.bwa.MXL.exome.20120522	102	0	0	62	122	121	122	121	135	0	0	0	0	0	83	0	89
NA19731.mapped.ILLUMINA.bwa.MXL.exome.20120522	102	0	89	49	164	140	123	120	135	0	85	0	80	0	75	0	98
NA19732.mapped.ILLUMINA.bwa.MXL.exome.20120522	107	0	0	48	127	141	125	155	95	14	75	0	88	105	64	0	96
NA19734.mapped.ILLUMINA.bwa.MXL.exome.20130422	85	0	0	30	55	66	73	47	72	0	0	0	0	0	22	38	78
NA19735.mapped.ILLUMINA.bwa.MXL.exome.20130422	67	37	33	19	49	59	72	48	49	7	29	35	25	39	0	22	82
NA19740.mapped.ILLUMINA.bwa.MXL.exome.20130415	65	0	0	49	50	79	83	58	70	0	0	0	1	1	0	62	78
NA19741.mapped.ILLUMINA.bwa.MXL.exome.20130422	57	22	30	20	15	33	30	25	29	0	12	0	16	40	0	24	69
NA19746.mapped.ILLUMINA.bwa.MXL.exome.20120522	122	0	0	76	180	173	148	172	142	12	98	115	0	117	69	0	147
NA19747.mapped.ILLUMINA.bwa.MXL.exome.20120522	108	0	0	66	150	135	132	135	112	12	92	0	92	114	0	102	114
NA19749.mapped.ILLUMINA.bwa.MXL.exome.20130415	104	3	1	90	168	153	165	165	123	17	80	2	105	109	0	99	136
NA19750.mapped.ILLUMINA.bwa.MXL.exome.20120522	106	120	102	51	105	104	141	147	159	0	0	0	0	0	78	0	135
NA19752.mapped.ILLUMINA.bwa.MXL.exome.20130422	68	1	0	25	38	71	65	60	28	9	8	0	20	32	0	47	70
NA19755.mapped.ILLUMINA.bwa.MXL.exome.20120522	103	118	105	51	192	168	162	168	118	9	148	112	92	117	62	0	147
NA19756.mapped.ILLUMINA.bwa.MXL.exome.20120522	107	99	91	44	166	142	125	142	101	7	141	99	89	105	53	0	105
NA19758.mapped.ILLUMINA.bwa.MXL.exome.20120522	93	0	2	84	114	127	132	142	97	4	78	0	72	102	58	0	103
NA19759.mapped.ILLUMINA.bwa.MXL.exome.20120522	110	0	1	55	154	153	149	159	197	0	0	0	0	0	67	106	109
NA19761.mapped.ILLUMINA.bwa.MXL.exome.20120522	91	0	0	52	115	128	116	111	137	0	0	0	0	1	85	0	100
NA19762.mapped.ILLUMINA.bwa.MXL.exome.20120522	152	118	145	62	137	135	228	168	117	5	80	0	119	162	0	94	197
NA19764.mapped.ILLUMINA.bwa.MXL.exome.20130415	62	0	0	28	36	62	50	49	26	5	17	0	24	28	10	0	73
NA19770.mapped.ILLUMINA.bwa.MXL.exome.20120522	140	105	114	51	210	161	168	147	84	8	124	113	102	127	0	85	158
NA19771.mapped.ILLUMINA.bwa.MXL.exome.20120522	116	0	0	75	183	164	149	145	0	17	114	87	89	159	0	0	148
NA19773.mapped.ILLUMINA.bwa.MXL.exome.20120522	106	0	3	103	197	159	184	136	190	0	0	0	0	0	57	103	163
NA19774.mapped.ILLUMINA.bwa.MXL.exome.20120522	106	0	0	70	150	137	144	154	181	0	0	0	0	0	57	83	131
NA19776.mapped.ILLUMINA.bwa.MXL.exome.20120522	84	81	78	43	98	91	108	105	89	6	66	0	84	88	0	67	99
NA19777.mapped.ILLUMINA.bwa.MXL.exome.20120522	88	0	0	93	115	117	117	144	160	0	0	0	0	1	0	115	93
NA19779.mapped.ILLUMINA.bwa.MXL.exome.20120522	90	0	1	61	119	118	116	103	139	0	0	0	0	0	68	0	99
NA19780.mapped.ILLUMINA.bwa.MXL.exome.20120522	130	0	0	91	192	170	166	162	162	0	0	0	0	0	0	171	137
NA19782.mapped.ILLUMINA.bwa.MXL.exome.20120522	98	0	0	46	108	134	136	148	156	0	0	0	0	0	95	0	113
NA19783.mapped.ILLUMINA.bwa.MXL.exome.20120522	103	106	105	49	112	101	152	132	104	5	73	0	95	112	0	95	148
NA19785.mapped.ILLUMINA.bwa.MXL.exome.20120522	124	2	1	68	188	149	172	196	130	6	99	0	116	125	75	0	113
NA19786.mapped.ILLUMINA.bwa.MXL.exome.20120522	109	0	0	90	189	150	132	145	165	0	0	1	0	0	68	91	111
NA19788.mapped.ILLUMINA.bwa.MXL.exome.20120522	96	87	87	46	99	82	126	130	132	0	0	0	0	0	50	70	95
NA19789.mapped.ILLUMINA.bwa.MXL.exome.20120522	90	0	0	82	135	89	86	65	95	0	0	0	1	92	0	79	96
NA19792.mapped.ILLUMINA.bwa.MXL.exome.20121211	78	1	0	54	93	85	94	72	48	20	32	0	43	68	0	71	93
NA19794.mapped.ILLUMINA.bwa.MXL.exome.20130422	51	35	36	0	0	0	43	32	52	0	0	0	0	0	7	18	56
NA19795.mapped.ILLUMINA.bwa.MXL.exome.20130415	57	0	1	32	32	54	58	39	59	0	0	0	0	0	14	10	63
NA19818.mapped.ILLUMINA.bwa.ASW.exome.20120522	97	67	66	46	73	68	85	80	96	0	0	0	0	1	36	0	147
NA19819.mapped.ILLUMINA.bwa.ASW.exome.20120522	109	1	0	74	145	107	98	86	96	0	0	0	0	0	25	0	105
NA19834.mapped.ILLUMINA.bwa.ASW.exome.20120522	100	1	0	75	57	2	58	51	71	0	41	0	42	71	0	52	105
NA19835.mapped.ILLUMINA.bwa.ASW.exome.20120522	90	58	70	46	133	95	101	78	65	12	64	53	62	61	20	0	116
NA19900.mapped.ILLUMINA.bwa.ASW.exome.20121211	110	0	1	62	133	102	98	87	107	0	41	0	68	2	42	0	126
NA19901.mapped.ILLUMINA.bwa.ASW.exome.20120522	97	0	1	85	102	86	93	71	92	0	0	0	0	1	0	92	114
NA19904.mapped.ILLUMINA.bwa.ASW.exome.20120522	105	0	1	60	85	101	105	77	92	0	0	0	0	0	37	1	114
NA19908.mapped.ILLUMINA.bwa.ASW.exome.20120522	92	60	58	45	74	110	92	81	97	0	0	1	0	0	17	48	119
NA19909.mapped.ILLUMINA.bwa.ASW.exome.20120522	99	58	66	40	61	65	54	53	59	0	44	1	53	53	0	60	109
NA19913.mapped.ILLUMINA.bwa.ASW.exome.20130415	105	148	141	66	154	122	233	192	208	0	0	0	1	0	87	0	164
NA19914.mapped.ILLUMINA.bwa.ASW.exome.20120522	96	57	57	53	93	93	96	83	111	0	41	1	51	0	19	1	78
NA19916.mapped.ILLUMINA.bwa.ASW.exome.20120522	89	0	0	63	96	92	83	82	109	0	1	1	0	2	29	56	105
NA19917.mapped.ILLUMINA.bwa.ASW.exome.20120522	95	56	58	52	118	83	95	79	107	0	46	59	0	0	18	51	118
NA19920.mapped.ILLUMINA.bwa.ASW.exome.20120522	106	60	68	40	79	70	64	36	60	0	57	0	58	68	0	61	112
NA19921.mapped.ILLUMINA.bwa.ASW.exome.20120522	110	87	91	0	69	52	86	81	51	11	62	57	54	68	0	53	103
NA19922.mapped.ILLUMINA.bwa.ASW.exome.20130415	51	13	23	13	32	43	36	26	62	0	10	24	0	0	14	1	67
NA19923.mapped.ILLUMINA.bwa.ASW.exome.20130415	51	0	0	30	21	28	47	21	32	9	6	0	25	18	0	15	46
NA19982.mapped.ILLUMINA.bwa.ASW.exome.20120522	97	98	48	0	119	106	92	61	1	19	110	92	84	104	0	1	124
NA19984.mapped.ILLUMINA.bwa.ASW.exome.20130422	62	0	0	27	36	56	63	46	30	6	14	0	18	37	13	1	70
NA19985.mapped.ILLUMINA.bwa.ASW.exome.20120522	90	2	0	50	146	97	103	94	109	0	0	0	0	0	64	0	95
NA20126.mapped.ILLUMINA.bwa.ASW.exome.20120522	79	113	107	0	112	119	104	118	83	8	133	117	82	88	0	74	84
NA20127.mapped.ILLUMINA.bwa.ASW.exome.20120522	89	0	1	73	129	153	114	114	77	8	62	0	77	95	0	79	83
NA20274.mapped.ILLUMINA.bwa.ASW.exome.20130415	84	163	174	74	280	208	232	216	256	0	125	133	1	0	65	118	170
NA20276.mapped.ILLUMINA.bwa.ASW.exome.20120522	98	111	108	51	181	153	140	146	201	0	74	99	0	0	86	0	124
NA20278.mapped.ILLUMINA.bwa.ASW.exome.20120522	103	0	0	54	167	126	127	144	102	12	80	0	80	96	56	0	111
NA20281.mapped.ILLUMINA.bwa.ASW.exome.20120522	96	0	0	69	131	139	128	141	157	0	0	0	0	0	47	77	116
NA20282.mapped.ILLUMINA.bwa.ASW.exome.20120522	108	116	102	48	95	104	97	86	110	0	73	0	100	110	52	0	115
NA20287.mapped.ILLUMINA.bwa.ASW.exome.20120522	97	94	97	41	173	131	125	161	140	0	78	85	0	0	51	73	97
NA20289.mapped.ILLUMINA.bwa.ASW.exome.20120522	94	0	1	60	129	122	157	141	158	0	1	0	0	0	0	77	79
NA20291.mapped.ILLUMINA.bwa.ASW.exome.20120522	113	106	112	46	202	170	158	128	220	0	79	0	97	0	66	79	129
NA20294.mapped.ILLUMINA.bwa.ASW.exome.20120522	104	0	0	56	94	80	76	84	97	0	85	0	85	103	48	0	100
NA20296.mapped.ILLUMINA.bwa.ASW.exome.20120522	106	101	97	41	172	130	129	136	148	0	70	86	0	0	0	162	105
NA20298.mapped.ILLUMINA.bwa.ASW.exome.20130415	70	0	0	33	39	55	70	42	45	0	0	0	0	0	20	0	66
NA20299.mapped.ILLUMINA.bwa.ASW.exome.20120522	108	0	0	67	160	137	139	133	97	5	78	0	94	104	0	89	124
NA20314.mapped.ILLUMINA.bwa.ASW.exome.20120522	104	0	0	62	125	142	121	131	96	10	89	1	91	113	60	0	110

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA20317.mapped.ILLUMINA.bwa.ASW.exome.20120522	103	92	87	37	94	90	118	115	131	0	81	92	0	0	70	1	105
NA20318.mapped.ILLUMINA.bwa.ASW.exome.20130415	98	1	4	106	282	205	251	197	285	0	99	130	0	1	57	126	180
NA20320.mapped.ILLUMINA.bwa.ASW.exome.20130415	108	2	3	150	248	244	314	223	274	0	0	0	0	0	67	145	203
NA20321.mapped.ILLUMINA.bwa.ASW.exome.20130415	105	212	174	74	149	160	291	283	295	0	0	1	0	0	61	128	194
NA20322.mapped.ILLUMINA.bwa.ASW.exome.20120522	87	89	88	37	77	93	113	142	143	0	0	0	0	0	60	84	90
NA20332.mapped.ILLUMINA.bwa.ASW.exome.20120522	122	111	109	56	181	176	160	149	113	5	137	150	1	109	64	0	135
NA20334.mapped.ILLUMINA.bwa.ASW.exome.20120522	109	1	1	56	189	141	128	141	141	0	0	0	0	0	50	74	112
NA20336.mapped.ILLUMINA.bwa.ASW.exome.20120522	93	81	80	43	150	117	119	112	125	0	67	84	0	0	71	0	93
NA20339.mapped.ILLUMINA.bwa.ASW.exome.20130415	62	27	0	18	25	32	26	15	32	0	13	0	20	31	10	0	62
NA20340.mapped.ILLUMINA.bwa.ASW.exome.20120522	69	89	95	41	148	108	110	125	164	0	83	0	78	0	49	80	86
NA20341.mapped.ILLUMINA.bwa.ASW.exome.20120522	110	0	1	70	174	152	136	140	92	9	131	92	99	109	0	102	107
NA20342.mapped.ILLUMINA.bwa.ASW.exome.20120522	101	88	96	48	83	89	82	75	109	0	76	0	78	85	65	0	116
NA20344.mapped.ILLUMINA.bwa.ASW.exome.20120522	96	0	0	96	144	115	137	154	145	0	0	0	0	0	57	100	90
NA20346.mapped.ILLUMINA.bwa.ASW.exome.20120522	98	95	98	42	169	115	113	153	136	0	67	92	0	0	55	80	88
NA20348.mapped.ILLUMINA.bwa.ASW.exome.20120522	120	0	0	81	186	159	128	143	166	0	0	0	1	0	65	84	140
NA20351.mapped.ILLUMINA.bwa.ASW.exome.20130415	57	0	0	31	54	60	72	45	56	0	23	0	25	0	28	2	76
NA20355.mapped.ILLUMINA.bwa.ASW.exome.20130415	92	185	164	70	262	230	271	201	230	0	125	145	1	0	76	3	171
NA20356.mapped.ILLUMINA.bwa.ASW.exome.20120522	102	122	136	0	136	140	139	148	156	0	136	137	0	0	101	0	114
NA20357.mapped.ILLUMINA.bwa.ASW.exome.20130422	53	0	2	30	51	55	51	41	58	0	1	0	1	0	14	22	64
NA20359.mapped.ILLUMINA.bwa.ASW.exome.20130422	48	0	0	24	31	49	57	32	39	1	0	0	0	0	9	19	58
NA20362.mapped.ILLUMINA.bwa.ASW.exome.20130415	47	61	47	17	61	58	108	84	102	0	0	1	0	1	52	3	86
NA20412.mapped.ILLUMINA.bwa.ASW.exome.20130415	58	25	27	12	14	37	61	37	30	5	11	0	29	22	0	28	74
NA20502.mapped.ILLUMINA.bwa.TSI.exome.20130415	87	1	0	36	45	62	75	62	38	11	18	55	1	48	0	56	88
NA20503.mapped.ILLUMINA.bwa.TSI.exome.20130415	59	34	27	21	45	52	66	38	1	15	42	29	40	55	0	0	72
NA20504.mapped.ILLUMINA.bwa.TSI.exome.20130422	55	0	0	23	46	53	55	40	62	0	0	0	0	0	10	23	71
NA20505.mapped.ILLUMINA.bwa.TSI.exome.20130415	62	23	25	10	49	58	62	36	17	6	23	52	0	25	0	25	58
NA20506.mapped.ILLUMINA.bwa.TSI.exome.20130422	42	29	25	10	17	34	31	27	14	0	16	0	22	35	0	24	55
NA20507.mapped.ILLUMINA.bwa.TSI.exome.20130422	90	2	0	36	49	77	85	60	88	0	0	1	0	0	21	43	83
NA20508.mapped.ILLUMINA.bwa.TSI.exome.20130415	65	32	33	23	44	67	68	44	42	9	22	47	0	40	0	41	73
NA20509.mapped.ILLUMINA.bwa.TSI.exome.20130422	49	37	32	23	56	81	81	60	35	12	47	55	24	38	16	0	60
NA20510.mapped.ILLUMINA.bwa.TSI.exome.20130422	69	48	50	1	84	97	85	80	48	11	51	49	46	47	0	43	77
NA20511.mapped.ILLUMINA.bwa.TSI.exome.20130415	112	2	2	128	256	228	282	251	296	0	0	0	0	0	0	246	184
NA20512.mapped.ILLUMINA.bwa.TSI.exome.20130415	72	58	50	0	46	71	63	54	53	0	30	61	0	0	0	70	72
NA20513.mapped.ILLUMINA.bwa.TSI.exome.20130422	51	33	21	19	28	44	56	29	1	10	37	26	41	54	0	0	59
NA20514.mapped.ILLUMINA.bwa.TSI.exome.20130422	72	45	33	18	66	70	66	64	40	5	42	46	29	48	0	31	87
NA20515.mapped.ILLUMINA.bwa.TSI.exome.20130422	68	0	0	28	46	61	47	29	29	6	12	0	21	38	16	0	68
NA20516.mapped.ILLUMINA.bwa.TSI.exome.20130415	77	34	40	23	33	46	82	50	79	0	0	0	0	0	0	52	80
NA20517.mapped.ILLUMINA.bwa.TSI.exome.20130415	65	0	0	39	52	70	68	46	36	8	13	0	32	27	0	34	62
NA20518.mapped.ILLUMINA.bwa.TSI.exome.20130422	59	21	27	20	28	36	46	45	34	8	21	0	24	29	0	22	65
NA20519.mapped.ILLUMINA.bwa.TSI.exome.20130422	58	29	34	12	25	25	67	43	55	0	0	0	0	0	0	69	67
NA20520.mapped.ILLUMINA.bwa.TSI.exome.20130422	68	2	0	39	65	64	81	46	77	0	1	0	0	1	26	1	68
NA20521.mapped.ILLUMINA.bwa.TSI.exome.20130422	45	0	0	30	33	55	54	32	51	0	0	0	1	0	0	41	60
NA20522.mapped.ILLUMINA.bwa.TSI.exome.20130422	44	0	1	27	34	57	55	46	32	5	11	0	25	37	14	0	80
NA20524.mapped.ILLUMINA.bwa.TSI.exome.20130415	43	23	25	16	34	42	51	37	22	8	18	32	0	21	0	16	56
NA20525.mapped.ILLUMINA.bwa.TSI.exome.20130422	43	2	0	22	60	73	62	59	30	11	44	23	22	30	0	31	61
NA20526.mapped.ILLUMINA.bwa.TSI.exome.20130415	78	0	1	33	61	80	76	54	60	0	2	2	0	2	21	44	72
NA20527.mapped.ILLUMINA.bwa.TSI.exome.20130422	65	44	42	19	35	49	54	34	3	7	44	48	43	76	0	0	86
NA20528.mapped.ILLUMINA.bwa.TSI.exome.20130415	81	0	0	30	59	87	83	57	77	0	0	0	0	1	0	81	84
NA20529.mapped.ILLUMINA.bwa.TSI.exome.20130415	71	1	0	32	92	97	95	105	95	7	19	58	0	0	22	47	79
NA20530.mapped.ILLUMINA.bwa.TSI.exome.20130415	40	25	25	12	15	25	45	26	38	0	1	1	0	0	12	27	58
NA20531.mapped.ILLUMINA.bwa.TSI.exome.20130415	88	34	29	22	34	43	75	55	32	6	25	0	32	42	17	2	77
NA20532.mapped.ILLUMINA.bwa.TSI.exome.20130415	56	21	22	18	19	32	53	27	45	0	0	0	0	0	0	55	65
NA20533.mapped.ILLUMINA.bwa.TSI.exome.20130415	56	0	0	24	36	73	59	46	64	0	0	0	1	0	18	32	77
NA20534.mapped.ILLUMINA.bwa.TSI.exome.20130415	79	57	38	17	92	85	86	59	51	8	54	50	39	53	20	1	72
NA20535.mapped.ILLUMINA.bwa.TSI.exome.20130415	87	1	0	39	59	78	95	61	46	13	23	1	34	47	0	29	91
NA20536.mapped.ILLUMINA.bwa.TSI.exome.20130415	74	0	3	43	55	74	59	62	62	0	0	0	0	0	8	23	67
NA20538.mapped.ILLUMINA.bwa.TSI.exome.20130415	85	53	46	23	61	74	79	69	41	12	49	74	1	49	18	0	92
NA20539.mapped.ILLUMINA.bwa.TSI.exome.20130415	55	2	0	27	36	55	43	54	25	4	19	0	20	28	0	21	65
NA20540.mapped.ILLUMINA.bwa.TSI.exome.20130415	81	25	30	20	31	37	60	66	66	0	0	0	0	0	0	67	85
NA20541.mapped.ILLUMINA.bwa.TSI.exome.20130415	78	34	0	16	33	36	75	68	63	0	0	0	1	0	16	27	85
NA20542.mapped.ILLUMINA.bwa.TSI.exome.20121211	80	101	103	0	67	69	86	72	0	36	113	91	61	100	0	1	86
NA20543.mapped.ILLUMINA.bwa.TSI.exome.20121211	101	88	84	49	154	112	114	90	119	0	58	77	1	0	0	127	94
NA20544.mapped.ILLUMINA.bwa.TSI.exome.20121211	87	0	73	44	77	79	105	92	101	0	1	1	0	1	47	80	103
NA20581.mapped.ILLUMINA.bwa.TSI.exome.20121211	95	94	81	42	127	115	105	83	0	36	126	94	61	115	0	2	102
NA20582.mapped.ILLUMINA.bwa.TSI.exome.20120522	96	0	0	98	126	118	114	82	107	0	0	0	0	0	40	77	91
NA20585.mapped.ILLUMINA.bwa.TSI.exome.20121211	88	0	1	99	125	81	114	96	126	0	0	1	0	0	0	128	99
NA20586.mapped.ILLUMINA.bwa.TSI.exome.20120522	79	81	70	43	73	68	92	92	83	1	0	0	0	0	0	157	85
NA20587.mapped.ILLUMINA.bwa.TSI.exome.20121211	93	0	0	60	91	74	78	77	64	15	39	0	53	73	0	66	100
NA20588.mapped.ILLUMINA.bwa.TSI.exome.20121211	70	109	97	1	64	77	92	76	60	32	82	90	0	73	0	79	95
NA20589.mapped.ILLUMINA.bwa.TSI.exome.20121211	96	0	0	65	121	115	110	84	105	0	0	0	0	0	45	80	97
NA20752.mapped.ILLUMINA.bwa.TSI.exome.20121211	89	0	0	86	133	115	109	97	117	0	0	0	1	0	0	137	104
NA20753.mapped.ILLUMINA.bwa.TSI.exome.20121211	112	0	1	93	154	122	107	99	101	0	0	0	0	0	45	86	97
NA20754.mapped.ILLUMINA.bwa.TSI.exome.20121211	86	88	0	55	137	101	104	91	102	0	0	0	0	0	0	145	97
NA20755.mapped.ILLUMINA.bwa.TSI.exome.20121211	65	108	91	0	0	0	93	85	1	35	92	0	116	102	0	0	79
NA20756.mapped.ILLUMINA.bwa.TSI.exome.20121211	86	97	78	45	148	114	106	87	71	37	84	103	1	81	0	76	100
NA20757.mapped.ILLUMINA.bwa.TSI.exome.20121211	70	0	0	61	119	96	95	92	119	0	0	0	0	0	0	122	82
NA20758.mapped.ILLUMINA.bwa.TSI.exome.20121211	74	89	65	47	65	65	67	52	59	0	50	0	66	75	0	62	90
NA20759.mapped.ILLUMINA.bwa.TSI.exome.20121211	74	0	0	92	109	93	80	65	32	32	34	0	68	66	0	58	94
NA20760.mapped.ILLUMINA.bwa.TSI.exome.20120522	78	82	68	36	120	94	91	77	98	0	44	65	0	0	36	49	111
NA20761.mapped.ILLUMINA.bwa.TSI.exome.20121211	67	0	1	57	102	88	88	81	67	0	0	0	0	0	0	110	78
NA20762.mapped.ILLUMINA.bwa.TSI.exome.20130415	111	167	193	68	309	260	292	226	261	0	128	154	0	2	74	106	189
NA20763.mapped.ILLUMINA.bwa.TSI.exome.20130415	102	378	270	0	246	234	276	236	176	61	303	308	1	159	0	142	197
NA20764.mapped.ILLUMINA.bwa.TSI.exome.20130415	100	29	12	152	284	271	294	236	156	57	166	25	153	173	63	4	194
NA20765.mapped.ILLUMINA.bwa.TSI.exome.20121211	87	91	0	49	144	99	102	88	48	28	54	0	74	77	0	66	104
NA20766.mapped.ILLUMINA.bwa.TSI.exome.20121211	88	80	90	0	113	101	81	80	53	10	90	90	44	62	0	45	117
NA20767.mapped.ILLUMINA.bwa.TSI.exome.20130415	119	305	292	1	168	177	294	280	319	0	145	179	2	0	0	309	208
NA20768.mapped.ILLUMINA.bwa.TSI.exome.20121211	112	1	0	65	100	107	85	83	104	0	1	0	0	0	0	85	100
NA20769.mapped.ILLUMINA.bwa.TSI.exome.20120522	104	0	1	80	100	111	111	87	104	1	0	0	0	0	19	46	114
NA20770.mapped.ILLUMINA.bwa.TSI.exome.20121211	93	58	60	47	111	101	88	83	94	1	46	61	2	0	0	98	111
NA20771.mapped.ILLUMINA.bwa.TSI.exome.20121211	116	0	2	61	110	92	89	90	97	0	1	0	1	0	21	47	111
NA20772.mapped.ILLUMINA.bwa.TSI.exome.20121211	113	72	77	46	74	60	102	93	87	0	1	0	0	0	0	110	127
NA20773.mapped.ILLUMINA.bwa.TSI.exome.20121211	108	92	109	1	109	96	87	106	105	0	79	104	0	2	0	123	118
NA20774.mapped.ILLUMINA.bwa.TSI.exome.20121211	83	61	52	44	115	82	99	67	64	12	62	59	49	66	0	48	117
NA20775.mapped.ILLUMINA.bwa.TSI.exome.20121211	118	55	63	43	61	59	86	65	1	21	76	0	82	110	0	0	118
NA20778.mapped.ILLUMINA.bwa.TSI.exome.20121211	106	66	63	44	126	106	101	72	92	0	44	61	0	0	24	54	112
NA20783.mapped.ILLUMINA.bwa.TSI.exome.20121211	103	62	56	49	113	107	92	82	128	0	45	62	0	0	15	66	118

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA20785.mapped.ILLUMINA.bwa.TSI.exome.20121211	83	0	0	79	98	88	85	68	52	11	38	0	49	57	0	52	110
NA20786.mapped.ILLUMINA.bwa.TSI.exome.20121211	101	89	88	0	102	99	82	80	48	13	80	115	0	59	0	39	100
NA20787.mapped.ILLUMINA.bwa.TSI.exome.20121211	101	0	0	72	114	108	89	78	77	0	0	0	0	1	0	104	119
NA20790.mapped.ILLUMINA.bwa.TSI.exome.20121211	115	0	0	85	101	99	80	59	89	0	0	1	0	0	0	78	114
NA20792.mapped.ILLUMINA.bwa.TSI.exome.20120522	113	1	1	63	101	91	89	82	97	0	0	0	0	2	26	51	119
NA20795.mapped.ILLUMINA.bwa.TSI.exome.20121211	106	52	54	38	55	51	83	85	84	0	0	0	0	0	0	108	106
NA20796.mapped.ILLUMINA.bwa.TSI.exome.20120522	195	1	1	75	143	149	137	113	124	20	47	0	93	106	0	82	185
NA20797.mapped.ILLUMINA.bwa.TSI.exome.20121211	96	77	85	0	0	0	80	81	94	0	0	0	1	0	0	85	110
NA20798.mapped.ILLUMINA.bwa.TSI.exome.20121211	113	0	1	64	110	122	102	95	150	0	0	0	1	1	0	121	162
NA20799.mapped.ILLUMINA.bwa.TSI.exome.20121211	113	65	82	44	81	74	94	95	115	0	0	0	0	0	28	63	117
NA20800.mapped.ILLUMINA.bwa.TSI.exome.20120522	114	0	0	47	105	115	99	121	130	0	0	0	0	1	0	123	124
NA20801.mapped.ILLUMINA.bwa.TSI.exome.20121211	110	0	0	74	119	112	100	118	88	19	51	0	66	80	0	58	122
NA20802.mapped.ILLUMINA.bwa.TSI.exome.20120522	124	0	1	83	132	111	98	121	115	0	0	0	0	0	27	64	128
NA20803.mapped.ILLUMINA.bwa.TSI.exome.20121211	135	0	1	91	139	141	121	100	102	22	54	0	76	93	0	83	173
NA20804.mapped.ILLUMINA.bwa.TSI.exome.20121211	139	84	76	51	170	161	119	112	93	13	82	144	0	96	0	71	145
NA20805.mapped.ILLUMINA.bwa.TSI.exome.20121211	145	0	0	84	134	124	120	108	134	0	0	0	0	1	0	117	176
NA20806.mapped.ILLUMINA.bwa.TSI.exome.20121211	126	0	0	100	123	119	100	129	78	18	47	0	68	94	0	66	135
NA20807.mapped.ILLUMINA.bwa.TSI.exome.20121211	95	77	83	41	83	89	110	112	119	0	0	0	0	0	63	1	97
NA20808.mapped.ILLUMINA.bwa.TSI.exome.20121211	92	0	0	44	130	114	111	114	137	0	0	0	0	0	0	128	105
NA20809.mapped.ILLUMINA.bwa.TSI.exome.20121211	98	0	0	49	130	123	130	158	181	0	0	0	0	1	0	169	122
NA20810.mapped.ILLUMINA.bwa.TSI.exome.20121211	92	86	86	45	159	126	110	120	94	7	136	88	73	99	48	0	103
NA20811.mapped.ILLUMINA.bwa.TSI.exome.20121211	81	90	98	37	157	128	133	123	105	10	108	117	0	98	0	84	90
NA20812.mapped.ILLUMINA.bwa.TSI.exome.20121211	116	117	122	56	190	173	151	132	165	0	99	102	0	0	0	158	137
NA20813.mapped.ILLUMINA.bwa.TSI.exome.20121211	130	118	115	57	195	186	168	130	105	5	141	101	106	120	0	95	142
NA20814.mapped.ILLUMINA.bwa.TSI.exome.20121211	108	109	99	47	184	139	142	163	100	6	126	134	0	102	0	106	115
NA20815.mapped.ILLUMINA.bwa.TSI.exome.20121211	143	122	115	46	134	118	167	229	224	0	0	0	0	0	0	242	151
NA20818.mapped.ILLUMINA.bwa.TSI.exome.20121211	150	1	1	118	292	246	213	255	240	13	107	131	0	1	78	125	135
NA20819.mapped.ILLUMINA.bwa.TSI.exome.20121211	108	111	105	49	205	157	152	145	0	10	177	127	106	182	0	0	131
NA20821.mapped.ILLUMINA.bwa.TSI.exome.20130415	91	0	2	77	149	155	167	148	220	0	0	0	0	0	0	137	107
NA20822.mapped.ILLUMINA.bwa.TSI.exome.20130415	90	0	1	78	158	152	155	198	135	24	106	1	127	135	0	114	126
NA20826.mapped.ILLUMINA.bwa.TSI.exome.20121211	134	135	142	63	135	135	197	165	222	0	0	1	0	1	0	186	143
NA20827.mapped.ILLUMINA.bwa.TSI.exome.20130415	32	62	54	0	8	7	49	34	55	0	34	0	23	44	0	30	65
NA20828.mapped.ILLUMINA.bwa.TSI.exome.20121211	149	116	116	62	140	115	158	188	217	0	0	0	0	0	67	102	143
NA20832.mapped.ILLUMINA.bwa.TSI.exome.20130415	39	1	0	37	82	83	86	73	73	10	38	1	50	55	40	0	70
NA20845.mapped.ILLUMINA.bwa.GIH.exome.20120522	177	76	91	65	92	126	115	112	124	0	1	0	0	1	0	119	158
NA20846.mapped.ILLUMINA.bwa.GIH.exome.20120522	154	2	0	112	134	130	112	142	95	18	67	0	80	101	0	80	166
NA20847.mapped.ILLUMINA.bwa.GIH.exome.20120522	136	82	88	68	138	127	121	115	122	0	56	62	0	0	0	112	127
NA20849.mapped.ILLUMINA.bwa.GIH.exome.20120522	126	83	100	62	106	87	130	108	93	20	58	1	74	98	0	74	154
NA20850.mapped.ILLUMINA.bwa.GIH.exome.20120522	135	99	112	2	95	108	124	104	126	0	63	76	0	1	0	121	149
NA20851.mapped.ILLUMINA.bwa.GIH.exome.20120522	146	94	93	71	160	118	113	130	108	20	98	86	82	105	32	1	155
NA20852.mapped.ILLUMINA.bwa.GIH.exome.20120522	135	0	1	127	122	119	115	136	123	0	0	1	0	2	35	86	157
NA20853.mapped.ILLUMINA.bwa.GIH.exome.20120522	123	109	100	0	79	82	100	103	85	17	74	75	63	82	0	78	141
NA20854.mapped.ILLUMINA.bwa.GIH.exome.20121211	161	89	93	70	170	118	121	119	103	19	93	77	89	95	0	78	162
NA20856.mapped.ILLUMINA.bwa.GIH.exome.20120522	182	85	89	57	139	115	100	139	96	20	88	88	73	88	41	0	144
NA20858.mapped.ILLUMINA.bwa.GIH.exome.20120522	138	124	114	0	0	138	116	122	143	0	0	1	0	2	0	134	192
NA20859.mapped.ILLUMINA.bwa.GIH.exome.20120522	141	85	92	58	151	126	112	132	122	0	63	80	1	1	35	75	159
NA20861.mapped.ILLUMINA.bwa.GIH.exome.20121211	159	121	116	1	94	87	110	115	102	23	89	120	1	92	0	70	159
NA20862.mapped.ILLUMINA.bwa.GIH.exome.20120522	161	2	3	83	140	122	124	126	3	25	95	90	79	134	0	0	156
NA20863.mapped.ILLUMINA.bwa.GIH.exome.20121211	94	89	74	42	84	66	104	86	88	0	0	0	0	0	0	114	84
NA20864.mapped.ILLUMINA.bwa.GIH.exome.20121211	78	0	0	54	126	105	88	84	105	0	0	0	0	0	0	109	82
NA20866.mapped.ILLUMINA.bwa.GIH.exome.20120522	148	114	127	2	2	92	119	117	135	0	0	1	0	2	0	114	167
NA20867.mapped.ILLUMINA.bwa.GIH.exome.20120522	85	107	111	0	143	103	105	89	0	38	140	107	84	118	0	0	92
NA20868.mapped.ILLUMINA.bwa.GIH.exome.20120522	69	85	65	38	79	84	75	53	0	28	74	0	103	108	0	0	96
NA20869.mapped.ILLUMINA.bwa.GIH.exome.20120522	130	94	86	63	96	92	85	82	3	14	89	0	101	129	0	0	150
NA20870.mapped.ILLUMINA.bwa.GIH.exome.20120522	136	122	119	2	139	109	121	115	128	0	98	106	2	3	0	115	143
NA20871.mapped.ILLUMINA.bwa.GIH.exome.20120522	186	0	1	118	131	115	126	110	1	31	86	1	111	128	0	1	163
NA20872.mapped.ILLUMINA.bwa.GIH.exome.20120522	143	0	1	86	136	109	110	136	80	22	57	0	71	91	0	77	152
NA20874.mapped.ILLUMINA.bwa.GIH.exome.20120522	133	112	115	2	102	91	106	122	93	17	84	105	0	103	0	82	134
NA20875.mapped.ILLUMINA.bwa.GIH.exome.20120522	139	89	88	61	106	89	121	127	134	0	0	0	0	0	0	112	180
NA20876.mapped.ILLUMINA.bwa.GIH.exome.20120522	145	83	86	70	101	100	134	112	94	22	66	0	77	93	0	80	164
NA20877.mapped.ILLUMINA.bwa.GIH.exome.20120522	140	0	1	84	132	122	116	130	128	1	0	0	1	2	29	61	149
NA20878.mapped.ILLUMINA.bwa.GIH.exome.20120522	121	77	72	57	80	77	80	65	87	0	53	0	65	87	0	77	136
NA20881.mapped.ILLUMINA.bwa.GIH.exome.20120522	129	0	2	114	99	122	132	120	131	0	0	1	0	1	0	149	155
NA20882.mapped.ILLUMINA.bwa.GIH.exome.20130415	41	38	57	0	22	23	51	36	36	5	37	53	0	38	0	18	53
NA20884.mapped.ILLUMINA.bwa.GIH.exome.20130415	56	34	29	14	46	62	52	47	34	6	27	28	27	32	0	32	65
NA20885.mapped.ILLUMINA.bwa.GIH.exome.20120522	130	0	0	75	133	124	116	104	141	0	0	0	0	2	0	105	160
NA20886.mapped.ILLUMINA.bwa.GIH.exome.20120522	136	80	86	62	92	95	129	159	144	0	1	1	0	1	0	166	168
NA20887.mapped.ILLUMINA.bwa.GIH.exome.20120522	143	83	81	72	157	126	116	126	4	30	104	89	102	136	0	2	178
NA20888.mapped.ILLUMINA.bwa.GIH.exome.20120522	138	90	93	52	103	98	104	87	95	0	57	0	74	125	0	98	174
NA20889.mapped.ILLUMINA.bwa.GIH.exome.20120522	144	86	89	63	161	144	125	122	92	27	101	80	86	96	0	80	158
NA20890.mapped.ILLUMINA.bwa.GIH.exome.20120522	163	0	6	84	195	150	137	164	138	17	64	81	1	0	39	80	139
NA20891.mapped.ILLUMINA.bwa.GIH.exome.20120522	135	1	3	114	133	121	113	120	135	0	0	0	0	0	0	114	147
NA20892.mapped.ILLUMINA.bwa.GIH.exome.20120522	146	88	83	60	92	91	120	116	141	0	0	1	0	1	0	120	146
NA20893.mapped.ILLUMINA.bwa.GIH.exome.20120522	145	0	2	71	101	105	93	126	148	0	0	0	0	1	0	134	123
NA20894.mapped.ILLUMINA.bwa.GIH.exome.20120522	165	87	95	57	84	92	95	75	1	23	84	0	113	123	0	1	145
NA20895.mapped.ILLUMINA.bwa.GIH.exome.20120522	179	77	94	62	94	91	93	83	93	0	57	0	84	99	0	89	150
NA20896.mapped.ILLUMINA.bwa.GIH.exome.20120522	135	113	86	1	94	97	111	145	132	0	0	1	0	1	0	126	144
NA20897.mapped.ILLUMINA.bwa.GIH.exome.20120522	159	2	3	123	131	129	121	127	96	20	60	1	72	96	0	83	164
NA20898.mapped.ILLUMINA.bwa.GIH.exome.20120522	129	81	94	74	162	131	137	142	142	0	61	85	1	2	0	123	148
NA20899.mapped.ILLUMINA.bwa.GIH.exome.20120522	141	125	123	1	2	4	4	2	2	0	80	0	105	148	0	1	148
NA20900.mapped.ILLUMINA.bwa.GIH.exome.20130415	94	141	116	65	220	166	181	136	128	33	138	157	0	116	0	112	127
NA20901.mapped.ILLUMINA.bwa.GIH.exome.20120522	171	81	88	59	143	118	123	108	4	27	121	85	94	136	0	0	148
NA20902.mapped.ILLUMINA.bwa.GIH.exome.20120522	147	2	0	111	128	129	110	109	3	26	90	0	92	132	0	1	161
NA20903.mapped.ILLUMINA.bwa.GIH.exome.20120522	151	0	3	118	137	127	131	115	2	32	88	0	103	135	0	0	153
NA20904.mapped.ILLUMINA.bwa.GIH.exome.20120522	168	2	0	76	138	124	109	155	145	0	1	1	1	3	33	87	150
NA20905.mapped.ILLUMINA.bwa.GIH.exome.20120522	132	101	104	1	110	92	106	94	123	0	84	119	0	1	0	103	118
NA20906.mapped.ILLUMINA.bwa.GIH.exome.20120522	148	88	84	68	176	126	111	123	112	19	103	96	97	103	0	90	181
NA20908.mapped.ILLUMINA.bwa.GIH.exome.20120522	141	91	98	55	152	123	119	146	124	0	59	74	0	0	34	77	151
NA20910.mapped.ILLUMINA.bwa.GIH.exome.20120522	143	2	0	91	134	123	128	138	213	0	0	0	0	0	0	100	188
NA20911.mapped.ILLUMINA.bwa.GIH.exome.20120522	130	88	1	75	155	121	115	115	93	21	57	4	75	86	0	78	161
NA21086.mapped.ILLUMINA.bwa.GIH.exome.20120522	138	0	1	99	132	115	111	134	135	0	0	0	0	0	0	116	169
NA21087.mapped.ILLUMINA.bwa.GIH.exome.20120522	120	76	74	59	97	85	78	70	1	15	82	0	98	132	0	0	146
NA21088.mapped.ILLUMINA.bwa.GIH.exome.20120522	145	0	2	85	143	119	112	124	95	23	56	0	63	94	0	78	146
NA21089.mapped.ILLUMINA.bwa.GIH.exome.20120522	126	110	0	44	209	169	144	128	117	12	73	0	97	108	0	93	133
NA21090.mapped.ILLUMINA.bwa.GIH.exome.20120522	129	0	0	95	165	165	153	162	173	0	0	0	0	0	0	156	142
NA21091.mapped.ILLUMINA.bwa.GIH.exome.20120522	127	104	109	47	105	99	102	73	0	11	116	0	146	175	0	0	138

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA21092.mapped.ILLUMINA.bwa.GIH.exome.20120522	133	162	182	0	0	2	116	89	119	0	89	0	116	128	0	98	142
NA21093.mapped.ILLUMINA.bwa.GIH.exome.20120522	128	1	1	86	118	103	110	136	120	0	0	0	0	2	0	101	129
NA21094.mapped.ILLUMINA.bwa.GIH.exome.20121211	124	106	115	49	183	138	163	148	161	0	87	101	0	1	0	145	114
NA21095.mapped.ILLUMINA.bwa.GIH.exome.20121211	129	69	83	61	153	105	98	107	118	0	57	70	1	2	0	145	133
NA21097.mapped.ILLUMINA.bwa.GIH.exome.20120522	147	201	230	0	0	0	1	0	0	0	157	0	198	223	0	0	189
NA21098.mapped.ILLUMINA.bwa.GIH.exome.20120522	134	192	182	0	126	124	187	165	172	0	74	112	0	1	63	99	155
NA21099.mapped.ILLUMINA.bwa.GIH.exome.20120522	111	121	112	49	209	170	155	142	122	12	146	120	109	124	0	96	142
NA21100.mapped.ILLUMINA.bwa.GIH.exome.20120522	138	165	139	0	129	129	113	98	0	18	201	129	157	184	0	0	148
NA21101.mapped.ILLUMINA.bwa.GIH.exome.20120522	126	150	158	0	110	115	163	125	113	10	136	117	95	125	0	91	133
NA21102.mapped.ILLUMINA.bwa.GIH.exome.20120522	136	0	1	97	188	187	199	180	201	0	0	1	0	0	59	117	143
NA21103.mapped.ILLUMINA.bwa.GIH.exome.20120522	113	0	0	63	153	160	155	169	187	0	0	0	0	0	0	185	132
NA21104.mapped.ILLUMINA.bwa.GIH.exome.20130415	52	23	27	11	23	29	55	40	52	0	0	0	0	0	3	29	67
NA21105.mapped.ILLUMINA.bwa.GIH.exome.20130415	69	36	1	35	48	69	92	67	59	9	0	0	0	0	0	49	72
NA21106.mapped.ILLUMINA.bwa.GIH.exome.20130415	64	25	0	30	43	62	77	41	28	7	13	0	25	40	0	30	88
NA21107.mapped.ILLUMINA.bwa.GIH.exome.20130415	74	34	23	16	58	72	72	58	42	7	38	34	21	47	13	0	85
NA21108.mapped.ILLUMINA.bwa.GIH.exome.20130415	74	0	0	27	56	71	65	65	60	0	0	0	0	1	0	69	82
NA21109.mapped.ILLUMINA.bwa.GIH.exome.20130415	66	37	38	8	34	39	46	25	28	0	25	0	32	42	0	44	74
NA21110.mapped.ILLUMINA.bwa.GIH.exome.20130415	72	0	0	41	56	60	83	63	45	6	24	0	35	38	12	0	79
NA21111.mapped.ILLUMINA.bwa.GIH.exome.20130415	62	0	0	36	43	66	72	46	65	0	0	0	0	0	0	64	80
NA21112.mapped.ILLUMINA.bwa.GIH.exome.20130415	69	25	25	14	40	41	73	59	0	14	40	0	48	71	0	0	83
NA21113.mapped.ILLUMINA.bwa.GIH.exome.20130415	53	0	1	18	39	50	48	37	36	0	0	0	0	0	0	49	66
NA21114.mapped.ILLUMINA.bwa.GIH.exome.20120522	132	97	103	1	88	76	103	128	126	0	57	76	0	0	31	73	126
NA21115.mapped.ILLUMINA.bwa.GIH.exome.20130415	75	31	21	14	23	41	50	38	61	0	0	0	0	0	12	31	65
NA21116.mapped.ILLUMINA.bwa.GIH.exome.20130415	68	0	0	25	43	58	55	42	50	4	14	0	26	34	8	0	70
NA21117.mapped.ILLUMINA.bwa.GIH.exome.20130415	56	27	19	16	30	27	55	35	35	6	10	0	21	28	0	24	56
NA21118.mapped.ILLUMINA.bwa.GIH.exome.20130415	66	0	0	24	38	60	41	41	19	4	15	1	24	31	6	0	63
NA21119.mapped.ILLUMINA.bwa.GIH.exome.20130415	57	0	0	41	27	71	43	38	47	0	0	0	0	1	10	32	56
NA21120.mapped.ILLUMINA.bwa.GIH.exome.20130415	49	0	0	22	41	50	37	38	25	6	6	0	26	24	8	1	56
NA21122.mapped.ILLUMINA.bwa.GIH.exome.20130415	61	29	38	17	22	39	63	37	53	0	0	0	1	1	0	50	61
NA21123.mapped.ILLUMINA.bwa.GIH.exome.20130415	71	38	35	11	40	55	59	37	25	8	22	26	20	25	0	29	57
NA21124.mapped.ILLUMINA.bwa.GIH.exome.20130415	92	83	89	1	81	70	70	49	2	15	80	56	67	89	0	0	101
NA21125.mapped.ILLUMINA.bwa.GIH.exome.20130415	70	22	24	12	29	22	35	21	0	9	24	0	40	48	0	0	68
NA21126.mapped.ILLUMINA.bwa.GIH.exome.20121211	103	78	82	0	80	80	80	88	89	0	48	62	0	2	31	65	128
NA21127.mapped.ILLUMINA.bwa.GIH.exome.20130415	95	144	147	0	0	0	150	199	122	24	106	0	106	109	0	103	112
NA21128.mapped.ILLUMINA.bwa.GIH.exome.20130415	111	167	174	71	286	247	291	227	161	39	254	184	157	145	0	131	228
NA21129.mapped.ILLUMINA.bwa.GIH.exome.20130415	80	55	44	45	68	52	72	64	83	0	1	2	0	1	36	0	97
NA21130.mapped.ILLUMINA.bwa.GIH.exome.20130415	106	175	199	68	395	288	404	310	247	46	206	273	2	1	0	228	197
NA21133.mapped.ILLUMINA.bwa.GIH.exome.20130415	83	134	126	50	238	162	177	203	161	0	109	131	0	1	56	103	125
NA21135.mapped.ILLUMINA.bwa.GIH.exome.20130415	88	195	183	0	128	124	139	120	0	39	241	177	146	163	0	1	125
NA21137.mapped.ILLUMINA.bwa.GIH.exome.20120522	182	0	0	84	134	121	113	121	144	0	0	0	0	0	0	118	175
NA21141.mapped.ILLUMINA.bwa.GIH.exome.20121211	81	81	71	42	66	69	106	81	87	0	0	0	0	0	0	122	92
NA21142.mapped.ILLUMINA.bwa.GIH.exome.20121211	90	1	1	88	113	97	104	86	103	0	0	0	0	0	0	129	98
NA21143.mapped.ILLUMINA.bwa.GIH.exome.20121211	82	0	0	98	125	118	109	97	64	35	54	0	75	78	0	81	101
NA21144.mapped.ILLUMINA.bwa.GIH.exome.20121211	100	115	115	1	111	106	112	89	63	31	118	106	73	73	0	76	103
TCGA-02-0003-10A-01D-1490-08_GBM	125	0	0	70	117	115	94	135	106	0	0	0	0	1	0	168	115
TCGA-02-0033-10A-01D-1490-08_GBM	117	84	74	48	96	99	80	88	91	0	66	1	80	91	39	2	134
TCGA-02-0047-10A-01D-1490-08_GBM	140	79	82	48	86	75	98	142	125	0	0	0	0	0	41	89	109
TCGA-02-0055-10A-01D-1490-08_GBM	114	69	81	46	82	73	91	138	103	0	0	0	0	1	36	76	121
TCGA-02-2470-10A-01D-1494-08_GBM	136	0	1	75	125	101	109	104	83	23	61	0	75	88	0	84	140
TCGA-02-2483-10A-01D-1494-08_GBM	110	2	0	53	112	119	93	111	1	28	86	0	89	107	0	0	115
TCGA-02-2485-10A-01D-1494-08_GBM	116	0	4	87	119	115	87	153	135	0	0	0	1	0	0	128	131
TCGA-02-2486-10A-01D-1494-08_GBM	127	95	96	3	5	2	111	119	120	0	0	2	0	2	49	1	129
TCGA-05-4244-10A-01D-1105-08_LUAD	105	78	77	45	91	78	95	99	84	17	51	0	65	81	0	69	119
TCGA-05-4249-10A-01D-1105-08_LUAD	116	0	0	62	111	115	97	124	104	0	0	0	0	1	0	88	116
TCGA-05-4250-10A-01D-1105-08_LUAD	113	0	0	82	109	120	93	94	126	0	0	0	0	2	0	124	107
TCGA-05-4382-10A-01D-1265-08_LUAD	98	71	75	44	87	82	90	94	74	16	47	0	58	78	26	1	107
TCGA-05-4384-10A-01D-1753-08_LUAD	93	0	0	61	86	101	82	71	84	0	0	0	0	1	0	71	129
TCGA-05-4389-10A-01D-1265-08_LUAD	116	62	79	49	153	128	96	97	3	30	89	100	64	115	0	0	128
TCGA-05-4390-10A-01D-1753-08_LUAD	93	0	1	73	83	91	106	91	57	16	31	0	40	70	0	44	105
TCGA-05-4395-10A-01D-1265-08_LUAD	133	1	0	82	112	113	103	109	119	0	1	1	1	1	0	100	121
TCGA-05-4396-10A-01D-1855-08_LUAD	153	1	1	76	166	123	133	120	72	22	79	85	62	80	0	65	123
TCGA-05-4397-10A-01D-1265-08_LUAD	121	0	0	58	123	121	110	111	100	0	0	0	1	1	0	89	131
TCGA-05-4398-10A-01D-1265-08_LUAD	150	0	0	77	133	109	93	110	117	0	0	1	1	0	49	0	120
TCGA-05-4402-10A-01D-1265-08_LUAD	132	1	0	62	111	79	76	85	88	0	0	0	0	91	30	0	88
TCGA-05-4403-10A-01D-1265-08_LUAD	118	97	89	1	95	95	106	118	69	19	73	87	70	77	0	70	119
TCGA-05-4405-10A-01D-1855-08_LUAD	137	0	1	65	103	90	95	115	127	0	1	0	0	0	25	68	125
TCGA-05-4410-10A-01D-1855-08_LUAD	155	71	69	47	72	76	101	111	116	0	0	0	0	0	35	66	121
TCGA-05-4415-10A-01D-1855-08_LUAD	122	0	0	76	108	79	108	121	101	0	0	0	0	1	0	132	117
TCGA-05-4417-10A-01D-1855-08_LUAD	119	70	71	55	150	74	76	66	1	19	88	101	0	106	0	0	93
TCGA-05-4418-10A-01D-1265-08_LUAD	124	72	83	51	152	112	103	104	93	20	80	86	74	90	0	58	127
TCGA-05-4420-10A-01D-1265-08_LUAD	121	0	0	85	124	109	107	96	93	16	47	0	68	86	0	75	121
TCGA-05-4422-10A-01D-1265-08_LUAD	124	81	78	43	95	85	99	107	129	0	0	0	0	2	0	98	127
TCGA-05-4424-10A-01D-1855-08_LUAD	145	0	1	104	110	104	95	95	132	0	0	0	0	2	0	91	118
TCGA-05-4425-10A-01D-1753-08_LUAD	103	66	76	44	67	62	89	87	86	0	0	2	0	1	0	95	122
TCGA-05-4426-10A-01D-1265-08_LUAD	126	94	105	1	131	108	103	96	3	25	106	128	68	112	0	1	122
TCGA-05-4427-10A-01D-1855-08_LUAD	122	80	72	60	85	77	91	119	116	0	0	0	0	0	0	120	140
TCGA-05-4430-10A-01D-1265-08_LUAD	118	0	2	60	112	107	105	89	95	18	50	0	74	93	0	74	110
TCGA-05-4432-10A-01D-1265-08_LUAD	122	3	0	54	119	103	92	131	137	0	2	4	2	5	0	120	118
TCGA-05-4433-10A-01D-1855-08_LUAD	104	76	72	57	125	98	105	88	85	0	47	67	0	1	0	90	108
TCGA-05-4434-10A-01D-1265-08_LUAD	158	0	1	89	125	112	104	96	87	23	47	0	77	96	0	68	126
TCGA-05-5423-10A-01D-1625-08_LUAD	113	0	0	73	106	95	105	92	99	0	0	0	3	0	0	95	122
TCGA-05-5425-10A-01D-1625-08_LUAD	136	1	1	77	110	101	99	94	130	0	0	0	0	1	0	105	120
TCGA-05-5428-10A-01D-1625-08_LUAD	105	0	2	79	110	97	108	86	83	13	33	0	53	68	0	61	126
TCGA-05-5429-10A-01D-1625-08_LUAD	100	66	69	41	62	66	110	92	101	0	0	0	0	1	0	100	126
TCGA-05-5715-10A-01D-1625-08_LUAD	111	71	72	42	67	85	102	82	74	15	40	1	61	82	0	49	126
TCGA-06-0119-10A-01D-1490-08_GBM	104	1	2	60	112	99	95	97	78	16	49	3	71	80	0	75	121
TCGA-06-0122-10A-01D-1490-08_GBM	101	73	78	41	78	81	90	117	100	0	1	0	0	2	34	73	116
TCGA-06-0124-10A-01D-1490-08_GBM	104	72	102	47	78	77	109	116	80	23	71	1	91	74	0	69	106
TCGA-06-0125-10A-01D-1490-08_GBM	112	78	75	43	132	102	102	122	97	1	58	77	2	1	0	128	118
TCGA-06-0126-10A-01D-1490-08_GBM	93	69	71	47	69	67	88	116	71	17	53	70	1	82	0	61	103
TCGA-06-0128-10A-01D-1490-08_GBM	106	1	0	56	113	105	86	102	131	0	1	1	0	3	0	99	124
TCGA-06-0129-10A-01D-1490-08_GBM	136	74	79	54	135	106	106	136	88	19	71	87	69	83	32	0	108
TCGA-06-0130-10A-01D-1490-08_GBM	101	84	67	43	83	86	85	108	116	0	0	1	0	0	33	68	111
TCGA-06-0132-10A-01D-1491-08_GBM	97	68	72	40	81	81	90	117	92	0	0	1	1	1	0	93	101
TCGA-06-0137-10A-01D-1490-08_GBM	99	68	76	43	80	76	92	92	108	0	0	0	0	0	54	3	105
TCGA-06-0139-10A-01D-1490-08_GBM	109	71	77	45	132	107	103	113	80	16	73	105	0	85	0	71	122

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-06-0140-10A-01D-1490-08_GBM	105	0	0	83	104	100	90	83	121	1	0	0	2	1	0	90	116
TCGA-06-0141-10A-01D-1490-08_GBM	84	46	49	24	54	52	77	77	53	18	25	59	0	63	0	38	85
TCGA-06-0142-10A-01D-1490-08_GBM	131	60	67	41	113	83	86	105	74	16	73	65	59	71	0	69	105
TCGA-06-0145-10A-01D-1490-08_GBM	113	0	1	59	114	99	94	88	100	0	0	0	0	1	0	95	114
TCGA-06-0151-10A-01D-1491-08_GBM	96	0	0	49	97	100	90	127	64	23	52	0	57	77	0	74	100
TCGA-06-0152-10A-01D-1492-08_GBM	97	0	1	57	105	90	82	90	75	21	60	0	71	66	0	86	100
TCGA-06-0154-10A-01D-1491-08_GBM	119	73	88	58	107	78	112	115	102	24	70	2	84	83	0	76	106
TCGA-06-0155-10A-01D-1492-08_GBM	110	78	77	45	86	92	99	108	112	0	0	1	0	0	33	75	121
TCGA-06-0157-10A-01D-1491-08_GBM	99	1	1	47	106	91	87	143	120	0	0	1	0	0	0	152	105
TCGA-06-0158-10A-01D-1491-08_GBM	111	0	0	64	104	83	76	80	2	22	54	0	70	111	0	1	81
TCGA-06-0165-10A-01D-1491-08_GBM	105	0	1	83	95	107	90	89	84	20	56	1	67	84	0	79	101
TCGA-06-0166-10A-01D-1491-08_GBM	104	66	75	49	91	77	88	101	98	0	0	1	1	1	48	0	93
TCGA-06-0167-10A-01D-1491-08_GBM	126	2	0	57	111	95	103	122	105	0	1	1	0	0	42	82	108
TCGA-06-0168-10A-01D-1491-08_GBM	95	1	0	43	105	93	89	100	69	22	55	0	58	90	0	81	97
TCGA-06-0169-10A-01D-1490-08_GBM	105	1	5	84	107	94	93	109	121	0	0	1	1	1	35	75	108
TCGA-06-0171-10A-01D-1491-08_GBM	111	71	0	44	137	95	88	135	80	20	64	0	71	82	33	0	96
TCGA-06-0173-10B-01D-1491-08_GBM	91	67	80	42	121	101	85	135	112	0	46	74	0	0	33	74	109
TCGA-06-0174-10B-01D-1491-08_GBM	97	91	102	0	104	102	85	82	72	20	80	105	0	83	0	69	125
TCGA-06-0178-10B-01D-1491-08_GBM	108	0	0	57	106	103	84	127	97	0	0	0	0	0	0	147	105
TCGA-06-0184-10B-01D-1491-08_GBM	128	74	74	41	82	80	86	101	2	24	70	0	84	93	0	2	101
TCGA-06-0185-10B-01D-1491-08_GBM	124	0	0	81	100	91	80	148	108	0	0	0	0	1	35	74	106
TCGA-06-0187-10B-01D-1491-08_GBM	108	74	77	43	81	76	85	111	127	0	0	0	1	0	37	80	112
TCGA-06-0188-10B-01D-1491-08_GBM	101	0	2	63	95	94	89	106	118	0	0	0	0	1	34	80	109
TCGA-06-0189-10A-01D-1491-08_GBM	135	68	65	59	72	79	83	98	99	0	1	0	0	4	49	11	99
TCGA-06-0190-10B-01D-1491-08_GBM	130	85	98	59	171	128	116	145	86	21	93	100	89	103	34	4	155
TCGA-06-0192-10A-01D-1492-08_GBM	114	73	75	48	158	119	95	151	127	0	63	94	0	1	0	167	109
TCGA-06-0195-10A-01D-1491-08_GBM	104	0	2	51	95	60	63	58	72	0	0	0	0	73	0	70	82
TCGA-06-0209-10A-01D-1491-08_GBM	149	0	2	79	107	100	88	97	94	0	1	0	0	0	35	74	111
TCGA-06-0210-10A-01D-1491-08_GBM	117	1	3	83	100	90	83	102	85	17	61	82	2	77	0	77	123
TCGA-06-0211-10A-01D-1491-08_GBM	93	0	0	54	100	100	90	106	94	0	0	0	0	1	0	102	98
TCGA-06-0213-10A-01D-1491-08_GBM	120	0	0	75	105	85	79	93	91	0	0	0	1	1	54	1	88
TCGA-06-0214-10A-01D-1491-08_GBM	111	72	75	43	88	74	92	114	79	20	56	0	76	87	0	79	106
TCGA-06-0216-10A-01D-1492-08_GBM	103	3	0	77	97	90	85	138	104	1	1	0	0	1	0	147	101
TCGA-06-0219-10A-01D-1491-08_GBM	134	0	2	82	99	99	96	97	122	0	1	4	1	0	0	140	110
TCGA-06-0221-10A-01D-1491-08_GBM	112	71	74	47	118	97	83	121	81	21	79	84	71	83	0	85	108
TCGA-06-0237-10A-01D-1491-08_GBM	93	72	64	51	130	88	88	110	83	16	62	104	0	79	31	3	107
TCGA-06-0238-10A-01D-1492-08_GBM	103	73	72	43	84	82	89	103	112	0	0	1	1	0	0	110	106
TCGA-06-0240-10A-01D-1491-08_GBM	101	0	0	51	108	94	85	134	82	18	53	0	72	80	0	83	106
TCGA-06-0241-10A-01D-1491-08_GBM	99	85	84	1	78	85	93	92	122	1	49	81	0	1	0	116	108
TCGA-06-0644-10A-01D-1492-08_GBM	91	75	88	0	78	65	85	119	83	24	75	86	0	73	33	0	105
TCGA-06-0645-10A-01D-1492-08_GBM	98	70	72	47	80	68	78	119	114	0	0	1	2	0	31	83	93
TCGA-06-0646-10A-01D-1492-08_GBM	88	70	73	46	78	81	80	115	114	0	0	1	0	0	0	131	98
TCGA-06-0648-10A-01D-1492-08_GBM	132	1	2	76	108	93	88	126	83	0	0	0	0	1	0	142	102
TCGA-06-0649-10A-01D-1492-08_GBM	120	74	80	46	141	103	93	145	121	0	63	86	0	2	0	105	103
TCGA-06-0650-10A-01D-1696-08_GBM	127	68	64	51	75	73	87	102	104	0	1	1	0	0	28	57	112
TCGA-06-0686-10A-01D-1492-08_GBM	142	1	0	88	136	114	100	140	107	0	0	1	0	2	0	165	133
TCGA-06-0743-10A-01D-1492-08_GBM	114	78	71	47	140	102	96	111	122	0	57	78	0	0	0	117	124
TCGA-06-0744-10A-01D-1492-08_GBM	113	89	100	5	2	6	89	127	77	14	60	1	61	87	32	1	108
TCGA-06-0745-10A-01D-1492-08_GBM	115	2	2	80	123	112	86	141	74	17	54	1	72	75	0	90	122
TCGA-06-0747-10A-01D-1492-08_GBM	96	74	69	45	83	78	84	118	120	0	0	1	0	0	35	76	108
TCGA-06-0749-10A-01D-1492-08_GBM	116	1	2	54	118	99	104	117	81	21	62	0	69	92	32	1	112
TCGA-06-0750-10A-01D-1492-08_GBM	107	67	71	42	134	102	84	131	75	20	91	109	0	72	0	72	113
TCGA-06-0875-10A-01D-1492-08_GBM	114	79	86	47	156	115	100	100	114	0	52	93	0	0	54	1	132
TCGA-06-0876-10A-01D-1492-08_GBM	107	62	65	45	80	77	92	120	73	21	68	0	59	75	36	1	108
TCGA-06-0877-10A-01D-1492-08_GBM	112	99	87	1	97	85	103	154	78	21	88	77	76	85	0	89	120
TCGA-06-0878-10A-01D-1492-08_GBM	100	0	3	48	107	110	116	124	89	19	69	0	72	95	36	2	104
TCGA-06-0879-10A-01D-1492-08_GBM	112	72	76	53	158	111	98	141	102	0	68	78	0	1	0	170	117
TCGA-06-0881-10A-01D-1492-08_GBM	118	81	74	51	153	105	94	108	116	0	57	93	0	0	51	1	118
TCGA-06-0882-10A-01D-1492-08_GBM	123	2	4	58	103	105	103	106	126	0	1	1	1	0	0	121	109
TCGA-06-0939-10A-01D-1353-08_GBM	145	73	92	46	182	133	120	140	92	23	80	98	71	90	0	81	149
TCGA-06-1804-10A-01D-1696-08_GBM	97	58	80	49	78	69	95	113	108	0	0	0	0	2	32	60	121
TCGA-06-1806-10B-01D-1845-08_GBM	124	0	0	90	108	108	97	114	118	0	0	0	0	1	34	70	129
TCGA-06-2557-10A-01D-1494-08_GBM	108	0	2	78	119	106	103	143	97	0	0	0	0	3	31	0	92
TCGA-06-2558-10A-01D-1494-08_GBM	151	74	82	48	126	114	108	95	106	0	50	78	0	0	53	3	129
TCGA-06-2559-10A-01D-1494-08_GBM	112	1	1	63	112	114	98	128	118	0	0	0	0	1	32	81	108
TCGA-06-2561-10A-01D-1494-08_GBM	117	0	0	57	118	116	102	95	78	21	49	91	1	79	0	73	114
TCGA-06-2562-10A-01D-1494-08_GBM	120	0	2	69	107	119	102	118	109	0	0	0	3	2	44	2	129
TCGA-06-2563-10A-01D-1494-08_GBM	113	2	2	87	130	109	99	133	96	22	56	0	67	98	37	3	135
TCGA-06-2564-10A-01D-1494-08_GBM	125	76	83	52	145	111	104	132	88	20	80	89	74	85	36	1	132
TCGA-06-2565-10A-01D-1494-08_GBM	98	127	79	0	87	83	77	75	4	21	93	69	80	110	0	0	120
TCGA-06-2567-10A-01D-1494-08_GBM	125	95	109	0	3	2	100	138	130	0	0	0	0	1	37	73	126
TCGA-06-2569-10A-01D-1494-08_GBM	119	75	77	49	84	83	94	117	81	20	60	1	73	94	0	70	129
TCGA-06-2570-10A-01D-1495-08_GBM	123	2	2	87	134	103	96	115	114	0	0	1	0	1	0	112	136
TCGA-06-5408-10A-01D-1696-08_GBM	103	68	74	42	120	98	87	93	106	0	39	71	1	1	0	121	117
TCGA-06-5410-10A-01D-1696-08_GBM	133	70	65	40	123	101	105	95	76	27	75	58	51	84	0	67	111
TCGA-06-5411-10A-01D-1696-08_GBM	134	1	0	62	105	93	84	87	99	0	0	0	0	2	26	63	115
TCGA-06-5412-10A-01D-1696-08_GBM	100	50	61	47	61	60	61	60	69	0	43	0	57	73	27	1	119
TCGA-06-5413-10A-01D-1696-08_GBM	107	2	1	79	96	93	91	122	116	0	0	0	0	2	26	57	119
TCGA-06-5414-10A-01D-1486-08_GBM	107	74	73	55	142	101	98	91	75	20	75	77	66	88	0	74	116
TCGA-06-5415-10A-01D-1486-08_GBM	116	76	78	58	143	109	105	157	135	0	64	88	0	3	0	160	129
TCGA-06-5416-10A-01D-1486-08_GBM	142	0	2	80	96	91	99	87	130	0	1	1	0	2	0	100	131
TCGA-06-5417-10A-01D-1486-08_GBM	110	0	1	87	105	89	100	155	127	0	2	1	0	1	37	88	120
TCGA-06-5418-10A-01D-1486-08_GBM	118	73	76	47	147	104	96	114	84	22	89	86	72	79	0	81	127
TCGA-06-5856-10A-01D-1696-08_GBM	94	0	0	61	89	101	87	105	98	0	0	0	1	1	34	59	115
TCGA-06-5858-10A-01D-1696-08_GBM	102	0	1	76	96	85	85	98	112	0	2	3	0	3	29	56	108
TCGA-06-5859-10A-01D-1696-08_GBM	99	0	0	66	107	95	87	98	107	0	0	0	0	1	0	80	106
TCGA-06-6388-10A-01D-1845-08_GBM	113	69	78	53	134	97	107	121	81	14	88	72	66	85	33	0	140
TCGA-06-6389-10A-01D-1696-08_GBM	92	66	65	36	76	71	77	90	64	16	37	1	62	78	0	70	113
TCGA-06-6390-10A-01D-1696-08_GBM	127	64	67	51	72	86	85	109	118	0	0	0	0	1	23	54	120
TCGA-06-6391-10A-01D-1696-08_GBM	95	1	1	60	103	90	79	102	69	15	44	3	48	71	0	74	117
TCGA-06-6693-10A-01D-1845-08_GBM	123	73	75	49	121	108	117	114	70	17	101	75	67	87	0	62	143
TCGA-06-6694-10A-01D-1845-08_GBM	123	81	94	57	85	1	96	102	1	26	82	1	98	105	0	0	95
TCGA-06-6695-10A-01D-1845-08_GBM	129	0	2	101	122	99	114	147	122	0	0	0	2	0	0	128	127
TCGA-06-6697-10A-01D-1845-08_GBM	129	0	0	100	113	109	91	135	122	0	0	2	0	0	0	129	148
TCGA-06-6698-10A-01D-1845-08_GBM	102	64	64	52	63	69	100	129	134	0	0	1	0	0	33	64	120
TCGA-06-6699-10A-01D-1845-08_GBM	118	79	78	0	78	76	100	144	134	0	1	0	0	0	32	79	122

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-06-6700-10A-01D-1845-08_GBM	130	72	70	54	73	76	74	68	75	0	53	0	72	91	0	73	126
TCGA-06-6701-10A-01D-1845-08_GBM	125	77	70	53	76	82	94	105	130	0	1	0	0	0	0	100	132
TCGA-06-A5U0-10A-01D-A33W-08_GBM	76	58	53	40	61	81	72	66	80	0	0	0	0	0	34	0	83
TCGA-06-A5U1-10A-01D-A33W-08_GBM	85	0	0	70	77	87	71	88	83	0	0	0	0	0	20	52	85
TCGA-06-A6S0-10A-01D-A33W-08_GBM	77	73	47	0	81	73	67	78	55	18	66	46	53	63	0	47	85
TCGA-06-A6S1-10A-01D-A33W-08_GBM	82	0	1	52	103	75	71	72	88	0	35	51	0	0	34	0	89
TCGA-09-2044-10A-01D-0704-01_OV	126	83	77	52	76	74	92	94	79	20	54	0	66	84	0	68	130
TCGA-12-0615-10A-01D-1492-08_GBM	94	0	1	50	90	92	91	128	108	0	0	0	0	2	0	135	106
TCGA-12-0616-10A-01D-1492-08_GBM	104	71	67	44	83	72	80	123	119	0	1	0	0	5	41	80	106
TCGA-12-0618-10A-01D-1492-08_GBM	91	1	1	76	91	87	76	114	91	0	0	0	0	0	35	66	91
TCGA-12-0619-10A-01D-1492-08_GBM	95	61	65	41	71	70	88	124	100	1	0	1	0	0	0	140	101
TCGA-12-0688-10A-01D-1492-08_GBM	117	69	82	47	83	82	97	136	131	0	1	0	0	0	41	85	124
TCGA-12-0692-10A-01D-1492-08_GBM	80	1	0	50	82	67	68	71	66	0	0	0	1	0	0	62	70
TCGA-12-0821-10A-01D-1492-08_GBM	117	70	78	48	91	6	70	78	87	0	1	0	0	86	35	4	88
TCGA-12-1597-10A-01D-1495-08_GBM	115	61	75	40	84	70	67	64	76	0	45	0	62	73	0	68	103
TCGA-12-3649-10A-01D-1495-08_GBM	96	2	4	88	99	94	97	92	115	1	1	1	0	4	0	114	113
TCGA-12-3650-10A-01D-1495-08_GBM	94	64	76	42	120	79	90	98	81	16	71	82	59	74	0	61	93
TCGA-12-3652-10A-01D-1495-08_GBM	112	92	91	0	103	108	85	132	83	17	89	102	71	82	0	76	121
TCGA-12-3653-10A-01D-1495-08_GBM	102	66	81	45	118	103	98	125	80	19	75	72	74	83	0	64	104
TCGA-12-5295-10A-01D-1486-08_GBM	119	0	0	64	114	112	102	112	120	0	2	1	2	0	43	2	124
TCGA-12-5299-10A-01D-1486-08_GBM	154	95	102	2	2	1	106	133	100	21	72	1	78	85	32	0	128
TCGA-12-5301-10A-01D-1486-08_GBM	110	2	2	67	136	109	102	118	84	15	49	0	68	85	33	6	121
TCGA-13-0751-10A-01D-0446-08_OV	218	0	0	103	199	199	152	143	1	34	112	0	145	183	0	0	238
TCGA-13-0757-10A-01D-0356-01_OV	191	85	87	50	170	105	110	152	99	26	93	104	77	97	39	0	146
TCGA-13-0758-10A-01D-0356-01_OV	224	135	113	58	247	165	135	140	175	0	95	133	0	4	58	2	219
TCGA-13-0883-10A-01D-0399-01_OV	411	191	206	66	417	363	219	202	202	27	213	301	1	235	0	203	392
TCGA-13-0886-10A-01D-0399-01_OV	271	0	2	88	242	214	149	206	269	0	0	2	0	5	0	290	245
TCGA-13-0888-10A-01D-0399-01_OV	246	126	114	52	137	112	151	188	143	0	0	0	0	2	0	229	213
TCGA-13-0891-10A-01D-0399-01_OV	199	119	114	56	117	107	138	171	131	0	0	0	0	1	0	245	155
TCGA-13-0899-10A-01D-0399-01_OV	301	127	120	58	130	126	141	166	128	27	92	0	101	131	53	0	224
TCGA-13-0904-10A-01D-0399-01_OV	270	156	124	57	181	158	143	146	256	0	0	0	0	2	0	222	266
TCGA-13-0911-10A-01D-0399-01_OV	215	1	0	97	185	163	126	155	217	0	0	0	0	1	68	0	198
TCGA-13-0913-10A-01D-0399-01_OV	212	103	106	47	129	120	141	194	184	0	0	0	0	1	0	279	190
TCGA-13-0916-10A-01D-0399-01_OV	273	0	1	68	237	146	107	151	163	0	0	0	0	0	0	221	161
TCGA-13-0921-10A-01D-0399-01_OV	277	131	118	50	139	134	192	178	195	0	0	0	0	3	0	152	243
TCGA-13-0923-10A-01D-0399-01_OV	296	0	0	74	226	223	163	142	161	30	99	0	118	121	0	129	216
TCGA-13-1477-10A-01D-0472-01_OV	229	154	133	0	180	139	137	163	124	23	158	181	0	119	0	98	167
TCGA-13-1485-10A-01D-0472-01_OV	199	99	111	48	200	167	125	123	139	0	92	105	0	1	0	137	161
TCGA-13-1495-10A-01D-0472-01_OV	315	0	0	101	204	193	163	254	221	0	0	0	0	1	0	261	275
TCGA-13-1500-10A-01D-0472-01_OV	197	1	1	69	165	145	130	132	104	27	74	2	88	126	0	99	198
TCGA-13-1505-10A-01D-0472-01_OV	243	0	0	69	183	161	133	181	155	0	0	0	0	0	0	260	212
TCGA-13-2057-10A-01D-1526-09_OV	141	154	145	0	0	1	108	81	87	0	106	0	102	115	0	124	117
TCGA-13-2059-10A-01D-1526-09_OV	96	0	0	99	132	117	120	134	77	21	72	0	93	107	0	92	102
TCGA-13-2061-10A-01D-1526-09_OV	117	0	1	116	162	161	151	129	135	0	0	0	0	0	0	190	156
TCGA-13-2065-10A-01D-1526-09_OV	161	0	1	103	210	192	182	190	158	0	0	0	0	0	93	156	153
TCGA-13-2066-10A-01D-1526-09_OV	122	0	0	113	162	158	136	180	124	0	0	0	0	0	0	198	117
TCGA-13-2071-10A-01D-1526-09_OV	146	133	122	59	205	184	147	183	0	31	259	139	172	181	0	0	134
TCGA-14-0736-10C-01D-2280-08_GBM	99	85	77	0	88	74	83	80	108	0	35	0	51	1	35	0	111
TCGA-14-0740-10B-01D-1845-08_GBM	142	0	1	85	114	117	115	116	128	0	0	0	0	0	43	3	137
TCGA-14-0781-10A-01D-1696-08_GBM	95	64	65	42	103	90	86	87	109	0	41	66	0	1	36	2	113
TCGA-14-0786-10A-01D-1492-08_GBM	127	95	100	1	1	4	100	137	132	0	0	1	0	1	0	159	129
TCGA-14-0787-10A-01D-1492-08_GBM	122	80	85	46	90	91	99	141	98	20	68	0	74	79	43	0	122
TCGA-14-0789-10A-01D-1492-08_GBM	109	0	1	81	99	94	82	106	105	0	0	0	0	3	31	71	112
TCGA-14-0790-10A-01D-1494-08_GBM	145	1	2	85	113	101	104	120	85	20	49	2	68	87	0	76	139
TCGA-14-0813-10A-01D-1492-08_GBM	104	2	1	88	109	96	84	146	113	0	0	0	0	0	34	63	125
TCGA-14-0817-10A-01D-1492-08_GBM	100	2	1	62	115	96	83	101	89	0	0	0	0	0	0	100	107
TCGA-14-0862-10C-01D-1845-08_GBM	110	0	0	90	104	98	92	121	115	0	1	0	0	0	35	64	110
TCGA-14-0871-10A-01D-1492-08_GBM	119	95	98	2	84	83	90	95	1	32	100	111	74	103	0	1	124
TCGA-14-1034-10A-01D-1492-08_GBM	122	0	1	88	124	123	104	131	145	0	0	0	2	3	35	74	129
TCGA-14-1043-10A-01D-1845-08_GBM	129	73	74	58	81	77	103	135	133	0	0	1	0	0	36	67	139
TCGA-14-1395-10A-01D-1845-08_GBM	111	0	0	98	107	117	105	95	140	0	0	0	1	1	0	95	135
TCGA-14-1450-10B-01D-1845-08_GBM	112	99	108	0	101	137	108	121	80	12	96	96	65	73	30	0	119
TCGA-14-1456-10A-01D-1494-08_GBM	120	0	1	92	126	122	94	134	121	0	0	0	1	0	31	70	138
TCGA-14-1823-10A-01D-1494-08_GBM	116	3	1	54	95	101	82	101	113	0	1	3	0	2	31	71	91
TCGA-14-1825-10A-01D-1494-08_GBM	116	0	2	84	113	106	91	128	88	22	57	2	78	95	0	79	119
TCGA-14-1829-10A-01D-1494-08_GBM	128	77	84	49	142	120	96	117	117	0	64	83	2	1	68	0	119
TCGA-14-2554-10A-01D-1494-08_GBM	122	83	82	55	91	97	76	90	101	1	51	90	1	92	0	86	129
TCGA-14-3476-10A-01D-1353-08_GBM	118	73	78	58	145	125	151	125	79	22	70	124	0	90	0	71	132
TCGA-14-4157-10A-01D-1353-08_GBM	137	109	111	2	101	95	106	114	119	0	48	89	0	0	0	123	152
TCGA-15-0742-10A-01D-1492-08_GBM	119	78	82	47	81	79	99	107	89	0	0	1	1	0	0	118	117
TCGA-15-1444-10A-01D-1696-08_GBM	100	90	85	2	62	74	83	96	111	0	44	67	1	1	0	89	116
TCGA-16-0846-10A-01D-1492-08_GBM	102	87	86	1	84	80	102	120	96	12	56	76	0	1	0	105	99
TCGA-16-0848-10A-01D-1492-08_GBM	102	3	0	81	125	117	90	107	101	0	2	0	0	4	36	82	99
TCGA-16-0861-10A-01D-1492-08_GBM	105	2	2	66	113	107	77	142	89	20	67	2	67	96	0	90	126
TCGA-16-1045-10B-01D-1492-08_GBM	114	1	1	64	119	117	105	118	2	31	77	82	70	118	0	0	119
TCGA-16-1048-10A-01D-1353-08_GBM	167	0	1	93	140	133	124	158	118	0	0	1	0	1	0	148	170
TCGA-19-1390-10C-01D-1495-08_GBM	107	78	1	49	137	100	91	93	82	17	56	1	68	85	0	80	121
TCGA-19-1787-10A-01D-1495-08_GBM	127	0	0	80	101	99	82	112	126	0	0	0	0	0	39	74	118
TCGA-19-1790-10B-01D-1353-08_GBM	135	0	2	99	157	140	123	159	171	0	0	0	0	0	41	92	157
TCGA-19-2619-10A-01D-1495-08_GBM	104	71	77	46	136	102	106	135	80	27	78	76	61	77	31	13	114
TCGA-19-2620-10A-01D-1495-08_GBM	109	1	4	75	98	91	95	118	101	0	0	0	0	1	30	72	113
TCGA-19-2623-10A-01D-1495-08_GBM	112	70	74	44	89	78	87	110	125	0	1	0	0	0	0	139	115
TCGA-19-2624-10A-01D-1495-08_GBM	108	1	1	83	100	81	78	83	84	0	0	0	0	76	29	1	90
TCGA-19-2625-10A-01D-1495-08_GBM	132	1	4	87	164	112	109	102	75	28	78	75	66	79	0	72	109
TCGA-19-2629-10A-01D-1495-08_GBM	97	79	76	45	145	99	95	90	102	0	57	81	2	2	49	0	103
TCGA-19-2631-10B-01D-1353-08_GBM	136	1	1	67	130	124	113	145	153	0	1	0	1	2	35	73	147
TCGA-19-4065-10A-01D-2280-08_GBM	127	56	57	46	81	67	78	89	92	0	0	0	0	1	25	59	99
TCGA-19-4068-10A-01D-1353-08_GBM	131	84	93	59	153	124	99	132	138	0	44	81	1	2	37	74	140
TCGA-19-5947-10A-01D-1696-08_GBM	101	0	0	57	121	105	85	116	118	0	0	0	0	3	42	64	124
TCGA-19-5950-10A-01D-1696-08_GBM	97	0	1	59	109	106	91	119	115	1	1	0	0	1	0	111	107
TCGA-19-5951-10A-01D-1696-08_GBM	106	1	3	62	102	80	115	135	69	27	52	1	53	71	0	62	127
TCGA-19-5952-10A-01D-1696-08_GBM	107	73	63	37	122	100	93	108	99	0	45	64	1	1	25	69	123
TCGA-19-5953-10A-01D-1845-08_GBM	121	102	106	0	81	68	95	100	127	0	60	88	1	1	0	110	162
TCGA-19-5954-10A-01D-1696-08_GBM	108	65	67	40	111	98	91	102	64	21	67	96	0	80	0	61	128
TCGA-19-5955-10A-01D-1696-08_GBM	107	0	1	74	93	91	88	99	72	11	46	0	55	72	0	60	105
TCGA-19-5956-10A-01D-1696-08_GBM	146	66	89	50	74	71	94	100	116	0	1	0	1	0	37	72	125

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-19-5958-10A-01D-1696-08_GBM	118	69	71	42	72	66	86	100	69	15	41	3	59	74	0	66	111
TCGA-19-5959-10A-01D-1696-08_GBM	110	0	0	57	100	85	77	71	64	13	31	63	0	69	0	39	106
TCGA-19-5960-10A-01D-1696-08_GBM	101	65	61	42	69	62	95	99	64	13	37	4	51	73	0	51	108
TCGA-19-A60I-10A-01D-A33W-08_GBM	85	61	63	46	101	79	73	82	78	0	42	62	0	0	29	62	86
TCGA-19-A6J4-10A-01D-A33W-08_GBM	81	0	1	69	82	76	67	80	101	0	0	0	0	0	0	76	90
TCGA-19-A6J5-10A-01D-A33W-08_GBM	67	52	48	39	70	73	61	75	77	0	36	0	42	0	30	0	61
TCGA-20-0991-10A-01D-0428-01_OV	155	0	3	55	166	133	120	209	153	0	0	0	0	0	0	221	162
TCGA-21-1081-10B-01D-1521-08_LUSC	125	79	84	60	149	109	102	140	105	1	70	100	0	3	0	175	154
TCGA-21-1082-10B-01D-1521-08_LUSC	112	0	2	61	122	107	106	102	113	0	0	1	1	1	0	109	129
TCGA-21-5782-10A-01D-1632-08_LUSC	106	99	90	2	62	63	89	85	73	16	58	107	1	67	0	50	123
TCGA-21-5783-10A-01D-2184-08_LUSC	105	0	0	53	70	84	76	75	56	12	39	0	44	65	0	56	93
TCGA-21-5784-10A-01D-1632-08_LUSC	89	59	64	35	65	59	96	80	1	18	58	1	78	105	0	2	119
TCGA-21-5786-10A-01D-1632-08_LUSC	117	0	1	73	115	106	98	87	118	0	0	0	0	0	23	62	114
TCGA-21-5787-10A-01D-1632-08_LUSC	103	55	67	38	73	56	90	82	110	0	0	2	0	0	21	59	123
TCGA-21-A5DI-10A-01D-A26K-08_LUSC	100	0	1	76	93	88	96	91	69	9	42	1	56	70	30	2	110
TCGA-22-A5C4-10A-01D-A27N-08_LUSC	78	0	1	64	81	79	67	77	95	0	1	0	0	0	0	98	82
TCGA-23-1110-10A-01D-0428-01_OV	237	0	3	66	152	156	142	170	194	0	0	0	0	1	52	124	220
TCGA-23-2641-10A-01D-1526-09_OV	111	112	107	58	99	100	130	129	149	0	0	0	0	0	0	167	111
TCGA-23-2643-10A-01D-1526-09_OV	112	117	126	0	96	112	112	185	162	0	105	103	0	0	87	137	98
TCGA-23-2647-10A-01D-1526-09_OV	164	118	98	61	189	177	133	104	104	0	66	87	0	0	98	111	127
TCGA-23-2649-10A-01D-1526-09_OV	108	136	129	0	104	100	119	146	147	0	97	93	0	0	74	118	100
TCGA-24-1430-10A-01D-0472-01_OV	314	216	194	2	1	2	149	136	154	0	101	0	107	130	0	138	268
TCGA-24-1431-10A-01D-0472-01_OV	243	0	1	109	194	183	124	209	121	26	103	0	117	135	0	138	224
TCGA-25-1319-10A-01D-0452-01_OV	150	0	0	83	126	112	90	152	133	0	0	0	0	0	45	84	109
TCGA-25-2397-10A-01D-0704-01_OV	122	70	72	43	87	69	89	107	73	18	51	0	72	76	0	75	106
TCGA-25-2398-10A-01D-0704-01_OV	154	0	1	107	152	119	108	164	143	0	0	0	0	0	0	178	180
TCGA-26-1439-10A-01D-1353-08_GBM	114	61	81	52	92	80	95	100	101	0	2	1	0	0	25	67	136
TCGA-26-1442-10A-01D-1696-08_GBM	91	77	80	0	65	58	108	121	92	14	41	62	1	1	30	63	109
TCGA-26-5132-10A-01D-1486-08_GBM	143	75	72	43	143	103	100	92	110	0	64	82	1	1	45	10	118
TCGA-26-5133-10A-01D-1486-08_GBM	152	81	80	50	83	84	88	101	127	0	0	0	1	2	0	101	119
TCGA-26-5134-10A-01D-1486-08_GBM	100	3	2	62	118	111	84	131	103	0	0	1	3	2	0	158	119
TCGA-26-5135-10A-01D-1486-08_GBM	119	2	2	60	112	111	99	103	91	0	1	0	0	0	0	105	119
TCGA-26-5136-10A-01D-1486-08_GBM	105	65	76	48	79	80	89	103	97	0	0	0	0	1	0	107	113
TCGA-26-5139-10A-01D-1486-08_GBM	129	1	0	66	113	103	109	142	91	17	62	0	75	89	42	0	137
TCGA-26-6173-10A-01D-1845-08_GBM	120	1	2	112	111	108	106	97	77	16	56	1	64	87	0	73	129
TCGA-26-6174-10A-01D-1845-08_GBM	123	108	116	2	95	83	104	124	100	14	84	103	0	89	0	82	140
TCGA-27-1830-10A-01D-1494-08_GBM	127	0	0	87	121	118	94	116	135	0	1	1	0	0	0	134	121
TCGA-27-1831-10A-01D-1494-08_GBM	124	81	85	53	100	94	78	77	5	18	81	0	93	129	0	0	130
TCGA-27-1832-10A-01D-1494-08_GBM	120	1	1	78	124	102	81	79	74	0	0	0	0	2	0	74	82
TCGA-27-1833-10A-01D-1494-08_GBM	125	74	80	53	91	93	97	161	132	0	1	0	1	2	41	89	127
TCGA-27-1834-10A-01D-1494-08_GBM	114	0	1	54	111	119	90	151	120	0	0	0	0	1	0	138	118
TCGA-27-1835-10A-01D-1494-08_GBM	122	75	82	52	153	116	99	155	136	1	53	93	0	0	0	161	124
TCGA-27-1836-10A-01D-1494-08_GBM	120	0	0	97	131	111	94	104	108	0	0	0	1	1	47	0	128
TCGA-27-1837-10A-01D-1494-08_GBM	113	77	80	51	94	85	107	106	121	0	0	0	0	0	0	110	136
TCGA-27-1838-10A-01D-1494-08_GBM	137	76	89	51	106	80	96	122	121	0	0	0	0	2	0	119	137
TCGA-27-2518-10A-01D-1494-08_GBM	120	77	86	53	96	87	95	126	113	0	0	1	1	0	39	77	122
TCGA-27-2519-10A-01D-1494-08_GBM	117	85	77	54	94	79	73	85	4	19	70	0	94	116	0	2	119
TCGA-27-2521-10A-01D-1494-08_GBM	136	0	4	89	127	111	109	118	122	0	0	0	0	0	0	120	134
TCGA-27-2523-10A-01D-1494-08_GBM	110	1	1	72	113	112	111	122	119	1	1	1	0	0	0	158	120
TCGA-27-2524-10A-01D-1494-08_GBM	117	1	5	59	126	105	108	130	116	0	2	0	3	4	36	80	123
TCGA-27-2526-10A-01D-1494-08_GBM	113	1	2	94	119	104	91	107	123	0	0	0	2	0	0	93	128
TCGA-27-2527-10A-01D-1494-08_GBM	130	87	82	50	147	109	82	86	2	24	90	91	79	94	0	1	120
TCGA-27-2528-10A-01D-1494-08_GBM	116	0	1	61	148	112	111	122	92	24	61	1	81	84	35	0	138
TCGA-28-1747-10B-01D-1494-08_GBM	132	1	0	70	116	113	96	129	139	0	0	0	0	1	29	77	128
TCGA-28-1753-10B-01D-1494-08_GBM	124	2	1	100	132	130	107	139	96	0	1	0	0	1	37	78	113
TCGA-28-2499-10A-01D-1494-08_GBM	106	2	0	59	120	111	92	151	134	0	1	0	0	1	0	139	122
TCGA-28-2501-10A-01D-1696-08_GBM	89	1	1	54	100	88	83	74	1	19	59	0	78	102	0	0	106
TCGA-28-2502-10A-01D-1494-08_GBM	134	81	79	51	173	123	112	151	118	0	64	92	1	0	0	161	132
TCGA-28-2509-10A-01D-1494-08_GBM	149	103	99	2	80	88	90	110	86	22	72	98	4	92	36	0	121
TCGA-28-2510-10A-01D-1696-08_GBM	112	62	66	41	121	97	97	82	103	0	28	65	0	1	39	1	115
TCGA-28-2513-10A-01D-1494-08_GBM	112	1	2	73	145	124	112	137	125	0	0	0	0	0	41	79	144
TCGA-28-2514-10A-01D-1494-08_GBM	126	0	2	63	114	112	91	107	127	0	0	1	1	2	0	101	127
TCGA-28-5204-10A-01D-1486-08_GBM	105	99	108	2	86	87	101	129	85	17	84	79	73	86	0	78	129
TCGA-28-5207-10A-01D-1486-08_GBM	125	7	8	64	120	98	110	102	112	0	2	7	1	8	0	107	150
TCGA-28-5208-10A-01D-1486-08_GBM	119	88	85	47	93	88	148	127	132	0	0	2	1	1	0	155	143
TCGA-28-5209-10A-01D-1486-08_GBM	133	0	1	95	204	142	139	176	89	26	95	86	81	89	0	88	169
TCGA-28-5211-10B-01D-1845-08_GBM	118	0	1	78	105	103	98	96	108	0	0	1	0	0	47	0	137
TCGA-28-5213-10A-01D-1486-08_GBM	118	85	87	58	138	113	107	139	123	0	59	86	0	2	0	163	131
TCGA-28-5214-10A-01D-1486-08_GBM	126	86	83	53	106	86	99	114	110	0	0	2	1	2	49	1	147
TCGA-28-5215-10A-01D-1486-08_GBM	120	75	84	44	88	83	98	103	109	0	0	0	0	2	51	0	127
TCGA-28-5216-10A-01D-1486-08_GBM	113	82	86	55	87	90	97	111	125	0	1	0	0	1	0	116	121
TCGA-28-5218-10A-01D-1486-08_GBM	131	82	75	57	90	86	107	118	3	28	85	0	101	118	0	1	132
TCGA-28-5219-10A-01D-1486-08_GBM	118	2	0	66	120	113	102	133	128	1	1	1	1	3	37	74	119
TCGA-28-5220-10A-01D-1486-08_GBM	120	1	0	78	107	111	109	134	122	0	0	0	1	2	39	71	129
TCGA-28-6450-10A-01D-1696-08_GBM	91	91	92	3	103	102	96	86	74	18	78	116	3	68	0	61	113
TCGA-29-2429-10A-01D-1526-09_OV	117	115	101	49	105	106	133	144	161	0	0	0	0	0	70	107	110
TCGA-29-2431-10A-01D-1526-09_OV	124	117	92	61	106	103	143	135	133	0	0	0	0	0	0	191	121
TCGA-29-2432-10A-01D-1526-09_OV	109	0	1	108	138	138	131	128	146	0	0	0	0	0	0	199	104
TCGA-29-2434-10A-01D-1526-09_OV	131	0	0	106	157	160	126	147	113	0	0	0	0	0	0	202	105
TCGA-29-2436-10A-01D-1526-09_OV	140	0	0	89	179	174	136	205	131	0	0	0	0	0	0	296	120
TCGA-32-1970-10A-01D-1494-08_GBM	131	74	81	49	140	124	101	148	117	0	56	93	1	2	0	144	128
TCGA-32-1977-10C-01D-1353-08_GBM	130	75	74	48	153	124	101	95	87	25	65	90	71	96	0	66	127
TCGA-32-1979-10A-01D-1696-08_GBM	111	0	1	85	90	92	89	97	84	0	0	0	0	1	0	116	113
TCGA-32-1980-10A-01D-1696-08_GBM	95	73	65	43	63	66	89	78	101	0	0	1	0	6	35	0	100
TCGA-32-1982-10A-01D-1494-08_GBM	139	93	106	0	91	93	103	139	114	1	64	0	0	0	0	153	130
TCGA-32-1986-10A-01D-1494-08_GBM	119	0	1	52	116	103	98	125	134	0	0	1	1	0	0	136	126
TCGA-32-1991-10C-01D-1353-08_GBM	135	1	0	95	125	127	109	130	103	0	0	0	1	0	0	153	145
TCGA-32-2491-10A-01D-1353-08_GBM	113	74	80	46	144	110	121	109	86	20	74	132	0	78	0	67	134
TCGA-32-2494-10A-01D-1353-08_GBM	135	73	72	50	91	76	106	133	98	25	46	0	67	98	30	1	142
TCGA-32-2495-10B-01D-1353-08_GBM	133	75	82	53	98	92	104	121	146	0	0	0	0	2	0	104	134
TCGA-32-2498-10B-01D-1353-08_GBM	125	83	82	53	159	111	107	111	87	21	69	124	0	103	33	0	126
TCGA-32-2615-10A-01D-1495-08_GBM	99	0	2	57	91	92	94	113	98	0	1	0	0	0	0	91	127
TCGA-32-2616-10A-01D-1495-08_GBM	100	1	5	53	104	99	85	111	86	16	57	71	9	80	34	5	105
TCGA-32-2632-10A-01D-1495-08_GBM	140	74	67	51	80	88	102	97	1	27	78	1	84	115	0	1	121
TCGA-32-2634-10A-01D-1495-08_GBM	93	87	90	0	74	65	84	84	79	17	70	77	64	75	0	68	105
TCGA-32-2638-10A-01D-1495-08_GBM	104	70	74	36	130	85	93	112	81	19	70	92	0	79	34	0	111

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-32-4208-10A-01D-1353-08_GBM	145	0	0	70	125	131	113	115	155	0	1	1	0	3	0	113	149
TCGA-32-4209-10A-01D-1353-08_GBM	135	81	85	54	88	90	107	115	126	0	1	0	0	2	49	0	146
TCGA-32-4210-10A-01D-1353-08_GBM	126	76	86	50	141	114	135	175	150	20	52	90	1	2	38	73	137
TCGA-32-4211-10A-01D-1353-08_GBM	144	0	0	91	130	118	111	99	95	21	43	0	74	91	0	74	145
TCGA-32-4213-10A-01D-1353-08_GBM	117	100	108	2	83	85	95	123	85	23	70	86	70	94	28	1	132
TCGA-32-4719-10A-01D-1353-08_GBM	146	2	2	70	140	108	109	118	136	0	1	0	0	3	47	0	150
TCGA-32-5222-10A-01D-1486-08_GBM	123	82	88	55	151	107	105	141	88	21	80	133	0	89	37	4	128
TCGA-33-A4WN-10A-01D-A25L-08_LUSC	84	61	59	37	117	79	76	87	61	18	60	59	58	60	0	58	98
TCGA-33-A5GW-10A-01D-A27N-08_LUSC	82	1	2	46	87	78	82	67	100	0	0	0	0	0	0	81	87
TCGA-34-5231-10A-01D-1817-08_LUSC	98	0	0	77	104	105	86	121	121	0	0	0	1	0	29	66	106
TCGA-34-5232-10A-01D-1817-08_LUSC	100	0	2	72	128	100	104	120	90	20	0	0	0	0	36	0	112
TCGA-34-5234-10A-01D-1632-08_LUSC	119	104	99	1	98	108	96	81	125	0	56	100	0	2	0	85	133
TCGA-34-5236-10A-01D-1817-08_LUSC	107	1	4	63	93	86	85	89	96	0	1	0	0	2	33	64	106
TCGA-34-5239-10A-01D-1817-08_LUSC	98	95	89	1	0	4	91	86	74	19	50	0	62	72	0	68	114
TCGA-34-5240-10A-01D-1441-08_LUSC	106	0	1	58	97	92	90	121	73	21	53	0	58	73	36	2	97
TCGA-34-5241-10A-01D-1441-08_LUSC	111	3	1	50	100	89	92	112	119	0	0	0	0	2	32	84	98
TCGA-34-5927-10A-01D-1817-08_LUSC	105	1	0	88	88	98	82	86	99	0	0	1	0	2	0	84	120
TCGA-34-5928-10A-01D-1817-08_LUSC	128	77	63	51	69	72	73	64	72	0	47	65	0	75	0	54	93
TCGA-34-7107-10A-01D-1945-08_LUSC	114	64	72	52	80	76	108	90	69	18	60	69	0	88	0	68	119
TCGA-34-8454-10A-01D-2323-08_LUSC	115	82	79	50	144	102	96	116	97	19	76	84	65	90	34	0	132
TCGA-34-8455-10A-01D-2323-08_LUSC	125	109	106	2	81	76	120	101	87	20	73	111	0	90	0	75	134
TCGA-34-8456-10A-01D-2323-08_LUSC	77	0	2	71	85	89	81	85	83	0	0	1	0	0	24	49	97
TCGA-34-A5IX-10A-01D-A27N-08_LUSC	84	0	1	55	86	88	83	80	89	0	0	0	0	1	31	0	102
TCGA-35-3615-10A-01D-1489-08_LUAD	140	18	4	89	112	127	116	125	130	1	3	6	1	8	44	83	124
TCGA-35-4122-10A-01D-1105-08_LUAD	115	0	1	91	126	127	97	94	1	27	82	84	80	112	0	1	124
TCGA-35-4123-10A-01D-1105-08_LUAD	116	74	73	51	90	88	97	111	109	0	2	1	0	0	0	104	122
TCGA-35-5375-10A-01D-1625-08_LUAD	103	60	68	48	116	116	101	99	66	12	59	89	0	74	0	63	122
TCGA-36-2530-10A-01D-1526-09_OV	129	3	0	70	136	132	109	88	67	16	60	0	77	103	0	106	108
TCGA-36-2532-10A-01D-1526-09_OV	104	1	0	101	143	133	123	139	79	20	111	1	98	105	90	0	104
TCGA-36-2533-10A-01D-1526-09_OV	98	0	0	62	91	119	55	17	19	12	14	0	44	66	0	69	90
TCGA-36-2534-10A-01D-1526-09_OV	141	0	0	97	174	175	163	162	179	0	0	0	0	0	141	0	152
TCGA-36-2537-10A-01D-1526-09_OV	136	0	1	57	154	157	134	121	125	0	0	0	0	0	117	0	111
TCGA-36-2538-10A-01D-1526-09_OV	150	0	0	103	189	209	224	226	100	48	120	0	132	139	0	146	164
TCGA-36-2539-10A-01D-1526-09_OV	135	0	0	126	178	171	146	159	157	0	0	0	0	0	74	120	146
TCGA-36-2540-10A-01D-1526-09_OV	125	112	106	58	119	101	138	205	153	0	0	0	0	0	86	125	110
TCGA-36-2542-10A-01D-1526-09_OV	119	154	135	0	90	95	117	96	67	19	111	137	0	106	0	128	105
TCGA-36-2543-10A-01D-1526-09_OV	111	102	101	50	93	92	106	93	99	0	0	0	0	0	85	100	110
TCGA-36-2544-10A-01D-1526-09_OV	121	153	140	0	88	85	123	120	112	0	72	96	0	0	0	135	105
TCGA-36-2545-10A-01D-1526-09_OV	124	0	0	83	153	154	142	156	150	0	0	0	0	0	71	127	118
TCGA-36-2547-10A-01D-1526-09_OV	128	117	97	57	110	111	135	174	89	27	97	0	104	106	108	0	115
TCGA-36-2548-10A-01D-1526-09_OV	135	0	0	128	168	175	143	163	146	0	0	0	0	0	75	103	135
TCGA-36-2551-10A-01D-1526-09_OV	130	111	112	60	107	92	143	170	105	20	117	0	104	113	0	146	115
TCGA-36-2552-10A-01D-1526-09_OV	106	81	82	45	141	111	109	105	95	0	59	76	0	0	62	84	88
TCGA-37-3783-10A-01D-1267-08_LUSC	209	0	0	131	219	133	107	99	110	0	0	0	0	141	0	119	142
TCGA-37-3789-10A-01D-0983-08_LUSC	137	80	77	60	183	127	138	96	125	0	65	69	1	1	0	122	155
TCGA-37-3792-10A-01D-0983-08_LUSC	130	87	74	49	99	83	70	58	88	0	43	0	76	75	27	0	140
TCGA-37-4129-10A-01D-1352-08_LUSC	172	0	1	90	218	190	164	118	191	0	0	0	0	0	0	113	234
TCGA-37-4130-10A-01D-1352-08_LUSC	244	105	118	72	172	157	196	174	184	0	0	2	0	0	0	202	262
TCGA-37-4132-10A-01D-1352-08_LUSC	208	0	1	142	205	172	183	177	162	0	1	1	0	2	37	106	189
TCGA-37-4133-10A-01D-1352-08_LUSC	229	119	122	102	131	137	197	170	219	0	0	0	1	0	0	171	299
TCGA-37-4135-10A-01D-1352-08_LUSC	181	1	0	116	191	196	170	177	184	0	0	0	0	1	0	151	204
TCGA-37-4141-10A-01D-1352-08_LUSC	217	0	1	129	213	181	160	144	173	0	0	1	0	2	0	165	220
TCGA-37-5819-10A-01D-1632-08_LUSC	135	63	69	47	70	68	98	100	114	0	0	0	0	2	0	101	135
TCGA-37-A5EL-10A-01D-A26K-08_LUSC	81	68	70	35	101	86	86	86	60	13	76	98	3	64	0	59	104
TCGA-37-A5EM-10A-01D-A27N-08_LUSC	83	56	64	34	107	74	69	90	62	16	74	61	62	71	23	1	90
TCGA-37-A5EN-10A-01D-A26K-08_LUSC	118	67	77	60	132	107	102	101	114	0	42	84	0	1	0	85	128
TCGA-38-6178-10A-01D-1753-08_LUAD	97	0	0	77	93	106	85	80	102	0	0	0	0	0	28	43	114
TCGA-38-A44F-10A-01D-A24F-08_LUAD	95	69	74	44	78	66	57	59	7	15	68	0	80	88	0	1	96
TCGA-41-2571-10A-01D-1495-08_GBM	103	72	75	53	140	105	93	119	72	19	92	76	73	88	0	60	110
TCGA-41-2572-10A-01D-1353-08_GBM	149	80	92	58	93	86	108	130	140	0	0	1	0	0	36	70	140
TCGA-41-2573-10A-01D-1495-08_GBM	96	72	73	45	122	92	89	89	86	20	71	75	65	76	0	55	101
TCGA-41-2575-10A-01D-1495-08_GBM	101	76	72	46	82	75	89	91	107	0	0	0	0	0	39	3	112
TCGA-41-3392-10A-01D-1495-08_GBM	125	64	68	43	75	83	88	141	111	0	0	0	0	1	32	59	106
TCGA-41-3393-10A-01D-1353-08_GBM	133	2	2	98	121	104	109	118	149	0	2	0	1	3	0	114	144
TCGA-41-3915-10A-01D-1353-08_GBM	140	0	1	77	136	129	87	139	108	30	56	0	78	93	0	74	146
TCGA-41-4097-10A-01D-1353-08_GBM	130	0	1	96	133	115	115	126	98	24	39	0	70	86	0	87	152
TCGA-41-5651-10A-01D-1696-08_GBM	105	60	68	38	72	70	83	115	107	0	0	0	0	0	31	60	99
TCGA-41-6646-10A-01D-1845-08_GBM	134	2	0	60	109	95	102	126	76	19	58	1	80	82	0	79	145
TCGA-42-2582-10A-01D-1526-09_OV	147	0	0	143	175	166	150	160	135	0	0	0	1	0	0	270	137
TCGA-42-2587-10A-01D-1526-09_OV	136	107	106	51	117	101	122	147	123	0	0	0	0	0	82	132	99
TCGA-42-2588-10A-01D-1526-09_OV	115	143	126	0	0	0	109	104	101	0	0	0	0	0	63	110	114
TCGA-42-2589-10A-01D-1526-09_OV	114	116	123	50	118	131	137	189	145	0	0	1	0	0	92	130	124
TCGA-42-2590-10A-01D-1526-09_OV	175	0	0	82	169	171	154	162	143	0	0	0	0	0	87	146	133
TCGA-42-2591-10A-01D-1526-09_OV	106	127	143	0	1	1	123	141	100	30	91	113	0	100	0	138	117
TCGA-42-2593-10A-01D-1764-09_OV	151	0	0	122	162	156	143	199	111	22	125	0	102	116	92	0	125
TCGA-43-3394-10A-01D-0983-08_LUSC	127	80	1	62	106	86	78	58	97	0	94	82	80	91	31	1	177
TCGA-43-3920-10A-01D-0983-08_LUSC	142	72	76	52	155	134	131	90	109	0	53	74	0	0	0	114	165
TCGA-43-5668-10A-01D-1632-08_LUSC	108	61	67	30	69	62	96	89	71	12	38	0	63	75	25	0	136
TCGA-43-5670-10A-01D-2122-08_LUSC	98	70	69	47	96	86	83	77	67	19	68	86	0	64	0	63	101
TCGA-43-6143-10A-01D-1817-08_LUSC	93	0	1	87	102	85	82	108	120	0	0	0	0	1	29	67	106
TCGA-43-6647-10A-01D-1817-08_LUSC	102	2	1	73	95	96	84	95	85	19	56	2	58	78	0	66	102
TCGA-43-6770-10A-01D-1817-08_LUSC	102	61	75	47	111	115	79	108	92	1	46	72	0	4	26	49	93
TCGA-43-6771-10A-01D-1817-08_LUSC	113	0	1	101	105	93	91	146	95	1	0	0	0	2	32	77	109
TCGA-43-6773-10A-01D-1945-08_LUSC	108	0	0	71	101	98	91	106	127	0	0	0	0	1	0	129	109
TCGA-43-7656-10A-01D-2122-08_LUSC	84	2	7	58	93	86	84	88	79	2	0	5	1	1	0	80	104
TCGA-43-7657-10A-01D-2122-08_LUSC	88	0	2	49	88	86	75	73	86	0	1	1	1	2	0	78	101
TCGA-43-7658-10A-01D-2122-08_LUSC	83	63	64	55	67	64	80	93	70	17	41	0	65	71	22	1	80
TCGA-43-8115-10A-01D-2244-08_LUSC	88	0	0	55	80	76	83	72	98	0	0	0	0	1	0	86	103
TCGA-43-8116-10A-01D-2244-08_LUSC	94	60	55	48	71	67	80	64	101	0	0	0	1	1	0	72	96
TCGA-43-8118-10A-01D-2395-08_LUSC	88	66	60	40	104	76	76	95	68	17	70	75	0	67	31	0	81
TCGA-43-A474-10A-01D-A24F-08_LUSC	73	5	5	58	80	77	75	69	96	0	1	0	0	0	0	73	93
TCGA-43-A475-10A-01D-A24F-08_LUSC	80	1	0	49	78	70	77	68	85	0	0	1	0	0	0	65	82
TCGA-43-A56U-10A-01D-A26K-08_LUSC	99	98	92	0	80	65	87	129	110	0	44	72	1	6	0	132	110
TCGA-43-A56V-10A-01D-A26K-08_LUSC	84	49	0	38	47	48	48	45	55	1	34	0	53	56	0	50	90
TCGA-44-2656-10A-01D-0969-08_LUAD	113	0	1	98	106	102	92	133	116	0	0	0	0	1	0	104	112
TCGA-44-2657-10A-01D-1105-08_LUAD	130	79	93	46	99	84	109	126	126	0	0	0	0	3	28	77	144

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-44-2659-10A-01D-0969-08_LUAD	119	77	86	52	84	82	105	98	84	21	62	85	0	77	0	78	111
TCGA-44-2661-10A-01D-1105-08_LUAD	130	88	107	0	2	1	100	91	136	0	0	0	0	1	0	106	126
TCGA-44-2662-10A-01D-0969-08_LUAD	123	81	89	54	86	97	104	148	143	0	1	0	1	0	37	90	153
TCGA-44-2665-10A-01D-1040-01_LUAD	112	94	105	0	90	86	100	136	84	17	80	115	1	97	0	74	138
TCGA-44-2666-10A-01D-A271-08_LUAD	103	0	0	83	99	99	96	90	101	0	0	0	0	1	0	85	118
TCGA-44-2668-10A-01D-1489-08_LUAD	133	0	0	66	123	107	99	116	99	28	62	0	86	92	0	86	125
TCGA-44-3396-10A-01D-1265-08_LUAD	138	0	1	56	142	135	104	100	122	0	1	0	0	2	50	1	128
TCGA-44-3398-10A-01D-1105-08_LUAD	159	0	1	59	131	118	108	123	140	0	0	1	1	2	0	129	130
TCGA-44-3917-10A-01D-A271-08_LUAD	93	1	0	82	97	100	92	92	113	0	0	0	0	0	0	112	98
TCGA-44-3918-10A-01D-A271-08_LUAD	101	1	1	57	101	98	97	105	124	0	1	0	0	0	0	95	112
TCGA-44-3919-10A-01D-1458-08_LUAD	122	73	84	49	95	91	105	142	116	0	0	0	0	0	42	80	137
TCGA-44-4112-10A-01D-1458-08_LUAD	145	93	87	51	169	115	107	132	93	20	94	92	81	94	38	0	130
TCGA-44-5643-10A-01D-1625-08_LUAD	105	0	2	75	104	95	89	97	88	13	35	0	67	74	28	0	140
TCGA-44-5644-10A-01D-2036-08_LUAD	106	0	1	85	106	100	98	130	126	0	1	0	2	1	0	133	119
TCGA-44-5645-10A-01D-1625-08_LUAD	123	1	1	61	89	94	88	94	129	0	0	0	0	1	19	47	141
TCGA-44-6144-10A-01D-1753-08_LUAD	108	0	1	75	92	83	101	80	106	1	0	1	0	1	0	68	122
TCGA-44-6145-10A-01D-1753-08_LUAD	97	62	60	42	121	101	83	78	70	19	57	86	0	72	0	52	124
TCGA-44-6146-10A-01D-1753-08_LUAD	100	66	69	38	119	95	91	80	1	26	72	90	55	109	0	0	95
TCGA-44-6147-10A-01D-1753-08_LUAD	92	1	0	59	107	99	79	69	93	0	0	0	0	0	0	99	129
TCGA-44-6148-10A-01D-1753-08_LUAD	101	2	1	74	109	92	86	81	107	0	0	0	1	0	0	73	121
TCGA-44-6774-10A-01D-1855-08_LUAD	118	98	100	1	0	2	93	117	82	16	60	0	73	82	32	7	124
TCGA-44-6775-10A-01D-1855-08_LUAD	116	75	78	54	139	94	91	130	117	0	49	82	0	1	0	131	120
TCGA-44-6776-10A-01D-1855-08_LUAD	116	101	109	0	77	86	92	154	130	0	53	89	0	0	30	75	128
TCGA-44-6777-10A-01D-1855-08_LUAD	136	0	0	91	102	91	87	122	125	0	1	0	0	0	0	117	118
TCGA-44-6778-10A-01D-1855-08_LUAD	109	0	0	62	139	99	107	118	126	0	55	0	72	0	25	77	113
TCGA-44-7659-10A-01D-2063-08_LUAD	95	63	66	46	71	70	84	86	90	0	0	0	1	0	0	85	98
TCGA-44-7660-10A-01D-2063-08_LUAD	87	99	90	2	2	4	87	117	95	0	0	2	0	1	30	69	103
TCGA-44-7661-10A-01D-2063-08_LUAD	122	68	63	44	69	71	96	91	4	23	77	0	85	110	0	1	126
TCGA-44-7662-10A-01D-2063-08_LUAD	91	84	83	0	67	68	98	123	110	0	49	75	0	0	33	76	110
TCGA-44-7667-10A-01D-2063-08_LUAD	121	2	4	88	97	85	96	106	118	0	0	3	0	0	30	67	115
TCGA-44-7669-10A-01D-2063-08_LUAD	86	83	90	0	73	60	94	101	110	0	46	72	1	2	0	90	105
TCGA-44-7670-10A-01D-2063-08_LUAD	93	3	4	61	98	90	83	83	112	0	0	2	0	1	0	85	109
TCGA-44-7671-10A-01D-2063-08_LUAD	96	1	3	60	129	89	83	81	92	0	0	3	1	3	32	81	111
TCGA-44-7672-10A-01D-2063-08_LUAD	94	0	1	64	96	89	83	118	117	0	0	1	0	1	35	60	111
TCGA-44-8117-10A-01D-2238-08_LUAD	98	0	0	57	96	87	95	93	111	0	0	0	0	0	0	128	106
TCGA-44-8119-10A-01D-2238-08_LUAD	80	56	58	42	63	73	59	51	68	0	42	0	43	73	20	2	103
TCGA-44-8120-10A-01D-2238-08_LUAD	88	72	68	3	58	59	87	82	68	8	52	67	40	74	0	54	104
TCGA-44-A479-10A-01D-A24F-08_LUAD	87	66	64	43	83	77	76	76	93	0	45	1	74	6	33	1	88
TCGA-44-A47A-10A-01D-A24F-08_LUAD	114	1	4	45	80	74	83	83	86	0	4	0	2	5	27	54	88
TCGA-44-A47B-10A-01D-A24F-08_LUAD	79	49	55	38	56	58	69	87	68	15	45	51	0	63	27	0	79
TCGA-44-A47F-10A-01D-A24F-08_LUAD	70	64	64	39	106	82	74	59	59	13	69	67	52	67	0	57	90
TCGA-44-A47G-10A-01D-A24F-08_LUAD	81	1	3	50	77	71	66	80	57	17	41	59	2	65	0	64	93
TCGA-44-A4SS-10A-01D-A24P-08_LUAD	85	0	1	48	78	80	69	103	80	0	0	0	4	1	0	115	90
TCGA-44-A4SU-10A-01D-A24P-08_LUAD	81	3	5	58	82	79	79	94	99	0	3	0	3	7	34	72	84
TCGA-46-3765-10A-01D-0983-08_LUSC	142	117	131	0	97	74	123	120	125	0	60	69	0	0	29	60	144
TCGA-46-3766-10A-01D-0983-08_LUSC	129	75	82	58	85	80	123	99	139	0	0	0	0	0	25	68	157
TCGA-46-3767-10A-01D-0983-08_LUSC	116	1	0	120	143	140	128	108	65	15	50	0	66	80	0	72	149
TCGA-46-3768-10A-01D-0983-08_LUSC	128	72	84	65	81	65	123	87	136	0	0	0	0	1	24	54	176
TCGA-46-3769-10A-01D-0983-08_LUSC	129	66	67	58	83	76	126	98	144	0	0	1	0	1	0	131	146
TCGA-46-6025-10A-01D-1817-08_LUSC	108	66	71	52	129	96	97	96	72	31	84	73	66	76	0	64	112
TCGA-46-6026-10A-01D-1817-08_LUSC	107	72	69	49	71	77	87	116	109	0	0	1	1	2	33	60	110
TCGA-50-5044-10A-01D-1855-08_LUAD	121	76	73	58	116	93	91	110	77	16	73	77	65	74	0	64	123
TCGA-50-5045-10A-01D-1625-08_LUAD	114	0	0	74	98	90	98	89	110	0	0	1	0	1	0	96	128
TCGA-50-5049-10A-01D-1625-08_LUAD	90	55	75	35	74	74	94	88	126	0	0	1	0	1	0	98	112
TCGA-50-5051-10A-01D-1855-08_LUAD	132	72	78	56	142	104	102	95	130	0	58	72	0	3	0	93	132
TCGA-50-5055-10A-01D-1625-08_LUAD	97	59	74	49	115	78	76	88	75	16	72	63	47	71	0	69	95
TCGA-50-5066-10A-01D-1625-08_LUAD	118	65	72	47	73	74	102	127	141	0	0	0	0	0	27	62	148
TCGA-50-5068-10A-01D-1625-08_LUAD	99	0	2	62	105	100	97	97	116	0	0	0	1	0	0	98	123
TCGA-50-5072-10A-01D-1855-08_LUAD	119	0	1	78	117	95	103	94	110	0	1	0	0	0	40	0	137
TCGA-50-5941-10A-01D-1753-08_LUAD	113	0	1	75	90	91	87	79	115	0	1	0	0	0	18	58	111
TCGA-50-5942-10A-01D-1753-08_LUAD	97	0	0	58	106	106	88	87	106	0	0	0	0	1	27	56	113
TCGA-50-5944-10A-01D-1753-08_LUAD	91	61	69	50	83	68	77	81	59	19	40	76	0	71	0	53	109
TCGA-50-5946-10A-01D-1753-08_LUAD	103	70	64	48	126	94	97	97	70	18	63	103	0	82	28	0	126
TCGA-50-6597-10A-01D-1855-08_LUAD	109	75	80	52	77	83	61	80	91	0	62	79	1	80	29	0	115
TCGA-50-8457-10A-01D-2323-08_LUAD	123	0	0	66	116	112	105	112	125	0	0	0	1	0	31	71	118
TCGA-50-8459-10A-01D-2323-08_LUAD	103	107	101	0	2	0	98	99	112	0	0	0	0	0	31	70	155
TCGA-50-8460-10A-01D-2323-08_LUAD	150	132	126	0	143	129	131	114	96	20	101	154	0	95	0	65	153
TCGA-52-7622-10A-01D-2122-08_LUSC	112	1	0	49	88	86	80	96	87	0	0	0	0	2	29	57	92
TCGA-52-7809-10A-01D-2122-08_LUSC	89	65	66	43	67	68	75	93	87	0	2	0	1	6	0	109	102
TCGA-52-7810-10A-01D-2122-08_LUSC	83	1	4	54	93	88	81	74	4	22	66	0	71	86	0	3	100
TCGA-52-7811-10A-01D-2122-08_LUSC	84	0	1	90	101	96	84	111	115	0	0	0	0	2	0	130	102
TCGA-52-7812-10A-01D-2122-08_LUSC	120	5	5	58	144	148	104	98	73	25	69	74	66	70	0	75	107
TCGA-53-7624-10A-01D-2063-08_LUAD	108	68	60	52	76	62	100	78	117	0	0	0	0	0	0	83	144
TCGA-53-7626-10A-01D-2063-08_LUAD	96	0	1	75	99	81	82	87	106	0	0	0	0	0	25	55	101
TCGA-53-7813-10A-01D-2167-08_LUAD	105	56	57	46	69	60	61	36	64	0	33	1	40	71	0	60	124
TCGA-53-A4EZ-10A-01D-A24P-08_LUAD	80	69	71	46	64	68	73	98	82	0	1	0	7	5	30	68	89
TCGA-55-5899-10A-01D-1625-08_LUAD	109	0	0	78	105	105	93	97	61	12	34	79	0	69	0	52	119
TCGA-55-6543-10A-01D-1753-08_LUAD	92	54	66	38	68	72	86	58	82	0	0	1	0	0	0	77	102
TCGA-55-6712-10A-01D-1855-08_LUAD	120	77	80	57	135	96	94	124	63	17	76	98	1	82	0	68	113
TCGA-55-7227-10A-01D-2036-08_LUAD	95	61	70	41	69	64	87	78	100	0	0	0	0	0	34	1	109
TCGA-55-7281-10A-01D-2036-08_LUAD	92	3	2	85	121	91	102	101	110	0	0	0	0	0	0	108	109
TCGA-55-7283-10A-01D-2036-08_LUAD	108	58	73	50	117	90	89	98	111	0	47	78	0	0	27	53	114
TCGA-55-7284-10A-01D-2238-08_LUAD	91	0	1	61	127	95	86	89	85	17	50	3	55	68	32	0	121
TCGA-55-7570-10A-01D-2036-08_LUAD	92	3	2	55	87	81	84	112	103	0	1	1	1	4	31	56	104
TCGA-55-7574-10A-01D-2036-08_LUAD	101	0	0	61	96	88	81	128	110	0	0	0	0	0	0	126	116
TCGA-55-7576-10A-01D-2063-08_LUAD	122	0	0	74	135	91	98	75	112	0	2	0	1	6	20	42	147
TCGA-55-7724-10A-01D-2167-08_LUAD	120	0	0	78	113	100	107	93	89	0	0	0	1	2	0	96	138
TCGA-55-7725-10A-01D-2167-08_LUAD	106	0	0	94	113	97	99	84	98	0	0	1	1	0	32	70	128
TCGA-55-7726-10A-01D-2167-08_LUAD	85	0	0	57	96	91	87	67	110	0	0	2	0	0	25	49	105
TCGA-55-7727-10A-01D-2167-08_LUAD	98	0	0	99	103	108	98	72	3	26	63	76	58	100	0	0	124
TCGA-55-7728-10A-01D-2184-08_LUAD	97	1	0	55	90	92	76	72	109	1	2	0	0	0	0	82	98
TCGA-55-7815-10A-01D-2167-08_LUAD	107	0	0	86	124	108	95	77	123	1	0	0	1	3	0	89	137
TCGA-55-7816-10A-01D-2167-08_LUAD	96	50	57	47	119	106	105	76	104	0	33	60	0	0	28	65	130
TCGA-55-7903-10A-01D-2167-08_LUAD	93	60	54	55	147	128	107	85	79	24	76	103	46	74	0	57	146
TCGA-55-7907-10A-01D-2167-08_LUAD	102	0	1	95	105	95	97	79	115	0	0	0	0	0	0	89	118
TCGA-55-7911-10A-01D-2167-08_LUAD	91	51	54	47	69	82	86	81	97	0	0	0	0	1	23	50	127

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-55-7913-10A-01D-2238-08_LUAD	94	78	76	1	72	60	78	82	115	0	53	0	56	1	0	92	110
TCGA-55-7914-10A-01D-2167-08_LUAD	95	49	55	50	70	65	80	59	93	0	0	2	0	0	17	47	115
TCGA-55-7994-10A-01D-2184-08_LUAD	88	83	79	1	72	63	82	88	96	0	42	67	0	0	0	105	103
TCGA-55-7995-10A-01D-2184-08_LUAD	95	1	2	82	86	94	92	65	75	0	0	0	0	2	0	82	119
TCGA-55-8085-10A-01D-2238-08_LUAD	85	0	1	61	92	96	88	92	65	14	46	0	57	71	0	68	108
TCGA-55-8087-10A-01D-2238-08_LUAD	92	69	65	53	79	79	81	83	78	17	48	0	49	82	29	0	103
TCGA-55-8089-10A-01D-2238-08_LUAD	91	63	68	45	77	74	86	84	96	0	0	0	0	1	41	1	107
TCGA-55-8090-10A-01D-2238-08_LUAD	89	1	4	57	93	101	88	92	79	15	49	1	55	86	28	1	111
TCGA-55-8091-10A-01D-2238-08_LUAD	76	0	1	63	95	85	87	75	107	0	2	0	0	3	0	81	102
TCGA-55-8092-10A-01D-2238-08_LUAD	97	0	0	54	87	82	84	94	76	0	0	0	0	1	0	134	128
TCGA-55-8094-10A-01D-2238-08_LUAD	99	0	1	87	99	93	79	113	121	0	0	0	0	1	0	139	108
TCGA-55-8096-10A-01D-2238-08_LUAD	110	58	74	55	78	68	90	101	104	0	0	0	0	0	35	60	118
TCGA-55-8097-10A-01D-2238-08_LUAD	96	0	0	67	92	90	84	80	4	23	74	1	72	96	0	1	108
TCGA-55-8203-10A-01D-2238-08_LUAD	98	0	1	63	98	86	92	97	82	0	0	1	1	0	0	128	106
TCGA-55-8204-10A-01D-2238-08_LUAD	94	0	0	65	97	99	92	113	122	0	1	0	1	2	0	143	114
TCGA-55-8205-10A-01D-2238-08_LUAD	89	64	57	45	71	69	77	81	78	23	50	3	64	69	0	70	110
TCGA-55-8206-10A-01D-2238-08_LUAD	99	0	1	63	93	92	96	97	77	0	1	0	1	1	0	126	129
TCGA-55-8207-10A-01D-2238-08_LUAD	96	66	61	50	81	74	103	71	94	0	0	0	0	2	0	97	116
TCGA-55-8208-10A-01D-2238-08_LUAD	89	69	63	52	72	79	96	91	114	0	0	0	0	1	33	68	114
TCGA-55-8299-10B-01D-2323-08_LUAD	126	110	116	1	0	0	116	119	123	0	1	0	0	1	37	72	126
TCGA-55-8301-10A-01D-2284-08_LUAD	138	0	0	97	154	124	118	102	90	23	72	74	59	87	0	66	128
TCGA-55-8302-10A-01D-2323-08_LUAD	107	72	78	57	81	97	99	126	138	0	0	0	0	0	32	63	137
TCGA-55-8505-10A-01D-2393-08_LUAD	87	64	68	45	119	92	78	112	76	20	68	73	59	67	0	69	94
TCGA-55-8506-10A-01D-2393-08_LUAD	124	75	80	52	70	78	93	137	112	0	0	0	0	1	37	81	102
TCGA-55-8507-10A-01D-2393-08_LUAD	115	113	112	2	0	0	109	125	138	0	0	0	0	1	0	148	138
TCGA-55-8508-10A-01D-2393-08_LUAD	102	80	80	43	125	103	90	122	98	0	63	83	0	1	36	78	117
TCGA-55-8510-10A-01D-2393-08_LUAD	107	102	105	0	79	89	113	85	116	0	40	90	1	0	47	1	131
TCGA-55-8511-10A-01D-2393-08_LUAD	106	0	0	72	114	104	113	95	71	15	40	0	63	88	0	60	129
TCGA-55-8512-10A-01D-2393-08_LUAD	102	78	82	54	131	100	82	102	83	17	80	100	1	73	28	5	101
TCGA-55-8513-10A-01D-2393-08_LUAD	82	0	1	44	81	79	72	64	104	1	0	0	0	0	0	72	83
TCGA-55-8514-10A-01D-2393-08_LUAD	101	73	67	48	84	81	114	110	132	0	0	0	0	1	0	129	120
TCGA-55-8614-10A-01D-2393-08_LUAD	109	0	1	95	113	102	101	116	77	19	46	0	71	82	0	67	135
TCGA-55-8615-10A-01D-2393-08_LUAD	90	3	6	63	140	87	87	88	80	20	69	0	73	75	0	65	106
TCGA-55-8616-10A-01D-2393-08_LUAD	113	69	78	55	143	158	102	90	71	19	79	70	74	90	0	65	119
TCGA-55-8619-10A-01D-2393-08_LUAD	86	86	86	2	62	78	84	97	67	17	64	97	0	75	0	72	96
TCGA-55-8620-10A-01D-2393-08_LUAD	100	0	0	59	112	103	89	86	82	16	38	0	62	87	0	59	145
TCGA-55-8621-10A-01D-2393-08_LUAD	113	0	1	69	134	104	110	95	74	19	48	0	69	89	0	65	132
TCGA-55-A48X-10A-01D-A24F-08_LUAD	106	1	1	52	82	73	79	75	64	16	48	0	57	73	0	60	89
TCGA-55-A48Y-10A-01D-A24F-08_LUAD	106	1	5	72	84	79	77	87	72	0	8	9	0	2	0	110	77
TCGA-55-A48Z-10A-01D-A24P-08_LUAD	90	68	69	46	74	63	74	73	84	0	0	0	1	0	0	84	85
TCGA-55-A490-10A-01D-A24F-08_LUAD	113	3	5	43	117	88	74	87	58	21	72	70	67	69	0	62	89
TCGA-55-A491-10A-01D-A24F-08_LUAD	83	61	66	42	67	70	71	81	76	0	1	1	0	0	0	83	90
TCGA-55-A492-10A-01D-A24F-08_LUAD	77	4	3	49	78	82	84	80	92	0	1	6	0	4	0	72	82
TCGA-55-A493-10A-01D-A24F-08_LUAD	86	79	82	1	70	66	79	80	81	0	44	64	0	1	39	0	89
TCGA-55-A494-10A-01D-A24P-08_LUAD	82	7	4	51	91	77	78	84	71	13	47	3	62	70	0	58	97
TCGA-55-A4DF-10A-01D-A24F-08_LUAD	105	96	98	1	107	101	107	128	83	15	87	130	0	72	30	1	123
TCGA-55-A4DG-10A-01D-A24F-08_LUAD	96	67	80	47	131	108	97	88	0	20	90	97	63	108	0	0	121
TCGA-56-5897-10A-01D-1632-08_LUSC	103	0	3	47	110	110	94	86	110	0	1	0	0	1	26	59	134
TCGA-56-5898-10A-01D-1632-08_LUSC	98	0	1	80	98	100	88	90	58	8	37	0	54	64	0	54	107
TCGA-56-6545-10A-01D-1817-08_LUSC	97	76	68	43	71	65	97	101	96	0	0	0	0	1	36	56	110
TCGA-56-6546-10A-01D-1817-08_LUSC	101	1	1	60	95	92	91	90	79	17	53	0	63	72	0	65	98
TCGA-56-7221-10A-01D-2042-08_LUSC	94	66	57	45	106	84	82	86	86	0	47	70	0	0	0	84	102
TCGA-56-7222-10A-01D-2042-08_LUSC	101	0	0	53	87	97	84	107	91	0	1	1	0	1	0	131	105
TCGA-56-7223-10A-01D-2042-08_LUSC	104	69	65	44	123	87	87	104	113	0	49	81	0	0	31	61	121
TCGA-56-7579-10A-01D-2042-08_LUSC	106	65	69	39	113	92	104	121	87	12	48	69	0	0	29	59	115
TCGA-56-7580-10A-01D-2042-08_LUSC	99	72	72	43	73	67	85	77	70	18	50	0	62	72	0	70	124
TCGA-56-7582-10A-01D-2042-08_LUSC	114	0	0	62	100	96	99	118	121	0	0	1	0	0	26	58	122
TCGA-56-7731-10A-01D-2122-08_LUSC	84	0	0	68	87	74	76	100	83	0	0	0	1	4	0	92	93
TCGA-56-7822-10A-01D-2122-08_LUSC	83	64	75	39	112	75	80	77	84	1	50	66	3	7	0	115	107
TCGA-56-7823-10A-01D-2244-08_LUSC	119	93	91	64	137	116	101	96	95	24	94	86	83	87	0	91	136
TCGA-56-8082-10A-01D-2244-08_LUSC	85	1	0	55	88	86	77	72	100	1	0	0	0	1	0	71	90
TCGA-56-8083-10A-01D-2244-08_LUSC	116	2	0	80	81	82	76	86	66	20	34	0	48	66	23	0	95
TCGA-56-8201-10A-01D-2244-08_LUSC	87	54	53	42	118	79	77	77	62	12	59	69	48	70	0	55	103
TCGA-56-8304-10A-01D-2323-08_LUSC	85	87	80	0	76	67	86	103	113	0	59	67	0	1	0	120	98
TCGA-56-8307-10A-01D-2293-08_LUSC	103	2	0	60	84	86	86	79	111	0	0	0	0	0	0	89	107
TCGA-56-8308-10A-01D-2293-08_LUSC	90	0	1	63	93	88	87	95	71	17	51	0	53	72	0	63	117
TCGA-56-8309-10A-01D-2293-08_LUSC	88	0	0	79	80	84	97	71	97	0	0	0	0	1	0	82	107
TCGA-56-8503-10A-01D-2395-08_LUSC	85	86	84	5	8	5	79	77	6	24	61	1	74	86	0	3	95
TCGA-56-8504-10A-01D-2395-08_LUSC	83	68	68	42	114	88	86	99	97	1	52	57	1	4	28	75	89
TCGA-56-8622-10A-01D-2395-08_LUSC	91	65	71	43	64	71	80	98	105	0	2	1	0	2	0	118	93
TCGA-56-8623-10A-01D-2395-08_LUSC	121	5	3	79	86	95	85	119	103	0	0	4	0	0	30	63	105
TCGA-56-8624-10A-01D-2395-08_LUSC	88	77	92	2	74	78	92	107	88	21	54	65	0	1	30	67	105
TCGA-56-8625-10A-01D-2395-08_LUSC	86	4	1	59	86	86	88	98	76	0	1	2	4	0	0	114	92
TCGA-56-8626-10A-01D-2395-08_LUSC	105	81	85	48	93	80	105	107	122	0	0	0	0	0	0	93	134
TCGA-56-8628-10A-01D-2395-08_LUSC	92	68	75	46	113	81	81	74	8	22	82	61	75	78	0	4	95
TCGA-56-8629-10A-01D-2395-08_LUSC	110	3	4	54	88	94	83	103	97	1	2	4	3	4	0	118	102
TCGA-56-A49D-10A-01D-A24F-08_LUSC	78	1	0	62	83	78	68	67	80	0	1	0	0	1	0	66	84
TCGA-56-A4BW-10A-01D-A24F-08_LUSC	82	63	59	40	57	59	76	77	74	11	39	0	49	64	24	1	88
TCGA-56-A4BX-10A-01D-A24F-08_LUSC	111	72	76	48	129	95	102	83	75	20	72	73	64	80	0	71	137
TCGA-56-A4BY-10A-01D-A24F-08_LUSC	82	81	76	1	3	1	78	99	92	2	1	1	2	3	29	53	84
TCGA-56-A4ZJ-10A-01D-A25L-08_LUSC	84	90	95	3	8	6	95	122	98	15	51	9	53	4	32	71	105
TCGA-56-A4ZK-10A-01D-A25L-08_LUSC	105	2	0	67	93	87	70	118	79	14	49	0	64	83	30	8	113
TCGA-56-A5DR-10A-01D-A27N-08_LUSC	88	69	63	45	68	73	75	71	0	20	61	0	79	83	0	1	89
TCGA-56-A5DS-10A-01D-A27N-08_LUSC	86	0	0	52	91	87	83	104	83	0	0	0	0	0	0	124	95
TCGA-58-8386-10A-01D-2293-08_LUSC	106	63	70	46	76	76	81	85	72	21	47	1	55	84	0	71	121
TCGA-58-8387-10A-01D-2293-08_LUSC	79	51	55	42	116	83	80	89	105	0	35	60	0	1	0	108	109
TCGA-58-8388-10A-01D-2323-08_LUSC	108	85	2	43	138	112	93	107	68	17	51	0	68	84	0	69	129
TCGA-58-8390-10A-01D-2323-08_LUSC	119	0	0	68	104	95	102	103	133	0	0	0	0	0	0	120	112
TCGA-58-8391-10A-01D-2323-08_LUSC	117	0	1	97	105	106	106	96	136	0	0	0	0	0	0	97	138
TCGA-58-8392-10A-01D-2323-08_LUSC	139	1	0	74	128	126	127	102	126	20	54	72	0	93	0	59	118
TCGA-58-8393-10A-01D-2323-08_LUSC	123	73	79	50	127	107	108	113	131	0	49	80	0	1	0	87	133
TCGA-58-A46J-10A-01D-A24F-08_LUSC	90	88	92	0	80	73	81	87	81	16	82	73	66	79	0	67	111
TCGA-58-A46K-10A-01D-A24F-08_LUSC	84	58	59	44	110	87	79	96	102	0	47	73	0	5	30	59	93
TCGA-58-A46L-10A-01D-A24F-08_LUSC	89	62	66	37	78	68	85	118	67	9	53	3	71	72	0	69	88
TCGA-58-A46M-10A-01D-A24F-08_LUSC	78	0	1	45	88	78	74	101	106	1	5	0	4	4	0	99	94
TCGA-58-A46N-10A-01D-A24F-08_LUSC	78	66	57	37	106	74	78	96	66	15	65	82	0	69	0	52	84

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-59-2372-10A-01D-1526-09_OV	118	161	143	0	173	158	134	146	173	0	183	163	0	0	0	232	136
TCGA-62-8394-10A-01D-2323-08_LUAD	183	1	0	116	144	143	150	139	163	0	0	0	1	1	35	96	163
TCGA-62-8395-10A-01D-2323-08_LUAD	153	0	2	115	143	139	129	116	94	16	54	0	85	97	0	92	172
TCGA-62-8397-10A-01D-2323-08_LUAD	117	0	0	84	121	113	102	114	87	15	50	0	77	94	29	0	124
TCGA-62-8398-10A-01D-2323-08_LUAD	110	60	64	50	63	75	67	59	65	0	41	0	60	90	0	64	116
TCGA-62-8399-10A-01D-2323-08_LUAD	107	83	89	49	78	75	108	95	130	0	0	0	0	1	0	96	143
TCGA-62-8402-10A-01D-2323-08_LUAD	114	73	84	54	136	117	101	127	70	19	89	116	0	88	0	69	141
TCGA-62-A46O-10A-01D-A24F-08_LUAD	84	51	64	46	66	67	77	72	68	16	43	1	56	65	0	51	89
TCGA-62-A46P-10A-01D-A24F-08_LUAD	115	76	84	49	91	79	116	115	98	0	0	0	1	0	0	126	141
TCGA-62-A46R-10A-01D-A24F-08_LUAD	83	62	62	37	71	72	71	72	5	22	69	70	61	80	0	1	80
TCGA-62-A46S-10A-01D-A24F-08_LUAD	83	1	2	65	78	78	73	71	71	16	38	0	50	64	0	51	82
TCGA-62-A46U-10A-01D-A24F-08_LUAD	70	81	80	1	65	59	75	70	64	15	71	72	0	66	0	58	84
TCGA-62-A46V-10A-01D-A24F-08_LUAD	103	4	3	46	79	72	74	91	67	16	44	1	61	72	0	57	82
TCGA-62-A46Y-10A-01D-A24F-08_LUAD	108	62	56	3	3	1	63	61	68	0	0	0	0	65	0	56	98
TCGA-62-A470-10A-01D-A24F-08_LUAD	82	67	64	41	115	76	78	94	72	15	74	63	62	70	32	1	86
TCGA-62-A471-10A-01D-A24F-08_LUAD	82	60	71	43	110	84	73	92	69	14	81	67	55	64	35	3	88
TCGA-62-A472-10A-01D-A24F-08_LUAD	74	0	0	50	74	67	69	92	48	11	43	51	0	53	0	50	71
TCGA-63-5128-10A-01D-1441-08_LUSC	100	1	0	52	94	80	82	104	97	0	0	0	0	0	0	99	120
TCGA-63-5131-10A-01D-1441-08_LUSC	145	78	0	41	125	94	87	90	90	20	52	0	64	81	0	73	125
TCGA-63-6202-10A-01D-1817-08_LUSC	128	1	1	77	93	89	86	104	104	1	0	0	0	2	0	81	97
TCGA-63-7020-10A-01D-1945-08_LUSC	109	93	92	0	110	85	91	113	106	0	78	98	0	0	0	128	122
TCGA-63-7021-10A-01D-1945-08_LUSC	110	1	0	74	101	95	110	112	94	0	1	0	0	0	0	139	125
TCGA-63-7022-10A-01D-1945-08_LUSC	119	0	2	107	134	108	110	114	134	0	0	0	0	1	44	3	143
TCGA-63-7023-10A-01D-1945-08_LUSC	102	0	0	92	102	99	88	94	128	1	0	1	0	0	0	119	109
TCGA-63-A5M9-10A-01D-A26K-08_LUSC	94	3	1	86	91	89	92	90	105	0	1	0	5	1	0	90	110
TCGA-63-A5MB-10A-01D-A26K-08_LUSC	95	53	53	44	65	75	93	83	89	0	0	0	0	4	0	95	95
TCGA-63-A5MG-10A-01D-A27N-08_LUSC	90	70	63	42	72	63	75	96	87	0	2	0	0	0	30	61	101
TCGA-63-A5MH-10A-01D-A27N-08_LUSC	111	1	1	72	86	77	73	95	106	0	0	0	0	1	24	54	92
TCGA-63-A5MI-10A-01D-A27N-08_LUSC	75	63	69	44	76	63	73	115	106	0	0	0	0	0	32	57	97
TCGA-63-A5MJ-10A-01D-A27N-08_LUSC	120	0	0	50	84	85	83	75	1	23	62	0	75	85	0	0	100
TCGA-63-A5ML-10A-01D-A27N-08_LUSC	85	63	65	42	116	78	81	95	95	0	44	67	0	0	25	61	86
TCGA-63-A5MM-10A-01D-A26K-08_LUSC	102	0	1	52	95	138	88	107	109	0	1	0	0	0	0	89	104
TCGA-63-A5MN-10A-01D-A27N-08_LUSC	123	0	0	54	85	84	80	94	107	0	0	0	0	0	0	78	94
TCGA-63-A5MP-10A-01D-A26K-08_LUSC	92	0	0	54	77	91	85	81	84	0	0	0	2	3	39	1	108
TCGA-63-A5MR-10A-01D-A27N-08_LUSC	93	61	61	41	69	67	79	69	86	0	0	0	0	0	34	1	87
TCGA-63-A5MS-10A-01D-A26K-08_LUSC	87	0	0	68	83	87	79	104	64	13	48	0	54	76	29	6	94
TCGA-63-A5MT-10A-01D-A26K-08_LUSC	96	54	58	47	72	67	86	97	70	12	52	0	65	67	31	6	111
TCGA-63-A5MU-10A-01D-A26K-08_LUSC	90	2	5	83	94	88	78	85	102	1	2	3	0	6	0	91	108
TCGA-63-A5MV-10A-01D-A26K-08_LUSC	91	91	93	1	73	62	93	89	6	20	84	84	55	100	0	5	111
TCGA-63-A5MW-10A-01D-A26K-08_LUSC	85	57	66	37	67	68	80	91	117	0	0	0	1	1	31	58	105
TCGA-63-A5MY-10A-01D-A26K-08_LUSC	103	2	0	79	86	84	86	87	88	0	0	0	1	3	0	91	105
TCGA-64-1676-10A-01D-0969-08_LUAD	138	1	0	88	115	130	90	117	88	18	53	0	76	75	0	88	113
TCGA-64-1678-10A-01D-1489-08_LUAD	128	0	0	59	103	111	100	131	97	19	60	1	64	95	0	78	143
TCGA-64-1679-10A-01D-2063-08_LUAD	92	64	68	44	65	68	84	93	93	0	0	0	0	1	0	76	102
TCGA-64-1680-10A-01D-1040-01_LUAD	74	70	78	0	56	49	65	77	85	0	26	50	0	0	24	49	93
TCGA-64-1681-10A-01D-2063-08_LUAD	91	0	1	59	96	100	93	98	123	0	0	0	1	0	26	58	120
TCGA-64-5774-10A-01D-1625-08_LUAD	118	1	1	83	94	105	100	110	123	0	0	0	0	1	23	63	131
TCGA-64-5775-10A-01D-1625-08_LUAD	112	3	0	68	107	106	106	103	77	20	43	2	57	79	25	0	129
TCGA-64-5778-10A-01D-1625-08_LUAD	120	75	70	41	136	115	86	95	4	16	92	99	72	113	0	0	133
TCGA-64-5779-10A-01D-1625-08_LUAD	120	92	97	1	74	96	91	108	115	0	30	73	0	0	23	60	128
TCGA-64-5781-10A-01D-1625-08_LUAD	98	1	1	61	95	92	94	74	64	11	46	0	57	57	0	58	118
TCGA-64-5815-10A-01D-1625-08_LUAD	132	58	70	48	135	73	66	52	0	16	66	77	65	108	0	1	104
TCGA-67-3770-10A-01D-0969-08_LUAD	115	0	2	54	124	104	103	100	112	0	2	0	0	0	47	3	131
TCGA-67-3771-10A-01D-1040-01_LUAD	131	99	117	0	2	3	102	168	145	0	1	0	1	1	45	81	144
TCGA-67-3773-10A-01D-1489-08_LUAD	126	1	2	89	111	102	93	115	141	0	0	0	1	0	0	108	125
TCGA-67-3774-10A-01D-1489-08_LUAD	165	1	1	95	118	113	101	131	108	0	0	1	2	1	37	95	146
TCGA-67-4679-10A-01D-1753-08_LUAD	92	56	66	36	120	91	87	84	110	1	36	69	0	2	0	104	123
TCGA-67-6215-10A-01D-1753-08_LUAD	96	63	64	39	119	93	96	79	79	12	65	59	54	69	0	49	121
TCGA-67-6216-10A-01D-1753-08_LUAD	95	59	71	0	62	79	81	83	71	9	24	0	51	76	0	42	123
TCGA-67-6217-10A-01D-1753-08_LUAD	127	0	2	68	110	98	90	92	111	0	0	0	0	1	24	44	133
TCGA-68-7755-10A-01D-2122-08_LUSC	113	0	3	47	91	73	70	87	73	15	38	1	59	60	24	2	88
TCGA-68-7756-10A-01D-2122-08_LUSC	123	2	1	91	94	91	119	89	2	22	70	0	79	102	0	0	103
TCGA-68-7757-10A-01D-2293-08_LUSC	85	61	59	44	70	64	76	91	69	18	42	72	0	71	0	57	107
TCGA-68-8250-10A-01D-2293-08_LUSC	92	1	1	87	103	88	87	98	94	0	1	1	0	0	36	77	109
TCGA-68-8251-10A-01D-2293-08_LUSC	93	79	77	1	0	5	91	111	118	0	0	0	0	0	30	63	103
TCGA-68-A59J-10A-01D-A26K-08_LUSC	89	0	0	84	89	81	89	79	73	14	46	0	51	65	0	64	108
TCGA-69-7760-10A-01D-2167-08_LUAD	101	63	53	56	135	94	104	74	67	16	67	93	0	73	0	75	132
TCGA-69-7761-10A-01D-2167-08_LUAD	99	0	1	80	103	101	82	69	94	0	0	0	0	0	30	57	134
TCGA-69-7763-10A-01D-2167-08_LUAD	99	56	51	54	127	104	111	75	66	17	59	61	51	83	0	50	127
TCGA-69-7764-10A-01D-2167-08_LUAD	108	100	87	0	85	68	119	94	124	0	45	73	1	2	32	71	141
TCGA-69-7765-10A-01D-2167-08_LUAD	100	50	47	48	135	93	85	81	97	0	28	0	45	0	27	1	91
TCGA-69-7973-10A-01D-2184-08_LUAD	82	56	67	46	103	89	81	76	1	25	85	64	65	86	0	2	105
TCGA-69-7974-10A-01D-2184-08_LUAD	87	0	3	88	90	83	79	83	75	14	39	0	52	69	30	1	90
TCGA-69-7978-10A-01D-2184-08_LUAD	93	85	81	1	98	94	90	113	106	0	59	75	0	0	0	127	112
TCGA-69-7979-10A-01D-2184-08_LUAD	86	71	79	0	70	67	101	108	84	15	34	69	0	1	37	1	101
TCGA-69-7980-10A-01D-2184-08_LUAD	122	66	59	50	116	86	74	86	65	16	60	86	0	70	0	55	102
TCGA-69-8253-10A-01D-2284-08_LUAD	81	61	56	33	63	62	75	92	78	1	6	0	2	6	28	52	95
TCGA-69-8254-10A-01D-2284-08_LUAD	108	64	75	37	129	84	118	121	107	13	39	74	0	0	44	0	122
TCGA-69-8255-10A-01D-2284-08_LUAD	97	0	1	59	108	122	103	90	117	0	0	0	0	0	44	0	128
TCGA-69-A59K-10A-01D-A25L-08_LUAD	87	0	0	82	125	87	84	83	93	0	0	1	0	1	37	4	104
TCGA-70-6722-10A-01D-1817-08_LUSC	138	0	0	83	98	89	88	89	73	20	57	0	63	92	0	59	110
TCGA-70-6723-10A-01D-1817-08_LUSC	131	70	73	49	79	70	102	87	115	0	0	0	0	1	43	2	130
TCGA-71-6725-10A-01D-1855-08_LUAD	104	0	2	69	114	101	95	122	112	0	0	0	1	2	36	70	113
TCGA-71-8520-10A-01D-2393-08_LUAD	138	69	66	41	126	111	86	88	69	15	62	74	63	85	0	57	125
TCGA-73-7498-10A-01D-2184-08_LUAD	91	1	0	54	93	86	83	91	95	0	0	0	0	0	0	125	95
TCGA-73-7499-10A-01D-2184-08_LUAD	83	1	0	76	90	76	78	60	79	0	0	0	0	0	0	88	98
TCGA-74-6575-10A-01D-1845-08_GBM	119	98	106	0	82	79	98	100	113	0	61	86	0	4	49	1	121
TCGA-74-6577-10A-01D-1845-08_GBM	126	88	72	57	98	83	113	131	142	0	0	0	0	0	34	67	150
TCGA-74-6578-10A-01D-1845-08_GBM	134	78	71	69	143	138	105	160	141	0	65	86	1	1	37	69	145
TCGA-74-6581-10A-01D-1845-08_GBM	155	1	0	108	109	108	121	131	142	0	0	0	0	1	40	81	133
TCGA-74-6584-10A-01D-1845-08_GBM	174	1	1	128	162	122	157	130	175	0	0	1	0	0	0	104	162
TCGA-75-5122-10A-01D-1753-08_LUAD	107	0	1	51	86	86	80	88	95	0	0	0	0	0	20	40	110
TCGA-75-5125-10A-01D-1753-08_LUAD	104	1	0	76	106	99	87	78	96	0	0	1	0	0	0	70	124
TCGA-75-5126-10A-01D-1753-08_LUAD	101	60	65	50	120	100	117	118	117	17	37	73	0	1	0	106	130
TCGA-75-5146-10A-01D-1625-08_LUAD	106	0	1	82	116	108	111	89	93	13	30	1	65	64	0	58	136
TCGA-75-5147-10A-01D-1625-08_LUAD	125	82	97	0	70	103	97	103	64	13	75	66	60	0	16	0	116

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-75-6203-10A-01D-1753-08_LUAD	94	59	59	37	73	65	88	76	108	0	1	0	1	1	0	72	114
TCGA-75-6205-10A-01D-1753-08_LUAD	95	0	0	62	97	103	88	83	103	0	0	1	0	0	28	51	123
TCGA-75-6206-10A-01D-1753-08_LUAD	97	68	0	41	133	94	78	73	73	21	40	1	55	77	0	51	106
TCGA-75-6207-10A-01D-1753-08_LUAD	107	1	0	58	100	95	86	96	119	0	0	0	0	0	29	54	103
TCGA-75-6211-10A-01D-1753-08_LUAD	112	67	83	41	118	96	98	101	64	14	60	104	0	82	0	50	105
TCGA-75-6212-10A-01D-1753-08_LUAD	96	0	1	81	95	91	91	92	113	1	2	3	0	1	0	116	110
TCGA-75-6214-10A-01D-1946-08_LUAD	96	0	1	59	96	92	82	111	75	18	45	0	66	78	27	0	111
TCGA-75-7025-10A-01D-1946-08_LUAD	89	0	5	83	100	84	91	80	120	0	0	0	1	1	0	91	105
TCGA-75-7027-10A-01D-1946-08_LUAD	153	1	1	105	137	133	128	109	162	0	1	0	0	2	0	105	168
TCGA-75-7030-10A-01D-1946-08_LUAD	115	1	0	63	101	67	65	59	70	0	0	1	0	69	23	0	84
TCGA-75-7031-10A-01D-1946-08_LUAD	161	86	87	59	85	91	124	105	91	13	55	1	73	89	0	84	155
TCGA-76-4925-10A-01D-1486-08_GBM	127	3	1	64	115	106	109	125	107	0	0	1	0	1	0	107	119
TCGA-76-4926-10A-01D-1486-08_GBM	130	1	1	89	112	132	105	91	84	25	53	87	0	88	0	86	128
TCGA-76-4927-10A-01D-1486-08_GBM	124	0	2	93	113	105	93	128	106	0	0	0	0	2	0	157	125
TCGA-76-4928-10A-01D-1486-08_GBM	118	0	1	64	122	105	112	153	130	0	1	0	0	0	0	165	126
TCGA-76-4929-10A-01D-1486-08_GBM	122	1	1	96	129	127	97	122	86	24	61	84	0	84	0	84	132
TCGA-76-4931-10A-01D-1486-08_GBM	128	111	105	1	1	3	98	118	89	19	61	1	82	87	0	78	139
TCGA-76-4932-10A-01D-1486-08_GBM	132	100	121	2	1	2	104	134	123	0	1	0	1	0	38	81	145
TCGA-76-4934-10A-01D-1486-08_GBM	112	80	72	50	140	109	94	94	2	27	100	102	63	109	0	1	124
TCGA-76-4935-10A-01D-1486-08_GBM	119	3	2	60	127	109	97	114	89	19	60	0	76	90	0	77	139
TCGA-76-6191-10A-01D-1696-08_GBM	94	1	3	58	106	101	96	93	88	1	1	0	0	1	0	107	119
TCGA-76-6192-10A-01D-1696-08_GBM	105	0	0	59	147	109	112	126	101	17	37	67	0	1	27	61	117
TCGA-76-6193-10A-01D-1696-08_GBM	132	0	0	55	106	81	89	101	92	0	0	0	0	2	0	113	115
TCGA-76-6280-10A-01D-1845-08_GBM	132	76	87	59	89	2	82	85	99	0	0	0	0	94	0	79	107
TCGA-76-6282-10A-01D-1696-08_GBM	98	0	1	80	107	90	91	87	80	15	42	78	0	65	0	63	116
TCGA-76-6283-10A-01D-1845-08_GBM	127	0	0	83	113	101	101	119	105	0	0	0	0	1	34	75	146
TCGA-76-6285-10A-01D-1696-08_GBM	106	68	63	35	78	62	87	87	71	15	40	4	58	75	25	0	113
TCGA-76-6286-10A-01D-1845-08_GBM	134	81	78	65	91	79	100	127	135	0	0	0	0	0	0	154	120
TCGA-76-6656-10A-01D-1845-08_GBM	119	0	0	65	115	103	91	113	74	18	46	0	75	80	0	68	140
TCGA-76-6657-10A-01D-1845-08_GBM	126	105	108	1	132	126	114	143	127	0	81	112	0	0	33	68	143
TCGA-76-6660-10A-01D-1845-08_GBM	119	68	81	52	83	81	107	107	125	0	0	0	1	2	0	98	122
TCGA-76-6661-10A-01D-1845-08_GBM	121	66	77	65	131	116	100	125	102	0	52	87	0	1	0	140	145
TCGA-76-6662-10A-01D-1845-08_GBM	134	74	82	61	85	85	107	152	142	0	1	0	0	0	39	77	150
TCGA-76-6663-10A-01D-1845-08_GBM	125	70	118	51	86	80	95	122	99	0	0	0	1	0	0	95	130
TCGA-76-6664-10A-01D-1845-08_GBM	134	69	74	55	81	90	112	112	109	0	0	0	0	0	40	2	139
TCGA-77-6842-10A-01D-1945-08_LUSC	105	61	72	42	134	110	83	116	115	0	34	69	0	1	30	54	96
TCGA-77-6843-10A-01D-1945-08_LUSC	91	65	60	44	107	92	82	100	104	0	32	59	0	0	32	55	99
TCGA-77-6844-10A-01D-1945-08_LUSC	98	76	73	40	117	98	93	88	121	0	51	74	0	3	0	85	108
TCGA-77-6845-10A-01D-1945-08_LUSC	84	0	1	76	79	67	66	82	78	0	0	0	0	1	26	52	90
TCGA-77-7138-10A-01D-2042-08_LUSC	91	0	0	51	94	87	89	100	73	10	45	1	66	68	35	0	122
TCGA-77-7139-10A-01D-2042-08_LUSC	94	1	2	82	90	98	93	106	112	0	0	0	0	0	28	69	100
TCGA-77-7140-10A-01D-2042-08_LUSC	93	58	65	49	78	57	77	92	91	0	0	0	0	1	29	65	100
TCGA-77-7463-10A-01D-2042-08_LUSC	98	58	60	45	72	62	80	110	90	0	0	0	0	0	0	130	111
TCGA-77-7465-10A-01D-2042-08_LUSC	89	0	0	62	88	82	90	109	71	15	49	0	51	72	0	63	105
TCGA-77-8128-10A-01D-2244-08_LUSC	118	57	0	49	110	82	80	74	112	0	0	0	0	0	0	82	112
TCGA-77-8130-10A-01D-2244-08_LUSC	87	0	0	76	90	68	84	70	85	0	0	0	1	0	0	74	100
TCGA-77-8131-10A-01D-2244-08_LUSC	88	57	51	45	101	90	82	84	107	0	33	60	1	3	25	54	96
TCGA-77-8133-10A-01D-2244-08_LUSC	114	52	60	42	68	65	73	61	83	0	0	0	1	0	33	0	88
TCGA-77-8136-10A-01D-2244-08_LUSC	131	7	5	116	137	102	127	127	153	2	4	3	3	14	41	83	171
TCGA-77-8138-10A-01D-2244-08_LUSC	87	78	78	1	89	80	89	94	65	25	67	86	0	73	0	68	106
TCGA-77-8139-10A-01D-2244-08_LUSC	76	0	0	51	87	73	82	74	87	0	1	0	0	0	23	64	87
TCGA-77-8140-10A-01D-2244-08_LUSC	87	51	69	43	63	63	83	68	75	0	0	1	0	0	0	69	90
TCGA-77-8143-10A-01D-2244-08_LUSC	83	2	1	59	93	75	79	58	74	0	0	0	0	2	0	75	97
TCGA-77-8144-10A-01D-2244-08_LUSC	106	59	61	37	84	74	80	106	76	15	47	0	53	67	31	0	91
TCGA-77-8145-10A-01D-2244-08_LUSC	85	1	0	67	75	78	77	73	92	0	0	0	0	0	0	102	92
TCGA-77-8146-10A-01D-2244-08_LUSC	81	53	54	42	116	80	77	56	0	19	62	67	61	91	0	0	97
TCGA-77-8148-10A-01D-2244-08_LUSC	91	61	60	46	117	67	60	42	79	1	40	67	0	76	27	0	104
TCGA-77-8150-10A-01D-2244-08_LUSC	107	1	0	49	85	69	79	82	97	13	0	0	0	2	25	42	92
TCGA-77-8154-10A-01D-2244-08_LUSC	121	52	53	44	74	66	78	86	65	18	36	0	50	67	25	0	97
TCGA-77-8156-10A-01D-2244-08_LUSC	87	55	53	43	108	88	87	65	88	0	41	65	0	2	0	74	99
TCGA-77-A5FZ-10A-01D-A27N-08_LUSC	79	55	64	32	70	63	71	70	75	0	0	0	0	0	0	72	85
TCGA-77-A5G1-10A-01D-A27N-08_LUSC	84	0	1	53	89	84	73	77	97	0	0	0	0	1	0	82	95
TCGA-77-A5G3-10A-01D-A27N-08_LUSC	87	71	66	42	73	68	84	75	80	0	0	0	0	0	0	79	100
TCGA-77-A5G6-10A-01D-A27N-08_LUSC	79	1	0	44	80	74	72	103	98	0	0	0	0	0	33	57	88
TCGA-77-A5G7-10A-01D-A27N-08_LUSC	102	57	65	38	64	65	74	98	98	0	0	0	0	0	27	55	86
TCGA-77-A5G8-10A-01D-A27N-08_LUSC	83	60	70	44	117	85	85	97	83	0	53	73	1	0	0	129	89
TCGA-77-A5GA-10A-01D-A27N-08_LUSC	85	0	2	81	83	85	79	107	109	0	0	0	0	1	0	82	102
TCGA-77-A5GB-10A-01D-A27N-08_LUSC	81	57	66	45	64	69	78	85	96	0	0	0	1	2	0	105	92
TCGA-77-A5GF-10A-01D-A27N-08_LUSC	88	81	91	0	83	76	83	106	65	18	68	65	62	79	0	58	97
TCGA-77-A5GH-10A-01D-A27N-08_LUSC	98	0	0	88	124	83	86	98	64	17	48	0	61	74	0	55	89
TCGA-78-7143-10A-01D-2036-08_LUAD	101	0	0	87	101	100	91	107	107	0	0	0	0	0	0	82	130
TCGA-78-7145-10A-01D-2036-08_LUAD	116	0	1	64	97	91	96	90	77	16	51	0	71	80	0	61	120
TCGA-78-7146-10A-01D-2036-08_LUAD	88	67	70	41	72	60	88	84	80	0	1	0	0	0	0	82	94
TCGA-78-7147-10A-01D-2036-08_LUAD	100	70	69	50	132	97	92	81	84	0	46	75	0	0	0	86	100
TCGA-78-7148-10A-01D-2036-08_LUAD	100	69	72	53	82	75	92	125	118	0	0	0	0	1	32	63	113
TCGA-78-7149-10A-01D-2036-08_LUAD	90	0	1	55	91	85	77	82	110	0	0	0	0	1	0	81	100
TCGA-78-7150-10A-01D-2036-08_LUAD	124	63	73	48	106	88	84	79	109	0	48	65	0	2	0	76	96
TCGA-78-7152-10A-01D-2036-08_LUAD	130	71	82	46	119	83	86	105	109	0	52	72	0	1	33	69	117
TCGA-78-7153-10A-01D-2036-08_LUAD	118	64	72	47	127	104	81	80	68	20	75	72	60	73	0	65	93
TCGA-78-7154-10A-01D-2036-08_LUAD	97	1	0	82	88	84	84	83	112	0	1	3	0	4	0	83	97
TCGA-78-7155-10A-01D-2036-08_LUAD	82	0	0	68	92	80	69	68	53	11	30	0	41	57	0	53	91
TCGA-78-7156-10A-01D-2036-08_LUAD	106	0	0	72	96	102	92	94	81	25	70	75	4	87	0	72	123
TCGA-78-7158-10A-01D-2036-08_LUAD	107	76	86	3	5	4	78	108	101	0	0	0	1	2	0	116	98
TCGA-78-7159-10A-01D-2036-08_LUAD	95	1	5	56	94	76	87	77	69	15	44	0	63	75	0	51	101
TCGA-78-7160-10A-01D-2036-08_LUAD	84	63	68	45	110	80	86	88	57	15	75	82	0	67	0	70	96
TCGA-78-7161-10A-01D-2036-08_LUAD	102	3	1	38	105	97	91	65	84	0	1	0	0	2	0	95	105
TCGA-78-7220-10A-01D-2036-08_LUAD	99	0	0	62	103	90	91	105	97	0	0	0	0	1	0	120	114
TCGA-78-7535-10A-01D-2063-08_LUAD	91	64	74	51	72	65	89	82	67	18	51	2	60	76	0	66	93
TCGA-78-7536-10A-01D-2063-08_LUAD	92	92	87	1	76	75	81	101	89	19	75	92	0	77	26	2	103
TCGA-78-7537-10A-01D-2063-08_LUAD	90	0	2	66	111	93	90	85	63	20	37	1	64	69	0	66	122
TCGA-78-7539-10A-01D-2063-08_LUAD	79	59	56	43	67	69	83	81	85	0	0	0	0	0	0	85	108
TCGA-78-7633-10A-01D-2063-08_LUAD	96	0	0	68	89	68	72	90	52	13	38	0	52	70	0	55	98
TCGA-78-8648-10A-01D-2393-08_LUAD	128	0	0	73	122	105	110	114	87	17	55	0	64	101	34	0	129
TCGA-78-8655-10A-01D-2393-08_LUAD	105	83	99	2	81	72	93	93	78	16	85	77	70	81	0	72	112
TCGA-78-8660-10A-01D-2393-08_LUAD	111	0	0	46	108	104	99	110	101	0	0	0	0	1	0	136	131
TCGA-78-8662-10A-01D-2393-08_LUAD	92	79	77	50	143	97	103	114	82	15	90	97	0	82	29	1	103

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-79-5596-10A-01D-1945-08_LUSC	98	62	66	45	111	86	78	72	71	11	59	89	0	70	0	60	107
TCGA-80-5607-10A-01D-1946-08_LUAD	126	0	0	92	122	110	111	88	115	0	0	0	0	1	0	108	142
TCGA-80-5608-10A-01D-1946-08_LUAD	134	1	3	102	125	107	112	108	84	19	44	0	74	94	0	81	154
TCGA-80-5611-10A-01D-1625-08_LUAD	105	58	57	36	63	69	94	95	128	1	1	0	0	0	12	42	108
TCGA-81-5910-10A-01D-1696-08_GBM	96	63	71	39	123	94	91	100	121	0	29	61	1	0	24	55	113
TCGA-81-5911-10A-01D-1845-08_GBM	105	0	1	104	122	115	106	110	82	16	44	0	60	77	0	67	127
TCGA-83-5908-10A-01D-2284-08_LUAD	84	68	62	49	78	68	86	88	70	20	47	0	56	75	0	65	97
TCGA-85-6175-10A-01D-1817-08_LUSC	145	77	0	54	154	107	113	106	86	24	56	0	63	92	24	0	127
TCGA-85-6560-10A-01D-1817-08_LUSC	103	92	86	2	73	73	84	91	92	21	77	78	63	80	0	71	105
TCGA-85-6561-10A-01D-1817-08_LUSC	104	68	69	54	79	71	85	105	98	0	0	0	0	1	27	63	98
TCGA-85-6798-10A-01D-1945-08_LUSC	161	105	101	0	3	0	118	122	151	0	0	1	0	2	0	109	150
TCGA-85-7696-10A-01D-2122-08_LUSC	101	70	82	40	77	79	105	122	84	21	69	3	88	81	21	3	105
TCGA-85-7697-10A-01D-2122-08_LUSC	130	68	69	50	125	80	88	101	69	19	70	97	0	75	0	68	106
TCGA-85-7698-10A-01D-2122-08_LUSC	90	6	6	88	97	93	80	94	96	0	3	1	5	8	0	129	111
TCGA-85-7699-10A-01D-2122-08_LUSC	138	84	90	63	164	134	134	114	92	28	101	131	1	116	0	101	166
TCGA-85-7710-10A-01D-2122-08_LUSC	91	86	99	0	83	54	106	89	3	27	79	92	52	120	0	0	126
TCGA-85-7843-10A-01D-2122-08_LUSC	79	66	64	46	124	82	78	96	82	0	44	67	0	1	0	112	93
TCGA-85-7844-10A-01D-2122-08_LUSC	80	61	63	41	77	71	80	71	86	1	1	0	1	2	0	76	97
TCGA-85-7950-10A-01D-2184-08_LUSC	79	66	63	48	111	81	75	78	66	14	70	66	51	75	0	50	105
TCGA-85-8048-10A-01D-2244-08_LUSC	86	63	56	40	72	64	62	37	66	0	31	0	53	68	0	56	108
TCGA-85-8049-10A-01D-2244-08_LUSC	76	51	46	40	93	76	67	103	76	0	52	52	0	0	28	59	77
TCGA-85-8052-10A-01D-2244-08_LUSC	83	49	58	43	110	56	64	55	68	0	36	64	1	68	29	0	81
TCGA-85-8070-10A-01D-2244-08_LUSC	118	0	0	71	87	84	82	64	99	0	0	0	0	0	0	75	100
TCGA-85-8071-10A-01D-2244-08_LUSC	86	0	0	51	85	81	72	59	58	16	34	0	48	60	0	61	91
TCGA-85-8072-10A-01D-2244-08_LUSC	80	0	0	55	81	81	77	82	77	0	0	0	0	0	0	109	100
TCGA-85-8276-10A-01D-2293-08_LUSC	87	0	1	43	95	102	77	87	76	14	52	0	64	73	0	68	96
TCGA-85-8277-10A-01D-2293-08_LUSC	119	65	72	48	70	77	79	84	89	0	0	0	0	0	0	129	103
TCGA-85-8287-10A-01D-2293-08_LUSC	121	63	58	44	112	99	90	77	2	30	85	86	57	90	0	0	105
TCGA-85-8288-10A-01D-2293-08_LUSC	95	76	63	46	75	74	80	95	82	0	0	0	0	0	0	125	99
TCGA-85-8350-10A-01D-2293-08_LUSC	93	0	1	64	95	84	92	106	94	0	0	0	0	0	0	83	122
TCGA-85-8351-10A-01D-2293-08_LUSC	93	2	2	102	113	106	103	129	127	19	1	1	1	1	32	66	111
TCGA-85-8352-10A-01D-2323-08_LUSC	112	78	81	49	87	89	106	94	89	10	46	0	79	84	0	70	143
TCGA-85-8353-10A-01D-2293-08_LUSC	92	0	0	93	89	83	82	102	123	0	0	0	0	0	0	122	112
TCGA-85-8354-10A-01D-2323-08_LUSC	116	0	0	98	174	128	115	152	128	14	43	81	1	0	0	118	119
TCGA-85-8355-10A-01D-2293-08_LUSC	92	1	1	82	96	88	78	116	114	0	1	0	0	1	0	127	113
TCGA-85-8479-10A-01D-2323-08_LUSC	116	98	113	0	113	112	105	97	114	0	66	107	0	0	48	0	123
TCGA-85-8481-10A-01D-2323-08_LUSC	110	104	119	2	88	79	77	70	1	23	111	84	108	125	0	0	127
TCGA-85-8580-10A-01D-2395-08_LUSC	122	66	65	47	116	90	81	96	104	0	46	74	0	1	35	68	100
TCGA-85-8582-10A-01D-2395-08_LUSC	89	69	68	44	111	82	86	81	74	17	72	65	57	76	0	71	94
TCGA-85-8584-10A-01D-2395-08_LUSC	89	54	56	41	99	87	73	85	76	2	48	62	0	1	0	81	94
TCGA-85-8664-10A-01D-2395-08_LUSC	86	5	4	81	86	87	76	75	100	0	0	0	0	1	0	81	94
TCGA-85-8666-10A-01D-2395-08_LUSC	85	58	62	43	105	72	83	116	112	0	57	70	3	0	26	61	98
TCGA-85-A4CL-10A-01D-A26K-08_LUSC	88	48	53	46	94	79	76	68	76	0	42	60	0	0	0	73	94
TCGA-85-A4CN-10A-01D-A24F-08_LUSC	78	61	60	37	66	51	71	88	78	0	4	3	0	0	0	71	90
TCGA-85-A4JB-10A-01D-A25L-08_LUSC	80	71	65	34	115	74	83	104	92	0	47	64	0	4	28	55	105
TCGA-85-A4JC-10A-01D-A25A-08_LUSC	91	67	83	0	84	80	82	86	67	20	77	75	51	61	32	0	97
TCGA-85-A4PA-10A-01D-A25A-08_LUSC	94	73	68	51	118	79	86	82	65	17	71	64	62	66	0	62	104
TCGA-85-A4QQ-10A-01D-A25L-08_LUSC	87	6	4	70	91	76	85	80	100	0	1	2	0	1	0	76	94
TCGA-85-A4QR-10A-01D-A25A-08_LUSC	97	62	64	47	63	8	57	67	61	0	0	2	0	70	0	63	71
TCGA-85-A50M-10A-01D-A25L-08_LUSC	98	0	0	54	99	94	86	105	96	0	1	0	1	1	32	65	105
TCGA-85-A50Z-10A-01D-A25L-08_LUSC	92	0	0	47	90	68	67	56	62	0	1	0	0	62	0	68	77
TCGA-85-A510-10A-01D-A26K-08_LUSC	112	2	4	58	98	93	88	91	98	0	0	0	0	0	0	90	110
TCGA-85-A511-10A-01D-A25L-08_LUSC	98	4	2	48	90	78	72	96	81	0	2	0	1	5	0	102	98
TCGA-85-A512-10A-01D-A26K-08_LUSC	111	59	69	54	81	78	106	99	119	0	0	0	0	0	29	63	116
TCGA-85-A513-10A-01D-A26K-08_LUSC	123	2	0	76	101	100	88	88	3	24	71	90	2	99	0	1	103
TCGA-85-A53L-10A-01D-A26K-08_LUSC	90	0	0	71	94	80	85	92	72	13	40	0	52	67	25	5	100
TCGA-85-A5B5-10A-01D-A26K-08_LUSC	101	60	66	39	120	92	90	105	64	14	61	87	1	78	0	65	103
TCGA-86-6562-10A-01D-1753-08_LUAD	92	0	2	62	104	94	90	93	107	0	0	1	2	0	27	46	117
TCGA-86-6851-10A-01D-1946-08_LUAD	144	1	1	104	123	117	108	102	97	1	1	0	0	0	0	101	143
TCGA-86-7701-10A-01D-2167-08_LUAD	124	48	59	68	73	87	101	68	115	0	0	1	0	0	0	84	135
TCGA-86-7711-10A-01D-2063-08_LUAD	91	60	50	38	105	97	101	80	105	0	32	58	1	1	20	46	107
TCGA-86-7713-10A-01D-2063-08_LUAD	129	67	68	52	78	80	91	136	117	1	0	0	0	2	30	71	113
TCGA-86-7714-10A-01D-2167-08_LUAD	104	48	51	0	89	92	80	63	107	0	37	0	38	0	26	55	118
TCGA-86-7953-10A-01D-2184-08_LUAD	96	1	0	84	96	90	83	61	72	14	35	1	50	81	0	51	109
TCGA-86-7954-10A-01D-2184-08_LUAD	91	75	74	1	1	3	74	78	86	0	1	0	0	1	36	3	101
TCGA-86-7955-10A-01D-2184-08_LUAD	81	1	0	57	93	71	72	68	57	19	49	0	49	76	0	58	100
TCGA-86-8054-10A-01D-2238-08_LUAD	100	1	1	62	101	71	72	54	72	0	1	0	0	69	0	64	97
TCGA-86-8055-10A-01D-2238-08_LUAD	103	1	0	63	105	92	97	106	121	0	2	0	0	2	0	86	109
TCGA-86-8056-10A-01D-2238-08_LUAD	96	62	69	50	112	87	81	100	72	22	78	70	48	74	33	0	120
TCGA-86-8073-10A-01D-2238-08_LUAD	85	61	59	50	77	72	87	94	71	16	52	0	53	78	32	0	111
TCGA-86-8074-10A-01D-2238-08_LUAD	102	85	85	1	80	75	93	107	76	18	71	88	0	81	36	1	114
TCGA-86-8075-10A-01D-2238-08_LUAD	88	63	90	46	135	91	78	79	80	15	80	99	0	79	0	68	116
TCGA-86-8076-10A-01D-2238-08_LUAD	96	1	1	61	91	77	71	49	69	0	0	1	0	79	0	57	84
TCGA-86-8278-10A-01D-2284-08_LUAD	112	78	89	47	81	81	108	109	126	0	0	0	0	0	28	66	124
TCGA-86-8279-10A-01D-2284-08_LUAD	114	0	0	64	108	101	99	105	114	0	0	0	0	0	25	64	118
TCGA-86-8280-10A-01D-2284-08_LUAD	112	0	0	85	101	77	72	51	86	0	0	0	0	76	0	66	108
TCGA-86-8281-10A-01D-2284-08_LUAD	94	46	69	51	77	68	90	91	85	0	0	0	0	0	0	103	108
TCGA-86-8358-10A-01D-2323-08_LUAD	109	75	88	53	150	109	110	130	101	0	46	89	0	0	0	141	140
TCGA-86-8359-10A-01D-2323-08_LUAD	159	2	0	94	152	150	132	153	104	25	66	3	83	119	0	85	177
TCGA-86-8585-10A-01D-2393-08_LUAD	91	77	76	58	75	76	87	112	112	0	4	6	0	0	32	67	112
TCGA-86-8668-10A-01D-2393-08_LUAD	89	90	90	7	10	8	90	110	125	0	0	3	2	5	0	69	99
TCGA-86-8669-10A-01D-2393-08_LUAD	94	8	7	54	106	102	96	107	99	1	3	7	1	3	0	91	106
TCGA-86-8671-10A-01D-2393-08_LUAD	110	72	66	43	120	82	89	91	99	6	59	75	2	10	0	127	99
TCGA-86-8672-10A-01D-2393-08_LUAD	96	73	74	51	128	88	97	103	81	26	86	100	7	75	0	82	106
TCGA-86-8673-10A-01D-2393-08_LUAD	105	75	79	51	84	81	97	109	117	5	2	1	4	5	0	137	111
TCGA-86-8674-10A-01D-2393-08_LUAD	105	0	0	95	116	116	101	103	107	0	0	0	0	0	0	104	142
TCGA-86-A456-10A-01D-A24F-08_LUAD	75	1	4	49	77	77	68	80	72	2	2	3	2	4	21	43	90
TCGA-86-A4D0-10A-01D-A24F-08_LUAD	72	5	9	42	79	71	70	84	91	0	1	5	1	5	0	71	83
TCGA-86-A4JF-10A-01D-A24P-08_LUAD	83	0	4	73	90	81	84	125	117	1	4	0	4	4	29	63	97
TCGA-86-A4P7-10A-01D-A24P-08_LUAD	84	86	83	1	5	5	78	107	85	0	0	0	1	0	29	64	98
TCGA-86-A4P8-10A-01D-A24P-08_LUAD	74	0	2	75	79	75	72	89	62	15	44	0	55	64	0	54	91
TCGA-87-5896-10A-01D-1696-08_GBM	86	62	66	39	62	63	78	85	98	0	0	0	1	5	27	51	106
TCGA-90-6837-10A-01D-1945-08_LUSC	169	110	99	79	183	123	177	205	104	36	111	121	81	110	39	3	185
TCGA-90-7766-10A-01D-2122-08_LUSC	94	63	72	42	77	62	83	95	78	17	46	0	61	74	24	6	100
TCGA-90-7767-10A-01D-2122-08_LUSC	95	70	53	47	68	61	79	92	69	14	43	0	57	59	20	3	117
TCGA-90-7769-10A-01D-2122-08_LUSC	94	1	0	90	93	86	81	111	117	0	0	1	0	2	25	60	107

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-90-7964-10A-01D-2184-08_LUSC	114	2	1	76	85	86	79	82	107	0	0	0	0	2	0	110	105
TCGA-90-A4ED-10A-01D-A25A-08_LUSC	111	74	71	47	73	69	89	90	79	13	50	0	61	66	0	66	99
TCGA-90-A4EE-10B-01D-A25A-08_LUSC	97	62	66	37	69	52	78	105	100	0	2	1	0	0	34	63	103
TCGA-90-A59Q-10A-01D-A26K-08_LUSC	92	1	0	55	87	82	72	81	79	1	1	0	1	1	0	94	104
TCGA-91-6828-10A-01D-1855-08_LUAD	117	0	0	92	105	98	96	103	130	0	0	0	0	1	29	55	114
TCGA-91-6840-10A-01D-1946-08_LUAD	101	89	93	1	71	71	94	113	116	14	43	63	0	1	23	58	125
TCGA-91-7771-10A-01D-2167-08_LUAD	117	0	1	74	89	79	89	116	113	0	0	0	0	3	33	62	107
TCGA-91-8496-10A-01D-2393-08_LUAD	128	0	0	77	109	106	100	101	133	0	0	0	0	0	0	79	118
TCGA-91-8497-10A-01D-2393-08_LUAD	80	43	56	36	61	56	79	104	57	21	49	0	54	68	27	9	89
TCGA-91-8499-10A-01D-2393-08_LUAD	127	0	1	65	97	91	89	144	125	0	0	1	0	1	0	149	115
TCGA-91-A4BC-10A-01D-A24F-08_LUAD	75	53	52	37	103	69	77	72	70	14	59	69	0	63	0	58	80
TCGA-91-A4BD-10A-01D-A24F-08_LUAD	75	58	64	37	104	80	71	71	64	16	66	61	59	67	0	55	87
TCGA-92-7340-10A-01D-2042-08_LUSC	91	1	0	81	86	87	87	85	58	17	46	0	66	68	0	59	108
TCGA-92-7341-10A-01D-2042-08_LUSC	93	88	87	2	3	0	79	84	90	0	1	1	0	1	0	92	117
TCGA-92-8063-10A-01D-2244-08_LUSC	78	50	51	45	105	83	71	71	73	13	50	65	52	64	23	2	82
TCGA-92-8064-10A-01D-2244-08_LUSC	78	0	0	52	79	88	77	68	102	0	0	0	0	2	29	56	86
TCGA-92-8065-10A-01D-2244-08_LUSC	82	3	0	78	100	86	79	64	104	0	0	0	0	1	0	74	100
TCGA-93-7347-10A-01D-2184-08_LUAD	132	0	0	68	102	89	81	77	91	0	0	0	0	0	33	1	103
TCGA-93-7348-10A-01D-2036-08_LUAD	99	71	58	48	70	66	89	82	82	0	0	1	0	2	0	81	109
TCGA-93-8067-10A-01D-2284-08_LUAD	108	0	0	80	106	110	106	80	82	21	40	1	63	88	0	64	120
TCGA-93-A4JN-10A-01D-A24P-08_LUAD	85	6	6	75	143	89	76	78	73	22	59	0	65	69	0	66	96
TCGA-93-A4JO-10A-01D-A24P-08_LUAD	112	0	1	54	79	75	75	126	111	0	1	0	0	0	0	119	89
TCGA-93-A4JP-10A-01D-A24P-08_LUAD	94	3	4	51	93	82	88	107	113	0	2	0	4	5	33	71	93
TCGA-93-A4JQ-10A-01D-A24P-08_LUAD	80	69	62	45	74	68	65	61	61	0	60	0	64	67	0	67	89
TCGA-94-7033-10A-01D-1946-08_LUSC	113	62	78	60	141	109	113	138	128	15	53	73	1	0	27	66	131
TCGA-94-7557-10A-01D-2122-08_LUSC	86	60	56	42	115	90	91	85	93	0	45	70	0	0	38	4	104
TCGA-94-7943-10A-01D-2184-08_LUSC	78	0	0	54	85	82	86	79	84	0	0	0	0	1	0	102	95
TCGA-94-8035-10A-01D-2244-08_LUSC	107	48	0	35	91	70	65	92	84	0	0	0	0	0	21	57	76
TCGA-94-8490-10A-01D-2323-08_LUSC	136	0	1	105	105	119	99	137	140	0	0	0	0	1	34	63	143
TCGA-94-8491-10A-01D-2323-08_LUSC	120	99	100	0	0	0	103	93	111	0	0	0	0	0	36	0	144
TCGA-94-A4VJ-10A-01D-A25A-08_LUSC	82	0	0	64	92	78	77	78	93	0	0	0	0	0	0	85	106
TCGA-94-A5I4-10A-01D-A26K-08_LUSC	130	1	2	72	106	90	100	111	123	0	1	3	0	0	0	128	118
TCGA-94-A5I6-10A-01D-A27N-08_LUSC	87	64	63	42	68	62	78	103	70	17	36	0	64	63	29	0	91
TCGA-95-7039-10A-01D-1946-08_LUAD	81	1	1	51	101	81	81	89	84	0	0	0	0	0	23	64	100
TCGA-95-7043-10A-01D-1946-08_LUAD	96	0	0	66	127	97	79	103	113	0	0	0	0	0	24	59	114
TCGA-95-7562-10B-01D-2238-08_LUAD	103	1	0	92	94	86	97	93	113	0	0	0	0	3	30	69	99
TCGA-95-7567-10A-01D-2063-08_LUAD	90	70	68	50	72	69	82	121	116	0	0	0	0	0	33	65	109
TCGA-95-7944-10A-01D-2184-08_LUAD	85	51	60	45	110	90	76	71	66	13	65	64	42	63	0	51	102
TCGA-95-7947-10A-01D-2184-08_LUAD	89	59	55	43	64	69	75	83	80	0	1	0	0	0	26	64	96
TCGA-95-7948-10A-01D-2184-08_LUAD	83	66	72	51	119	94	86	84	108	0	39	69	0	1	0	120	102
TCGA-95-8039-10A-01D-2238-08_LUAD	87	1	0	55	98	94	81	95	107	0	0	0	0	0	28	67	106
TCGA-95-8494-10A-01D-2323-08_LUAD	107	74	79	0	129	108	98	110	65	12	64	72	66	78	0	57	125
TCGA-95-A4VK-10A-01D-A25L-08_LUAD	92	1	0	75	94	89	85	89	104	0	4	3	2	3	0	114	99
TCGA-95-A4VN-10A-01D-A25L-08_LUAD	94	1	1	76	94	95	83	82	74	23	45	3	58	72	0	62	98
TCGA-95-A4VP-10A-01D-A25L-08_LUAD	109	2	5	54	98	79	88	86	90	0	3	5	0	0	29	56	100
TCGA-96-7544-10A-01D-2042-08_LUSC	101	0	1	61	94	92	74	93	78	16	47	1	62	70	0	67	103
TCGA-96-7545-10A-01D-2042-08_LUSC	96	0	1	52	127	72	83	77	114	0	0	1	0	0	0	83	117
TCGA-96-8169-10A-01D-2293-08_LUSC	79	0	1	91	102	96	89	104	117	0	2	2	0	0	35	61	120
TCGA-96-8170-10A-01D-2293-08_LUSC	84	63	62	45	73	69	77	91	106	0	0	0	0	1	25	51	109
TCGA-96-A4JK-10A-01D-A25A-08_LUSC	94	50	68	45	67	58	85	86	83	0	3	3	3	7	0	82	110
TCGA-96-A4JL-10A-01D-A25A-08_LUSC	140	2	0	86	100	100	91	124	65	20	53	1	55	70	32	2	107
TCGA-97-7546-10A-01D-2036-08_LUAD	88	59	65	41	70	63	73	99	82	0	0	1	4	4	31	62	102
TCGA-97-7547-10A-01D-2036-08_LUAD	93	0	1	87	87	86	86	92	77	11	45	3	48	71	0	64	111
TCGA-97-7552-10A-01D-2036-08_LUAD	102	2	2	84	97	87	97	102	94	0	0	0	1	1	0	134	108
TCGA-97-7553-10A-01D-2036-08_LUAD	117	71	75	46	112	91	98	102	76	16	68	74	62	71	28	1	105
TCGA-97-7554-10A-01D-2036-08_LUAD	102	0	0	49	94	84	85	98	61	9	37	0	64	68	27	0	117
TCGA-97-7937-10A-01D-2167-08_LUAD	109	0	0	78	104	101	102	79	1	25	59	0	66	106	0	2	118
TCGA-97-7938-10A-01D-2167-08_LUAD	113	0	0	71	93	105	93	73	63	17	47	0	47	69	0	58	100
TCGA-97-7941-10A-01D-2184-08_LUAD	87	1	1	76	89	82	69	89	79	0	0	0	0	1	28	65	102
TCGA-97-8171-10A-01D-2284-08_LUAD	105	73	70	49	86	75	102	104	104	0	0	0	0	1	30	57	126
TCGA-97-8172-10A-01D-2284-08_LUAD	107	65	74	52	87	89	99	97	93	20	46	0	62	87	26	0	133
TCGA-97-8174-10A-01D-2284-08_LUAD	111	63	73	47	71	71	105	95	90	17	33	0	65	84	0	44	123
TCGA-97-8175-10A-01D-2284-08_LUAD	92	52	59	42	71	67	91	79	67	11	31	0	52	77	0	50	114
TCGA-97-8176-10B-01D-2393-08_LUAD	118	0	0	61	101	107	97	116	137	0	0	0	0	0	0	116	121
TCGA-97-8177-10A-01D-2284-08_LUAD	102	1	0	68	105	107	97	97	130	0	0	0	0	0	0	107	117
TCGA-97-8179-10A-01D-2284-08_LUAD	110	0	0	91	115	110	104	86	107	0	0	0	0	0	0	89	131
TCGA-97-8547-10A-01D-2393-08_LUAD	88	4	4	49	87	80	88	83	78	1	3	2	6	8	0	119	87
TCGA-97-8552-10A-01D-2393-08_LUAD	127	80	85	48	84	78	95	113	118	0	0	0	0	0	0	101	124
TCGA-97-A4LX-10A-01D-A24P-08_LUAD	89	67	69	45	113	82	80	102	101	0	47	66	8	3	28	66	80
TCGA-97-A4M0-10A-01D-A24P-08_LUAD	89	0	1	52	90	84	75	101	56	11	41	0	54	67	0	54	96
TCGA-97-A4M1-10A-01D-A24P-08_LUAD	80	63	63	41	99	77	73	94	65	13	67	63	51	70	0	50	86
TCGA-97-A4M2-10A-01D-A24P-08_LUAD	75	63	66	42	59	66	69	103	70	14	52	0	54	62	25	3	88
TCGA-97-A4M3-10A-01D-A24P-08_LUAD	83	0	3	79	86	76	77	129	109	0	0	0	0	0	27	72	96
TCGA-97-A4M5-10A-01D-A24P-08_LUAD	82	67	69	47	70	66	69	56	70	0	43	0	57	69	0	60	95
TCGA-97-A4M6-10A-01D-A24P-08_LUAD	79	75	65	3	79	80	82	69	4	21	80	57	78	75	0	1	88
TCGA-97-A4M7-10A-01D-A24P-08_LUAD	91	4	3	45	87	80	80	111	113	0	1	1	0	2	31	69	94
TCGA-98-7454-10A-01D-2042-08_LUSC	105	0	1	91	100	82	85	85	116	0	0	0	0	0	0	91	112
TCGA-98-8020-10A-01D-2244-08_LUSC	97	58	59	42	106	112	80	77	102	1	38	65	0	0	0	68	106
TCGA-98-8021-10A-01D-2244-08_LUSC	78	0	0	75	86	83	57	44	67	0	0	0	0	0	26	0	77
TCGA-98-8022-10A-01D-2244-08_LUSC	85	0	0	74	84	83	81	74	72	0	0	2	0	1	0	89	99
TCGA-98-8023-10A-01D-2244-08_LUSC	85	0	0	50	79	90	75	71	58	16	33	0	40	70	0	63	97
TCGA-98-A538-10A-01D-A25L-08_LUSC	99	0	2	56	93	95	86	110	97	0	0	0	0	0	29	62	112
TCGA-98-A539-10A-01D-A25L-08_LUSC	84	0	0	72	81	80	81	93	94	0	0	1	0	0	31	61	104
TCGA-98-A53A-10A-01D-A25L-08_LUSC	91	63	69	41	72	66	77	111	96	0	2	4	0	1	25	6	78
TCGA-98-A53B-10A-01D-A25L-08_LUSC	86	71	75	34	71	64	81	96	85	0	1	2	0	2	0	116	99
TCGA-98-A53C-10A-01D-A25L-08_LUSC	79	66	59	32	52	54	76	77	47	15	45	0	44	67	0	61	104
TCGA-98-A53D-10A-01D-A25L-08_LUSC	117	0	0	75	95	85	82	116	92	0	0	0	0	0	0	127	101
TCGA-98-A53H-10A-01D-A25L-08_LUSC	79	56	55	35	55	55	71	99	54	13	46	6	53	54	0	43	99
TCGA-98-A53I-10A-01D-A25L-08_LUSC	128	66	69	42	79	63	94	94	73	15	50	0	69	70	0	65	107
TCGA-98-A53J-10A-01D-A26K-08_LUSC	88	0	0	75	94	88	93	84	92	1	1	0	3	6	0	86	107
TCGA-99-7458-10A-01D-2036-08_LUAD	109	0	1	86	113	102	103	109	77	19	53	0	65	88	35	3	114
TCGA-99-8025-10A-01D-2238-08_LUAD	90	0	0	60	98	87	78	79	98	0	0	0	1	0	29	53	99
TCGA-99-8028-10A-01D-2238-08_LUAD	90	0	1	93	108	98	90	122	118	0	0	2	0	0	39	66	120
TCGA-99-8032-10A-01D-2238-08_LUAD	97	0	0	64	98	89	87	103	119	0	1	0	0	1	33	69	115
TCGA-99-8033-10A-01D-2238-08_LUAD	105	0	1	94	99	103	90	119	110	0	0	0	0	1	0	134	100
TCGA-A1-A0SB-10B-01D-A142-09_BRCA	29	58	44	24	57	45	89	69	1	16	80	53	46	78	0	0	63

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-A1-A0SD-10A-01D-A110-09_BRCA	97	188	190	2	0	4	194	160	238	0	0	0	0	0	0	194	132
TCGA-A1-A0SE-10A-03D-A099-09_BRCA	66	111	108	52	175	149	185	134	0	30	189	150	100	152	0	0	119
TCGA-A1-A0SF-10B-01D-A142-09_BRCA	41	63	47	19	86	68	67	59	81	0	35	45	0	0	24	35	54
TCGA-A1-A0SG-10B-01D-A17G-09_BRCA	79	162	150	0	102	106	150	124	88	28	159	105	104	123	0	97	99
TCGA-A1-A0SH-10A-03D-A099-09_BRCA	75	147	127	60	228	198	246	150	1	66	220	181	143	242	0	0	137
TCGA-A1-A0SI-10B-01D-A142-09_BRCA	36	0	1	32	72	57	75	52	39	11	36	32	0	41	20	0	48
TCGA-A1-A0SJ-10A-02D-A099-09_BRCA	73	0	1	77	193	156	163	131	177	0	82	110	0	1	72	0	114
TCGA-A1-A0SK-10A-03D-A099-09_BRCA	86	0	0	62	148	151	185	131	166	0	0	0	0	0	62	0	121
TCGA-A1-A0SM-10A-02D-A10G-09_BRCA	88	106	111	47	187	127	136	163	174	0	78	109	0	0	47	93	100
TCGA-A1-A0SN-10B-01D-A142-09_BRCA	35	1	0	38	84	81	90	78	86	0	0	1	0	0	19	46	78
TCGA-A1-A0SO-10A-03D-A099-09_BRCA	53	89	85	34	149	99	129	96	93	19	108	81	70	82	0	67	76
TCGA-A1-A0SP-10A-02D-A099-09_BRCA	59	92	92	41	149	117	151	130	130	0	65	91	0	0	0	148	89
TCGA-A2-A04N-10A-01D-A110-09_BRCA	85	0	0	122	171	162	177	155	191	0	0	0	0	0	0	164	140
TCGA-A2-A04R-10B-01D-A10G-09_BRCA	55	89	83	34	100	99	106	89	78	20	93	0	102	66	31	3	79
TCGA-A2-A04U-10A-01D-A110-09_BRCA	76	0	0	97	145	145	165	151	148	0	0	0	0	0	58	95	115
TCGA-A2-A04W-10A-01D-A110-09_BRCA	76	0	0	67	158	150	196	160	166	0	0	0	0	0	57	92	105
TCGA-A2-A0CK-10A-01D-A22A-09_BRCA	35	64	65	3	63	64	62	61	53	4	59	66	3	43	0	28	52
TCGA-A2-A0CL-10A-01D-A110-09_BRCA	98	150	204	0	192	213	213	192	210	1	196	157	129	3	52	91	160
TCGA-A2-A0CO-10A-01D-A22A-09_BRCA	30	39	42	10	80	59	71	64	62	12	57	45	37	44	0	29	65
TCGA-A2-A0CR-10A-01D-A22A-09_BRCA	36	2	2	24	85	65	77	60	101	1	1	3	0	0	35	0	62
TCGA-A2-A0CS-10A-01D-A110-09_BRCA	69	0	0	57	173	137	172	147	108	29	103	1	105	106	0	113	123
TCGA-A2-A0CV-10A-01D-A110-09_BRCA	57	0	0	100	130	149	172	132	220	0	0	0	0	0	44	82	103
TCGA-A2-A0CW-10A-01D-A110-09_BRCA	140	138	137	70	155	156	218	188	239	0	0	0	0	0	100	0	142
TCGA-A2-A0D3-10A-01D-A110-09_BRCA	63	97	104	51	99	86	103	67	0	19	111	136	0	130	0	0	88
TCGA-A2-A0EN-10A-01D-A099-09_BRCA	70	118	117	45	89	102	151	162	109	28	76	0	98	103	0	88	105
TCGA-A2-A0EP-10A-01D-A22X-09_BRCA	47	2	2	29	88	84	95	94	123	0	0	0	0	0	0	86	77
TCGA-A2-A0ES-10A-01D-A110-09_BRCA	71	186	196	0	105	101	181	151	0	33	168	238	0	166	0	1	140
TCGA-A2-A0EW-10A-01D-A110-09_BRCA	92	120	131	52	123	133	173	188	208	0	0	0	0	0	59	112	132
TCGA-A2-A0ST-10A-01D-A099-09_BRCA	73	0	3	87	134	150	167	125	114	25	94	116	0	111	0	103	111
TCGA-A2-A0SU-10A-01D-A099-09_BRCA	73	0	0	85	188	151	188	162	111	26	81	1	106	104	32	0	139
TCGA-A2-A0SX-10A-01D-A099-09_BRCA	89	0	1	102	194	187	223	195	224	0	0	0	0	0	47	102	159
TCGA-A2-A0SY-10A-01D-A099-09_BRCA	76	119	130	58	125	115	169	126	166	0	0	0	0	0	0	159	121
TCGA-A2-A0T0-10A-01D-A099-09_BRCA	34	83	74	28	116	82	115	59	107	0	22	71	0	0	0	53	78
TCGA-A2-A0T1-10A-01D-A099-09_BRCA	83	158	171	0	99	112	160	121	129	26	132	166	0	116	0	98	113
TCGA-A2-A0T2-10A-01D-A099-09_BRCA	41	0	0	48	86	97	118	118	56	26	58	0	76	75	0	58	64
TCGA-A2-A0T3-10A-01D-A110-09_BRCA	60	80	96	42	142	118	119	115	153	0	57	76	0	0	0	137	88
TCGA-A2-A0T4-10A-01D-A099-09_BRCA	60	100	103	41	100	85	139	119	128	0	0	0	0	0	45	86	88
TCGA-A2-A0T5-10A-01D-A099-09_BRCA	78	98	91	54	158	133	123	113	97	30	104	120	1	95	0	60	86
TCGA-A2-A0T6-10A-01D-A099-09_BRCA	72	0	0	59	128	144	142	112	133	0	0	0	0	0	0	123	101
TCGA-A2-A0T7-10A-01D-A099-09_BRCA	72	0	1	57	144	127	138	155	108	25	88	0	107	112	50	0	103
TCGA-A2-A0YC-10A-01D-A10G-09_BRCA	62	89	91	36	75	69	134	125	149	0	0	0	0	0	42	70	90
TCGA-A2-A0YD-10A-01D-A10G-09_BRCA	64	0	0	61	128	114	130	106	150	0	0	0	0	1	0	118	91
TCGA-A2-A0YE-10A-01D-A10G-09_BRCA	88	0	1	96	143	134	163	184	180	1	0	2	4	4	48	92	122
TCGA-A2-A0YF-10A-01D-A10G-09_BRCA	26	73	70	23	99	95	97	58	83	0	38	3	51	1	13	27	64
TCGA-A2-A0YG-10A-01D-A10G-09_BRCA	43	0	0	51	90	94	117	72	107	0	0	0	0	0	0	72	74
TCGA-A2-A0YH-10A-01D-A10G-09_BRCA	59	0	0	92	125	124	151	137	159	0	0	0	0	1	0	161	105
TCGA-A2-A0YI-10A-01D-A10M-09_BRCA	82	0	0	64	174	151	172	126	162	0	0	0	0	0	62	95	118
TCGA-A2-A0YJ-10A-01D-A10G-09_BRCA	25	42	57	20	37	46	73	41	85	0	0	0	0	1	11	21	49
TCGA-A2-A0YK-10A-01D-A117-09_BRCA	96	0	2	101	232	228	273	196	253	0	0	0	1	1	0	202	207
TCGA-A2-A0YL-10A-01D-A10G-09_BRCA	75	1	0	62	142	130	154	133	115	20	95	0	105	102	0	78	107
TCGA-A2-A0YM-10A-01D-A10G-09_BRCA	59	64	78	35	131	100	111	104	71	19	90	101	0	62	0	56	79
TCGA-A2-A0YT-10A-01D-A10G-09_BRCA	62	102	108	41	95	105	130	185	175	0	0	0	0	0	49	89	97
TCGA-A2-A1FV-10A-01D-A13O-09_BRCA	53	0	0	43	89	91	100	95	107	0	0	0	0	0	37	54	70
TCGA-A2-A1FW-10A-01D-A13O-09_BRCA	49	54	45	25	51	52	81	87	98	0	2	0	0	0	33	46	64
TCGA-A2-A1FX-10A-01D-A13O-09_BRCA	45	71	60	36	54	60	83	85	96	0	0	0	0	0	0	75	67
TCGA-A2-A1FZ-10A-01D-A14G-09_BRCA	30	81	82	1	42	52	93	76	53	16	71	69	0	48	0	36	61
TCGA-A2-A1G0-10A-01D-A13O-09_BRCA	35	0	0	39	82	81	98	76	93	0	0	0	0	0	18	39	62
TCGA-A2-A1G1-10A-01D-A13O-09_BRCA	42	94	59	0	83	92	91	75	101	0	44	61	0	0	31	39	73
TCGA-A2-A1G6-10A-01D-A13O-09_BRCA	40	0	0	38	77	81	90	69	53	11	44	0	54	54	0	37	53
TCGA-A2-A259-10A-01D-A16D-09_BRCA	53	0	0	74	104	108	105	96	122	0	0	0	0	0	0	98	85
TCGA-A2-A25A-10A-01D-A16D-09_BRCA	47	0	0	56	87	72	113	87	86	0	0	0	0	0	0	63	66
TCGA-A2-A25B-10A-01D-A167-09_BRCA	38	0	0	52	97	102	95	85	99	0	0	0	0	0	51	0	75
TCGA-A2-A25C-10A-01D-A167-09_BRCA	38	0	0	35	54	55	57	64	67	0	0	0	1	0	0	58	43
TCGA-A2-A25D-10A-01D-A16D-09_BRCA	50	1	0	65	151	129	158	107	159	1	0	0	0	1	0	128	93
TCGA-A2-A25E-10A-01D-A167-09_BRCA	31	0	0	45	69	58	79	62	77	0	0	0	0	0	0	55	50
TCGA-A2-A25F-10A-01D-A167-09_BRCA	32	51	49	21	38	37	76	57	79	0	0	0	0	0	19	26	63
TCGA-A2-A3KC-10A-01D-A20S-09_BRCA	30	38	30	9	32	42	46	24	45	0	24	0	30	30	23	3	52
TCGA-A2-A3KD-10A-01D-A20S-09_BRCA	40	52	46	22	54	48	76	72	67	6	35	2	47	49	0	41	75
TCGA-A2-A3XS-10A-01D-A22X-09_BRCA	56	77	62	23	112	104	98	112	127	0	53	1	60	3	0	103	88
TCGA-A2-A3XT-10A-01D-A22X-09_BRCA	53	67	76	13	70	83	92	111	135	2	7	1	3	1	0	58	62
TCGA-A2-A3XU-10A-01D-A22X-09_BRCA	48	65	66	18	113	91	95	105	125	0	39	63	0	0	33	60	81
TCGA-A2-A3XV-10A-01D-A23C-09_BRCA	58	5	0	32	87	85	91	77	88	0	1	0	1	0	0	88	76
TCGA-A2-A3XW-10A-01D-A23C-09_BRCA	44	3	2	36	90	85	110	93	79	9	48	0	52	57	0	55	78
TCGA-A2-A3XX-10A-01D-A23C-09_BRCA	55	1	64	18	89	92	92	87	110	0	56	2	71	0	48	1	75
TCGA-A2-A3XY-10A-01D-A23C-09_BRCA	53	75	62	18	125	103	98	94	117	0	53	0	68	3	34	50	87
TCGA-A2-A3XZ-10A-01D-A23C-09_BRCA	64	3	4	48	136	99	119	99	133	3	3	3	4	0	41	75	82
TCGA-A2-A3Y0-10A-01D-A23C-09_BRCA	54	4	0	38	89	83	83	94	99	1	2	1	0	1	0	35	57
TCGA-A2-A4RW-10A-01D-A25Q-09_BRCA	43	1	4	20	83	85	94	89	66	9	33	48	0	46	0	39	62
TCGA-A2-A4RX-10A-01D-A25Q-09_BRCA	55	4	2	33	84	76	90	81	117	0	4	1	1	4	37	47	72
TCGA-A2-A4RY-10A-01D-A25Q-09_BRCA	65	66	59	12	65	66	100	86	87	13	42	0	66	70	0	60	81
TCGA-A2-A4S0-10A-01D-A25Q-09_BRCA	48	12	4	41	132	113	111	128	153	2	3	5	2	9	35	66	94
TCGA-A2-A4S1-10A-01D-A25Q-09_BRCA	81	62	67	25	58	69	106	92	114	1	0	1	0	1	0	97	88
TCGA-A2-A4S2-10A-01D-A25Q-09_BRCA	68	0	0	32	102	112	108	115	115	0	0	0	5	2	38	64	98
TCGA-A2-A4S3-10A-01D-A25Q-09_BRCA	42	3	3	26	91	91	96	87	96	0	0	1	0	0	40	4	72
TCGA-A4-7286-10A-01D-2136-08_KIRP	131	71	74	48	72	68	95	96	78	23	49	7	56	82	31	1	120
TCGA-A4-7287-10A-01D-2136-08_KIRP	97	1	6	76	88	83	79	98	82	0	0	0	1	1	0	117	90
TCGA-A4-7583-10A-01D-2136-08_KIRP	98	66	65	49	66	64	83	102	88	1	0	0	1	0	0	118	117
TCGA-A4-7584-10A-01D-2136-08_KIRP	104	2	6	83	106	91	91	92	93	1	1	1	2	1	0	96	131
TCGA-A4-7732-10A-01D-2136-08_KIRP	133	4	5	57	95	92	87	111	120	0	1	0	0	0	33	67	112
TCGA-A4-7734-10A-01D-2136-08_KIRP	89	2	4	61	88	96	84	79	67	19	54	1	59	80	0	71	115
TCGA-A4-7828-10A-01D-2136-08_KIRP	93	85	86	3	73	75	80	111	91	0	46	67	0	0	30	68	101
TCGA-A4-7915-10A-01D-2201-08_KIRP	94	1	0	56	100	89	90	107	95	0	0	0	0	0	31	69	112
TCGA-A4-7996-10A-01D-2201-08_KIRP	97	0	0	64	99	92	96	112	113	0	1	0	0	3	0	143	118
TCGA-A4-7997-10A-01D-2201-08_KIRP	114	0	0	59	90	95	88	94	95	0	0	0	1	0	32	60	105
TCGA-A4-8098-10A-01D-2396-08_KIRP	86	1	0	45	90	83	76	83	95	0	0	3	0	2	30	63	107
TCGA-A4-8310-10A-01D-2396-08_KIRP	83	58	66	35	65	67	73	108	97	0	1	3	0	0	0	129	98

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-A4-8311-10A-01D-2396-08_KIRP	115	65	67	45	69	63	75	75	82	0	0	1	3	4	38	0	95
TCGA-A4-8312-10A-01D-2396-08_KIRP	91	2	6	77	108	81	83	100	82	0	1	1	0	0	38	4	88
TCGA-A4-8515-10A-01D-2396-08_KIRP	90	3	3	56	131	96	93	84	67	29	71	86	0	84	0	69	106
TCGA-A4-8517-10A-01D-2396-08_KIRP	146	0	0	106	161	127	133	129	67	11	51	0	73	113	0	77	164
TCGA-A4-8518-10A-01D-2396-08_KIRP	148	92	85	65	85	79	126	156	84	22	54	0	74	98	0	82	167
TCGA-A4-8630-10A-01D-2396-08_KIRP	79	70	72	42	115	88	77	100	72	21	68	71	69	75	0	57	96
TCGA-A4-A48D-10A-01D-A25F-10_KIRP	76	58	48	33	84	98	92	75	94	0	29	52	0	1	20	35	88
TCGA-A4-A4ZT-10A-01D-A26P-10_KIRP	71	48	57	33	82	89	83	65	60	6	61	53	40	67	0	55	68
TCGA-A4-A57E-10A-01D-A26P-10_KIRP	66	49	45	28	74	84	81	87	87	0	33	40	0	0	0	80	62
TCGA-A4-A5DU-10A-01D-A28G-10_KIRP	74	42	44	31	68	94	88	76	58	3	55	86	1	50	0	55	69
TCGA-A4-A5XZ-10A-01D-A31X-10_KIRP	54	0	0	32	43	50	68	57	37	4	17	36	1	29	0	30	59
TCGA-A4-A6HP-10A-01D-A31X-10_KIRP	38	0	0	31	30	44	55	41	27	4	12	0	23	15	0	22	37
TCGA-A5-A0G1-10A-01D-A122-09_UCEC	115	0	1	130	198	189	199	160	146	28	102	146	0	135	0	126	120
TCGA-A5-A0GG-10A-01D-A122-09_UCEC	107	134	121	73	155	129	184	166	235	10	19	29	0	25	0	164	131
TCGA-A5-A0GQ-10A-01D-A122-09_UCEC	119	0	1	124	181	209	232	240	223	0	0	0	0	0	73	122	161
TCGA-A5-A0GR-10A-01D-A122-09_UCEC	97	125	146	61	257	218	195	220	236	0	124	142	0	1	69	102	131
TCGA-A5-A0R6-10A-01D-A10B-09_UCEC	63	105	108	67	84	96	149	135	175	0	0	0	0	0	32	67	99
TCGA-A5-A0R7-10A-01D-A10B-09_UCEC	77	114	112	44	112	110	133	133	119	20	101	0	105	106	0	101	90
TCGA-A5-A0R8-10A-01D-A10B-09_UCEC	36	0	0	47	85	68	77	73	103	0	0	0	0	0	0	68	59
TCGA-A5-A0R9-10A-01D-A10B-09_UCEC	77	99	103	46	176	112	129	110	113	23	108	128	0	106	0	91	96
TCGA-A5-A0RA-10A-01D-A10B-09_UCEC	50	104	106	0	0	0	111	104	77	18	72	0	75	83	26	0	75
TCGA-A5-A0VO-10A-01D-A10G-09_UCEC	78	99	106	48	179	123	133	128	107	24	136	105	106	93	0	78	99
TCGA-A5-A0VP-10A-01D-A10B-09_UCEC	66	111	100	42	173	133	151	168	176	0	69	100	0	1	46	90	91
TCGA-A5-A0VQ-10A-01D-A10B-09_UCEC	69	107	99	40	79	87	129	118	177	0	0	0	0	0	0	105	88
TCGA-A5-A1OF-10A-01D-A14G-09_UCEC	40	57	57	10	48	48	102	80	122	0	0	0	0	0	31	45	85
TCGA-A5-A1OG-10A-01D-A14G-09_UCEC	66	1	0	51	126	113	126	128	91	32	78	0	82	87	37	0	95
TCGA-A5-A1OH-10A-01D-A22A-09_UCEC	60	6	1	36	92	96	99	108	110	3	2	1	3	0	0	114	92
TCGA-A5-A1OJ-10A-01D-A14G-09_UCEC	40	1	1	26	72	73	84	75	100	0	0	0	0	0	32	40	65
TCGA-A5-A1OK-10A-01D-A14K-09_UCEC	53	0	0	27	91	48	82	77	1	14	70	50	57	86	0	2	67
TCGA-A5-A2K2-10A-01D-A18P-09_UCEC	47	56	51	16	46	49	91	76	93	0	1	0	1	0	0	66	65
TCGA-A5-A2K3-10A-01D-A17W-09_UCEC	50	0	1	31	96	95	88	82	62	13	41	0	56	67	0	46	71
TCGA-A5-A2K4-10B-01D-A18P-09_UCEC	48	2	3	31	86	81	80	99	67	13	45	2	49	62	0	47	69
TCGA-A5-A2K5-10A-01D-A17W-09_UCEC	53	58	47	16	45	53	85	75	1	14	66	1	79	75	0	0	66
TCGA-A5-A2K7-10A-01D-A17W-09_UCEC	43	55	50	8	47	54	58	43	61	1	41	1	53	57	33	1	65
TCGA-A5-A3LO-10A-01D-A22A-09_UCEC	43	72	65	0	32	51	83	61	49	13	58	36	36	43	0	39	63
TCGA-A5-A3LP-10A-01D-A22A-09_UCEC	47	73	60	19	74	68	96	111	128	0	0	0	1	0	0	120	82
TCGA-A6-2671-10A-01D-1408-10_COAD	38	0	0	37	46	37	58	29	58	0	0	0	0	0	0	40	54
TCGA-A6-2674-10A-01D-A270-10_COAD	64	0	2	50	71	88	89	75	73	0	0	0	0	1	0	75	71
TCGA-A6-2675-10A-01D-1719-10_COAD	147	1	1	114	170	159	180	150	212	0	0	0	0	0	31	53	184
TCGA-A6-2677-10A-01D-A270-10_COAD	48	60	45	0	49	64	64	56	0	8	66	76	28	64	0	0	48
TCGA-A6-2684-10A-01D-A270-10_COAD	42	30	22	18	29	31	53	51	2	6	28	1	49	53	0	0	44
TCGA-A6-3809-10A-01D-A270-10_COAD	43	41	50	0	28	30	76	72	25	7	41	20	19	37	12	0	49
TCGA-A6-3810-10A-01D-A270-10_COAD	65	40	34	32	32	44	74	63	71	0	1	0	2	0	0	72	59
TCGA-A6-4105-10A-01D-1771-10_COAD	82	0	0	45	93	102	82	63	64	16	33	0	41	47	0	58	99
TCGA-A6-5656-10A-01D-A270-10_COAD	70	0	0	45	50	69	82	65	29	7	16	0	34	54	0	36	60
TCGA-A6-5657-10A-01D-1650-10_COAD	128	0	102	52	167	144	203	142	168	0	57	0	79	0	29	0	110
TCGA-A6-5659-10A-01D-1650-10_COAD	94	0	0	56	93	57	112	80	123	0	0	0	0	0	0	66	110
TCGA-A6-5662-10A-01D-1650-10_COAD	158	0	2	84	173	175	212	157	205	0	0	0	0	0	0	117	193
TCGA-A6-5664-10A-01D-1835-10_COAD	41	0	0	21	28	34	33	36	31	0	0	0	0	0	0	4	36
TCGA-A6-5665-10A-01D-1650-10_COAD	115	0	0	85	137	136	179	115	189	0	0	0	0	1	0	99	183
TCGA-A6-5666-10A-01D-1650-10_COAD	104	0	0	74	113	102	129	99	129	0	0	0	0	0	31	41	113
TCGA-A6-6137-10A-01D-1806-10_COAD	70	0	0	48	72	70	81	63	82	0	0	0	0	0	0	64	83
TCGA-A6-6138-10A-01D-1771-10_COAD	95	77	81	0	47	44	136	108	105	12	20	50	0	0	19	53	99
TCGA-A6-6141-10A-01D-1771-10_COAD	68	40	33	34	38	55	46	42	45	0	22	0	34	35	0	30	79
TCGA-A6-6142-10A-01D-1771-10_COAD	56	0	0	51	61	53	73	52	73	0	0	0	0	1	0	53	68
TCGA-A6-6648-10A-01D-1771-10_COAD	65	28	38	29	28	28	81	41	50	13	25	0	26	35	0	23	60
TCGA-A6-6649-10A-01D-1771-10_COAD	56	0	0	29	48	50	60	38	30	8	21	0	12	28	0	33	55
TCGA-A6-6650-10A-01D-1771-10_COAD	24	0	0	21	26	41	38	25	40	0	0	0	0	1	9	0	41
TCGA-A6-6651-10A-01D-1835-10_COAD	41	9	1	15	37	31	33	24	21	4	9	0	5	28	0	14	43
TCGA-A6-6652-10A-01D-1771-10_COAD	59	22	0	24	30	24	45	21	45	0	23	0	22	30	0	41	75
TCGA-A6-6653-10A-01D-1771-10_COAD	70	51	70	0	0	1	42	35	44	0	19	1	27	45	0	36	68
TCGA-A6-6654-10A-01D-1835-10_COAD	75	0	0	54	74	93	78	78	103	0	0	0	0	0	16	51	82
TCGA-A6-6780-10A-01D-A270-10_COAD	46	0	0	46	40	43	73	66	0	11	30	0	53	41	0	0	46
TCGA-A6-6781-10A-01D-1924-10_COAD	56	2	0	39	60	50	66	68	33	15	18	0	19	25	0	32	65
TCGA-A6-6782-10A-01D-1835-10_COAD	25	18	11	9	20	15	39	27	22	6	10	15	0	10	9	0	32
TCGA-A6-A565-10A-01D-A28G-10_COAD	75	0	0	47	131	138	106	76	105	0	83	0	103	1	46	0	79
TCGA-A6-A566-10A-01D-A28G-10_COAD	61	0	1	55	91	106	106	84	104	0	0	0	1	0	0	108	78
TCGA-A6-A567-10A-01D-A28G-10_COAD	71	48	44	20	46	83	94	98	86	0	59	59	41	0	17	38	77
TCGA-A6-A56B-10A-01D-A28G-10_COAD	69	0	1	33	93	104	97	74	102	0	36	0	53	0	41	1	77
TCGA-A6-A5ZU-10A-01D-A28G-10_COAD	88	0	63	33	106	105	106	81	106	0	31	0	57	0	46	2	72
TCGA-A7-A0DA-10A-01D-A110-09_BRCA	136	1	1	138	270	246	284	208	290	0	2	0	1	0	67	154	195
TCGA-A7-A0DB-10A-02D-A272-09_BRCA	40	66	46	15	105	97	98	82	73	13	65	57	45	55	27	1	66
TCGA-A7-A13D-10A-02D-A12Q-09_BRCA	105	0	2	110	226	202	192	223	190	0	119	142	0	2	74	106	145
TCGA-A7-A13E-10A-01D-A12Q-09_BRCA	72	102	95	47	106	88	129	111	126	0	0	0	0	0	63	1	102
TCGA-A7-A13F-10A-01D-A12Q-09_BRCA	125	141	153	65	275	219	224	230	147	25	205	215	0	175	72	0	162
TCGA-A7-A13H-10A-01D-A22A-09_BRCA	57	0	2	27	97	93	95	103	133	0	1	0	0	3	0	88	99
TCGA-A7-A26E-10A-01D-A167-09_BRCA	50	1	0	33	149	99	103	99	3	22	98	56	79	82	0	0	64
TCGA-A7-A26F-10A-01D-A167-09_BRCA	22	0	0	23	55	56	72	44	57	0	0	0	0	0	21	21	41
TCGA-A7-A26G-10A-01D-A167-09_BRCA	47	72	1	22	57	55	56	48	60	0	44	0	63	55	0	54	72
TCGA-A7-A26H-10A-01D-A167-09_BRCA	35	75	48	23	72	55	96	75	110	0	0	0	0	0	24	40	70
TCGA-A7-A26I-10A-01D-A167-09_BRCA	31	61	58	34	59	67	105	69	115	0	0	0	1	0	0	84	68
TCGA-A7-A26J-10A-01D-A167-09_BRCA	40	1	0	53	107	89	101	87	107	0	0	0	0	0	0	98	60
TCGA-A7-A2KD-10A-01D-A21Q-09_BRCA	39	47	4	25	79	51	75	61	82	0	2	2	4	3	0	56	62
TCGA-A7-A3IY-10A-01D-A21Q-09_BRCA	50	5	2	28	74	67	80	69	88	0	0	0	0	0	0	64	68
TCGA-A7-A3IZ-10A-01D-A20S-09_BRCA	36	3	3	15	57	68	81	62	2	10	51	2	51	63	0	3	63
TCGA-A7-A3J0-10A-01D-A20S-09_BRCA	38	37	46	10	34	37	80	57	91	2	2	2	3	2	29	0	71
TCGA-A7-A3J1-10A-01D-A20S-09_BRCA	26	0	3	17	62	55	57	46	81	0	0	0	3	1	0	45	47
TCGA-A7-A3RF-10A-01D-A22A-09_BRCA	68	2	6	33	113	112	115	119	98	16	70	0	74	76	0	65	93
TCGA-A7-A425-10A-01D-A243-09_BRCA	37	14	10	19	55	63	77	65	84	2	4	5	6	7	0	31	63
TCGA-A7-A426-10A-01D-A243-09_BRCA	48	68	60	22	57	49	97	84	79	14	49	54	2	52	0	55	81
TCGA-A7-A4SA-10A-01D-A25Q-09_BRCA	42	62	59	20	103	92	98	107	118	0	45	54	3	3	41	51	73
TCGA-A7-A4SB-10A-01D-A25Q-09_BRCA	51	89	75	1	70	54	92	75	72	14	66	57	53	49	0	44	74
TCGA-A7-A4SC-10A-01D-A25Q-09_BRCA	42	2	0	32	89	83	94	83	107	1	0	0	1	0	27	45	72
TCGA-A7-A4SD-10A-01D-A25Q-09_BRCA	54	7	5	30	125	102	89	90	114	2	3	0	3	5	51	1	79
TCGA-A7-A4SE-10A-01D-A25Q-09_BRCA	65	3	2	45	138	108	118	99	145	0	1	1	0	2	55	0	103
TCGA-A7-A4SF-10A-01D-A25Q-09_BRCA	61	61	70	20	68	71	88	108	128	1	2	2	1	2	37	61	82

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-A7-A56D-10A-01D-A27P-09_BRCA	51	58	52	17	78	84	77	70	108	0	65	74	0	0	43	1	81
TCGA-A7-A5ZV-10A-01D-A28E-09_BRCA	42	1	0	22	107	107	97	99	142	0	0	1	0	0	32	56	83
TCGA-A7-A5ZW-10A-01D-A29N-09_BRCA	40	0	2	31	103	99	109	106	92	10	43	1	56	0	42	2	62
TCGA-A7-A5ZX-10A-01D-A29N-09_BRCA	56	70	67	17	110	102	85	110	110	0	47	55	0	0	0	106	84
TCGA-A8-A075-10B-01D-A099-09_BRCA	82	1	0	93	136	136	174	147	150	0	0	0	1	0	46	78	101
TCGA-A8-A07R-10B-01D-A047-09_BRCA	103	0	1	72	181	179	176	165	139	28	116	0	114	123	0	99	125
TCGA-A8-A097-10A-01D-A047-09_BRCA	99	0	0	71	188	165	176	152	231	0	0	0	0	1	0	160	123
TCGA-AC-A23C-10A-01D-A167-09_BRCA	36	57	43	23	52	52	86	54	98	0	0	0	0	0	23	38	60
TCGA-AC-A23E-10A-01D-A159-09_BRCA	62	73	75	26	122	95	103	84	60	22	84	79	68	69	0	55	68
TCGA-AC-A2B8-10A-01D-A17D-09_BRCA	36	0	0	33	72	80	72	59	45	12	35	0	40	46	0	34	54
TCGA-AC-A2QH-10A-01D-A18P-09_BRCA	49	92	80	0	52	62	103	88	94	0	53	55	0	0	0	78	59
TCGA-AC-A2QI-10A-01D-A19Y-09_BRCA	31	6	4	32	79	88	94	107	113	1	4	1	7	11	10	72	78
TCGA-AC-A3BB-10A-01D-A19Y-09_BRCA	34	1	2	30	70	67	77	60	117	0	2	2	1	0	0	12	70
TCGA-AC-A3HN-10A-01D-A20S-09_BRCA	35	1	2	15	58	64	64	68	78	1	3	4	0	1	20	19	59
TCGA-AC-A3QP-10B-01D-A22X-09_BRCA	47	50	45	18	85	68	66	73	53	11	58	40	50	44	0	39	70
TCGA-AC-A3TM-10A-01D-A22A-09_BRCA	33	51	58	0	8	11	70	53	50	5	34	0	28	34	19	2	51
TCGA-AC-A3TN-10A-01D-A22A-09_BRCA	36	1	1	28	76	89	121	101	71	17	25	3	48	61	29	0	75
TCGA-AC-A3W5-10A-01D-A22A-09_BRCA	53	1	2	31	99	81	84	74	96	2	2	2	2	3	54	7	84
TCGA-AC-A3W6-10A-01D-A22A-09_BRCA	53	53	0	14	86	73	76	76	65	10	38	0	42	40	0	43	70
TCGA-AC-A3W7-10A-01D-A22A-09_BRCA	51	101	54	26	109	104	109	81	5	17	109	68	96	104	0	1	92
TCGA-AC-A3YI-10A-01D-A23C-09_BRCA	44	71	62	0	87	77	95	81	69	8	58	49	56	58	0	53	72
TCGA-AC-A3YJ-10A-01D-A22X-09_BRCA	54	1	1	40	108	107	110	105	101	12	57	2	79	79	0	71	95
TCGA-AC-A5EH-10A-01D-A28E-09_BRCA	37	59	44	10	81	80	89	85	102	0	38	58	1	0	0	84	60
TCGA-AC-A5EI-10A-01D-A27P-09_BRCA	48	52	63	8	53	61	85	103	111	0	0	1	0	0	0	106	72
TCGA-AC-A5XS-10A-01D-A29N-09_BRCA	53	2	0	24	85	94	89	71	114	1	0	0	0	1	0	85	75
TCGA-AC-A5XU-10A-01D-A28E-09_BRCA	51	3	65	18	67	54	101	92	127	0	1	0	1	0	41	52	74
TCGA-AC-A62V-10A-01D-A31U-09_BRCA	37	0	55	16	63	56	67	46	85	0	42	0	55	62	37	0	93
TCGA-AC-A62X-10A-01D-A29N-09_BRCA	51	0	1	23	81	79	82	75	67	11	42	0	51	63	33	0	65
TCGA-AC-A62Y-10A-01D-A29N-09_BRCA	54	58	55	12	50	60	84	76	119	0	2	1	0	0	52	0	67
TCGA-AD-5900-10A-01D-1650-10_COAD	117	0	0	72	140	117	135	98	179	0	0	0	0	0	18	53	168
TCGA-AD-6548-10A-01D-1835-10_COAD	34	0	0	27	36	22	47	21	36	0	0	0	0	0	0	21	39
TCGA-AD-6888-10A-01D-1924-10_COAD	50	0	0	46	60	75	91	66	41	17	26	31	26	30	18	0	72
TCGA-AD-6889-10A-01D-1924-10_COAD	61	58	62	0	0	0	73	54	70	0	0	0	0	0	24	0	79
TCGA-AD-6890-10A-01D-1924-10_COAD	57	36	25	30	36	26	51	35	67	0	0	2	0	0	11	38	67
TCGA-AD-6895-10A-01D-1924-10_COAD	53	0	0	41	58	59	56	48	76	0	0	0	0	0	0	45	63
TCGA-AD-6899-10A-01D-1924-10_COAD	46	27	14	20	21	20	49	31	42	0	0	0	0	0	15	20	52
TCGA-AD-6901-10A-01D-1924-10_COAD	54	0	0	29	42	39	62	36	64	0	0	0	0	0	0	50	67
TCGA-AD-6963-10A-01D-1924-10_COAD	42	0	0	31	31	35	48	42	30	6	13	0	19	22	0	18	68
TCGA-AD-6964-10A-01D-1924-10_COAD	74	71	62	0	36	40	88	58	0	17	67	35	46	67	0	0	76
TCGA-AD-6965-10A-01D-1924-10_COAD	74	0	1	58	55	48	73	55	85	0	2	0	0	1	0	33	68
TCGA-AD-A5EK-10A-01D-A28G-10_COAD	85	0	63	29	53	76	109	86	99	0	41	57	1	0	39	0	85
TCGA-AF-2687-10A-01D-1733-10_READ	75	0	0	48	76	63	90	63	123	0	2	0	0	0	0	47	101
TCGA-AF-2690-10A-01D-1733-10_READ	65	0	1	33	81	82	93	85	105	0	0	0	0	0	16	40	113
TCGA-AF-2693-10A-01D-1733-10_READ	59	40	47	13	54	55	98	67	49	7	17	0	39	45	10	0	98
TCGA-AF-3911-10A-01D-1733-10_READ	70	0	0	45	70	76	108	70	103	0	0	0	0	0	0	62	97
TCGA-AF-4110-10A-01D-1733-10_READ	52	0	0	34	69	47	71	47	76	0	0	0	0	0	7	25	74
TCGA-AF-5654-10A-01D-1657-10_READ	68	58	63	36	96	75	93	71	103	0	24	44	2	0	0	66	94
TCGA-AG-3591-10A-01D-1733-10_READ	56	47	36	24	35	41	96	59	58	10	35	0	45	51	0	16	92
TCGA-AG-3592-10A-01D-1733-10_READ	78	2	0	48	68	83	87	58	72	13	19	0	37	37	0	25	99
TCGA-AG-4021-10A-01D-1733-10_READ	61	48	52	25	43	31	89	59	60	13	21	0	39	47	0	25	91
TCGA-AH-6544-10A-01D-1826-10_READ	51	25	31	23	25	32	53	45	39	9	21	0	22	29	0	36	61
TCGA-AH-6897-10A-01D-1924-10_READ	41	0	0	27	49	53	44	38	48	0	0	0	0	1	0	44	57
TCGA-AH-6903-10A-01D-1924-10_READ	41	18	23	18	45	42	43	37	31	7	16	49	0	23	0	18	51
TCGA-AJ-A23M-10A-01D-A159-09_UCEC	32	79	74	39	58	60	107	93	118	0	0	0	0	5	30	52	81
TCGA-AJ-A23N-10A-01D-A22A-09_UCEC	39	41	36	14	45	42	62	66	74	0	2	0	2	0	0	59	54
TCGA-AJ-A23O-10A-01D-A159-09_UCEC	46	0	0	35	79	78	92	70	93	0	1	0	0	1	49	1	69
TCGA-AJ-A2QK-10A-01D-A18P-09_UCEC	60	89	97	0	85	90	92	110	74	17	92	96	0	82	41	4	77
TCGA-AJ-A2QL-10A-01D-A18P-09_UCEC	60	77	72	17	66	6	77	67	84	1	2	1	2	73	37	0	90
TCGA-AJ-A2QM-10A-01D-A18P-09_UCEC	53	3	2	31	84	86	87	92	123	0	0	1	1	1	32	61	74
TCGA-AJ-A2QN-10A-01D-A18P-09_UCEC	45	59	51	14	94	88	85	87	115	0	47	58	0	0	32	47	64
TCGA-AJ-A2QO-10A-01D-A18P-09_UCEC	55	1	2	32	90	91	91	78	116	0	0	0	0	0	0	75	75
TCGA-AJ-A3BD-10A-01D-A19Y-09_UCEC	52	0	1	39	102	100	99	116	133	2	0	0	0	2	0	113	78
TCGA-AJ-A3BF-10A-01D-A20S-09_UCEC	49	92	84	0	80	65	89	110	109	0	50	60	0	0	31	62	77
TCGA-AJ-A3BG-10A-01D-A19Y-09_UCEC	48	3	1	33	94	83	88	84	74	11	45	2	47	59	0	50	67
TCGA-AJ-A3BH-10A-01D-A19Y-09_UCEC	53	60	47	20	109	95	82	107	65	10	81	77	0	63	0	52	74
TCGA-AJ-A3BI-10A-01D-A20S-09_UCEC	59	2	3	30	86	76	89	62	92	0	0	1	0	0	47	4	78
TCGA-AJ-A3BK-10A-01D-A19Y-09_UCEC	42	65	60	18	74	60	104	80	100	0	0	0	0	0	57	2	80
TCGA-AJ-A3EJ-10A-01D-A19Y-09_UCEC	64	1	5	38	116	113	128	122	156	0	0	0	0	0	0	129	86
TCGA-AJ-A3EL-10A-01D-A20S-09_UCEC	75	8	5	41	139	176	140	132	99	20	68	87	3	75	0	100	119
TCGA-AJ-A3I9-10A-01D-A22A-09_UCEC	75	3	5	38	100	113	116	109	130	0	0	0	0	1	42	51	78
TCGA-AJ-A3IA-10A-01D-A20S-09_UCEC	57	67	63	27	78	78	106	118	130	3	3	0	4	2	34	76	74
TCGA-AJ-A3NC-10A-01D-A22A-09_UCEC	51	4	1	33	87	98	102	94	73	10	55	0	57	62	0	63	79
TCGA-AJ-A3NE-10A-01D-A22A-09_UCEC	56	80	78	1	6	6	96	97	128	0	0	2	0	0	0	97	72
TCGA-AJ-A3NF-10A-01D-A22A-09_UCEC	65	5	5	33	93	89	108	84	118	1	0	1	2	5	42	7	73
TCGA-AJ-A3NG-10A-01D-A22A-09_UCEC	43	1	3	16	89	73	77	60	48	11	41	0	39	52	0	45	66
TCGA-AJ-A3NH-10A-01D-A22A-09_UCEC	68	2	2	39	104	107	129	83	111	0	0	1	0	0	52	3	76
TCGA-AJ-A3OJ-10A-01D-A22A-09_UCEC	41	2	1	19	74	76	78	81	62	13	29	0	43	57	0	38	63
TCGA-AJ-A3OK-10A-01D-A22A-09_UCEC	53	0	0	29	91	92	101	91	111	0	0	0	0	0	0	102	79
TCGA-AJ-A3OL-10A-01D-A22A-09_UCEC	65	78	62	22	122	116	114	95	126	0	59	68	0	0	0	98	96
TCGA-AJ-A3QS-10A-01D-A22A-09_UCEC	56	151	104	0	103	104	113	110	185	0	102	64	63	0	43	57	99
TCGA-AJ-A3TW-10A-01D-A22A-09_UCEC	48	69	65	0	32	25	58	57	81	0	38	32	0	0	13	29	47
TCGA-AJ-A5DV-10A-01D-A27P-09_UCEC	62	57	45	13	56	48	85	89	104	0	0	0	0	1	27	0	48
TCGA-AJ-A5DW-10A-01D-A27P-09_UCEC	54	64	62	18	66	75	73	57	82	0	52	0	54	64	0	64	67
TCGA-AK-3426-10A-01D-1251-10_KIRC	83	0	0	112	204	211	225	135	238	0	0	0	0	1	0	127	146
TCGA-AK-3427-10A-01D-0966-08_KIRC	129	86	87	49	107	87	90	89	87	0	59	0	78	96	39	1	143
TCGA-AK-3429-10A-01D-1251-10_KIRC	49	0	0	75	132	151	151	113	171	0	0	0	0	0	0	140	100
TCGA-AK-3430-10A-01D-1251-10_KIRC	46	0	0	62	96	119	128	103	74	30	43	0	77	70	0	38	91
TCGA-AK-3436-10A-01D-1251-10_KIRC	49	220	198	0	0	1	117	42	0	50	77	0	153	182	0	0	100
TCGA-AK-3440-10A-01D-0966-08_KIRC	122	77	105	49	94	84	112	156	86	26	77	0	91	85	0	83	129
TCGA-AK-3443-10A-01D-0966-08_KIRC	115	0	2	92	124	101	97	117	141	0	0	0	0	0	0	119	130
TCGA-AK-3444-10A-01D-0966-08_KIRC	157	82	78	44	96	96	108	145	117	0	1	0	1	0	0	126	148
TCGA-AK-3447-10A-01D-0966-08_KIRC	124	0	0	62	116	119	115	114	88	20	61	0	81	98	0	91	145
TCGA-AK-3451-10A-01D-1251-10_KIRC	67	0	2	104	167	182	273	192	227	63	0	0	0	0	50	0	149
TCGA-AK-3453-10A-01D-0966-08_KIRC	136	78	82	56	95	90	103	123	89	21	56	0	75	87	0	87	135
TCGA-AK-3455-10A-01D-0966-08_KIRC	111	102	92	2	2	3	93	131	109	0	0	0	0	0	32	79	117
TCGA-AK-3456-10A-01D-1251-10_KIRC	52	79	90	37	52	64	132	83	134	0	0	0	0	0	36	0	86

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-AK-3458-10A-01D-1501-10_KIRC	37	132	116	32	166	132	161	82	79	40	60	132	0	81	0	33	128
TCGA-AK-3465-10A-01D-0966-08_KIRC	133	1	0	59	132	116	99	111	114	0	0	1	0	1	35	76	132
TCGA-AL-3466-10A-01D-1252-08_KIRP	129	0	0	78	133	145	110	138	136	0	0	0	0	3	38	89	138
TCGA-AL-3467-10A-01D-1252-08_KIRP	152	0	1	70	124	142	107	163	150	0	0	0	1	3	0	184	138
TCGA-AL-3468-10A-01D-1252-08_KIRP	152	116	118	2	141	151	105	167	164	0	81	134	0	0	44	83	138
TCGA-AL-3472-10A-01D-1252-08_KIRP	135	81	78	54	91	88	102	167	141	0	0	0	0	0	33	87	136
TCGA-AL-3473-10A-01D-1252-08_KIRP	153	0	2	63	122	128	103	123	142	1	1	0	0	2	0	109	130
TCGA-AL-7173-10A-01D-2136-08_KIRP	80	61	66	38	57	71	76	100	87	0	0	1	0	0	28	65	89
TCGA-AL-A5DJ-10A-01D-A26P-10_KIRP	67	0	0	57	69	95	96	74	0	5	51	0	83	92	0	0	67
TCGA-AN-A04C-10A-01D-A047-09_BRCA	105	0	4	110	188	165	166	182	173	1	0	3	0	5	62	121	123
TCGA-AN-A0FY-10A-01D-A047-09_BRCA	116	0	3	97	218	169	230	217	245	0	0	1	0	0	58	123	121
TCGA-AN-A0XL-10A-01D-A10M-09_BRCA	72	96	83	51	183	104	163	115	144	0	56	66	0	0	0	96	80
TCGA-AN-A0XN-10A-01D-A10G-09_BRCA	94	164	166	56	233	227	275	169	277	0	89	179	3	0	61	110	169
TCGA-AN-A0XO-10A-01D-A10G-09_BRCA	39	62	66	0	16	60	91	103	43	20	104	34	41	37	15	0	54
TCGA-AN-A0XP-10A-01D-A10G-09_BRCA	61	18	10	68	127	113	129	122	127	0	5	17	1	0	0	141	97
TCGA-AN-A0XR-10A-01D-A117-09_BRCA	72	104	84	35	182	124	157	143	104	30	149	95	87	86	0	70	101
TCGA-AN-A0XS-10A-01D-A10G-09_BRCA	64	112	109	47	100	96	181	152	216	0	0	0	0	1	48	90	99
TCGA-AN-A0XT-10A-01D-A10G-09_BRCA	83	2	0	61	131	125	134	153	175	0	0	0	0	0	0	158	97
TCGA-AN-A0XU-10A-01D-A10G-09_BRCA	71	92	91	44	152	116	118	148	92	19	114	122	4	86	49	0	101
TCGA-AN-A0XV-10A-01D-A10G-09_BRCA	36	82	88	36	121	94	106	56	124	0	30	65	0	0	24	0	72
TCGA-AN-A0XW-10A-01D-A10G-09_BRCA	56	90	89	36	119	91	125	76	141	0	35	75	0	1	27	41	79
TCGA-AO-A03M-10A-01D-A10M-09_BRCA	86	113	115	49	118	112	142	132	0	37	169	124	102	131	0	0	100
TCGA-AO-A03N-10A-01D-A10M-09_BRCA	59	123	131	0	0	0	120	86	148	0	0	0	0	0	55	0	85
TCGA-AO-A03U-10A-01D-A10M-09_BRCA	32	0	0	46	101	99	102	62	80	24	30	0	74	80	0	27	69
TCGA-AO-A03V-10A-01D-A110-09_BRCA	63	0	0	58	134	117	131	121	94	25	84	0	76	87	0	68	82
TCGA-AO-A0JG-10A-01D-A099-09_BRCA	58	130	143	0	0	0	139	149	151	0	0	0	0	0	37	81	81
TCGA-AO-A124-10A-01D-A10M-09_BRCA	58	104	113	41	175	130	146	99	112	23	101	94	95	90	0	55	96
TCGA-AO-A125-10A-01D-A10M-09_BRCA	57	108	102	42	158	125	134	125	200	0	82	0	100	1	39	79	117
TCGA-AO-A126-10A-01D-A10M-09_BRCA	71	0	0	63	140	152	160	173	209	0	0	0	0	0	47	98	118
TCGA-AO-A128-10A-01D-A10M-09_BRCA	108	0	1	101	176	193	219	206	194	0	0	1	1	0	0	248	116
TCGA-AO-A129-10A-01D-A10M-09_BRCA	69	0	0	104	147	143	188	133	157	0	0	0	0	0	81	0	121
TCGA-AO-A12A-10A-01D-A110-09_BRCA	70	160	128	0	107	95	155	112	197	0	0	0	0	0	0	117	109
TCGA-AO-A12B-10A-01D-A10M-09_BRCA	74	113	115	56	119	93	121	69	98	0	77	92	0	96	0	79	113
TCGA-AO-A12D-10A-01D-A110-09_BRCA	111	0	0	121	225	238	262	164	244	0	1	1	0	1	0	204	144
TCGA-AO-A12E-10A-01D-A10M-09_BRCA	74	0	0	98	130	131	157	142	142	0	0	0	0	0	45	80	87
TCGA-AO-A12F-10A-01D-A110-09_BRCA	47	103	82	39	96	79	105	45	87	0	55	1	86	73	22	0	112
TCGA-AO-A12G-10A-01D-A10M-09_BRCA	37	114	90	50	93	76	137	61	131	0	0	0	1	0	33	0	105
TCGA-AO-A12H-10A-01D-A110-09_BRCA	89	1	121	63	124	103	152	168	143	27	107	2	108	131	43	2	120
TCGA-AO-A1KO-10A-01D-A13O-09_BRCA	49	76	75	29	74	64	104	102	103	0	0	0	0	0	26	61	76
TCGA-AO-A1KR-10A-01D-A142-09_BRCA	33	53	46	24	89	82	78	71	86	0	26	51	0	0	20	41	60
TCGA-AO-A1KT-10A-01D-A188-09_BRCA	70	118	94	0	70	84	123	118	112	0	0	0	0	0	44	74	92
TCGA-AP-A059-10A-01D-A122-09_UCEC	105	135	148	65	291	246	220	252	297	0	136	187	0	1	0	217	155
TCGA-AP-A05O-10A-01D-A122-09_UCEC	91	0	1	77	174	196	190	162	1	41	163	0	194	190	0	0	152
TCGA-AP-A0LE-10A-01D-A10B-09_UCEC	63	0	0	69	190	154	165	158	209	0	0	0	0	0	48	81	117
TCGA-AP-A0LF-10A-01D-A122-09_UCEC	89	129	134	64	125	124	129	124	113	0	107	0	125	129	0	92	134
TCGA-AP-A0LL-10A-01D-A10B-09_UCEC	78	0	1	60	138	139	143	133	208	0	0	0	0	1	0	132	111
TCGA-AP-A0LM-10A-01D-A122-09_UCEC	90	117	167	0	162	177	168	187	204	0	178	141	105	0	59	87	123
TCGA-AP-A0LP-10A-01D-A10B-09_UCEC	46	0	0	47	103	90	118	79	144	0	0	0	0	0	0	77	76
TCGA-AP-A0LQ-10A-01D-A10B-09_UCEC	99	214	216	1	210	185	219	189	1	42	307	316	1	194	0	0	160
TCGA-AP-A0LS-10B-01D-A14G-09_UCEC	49	65	55	15	61	42	52	34	61	0	40	0	52	47	27	1	69
TCGA-AP-A1DH-10A-01D-A135-09_UCEC	48	88	81	0	59	63	88	85	106	1	49	66	0	2	34	49	77
TCGA-AP-A1DK-10A-01D-A135-09_UCEC	52	1	3	24	90	60	58	50	71	1	1	3	0	50	0	51	50
TCGA-AP-A1DM-10A-01D-A135-09_UCEC	75	5	3	43	96	92	119	121	130	0	0	2	2	3	38	51	89
TCGA-AP-A1DO-10A-01D-A135-09_UCEC	47	56	64	23	109	92	77	92	79	13	79	63	55	60	34	1	76
TCGA-AP-A1DP-10A-01D-A135-09_UCEC	52	106	88	0	0	0	103	80	103	0	2	3	1	2	56	1	84
TCGA-AP-A1DQ-10A-01D-A135-09_UCEC	40	0	0	56	97	100	156	70	112	0	0	0	0	1	23	49	75
TCGA-AP-A1DR-10A-01D-A135-09_UCEC	34	66	74	0	52	48	85	73	107	0	38	0	48	0	29	40	62
TCGA-AP-A1DV-10A-01D-A135-09_UCEC	52	46	56	23	55	55	58	39	61	0	46	1	57	61	0	51	65
TCGA-AP-A1E0-10A-01D-A135-09_UCEC	51	0	0	18	76	70	77	77	93	0	2	0	3	1	0	74	74
TCGA-AP-A1E1-10A-01D-A135-09_UCEC	50	50	54	16	46	55	83	80	63	6	32	0	54	47	0	53	73
TCGA-AP-A1E3-10A-01D-A135-09_UCEC	50	0	3	25	86	88	99	68	2	15	67	1	83	85	0	0	77
TCGA-AP-A1E4-10A-01D-A135-09_UCEC	77	79	73	29	123	101	94	121	85	10	91	92	2	79	0	66	86
TCGA-AP-A3K1-10A-01D-A20S-09_UCEC	49	62	63	16	72	1	66	57	70	0	1	1	0	64	34	3	55
TCGA-AP-A5FX-10A-01D-A27P-09_UCEC	86	1	87	30	146	110	108	157	140	0	80	0	92	2	49	80	100
TCGA-AQ-A04H-10A-01D-A10M-09_BRCA	77	110	128	54	197	143	166	134	177	0	66	124	0	0	31	93	100
TCGA-AQ-A04L-10A-01D-A12J-09_BRCA	39	0	0	39	68	79	82	66	68	14	25	0	31	44	0	0	66
TCGA-AQ-A0Y5-10A-01D-A17G-09_BRCA	34	53	57	25	98	81	77	60	0	19	87	83	0	74	0	0	50
TCGA-AQ-A1H2-10A-01D-A13O-09_BRCA	57	0	0	58	123	107	115	120	88	27	79	0	78	65	0	54	92
TCGA-AQ-A1H3-10A-01D-A188-09_BRCA	39	0	0	63	114	80	96	94	61	20	47	0	55	50	0	42	73
TCGA-AQ-A54N-10A-01D-A25Q-09_BRCA	36	65	61	15	96	95	88	104	130	1	41	60	1	2	0	90	73
TCGA-AQ-A54O-10A-01D-A25Q-09_BRCA	63	1	2	36	120	96	138	113	140	14	36	0	70	2	44	52	82
TCGA-AR-A0TP-10A-01D-A099-09_BRCA	64	0	0	70	114	118	142	109	78	22	73	0	87	88	0	81	97
TCGA-AR-A0TQ-10A-01D-A099-09_BRCA	22	0	2	55	86	78	89	40	100	0	0	0	0	0	0	48	64
TCGA-AR-A0TR-10A-01D-A099-09_BRCA	52	114	119	1	71	74	107	133	81	21	112	74	72	81	0	67	84
TCGA-AR-A0TS-10A-01D-A110-09_BRCA	54	102	96	38	96	99	155	117	120	0	0	0	0	0	34	76	94
TCGA-AR-A0TT-10A-01D-A099-09_BRCA	64	0	2	73	168	151	191	149	203	0	0	0	2	1	44	83	125
TCGA-AR-A0TU-10A-01D-A10G-09_BRCA	29	0	1	41	83	86	99	64	60	23	29	2	53	56	0	23	76
TCGA-AR-A0TV-10A-01D-A099-09_BRCA	80	0	0	93	145	139	147	135	181	0	0	0	0	0	0	182	105
TCGA-AR-A0TW-10A-01D-A099-09_BRCA	23	0	0	37	42	60	60	35	30	19	12	0	34	40	0	17	55
TCGA-AR-A0TX-10A-01D-A099-09_BRCA	76	0	1	88	135	131	146	151	137	0	0	0	0	0	0	172	95
TCGA-AR-A0TY-10A-01D-A110-09_BRCA	125	0	0	132	204	211	238	253	157	29	133	0	154	147	85	0	147
TCGA-AR-A0TZ-10A-01D-A099-09_BRCA	79	0	1	121	239	129	159	96	170	0	0	0	1	142	0	81	111
TCGA-AR-A0U0-10A-01D-A10G-09_BRCA	60	2	1	73	104	101	117	106	134	0	0	0	0	1	35	60	85
TCGA-AR-A0U1-10A-01D-A110-09_BRCA	95	5	1	80	226	210	196	149	205	0	0	2	0	0	34	76	146
TCGA-AR-A0U2-10A-01D-A10G-09_BRCA	60	1	0	43	103	108	109	96	126	0	0	0	0	0	0	93	76
TCGA-AR-A0U3-10A-01D-A10G-09_BRCA	45	1	2	44	110	102	113	90	138	1	1	0	1	4	0	87	77
TCGA-AR-A0U4-10A-01D-A10G-09_BRCA	63	104	98	35	85	75	144	112	159	0	0	0	0	0	33	62	101
TCGA-AR-A1AH-10A-01D-A12B-09_BRCA	119	157	159	61	180	134	264	269	292	0	0	0	0	0	72	127	212
TCGA-AR-A1AI-10A-01D-A12Q-09_BRCA	104	125	175	66	156	149	248	240	140	62	198	0	223	132	0	117	118
TCGA-AR-A1AJ-10A-01D-A12Q-09_BRCA	99	0	0	118	196	176	195	230	221	0	0	0	0	1	68	130	138
TCGA-AR-A1AK-10A-01D-A12Q-09_BRCA	109	0	1	118	204	201	210	208	189	0	0	0	0	0	0	238	153
TCGA-AR-A1AL-10A-01D-A12Q-09_BRCA	93	129	129	60	116	129	177	176	239	0	0	0	0	0	50	109	121
TCGA-AR-A1AM-10A-01D-A22A-09_BRCA	37	78	61	3	11	11	79	66	83	2	4	4	3	10	0	35	68
TCGA-AR-A1AN-10A-01D-A12Q-09_BRCA	100	149	150	76	133	140	246	198	270	0	0	0	0	0	56	106	160
TCGA-AR-A1AO-10A-01D-A12Q-09_BRCA	91	134	0	64	240	199	193	227	237	0	0	0	0	0	0	242	131
TCGA-AR-A1AP-10A-01D-A12Q-09_BRCA	65	0	0	62	126	112	126	110	150	0	0	0	0	0	60	0	91

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-AR-A1AQ-10A-01D-A12Q-09_BRCA	110	118	134	52	236	171	234	290	191	21	125	141	1	0	130	0	117
TCGA-AR-A1AR-10A-01D-A135-09_BRCA	102	130	136	60	165	151	224	221	164	24	149	0	161	145	0	146	163
TCGA-AR-A1AS-10A-01D-A12Q-09_BRCA	94	123	124	67	236	202	193	201	135	31	234	153	131	138	0	102	135
TCGA-AR-A1AT-10A-01D-A12Q-09_BRCA	111	133	129	71	271	206	185	216	124	30	208	212	1	149	74	0	138
TCGA-AR-A1AU-10A-01D-A12Q-09_BRCA	92	0	0	120	195	160	175	167	178	0	0	0	0	0	90	1	121
TCGA-AR-A1AV-10A-01D-A12Q-09_BRCA	87	133	121	60	212	160	162	140	223	0	95	123	0	2	0	132	129
TCGA-AR-A1AW-10A-01D-A12Q-09_BRCA	59	1	1	96	125	3	119	86	120	0	0	1	0	116	0	40	92
TCGA-AR-A1AX-10A-01D-A12Q-09_BRCA	81	0	2	106	170	149	197	193	117	24	100	0	114	113	0	121	111
TCGA-AR-A1AY-10A-01D-A12Q-09_BRCA	76	0	0	59	138	152	149	117	153	0	0	0	0	0	0	137	116
TCGA-AR-A24H-10A-01D-A167-09_BRCA	52	91	84	28	67	80	117	93	102	0	0	0	0	0	65	0	86
TCGA-AR-A24K-10A-01D-A167-09_BRCA	29	0	0	26	60	46	63	53	55	0	0	0	0	0	0	50	54
TCGA-AR-A24L-10A-01D-A167-09_BRCA	51	0	0	81	116	107	108	108	71	24	65	0	79	84	43	2	77
TCGA-AR-A24M-10A-01D-A167-09_BRCA	33	0	0	21	66	80	89	69	93	0	0	0	0	0	0	74	61
TCGA-AR-A24N-10A-01D-A167-09_BRCA	55	66	63	29	113	99	111	100	98	0	51	63	0	0	0	105	79
TCGA-AR-A24O-10A-01D-A167-09_BRCA	31	61	51	27	90	72	88	95	94	0	35	57	0	0	24	48	59
TCGA-AR-A24P-10A-01D-A167-09_BRCA	45	63	52	32	56	58	103	97	98	0	0	0	0	0	25	43	69
TCGA-AR-A24Q-10A-01D-A167-09_BRCA	53	0	0	54	98	86	105	85	103	0	0	0	0	0	29	48	73
TCGA-AR-A24R-10A-01D-A167-09_BRCA	38	53	54	21	42	50	70	43	50	0	48	47	0	49	26	0	55
TCGA-AR-A24S-10A-01D-A167-09_BRCA	46	0	1	47	83	95	108	90	90	1	0	0	0	0	0	97	74
TCGA-AR-A24T-10A-01D-A167-09_BRCA	30	0	0	36	74	78	89	75	43	15	36	49	0	49	0	49	65
TCGA-AR-A24U-10A-01D-A167-09_BRCA	45	1	0	46	73	71	90	68	87	0	0	0	1	0	20	32	75
TCGA-AR-A24V-10A-01D-A167-09_BRCA	43	0	0	46	72	73	88	72	86	0	0	0	0	0	26	38	63
TCGA-AR-A24W-10A-01D-A167-09_BRCA	40	0	0	39	65	82	94	73	80	0	0	0	0	0	0	80	78
TCGA-AR-A24X-10A-01D-A167-09_BRCA	46	56	43	22	46	55	89	68	46	14	37	0	48	54	0	34	61
TCGA-AR-A24Z-10A-01D-A167-09_BRCA	35	1	0	43	74	65	75	76	78	0	0	0	0	1	0	82	60
TCGA-AR-A250-10A-01D-A167-09_BRCA	34	43	38	22	49	43	82	66	91	0	0	0	0	0	0	58	56
TCGA-AR-A251-10A-01D-A167-09_BRCA	29	0	0	46	80	67	91	73	88	0	0	0	0	0	0	57	64
TCGA-AR-A252-10A-01D-A167-09_BRCA	35	49	41	21	33	41	71	72	67	0	1	0	0	0	0	53	54
TCGA-AR-A254-10A-01D-A167-09_BRCA	46	0	0	39	74	74	98	63	77	0	1	1	0	0	0	67	76
TCGA-AR-A255-10A-01D-A167-09_BRCA	59	0	0	37	113	87	100	96	57	15	50	0	50	49	0	54	80
TCGA-AR-A256-10A-01D-A167-09_BRCA	38	60	52	21	104	82	94	82	104	1	40	54	0	0	0	80	71
TCGA-AR-A2LE-10A-01D-A17W-09_BRCA	47	65	72	34	61	1	72	43	62	0	0	0	0	64	35	0	51
TCGA-AR-A2LH-10A-01D-A18P-09_BRCA	31	0	0	38	81	70	88	82	85	0	0	0	0	0	25	42	55
TCGA-AR-A2LJ-10A-01D-A19Y-09_BRCA	34	50	37	13	38	40	76	48	58	8	27	0	36	46	0	37	57
TCGA-AR-A2LK-10A-01D-A17W-09_BRCA	64	1	0	55	111	79	125	99	126	0	0	1	1	2	0	102	97
TCGA-AR-A2LL-10A-01D-A17W-09_BRCA	44	0	0	42	92	98	89	102	63	17	43	0	55	62	0	47	70
TCGA-AR-A2LM-10A-01D-A17W-09_BRCA	67	102	96	46	152	124	137	135	132	0	69	100	0	0	42	78	99
TCGA-AR-A2LN-10A-01D-A18P-09_BRCA	40	0	2	52	99	105	119	110	108	0	0	0	1	0	0	110	79
TCGA-AR-A2LO-10A-01D-A18P-09_BRCA	37	0	3	46	91	84	93	91	100	1	0	1	0	0	32	56	79
TCGA-AR-A2LQ-10A-01D-A18P-09_BRCA	34	54	45	24	94	94	95	75	54	17	88	55	55	51	27	0	71
TCGA-AR-A2LR-10A-01D-A18P-09_BRCA	49	1	0	47	145	120	137	134	0	26	128	83	104	112	0	0	103
TCGA-AR-A5QM-10A-01D-A27P-09_BRCA	45	0	0	25	73	74	80	83	68	8	44	1	49	58	0	52	75
TCGA-AR-A5QN-10A-01D-A28E-09_BRCA	48	1	1	24	82	91	112	86	104	0	0	0	0	0	43	0	69
TCGA-AR-A5QP-10A-01D-A28E-09_BRCA	66	67	60	24	104	99	108	106	160	0	41	66	0	0	36	56	77
TCGA-AR-A5QQ-10A-01D-A28E-09_BRCA	47	0	1	45	96	90	98	91	107	0	0	0	0	0	0	77	85
TCGA-AS-3777-10A-01D-0966-08_KIRC	108	0	2	60	121	104	94	124	124	0	0	0	0	2	36	93	116
TCGA-AS-3778-10A-01D-0966-08_KIRC	95	1	0	55	104	105	91	92	105	0	0	0	0	0	0	118	114
TCGA-AT-A5NU-10A-01D-A28G-10_KIRP	66	48	46	25	52	74	121	93	86	0	0	0	0	0	0	96	80
TCGA-AU-3779-10A-01D-1719-10_COAD	100	0	0	88	161	152	184	142	187	0	0	0	0	0	0	107	170
TCGA-AU-6004-10A-01D-1719-10_COAD	47	0	0	32	71	80	89	49	93	0	0	0	0	0	0	36	85
TCGA-AW-A1PO-10A-01D-A159-09_UCEC	41	1	1	21	72	47	43	35	39	0	1	3	2	55	0	33	38
TCGA-AX-A06D-10A-01D-A122-09_UCEC	99	152	169	0	138	138	180	161	230	0	112	146	0	0	0	174	119
TCGA-AX-A06H-10A-01D-A122-09_UCEC	112	127	144	53	139	140	191	198	241	0	0	0	0	0	0	193	136
TCGA-AX-A06L-10A-01D-A122-09_UCEC	91	2	0	88	176	178	190	150	1	33	163	0	174	191	0	0	147
TCGA-AX-A0IS-10B-01D-A10M-09_UCEC	86	0	0	75	202	192	224	191	196	0	0	0	0	0	0	244	160
TCGA-AX-A0IU-10A-01D-A10B-09_UCEC	85	141	135	51	210	176	175	131	191	0	76	113	0	2	43	79	134
TCGA-AX-A0IZ-10A-01D-A122-09_UCEC	95	131	125	56	140	124	177	165	183	0	0	0	0	1	77	0	138
TCGA-AX-A1C4-10A-01D-A135-09_UCEC	43	49	50	9	88	75	77	71	1	12	80	67	50	74	0	1	63
TCGA-AX-A1C5-10A-01D-A135-09_UCEC	51	2	2	22	76	76	86	54	97	0	0	0	1	2	0	83	65
TCGA-AX-A1C7-10A-01D-A135-09_UCEC	43	0	0	63	101	113	137	89	130	0	0	0	0	0	24	50	87
TCGA-AX-A1C8-10A-01D-A135-09_UCEC	47	123	101	0	53	57	121	78	112	0	36	56	0	0	30	42	89
TCGA-AX-A1C9-10A-01D-A135-09_UCEC	54	71	52	16	60	56	54	30	74	0	43	0	54	70	28	0	77
TCGA-AX-A1CA-10A-01D-A135-09_UCEC	74	100	102	41	100	97	139	118	129	0	0	0	0	1	64	0	120
TCGA-AX-A1CC-10A-01D-A135-09_UCEC	26	0	0	35	35	60	80	66	65	0	0	0	0	0	10	15	56
TCGA-AX-A1CE-10A-01D-A135-09_UCEC	58	68	69	11	60	70	102	56	136	0	0	0	0	1	0	72	77
TCGA-AX-A1CN-10A-01D-A135-09_UCEC	46	56	49	15	58	56	97	93	92	0	0	2	0	0	0	106	75
TCGA-AX-A1CP-10A-01D-A135-09_UCEC	39	0	0	71	96	99	110	96	91	0	0	0	0	0	0	116	77
TCGA-AX-A2H7-10A-01D-A18P-09_UCEC	65	72	59	20	118	101	132	105	6	25	115	63	86	98	0	2	85
TCGA-AX-A2HF-10A-01D-A17D-09_UCEC	35	55	52	26	47	43	85	64	88	0	0	0	0	0	31	42	58
TCGA-AX-A2HG-10A-01D-A17D-09_UCEC	44	94	85	1	1	5	93	96	127	0	1	0	0	0	0	108	72
TCGA-AX-A2HH-10A-01D-A17D-09_UCEC	39	69	55	15	53	59	95	86	1	15	78	54	55	101	0	2	75
TCGA-AX-A2HJ-10A-01D-A17D-09_UCEC	44	1	0	19	80	84	80	74	98	0	0	1	0	0	42	2	68
TCGA-AX-A2HK-10A-01D-A17D-09_UCEC	46	54	42	13	51	67	76	66	99	0	3	1	1	4	29	44	71
TCGA-AX-A2IN-10A-01D-A17W-09_UCEC	37	51	38	13	48	53	75	71	84	0	0	0	2	1	35	38	73
TCGA-AX-A2IO-10A-01D-A17W-09_UCEC	68	2	0	41	110	104	92	115	85	11	56	0	66	73	40	3	83
TCGA-AX-A3FS-10A-01D-A22A-09_UCEC	47	7	4	25	64	70	82	62	93	1	3	0	1	0	0	55	61
TCGA-AX-A3FT-10A-01D-A22A-09_UCEC	52	1	0	34	83	85	88	89	77	0	0	1	0	0	0	90	57
TCGA-AX-A3FV-10A-01D-A22A-09_UCEC	37	53	60	10	58	50	79	83	99	1	2	0	1	1	28	49	71
TCGA-AX-A3FW-10A-01D-A22A-09_UCEC	40	0	6	24	93	101	105	100	88	0	1	0	0	1	0	94	79
TCGA-AX-A3FX-10A-01D-A22A-09_UCEC	55	1	0	23	103	92	91	110	112	0	0	0	0	0	0	103	72
TCGA-AX-A3FZ-10A-01D-A22A-09_UCEC	57	2	2	32	101	84	116	107	126	0	0	0	0	3	34	58	80
TCGA-AX-A3G1-10A-01D-A22A-09_UCEC	42	4	3	20	76	73	78	74	14	12	49	32	34	66	0	10	65
TCGA-AX-A3G3-10A-01D-A20S-09_UCEC	45	58	48	12	48	55	79	74	3	12	65	1	71	87	0	4	75
TCGA-AX-A3G4-10A-01D-A20S-09_UCEC	52	56	54	17	58	55	91	94	128	0	2	1	0	0	29	53	68
TCGA-AX-A3G6-10A-01D-A20S-09_UCEC	48	0	1	28	88	81	80	82	118	0	0	1	0	0	31	49	76
TCGA-AX-A3G7-10A-01D-A20S-09_UCEC	63	3	3	31	106	96	107	101	116	0	0	0	0	2	36	59	76
TCGA-AX-A3G8-10A-01D-A22A-09_UCEC	30	49	57	17	44	53	86	65	77	12	47	0	51	46	0	36	82
TCGA-AX-A3G9-10A-01D-A22A-09_UCEC	58	84	86	0	2	1	70	54	4	8	94	61	67	92	0	1	68
TCGA-AX-A3GB-10A-01D-A22A-09_UCEC	43	64	59	10	95	74	87	79	105	0	59	58	0	0	19	41	74
TCGA-AX-A3GI-10A-01D-A20S-09_UCEC	58	0	1	42	117	108	105	135	137	0	0	0	0	0	57	78	102
TCGA-AY-5543-10A-01D-1650-10_COAD	90	69	0	28	69	65	86	40	85	0	36	0	43	64	15	0	112
TCGA-AY-6197-10A-01D-1719-10_COAD	51	0	0	26	45	47	55	47	64	0	0	0	0	0	12	15	56
TCGA-AZ-4315-10A-01D-1408-10_COAD	98	0	0	53	124	120	129	96	144	0	0	0	0	0	0	78	110
TCGA-AZ-4323-10A-01D-1835-10_COAD	44	0	0	26	37	36	37	31	24	5	12	0	18	10	0	18	41
TCGA-AZ-4616-10A-01D-1835-10_COAD	58	0	0	63	57	30	38	28	44	0	0	0	0	50	0	30	36
TCGA-AZ-4681-10A-01D-1408-10_COAD	58	0	0	49	63	52	78	46	73	0	0	0	0	0	0	38	83

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-AZ-4682-10A-01D-1408-10_COAD	38	0	0	33	39	26	31	21	1	11	22	0	34	27	0	0	54
TCGA-AZ-5403-10A-01D-1650-10_COAD	84	0	1	56	99	96	133	97	137	0	0	0	0	1	16	28	115
TCGA-B0-5399-10A-01D-1501-10_KIRC	84	8	10	130	211	228	212	178	291	7	3	0	4	8	29	95	176
TCGA-B0-5698-10A-01D-1669-08_KIRC	116	106	110	0	1	2	102	133	122	0	1	0	0	2	30	65	140
TCGA-B1-5398-10A-01D-1589-08_KIRP	105	1	0	92	105	96	101	87	99	0	0	1	0	1	0	95	125
TCGA-B1-7332-10A-01D-2136-08_KIRP	100	70	75	45	103	104	85	94	119	0	55	65	1	0	40	3	114
TCGA-B1-A47M-10A-01D-A25F-10_KIRP	65	0	1	48	61	100	80	67	69	0	0	0	0	0	31	0	66
TCGA-B1-A47N-10A-01D-A25F-10_KIRP	78	52	53	24	99	97	109	99	97	0	33	62	0	0	0	103	87
TCGA-B1-A47O-10A-01D-A25F-10_KIRP	87	0	0	48	81	105	104	71	71	9	34	0	57	64	0	46	112
TCGA-B1-A654-10A-01D-A31X-10_KIRP	43	0	31	22	25	37	62	47	54	0	0	0	0	1	25	0	48
TCGA-B1-A655-10A-01D-A31X-10_KIRP	42	46	25	0	22	31	45	51	0	5	18	0	38	56	0	0	50
TCGA-B1-A656-10A-01D-A31X-10_KIRP	60	66	54	2	1	0	73	59	42	8	23	0	36	33	18	1	58
TCGA-B1-A657-10A-01D-A31X-10_KIRP	56	0	0	32	61	67	73	58	78	0	0	0	0	0	0	51	46
TCGA-B2-3923-10A-01D-1458-08_KIRC	124	94	106	0	3	0	115	113	120	0	0	0	0	0	46	0	130
TCGA-B2-3924-10A-01D-1458-08_KIRC	120	81	82	54	165	128	97	134	147	0	55	87	0	1	0	160	130
TCGA-B2-4098-10A-01D-1458-08_KIRC	123	1	3	64	128	124	104	107	145	0	0	1	5	3	0	118	132
TCGA-B2-4099-10A-01D-1458-08_KIRC	143	2	0	61	128	114	110	114	91	18	68	97	0	95	0	85	140
TCGA-B2-5633-10A-01D-1535-10_KIRC	74	0	2	162	242	184	219	160	220	0	0	0	0	0	0	167	137
TCGA-B2-5635-10A-01D-A270-10_KIRC	67	36	44	23	38	39	68	63	67	0	0	0	0	0	30	0	61
TCGA-B2-5636-10A-01D-1535-10_KIRC	56	0	1	109	169	124	173	127	129	28	0	0	0	2	0	101	95
TCGA-B2-5639-10A-01D-1535-10_KIRC	54	0	0	117	133	163	147	104	158	0	0	0	0	0	23	45	95
TCGA-B2-5641-10A-01D-1535-10_KIRC	52	0	1	93	139	130	152	109	191	0	0	0	0	1	16	44	102
TCGA-B2-A4SR-10A-01D-A25V-10_KIRC	101	0	0	60	105	101	117	75	136	0	0	0	0	0	27	61	120
TCGA-B3-3925-10A-01D-1458-08_KIRP	100	2	0	57	97	94	86	121	85	9	41	1	60	85	30	0	107
TCGA-B3-4103-10A-01D-1458-08_KIRP	115	0	2	69	118	121	109	134	118	0	0	0	1	0	0	111	135
TCGA-B3-4104-10A-01D-1458-08_KIRP	111	1	0	85	116	108	103	136	118	1	0	0	1	0	0	143	117
TCGA-B3-8121-10A-01D-2396-08_KIRP	97	1	69	48	120	78	80	75	83	0	46	0	66	3	38	0	102
TCGA-B4-5377-10A-01D-1501-10_KIRC	99	0	2	116	228	195	200	176	262	0	0	0	0	0	39	84	149
TCGA-B4-5378-10A-01D-1501-10_KIRC	55	0	0	54	128	136	152	101	145	0	0	0	0	0	43	0	117
TCGA-B4-5832-10A-01D-1669-08_KIRC	112	0	0	91	110	108	101	104	98	19	39	1	66	72	0	67	139
TCGA-B4-5834-10A-02D-1669-08_KIRC	119	70	76	52	77	86	97	103	128	0	0	0	0	0	0	141	143
TCGA-B4-5835-10A-01D-1669-08_KIRC	123	71	74	47	132	99	93	108	123	0	40	70	1	4	26	66	132
TCGA-B4-5836-10A-01D-1669-08_KIRC	114	75	0	49	129	114	89	94	73	20	33	0	64	76	0	71	149
TCGA-B4-5838-10A-01D-1669-08_KIRC	105	97	108	2	74	76	100	106	125	0	48	73	0	0	0	120	128
TCGA-B4-5843-10A-01D-1669-08_KIRC	123	0	0	90	111	112	94	93	132	0	0	0	0	1	0	108	132
TCGA-B4-5844-10A-01D-1669-08_KIRC	112	65	73	47	126	101	105	98	79	19	72	98	1	85	0	53	144
TCGA-B5-A0JN-10A-01D-A10O-09_UCEC	75	108	113	63	178	117	243	158	199	0	111	0	114	0	0	190	115
TCGA-B5-A0JS-10A-01D-A10O-09_UCEC	61	102	103	46	160	121	130	145	103	21	144	95	91	86	0	77	104
TCGA-B5-A0JT-10A-01D-A122-09_UCEC	86	0	0	120	155	159	206	179	182	0	0	0	0	0	0	217	135
TCGA-B5-A0JU-10A-01D-A14G-09_UCEC	61	71	63	24	141	103	114	94	133	0	53	0	61	0	63	0	95
TCGA-B5-A0JX-10B-01D-A14K-09_UCEC	50	60	65	19	66	66	91	73	113	0	0	0	1	0	0	87	75
TCGA-B5-A0JY-10A-01D-A10O-09_UCEC	83	0	0	89	127	136	153	168	189	0	0	0	0	0	0	175	104
TCGA-B5-A0K2-10A-01D-A10B-09_UCEC	78	123	119	49	114	113	153	133	118	24	104	0	104	104	0	87	106
TCGA-B5-A0K7-10A-02D-A10B-09_UCEC	64	94	94	42	87	75	123	101	147	0	0	0	0	0	0	103	84
TCGA-B5-A0K8-10B-01D-A14K-09_UCEC	41	60	62	35	113	103	114	91	58	25	86	72	61	75	24	1	81
TCGA-B5-A0K9-10A-02D-A10B-09_UCEC	91	0	1	74	178	166	184	175	197	0	0	0	0	0	0	216	124
TCGA-B5-A0KB-10A-01D-A14G-09_UCEC	43	1	0	25	134	88	112	96	123	14	41	0	50	0	49	41	71
TCGA-B5-A11E-10A-01D-A10M-09_UCEC	55	0	0	81	134	124	143	75	160	0	0	0	0	1	26	55	89
TCGA-B5-A11F-10A-01D-A10M-09_UCEC	103	138	147	59	245	185	220	222	174	25	190	218	2	146	0	137	145
TCGA-B5-A11G-10A-01D-A122-09_UCEC	105	0	0	71	184	161	197	217	192	0	0	1	0	0	81	119	133
TCGA-B5-A11H-10B-01D-A122-09_UCEC	102	137	139	63	232	177	203	186	150	24	169	183	0	141	0	116	141
TCGA-B5-A11I-10A-01D-A10M-09_UCEC	206	0	0	163	376	379	402	380	393	0	213	2	259	2	84	0	176
TCGA-B5-A11J-10A-01D-A122-09_UCEC	91	133	137	68	135	130	187	213	225	0	0	0	0	1	58	107	140
TCGA-B5-A11L-10A-01D-A13O-09_UCEC	46	71	64	15	66	66	91	91	72	17	41	1	60	58	37	2	76
TCGA-B5-A11M-10A-01D-A122-09_UCEC	84	135	123	0	133	119	181	165	120	30	116	0	138	136	0	110	113
TCGA-B5-A11N-10A-01D-A122-09_UCEC	104	0	1	78	186	153	199	240	195	0	0	0	0	0	0	259	120
TCGA-B5-A11O-10A-01D-A122-09_UCEC	113	0	1	88	168	178	202	232	236	0	0	0	0	0	63	124	134
TCGA-B5-A11P-10A-01D-A14G-09_UCEC	42	73	75	0	54	50	78	68	86	0	35	60	0	0	44	1	69
TCGA-B5-A11Q-10A-01D-A122-09_UCEC	99	0	0	67	154	144	164	179	220	0	0	0	0	0	63	109	125
TCGA-B5-A11R-10A-01D-A122-09_UCEC	77	0	0	102	222	161	158	176	213	0	0	0	1	1	0	189	123
TCGA-B5-A11S-10A-01D-A122-09_UCEC	115	128	136	53	225	179	219	252	244	0	135	131	0	1	69	132	130
TCGA-B5-A11U-10A-01D-A122-09_UCEC	99	0	0	65	176	169	165	221	176	0	0	0	0	0	0	234	110
TCGA-B5-A11V-10A-01D-A10M-09_UCEC	87	0	3	118	179	259	209	215	150	25	163	0	133	118	60	0	114
TCGA-B5-A11W-10A-01D-A122-09_UCEC	92	2	1	101	175	173	179	198	178	0	0	0	0	0	54	112	122
TCGA-B5-A11X-10A-01D-A10M-09_UCEC	85	126	128	49	202	145	165	130	174	0	95	123	0	0	64	115	109
TCGA-B5-A11Y-10A-01D-A10M-09_UCEC	120	161	185	61	295	280	320	246	318	0	155	199	0	0	0	325	215
TCGA-B5-A11Z-10A-01D-A10M-09_UCEC	116	144	1	51	151	132	244	249	166	26	146	156	0	131	70	0	172
TCGA-B5-A121-10A-01D-A122-09_UCEC	109	0	0	103	209	234	253	205	341	0	0	0	0	0	56	139	173
TCGA-B5-A1MR-10A-01D-A14G-09_UCEC	51	84	80	0	42	50	83	73	95	0	36	56	0	0	33	35	69
TCGA-B5-A1MS-10A-01D-A22A-09_UCEC	75	3	2	31	114	114	103	116	134	0	0	0	0	0	35	57	84
TCGA-B5-A1MU-10A-01D-A13O-09_UCEC	33	1	0	50	98	106	114	110	100	0	0	0	0	0	37	50	73
TCGA-B5-A1MV-10A-01D-A14G-09_UCEC	48	59	69	14	102	93	102	108	97	0	44	48	0	0	0	102	70
TCGA-B5-A1MW-10A-01D-A17D-09_UCEC	55	0	1	32	103	95	98	82	76	13	54	2	59	66	0	52	77
TCGA-B5-A1MX-10A-01D-A142-09_UCEC	58	0	2	50	89	85	89	96	123	0	0	0	0	1	37	59	73
TCGA-B5-A1MY-10A-01D-A142-09_UCEC	41	58	58	36	100	105	94	83	0	43	132	95	103	98	0	0	96
TCGA-B5-A1MZ-10A-01D-A142-09_UCEC	32	47	33	9	68	67	72	74	51	12	66	41	38	44	0	33	58
TCGA-B5-A1N2-10A-01D-A142-09_UCEC	49	51	2	17	43	53	66	59	54	0	45	0	44	52	19	0	68
TCGA-B5-A3F9-10A-01D-A22A-09_UCEC	48	0	3	44	98	98	101	111	146	0	0	0	0	0	0	115	85
TCGA-B5-A3FA-10A-01D-A19Y-09_UCEC	49	2	4	38	108	93	102	62	85	13	34	64	1	81	0	31	86
TCGA-B5-A3FB-10A-01D-A19Y-09_UCEC	55	0	64	19	100	103	104	70	131	0	88	64	62	0	50	1	78
TCGA-B5-A3FC-10A-01D-A22A-09_UCEC	66	1	1	36	152	105	116	121	148	0	0	0	0	0	68	73	96
TCGA-B5-A3FD-10A-01D-A19Y-09_UCEC	44	61	1	13	62	49	65	50	77	0	45	0	61	58	38	0	79
TCGA-B5-A3FH-10A-01D-A19Y-09_UCEC	50	67	66	22	57	68	104	77	115	0	0	0	0	0	0	91	87
TCGA-B5-A3S1-10A-01D-A22A-09_UCEC	37	32	33	13	44	38	77	53	75	2	0	2	1	5	26	32	48
TCGA-B5-A5OC-10A-01D-A27P-09_UCEC	61	52	52	17	68	65	94	88	124	0	48	0	48	0	0	61	54
TCGA-B5-A5OD-10A-01D-A31U-09_UCEC	38	0	0	23	90	75	84	65	105	0	0	0	0	0	48	0	79
TCGA-B5-A5OE-10A-01D-A31U-09_UCEC	39	0	0	32	104	76	86	95	113	0	0	0	0	0	0	99	82
TCGA-B6-A0I1-10A-01D-A21Q-09_BRCA	37	43	48	15	72	61	79	66	62	12	50	0	80	47	0	1	42
TCGA-B6-A0IH-10A-01D-A110-09_BRCA	83	5	3	83	177	192	196	169	206	0	1	3	0	0	0	148	126
TCGA-B6-A0RH-10A-01D-A110-09_BRCA	72	128	131	55	244	166	230	152	197	0	97	142	3	2	39	95	142
TCGA-B6-A0RL-10A-01D-A099-09_BRCA	72	122	110	46	100	100	164	146	118	21	136	0	160	94	36	1	110
TCGA-B6-A0RM-10A-01D-A099-09_BRCA	70	94	97	47	165	125	151	163	164	1	83	86	0	0	0	163	107
TCGA-B6-A0RN-10A-01D-A099-09_BRCA	67	105	0	49	102	97	148	128	176	0	0	0	0	0	47	75	105
TCGA-B6-A0RO-10A-01D-A099-09_BRCA	45	0	0	54	116	88	109	68	64	20	43	76	1	56	0	42	70
TCGA-B6-A0RP-10A-01D-A099-09_BRCA	53	0	0	55	111	101	129	69	148	0	0	0	0	1	0	70	70
TCGA-B6-A0RQ-10A-01D-A110-09_BRCA	116	0	1	117	169	186	189	181	127	25	121	0	124	124	0	101	120

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-B6-A0RT-10A-01D-A099-09_BRCA	90	0	0	103	180	151	187	136	129	23	111	1	129	109	42	0	105
TCGA-B6-A0RU-10A-01D-A099-09_BRCA	62	0	1	56	115	114	120	116	85	22	62	86	0	89	0	74	85
TCGA-B6-A0RV-10A-01D-A099-09_BRCA	74	0	0	65	138	149	163	147	157	0	0	0	0	1	48	93	100
TCGA-B6-A0WS-10A-01D-A110-09_BRCA	61	0	1	50	126	106	123	93	121	0	0	0	0	0	33	48	87
TCGA-B6-A0WT-10A-01D-A10G-09_BRCA	37	0	0	59	106	98	105	73	134	0	0	0	0	0	0	76	61
TCGA-B6-A0WV-10A-01D-A10G-09_BRCA	86	120	107	62	116	125	189	202	121	26	104	0	127	119	0	116	120
TCGA-B6-A0WW-10A-01D-A10G-09_BRCA	116	0	1	87	224	204	200	225	206	0	0	0	0	2	72	135	130
TCGA-B6-A0WX-10A-01D-A10G-09_BRCA	77	133	126	48	201	162	176	152	211	0	95	3	126	2	0	153	140
TCGA-B6-A0WY-10A-01D-A10G-09_BRCA	27	54	62	26	44	44	89	45	89	0	0	1	0	0	19	2	60
TCGA-B6-A0WZ-10A-01D-A10G-09_BRCA	33	0	0	55	112	101	116	56	112	1	0	0	0	0	45	0	76
TCGA-B6-A0X0-10A-01D-A110-09_BRCA	84	106	117	47	109	111	116	94	0	22	173	0	144	138	0	0	104
TCGA-B6-A0X1-10A-01D-A117-09_BRCA	45	106	111	0	118	120	108	86	106	0	78	108	0	0	0	103	87
TCGA-B6-A0X4-10A-01D-A10G-09_BRCA	21	0	0	30	58	79	71	58	91	0	0	0	0	0	13	29	47
TCGA-B6-A0X5-10A-01D-A10G-09_BRCA	35	113	112	0	55	58	107	54	73	22	70	60	63	53	0	0	68
TCGA-B6-A0X7-10A-01D-A10M-09_BRCA	97	177	175	0	190	184	186	144	121	26	217	194	122	131	0	115	159
TCGA-B6-A1KN-10A-01D-A188-09_BRCA	30	53	39	27	47	43	86	78	92	0	0	0	0	1	16	43	72
TCGA-B6-A2IU-10A-01D-A18P-09_BRCA	48	75	69	28	50	60	112	112	110	0	0	0	0	0	21	48	92
TCGA-B6-A3ZX-10A-01D-A23C-09_BRCA	51	2	0	25	89	91	93	88	113	1	4	2	2	4	30	35	77
TCGA-B6-A400-10A-01D-A23C-09_BRCA	53	1	1	32	84	90	88	78	108	0	1	0	0	0	53	5	78
TCGA-B6-A401-10A-01D-A23C-09_BRCA	50	67	57	22	117	92	106	89	65	13	76	50	56	60	34	1	78
TCGA-B6-A402-10A-01D-A23C-09_BRCA	49	72	64	22	101	82	89	86	104	0	37	46	1	0	27	39	78
TCGA-B6-A408-10A-01D-A243-09_BRCA	47	62	43	23	57	52	85	88	104	0	1	1	0	1	0	33	60
TCGA-B6-A409-10A-01D-A243-09_BRCA	42	1	1	15	44	76	86	66	93	0	26	3	44	3	37	5	61
TCGA-B6-A40B-10A-01D-A23C-09_BRCA	47	4	0	33	91	95	86	99	119	2	1	5	0	0	0	102	88
TCGA-B6-A40C-10A-01D-A23C-09_BRCA	38	49	48	7	49	40	83	66	105	0	1	1	2	1	0	64	58
TCGA-B7-5816-10A-01D-1600-08_STAD	119	75	85	54	90	93	115	114	110	0	0	0	0	0	0	116	143
TCGA-B7-5818-10A-01D-1600-08_STAD	122	74	81	50	168	117	106	94	147	0	53	90	0	0	0	103	120
TCGA-B7-A5TI-10A-01D-A31J-08_STAD	84	75	80	0	73	63	76	91	66	16	60	67	0	63	25	0	88
TCGA-B7-A5TJ-10A-01D-A31J-08_STAD	89	75	77	1	78	74	77	75	77	20	73	63	59	69	0	56	96
TCGA-B7-A5TK-10A-01D-A31J-08_STAD	86	0	0	73	84	78	76	62	96	0	0	0	0	0	0	69	85
TCGA-B7-A5TN-10A-01D-A31J-08_STAD	81	71	68	42	114	75	79	72	106	0	48	67	0	0	0	73	90
TCGA-B8-4146-10A-01D-1669-08_KIRC	116	84	86	46	148	115	117	107	152	0	48	83	0	1	0	99	140
TCGA-B8-4148-10A-01D-1251-10_KIRC	75	0	0	87	132	160	134	97	76	26	45	0	91	77	0	63	112
TCGA-B8-4151-10A-01D-1251-10_KIRC	50	130	117	43	65	89	176	117	145	0	0	0	0	0	24	61	117
TCGA-B8-4619-10A-01D-1251-10_KIRC	79	158	161	69	122	110	194	104	220	0	0	0	0	1	0	125	143
TCGA-B8-4620-10A-01D-1251-10_KIRC	50	0	0	73	131	128	137	104	157	0	0	0	0	0	23	69	104
TCGA-B8-4621-10A-01D-1501-10_KIRC	68	6	2	94	157	172	185	139	199	2	0	0	0	1	23	89	143
TCGA-B8-5158-10A-01D-1421-08_KIRC	147	0	1	100	148	123	128	135	107	0	0	0	1	0	0	164	141
TCGA-B8-5159-10A-01D-1421-08_KIRC	153	78	90	53	100	96	121	103	88	19	62	98	0	85	0	85	152
TCGA-B8-5162-10A-01D-1421-08_KIRC	125	70	77	42	89	87	103	106	78	17	49	0	76	82	0	70	121
TCGA-B8-5163-10A-01D-1421-08_KIRC	125	92	108	0	0	1	111	117	137	0	0	0	0	0	0	106	125
TCGA-B8-5164-10A-01D-1421-08_KIRC	147	87	88	50	106	100	114	127	98	19	49	0	68	94	0	79	158
TCGA-B8-5165-10A-01D-1421-08_KIRC	125	0	1	90	143	134	106	100	144	0	0	0	0	3	0	101	125
TCGA-B8-5545-10A-01D-1669-08_KIRC	116	1	1	69	101	102	102	147	133	0	0	0	0	0	33	72	122
TCGA-B8-5546-10A-01D-1535-10_KIRC	53	139	118	47	188	136	176	125	172	0	53	90	0	1	0	108	111
TCGA-B8-5549-10A-01D-1535-10_KIRC	37	0	1	81	125	127	128	61	67	43	37	0	78	86	0	47	105
TCGA-B8-5550-10A-01D-1535-10_KIRC	63	0	1	113	163	163	156	125	193	0	0	0	0	0	0	127	138
TCGA-B8-5551-10A-01D-1535-10_KIRC	65	0	0	89	148	168	168	114	173	0	0	0	0	2	35	0	135
TCGA-B8-5552-10A-01D-1669-08_KIRC	139	0	1	100	103	108	109	113	90	14	47	0	72	84	32	0	153
TCGA-B8-5553-10A-01D-1535-10_KIRC	82	0	1	137	209	210	245	131	223	0	0	0	0	3	51	0	182
TCGA-B8-A54D-10A-01D-A25V-10_KIRC	94	76	70	36	64	80	113	85	104	0	0	0	0	0	43	0	102
TCGA-B8-A54E-10A-01D-A25V-10_KIRC	75	52	56	32	91	101	94	81	91	0	36	53	0	0	22	48	76
TCGA-B8-A54F-10A-01D-A25V-10_KIRC	70	63	53	29	27	62	85	86	73	0	0	0	0	0	0	87	66
TCGA-B8-A54G-10A-01D-A25V-10_KIRC	75	0	57	25	39	78	95	82	87	0	0	0	0	0	31	57	80
TCGA-B9-4114-10A-01D-1252-08_KIRP	128	0	0	89	141	139	114	115	151	0	0	0	1	1	0	134	144
TCGA-B9-4115-10A-01D-1252-08_KIRP	137	10	10	94	135	128	110	122	142	0	9	1	10	9	51	2	135
TCGA-B9-4116-10A-01D-1252-08_KIRP	131	75	87	53	154	139	106	152	155	0	62	1	78	1	43	97	128
TCGA-B9-4117-10A-01D-1252-08_KIRP	105	63	64	44	130	98	64	56	73	0	65	0	81	72	30	0	105
TCGA-B9-4617-10A-01D-1252-08_KIRP	120	0	0	88	167	117	114	147	139	0	0	0	1	2	36	77	137
TCGA-B9-5155-10A-01D-1589-08_KIRP	89	70	63	46	84	66	69	57	72	0	48	3	68	68	0	69	110
TCGA-B9-5156-10A-01D-1589-08_KIRP	97	88	97	3	83	78	97	95	105	0	45	87	0	3	43	2	113
TCGA-B9-7268-10A-01D-2136-08_KIRP	88	54	58	45	116	87	96	106	85	16	48	70	0	0	29	61	95
TCGA-B9-A44B-10A-01D-A25F-10_KIRP	79	0	0	44	90	106	104	89	104	0	0	0	1	2	28	57	114
TCGA-B9-A5W7-10A-01D-A31X-10_KIRP	71	0	27	27	44	57	72	59	45	6	40	0	60	42	13	0	75
TCGA-B9-A5W8-10A-01D-A28G-10_KIRP	75	110	61	1	77	114	126	96	62	0	72	103	0	0	35	60	81
TCGA-B9-A5W9-10A-01D-A28G-10_KIRP	84	3	0	40	85	93	105	85	97	0	0	0	0	0	17	61	86
TCGA-B9-A69E-10A-01D-A31X-10_KIRP	66	44	40	32	44	57	55	57	43	4	39	30	46	32	0	38	71
TCGA-BA-4074-10A-01D-1434-08_HNSC	113	74	84	49	95	81	99	122	129	0	1	0	0	0	35	82	106
TCGA-BA-4075-10A-01D-1434-08_HNSC	105	0	0	85	99	96	96	98	106	1	0	0	0	2	50	1	106
TCGA-BA-4076-10A-01D-1434-08_HNSC	123	94	88	1	85	86	93	98	90	18	81	111	0	86	0	82	107
TCGA-BA-4077-10A-01D-1434-08_HNSC	111	66	69	44	129	100	102	104	97	0	46	87	1	2	43	1	101
TCGA-BA-4078-10A-01D-1434-08_HNSC	130	0	0	56	106	147	98	115	112	0	0	2	0	0	0	134	100
TCGA-BA-5149-10A-01D-1512-08_HNSC	161	80	85	46	90	75	100	151	134	0	1	2	0	2	36	83	112
TCGA-BA-5151-10A-01D-1434-08_HNSC	107	0	1	48	108	94	87	124	85	17	54	0	70	87	0	77	129
TCGA-BA-5152-10A-01D-1870-08_HNSC	125	72	88	50	81	82	103	137	77	22	74	0	69	84	0	72	138
TCGA-BA-5153-10A-01D-1434-08_HNSC	104	78	80	47	81	78	95	101	96	0	0	0	0	1	0	97	119
TCGA-BA-5555-10A-01D-1512-08_HNSC	103	71	72	42	128	100	84	86	110	0	44	83	1	1	46	2	93
TCGA-BA-5556-10A-01D-1512-08_HNSC	93	2	1	80	94	92	86	125	92	0	0	0	0	1	0	138	100
TCGA-BA-5557-10A-01D-1512-08_HNSC	98	1	2	51	96	88	84	114	100	0	0	0	1	0	33	66	104
TCGA-BA-5558-10A-01D-1512-08_HNSC	98	1	4	85	98	94	87	93	103	0	0	1	2	5	0	126	114
TCGA-BA-5559-10A-01D-1512-08_HNSC	134	1	0	52	101	94	99	118	77	16	60	1	61	78	0	66	113
TCGA-BA-6868-10A-01D-1912-08_HNSC	92	72	69	43	117	81	85	98	76	16	75	64	63	75	30	2	113
TCGA-BA-6869-10A-01D-1870-08_HNSC	118	76	69	58	75	72	110	131	128	0	0	0	0	0	38	69	120
TCGA-BA-6870-10A-01D-1870-08_HNSC	124	2	0	91	105	109	94	130	102	0	1	0	0	0	38	0	94
TCGA-BA-6871-10A-01D-1870-08_HNSC	122	0	0	75	113	93	104	91	123	0	0	0	0	1	0	96	125
TCGA-BA-6872-10A-01D-1870-08_HNSC	152	1	0	72	100	113	116	127	105	0	1	1	0	0	0	94	132
TCGA-BA-6873-10A-01D-1870-08_HNSC	118	0	0	76	107	109	101	98	80	20	65	1	68	87	0	65	132
TCGA-BA-7269-10A-01D-2013-08_HNSC	97	0	0	88	104	99	97	107	78	22	57	0	83	85	0	62	101
TCGA-BA-A4IF-10A-01D-A25Y-08_HNSC	89	68	77	44	112	95	88	101	106	1	67	70	2	3	0	129	100
TCGA-BA-A4IG-10A-01D-A25Y-08_HNSC	89	2	1	77	76	84	82	97	96	0	2	2	1	3	0	106	93
TCGA-BA-A4IH-10A-01D-A25Y-08_HNSC	90	0	0	50	87	91	74	92	93	1	1	0	3	3	0	110	99
TCGA-BA-A4II-10A-01D-A25Y-08_HNSC	116	60	62	37	99	82	81	96	91	0	48	51	1	2	27	65	103
TCGA-BA-A6D8-10A-01D-A31J-08_HNSC	91	0	0	52	85	79	81	80	85	0	0	0	0	0	37	0	88
TCGA-BA-A6DA-10A-01D-A31J-08_HNSC	75	0	0	74	85	81	79	95	106	0	0	0	0	2	0	120	94
TCGA-BA-A6DB-10A-01D-A30H-08_HNSC	107	75	82	54	139	107	107	122	93	0	49	99	0	1	0	136	136
TCGA-BA-A6DD-10A-01D-A31J-08_HNSC	85	45	62	41	68	59	78	87	86	0	0	0	0	0	22	51	92

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BA-A6DE-10A-01D-A31J-08_HNSC	79	0	0	52	84	87	78	78	62	12	46	0	59	73	0	57	103
TCGA-BA-A6DF-10A-01D-A30H-08_HNSC	133	0	1	97	117	117	104	94	1	28	82	0	91	118	0	0	132
TCGA-BA-A6DG-10A-01D-A30H-08_HNSC	126	75	81	54	93	75	110	119	77	17	47	0	67	93	0	79	130
TCGA-BA-A6DI-10A-01D-A30H-08_HNSC	113	75	83	50	77	81	98	84	83	22	59	0	66	79	0	66	123
TCGA-BA-A6DJ-10A-01D-A30H-08_HNSC	113	101	119	0	88	87	80	75	83	0	97	84	71	83	0	60	145
TCGA-BA-A6DL-10A-01D-A30H-08_HNSC	99	0	0	67	112	101	101	93	99	0	0	0	0	0	0	87	115
TCGA-BB-4217-10A-01D-2078-08_HNSC	81	0	4	75	78	94	72	71	79	1	0	0	0	1	31	0	86
TCGA-BB-4223-10A-01D-1434-08_HNSC	96	74	73	44	78	89	105	119	113	17	0	0	0	0	0	97	129
TCGA-BB-4224-10A-01D-1434-08_HNSC	105	0	1	54	99	100	90	89	77	24	52	0	71	83	0	80	112
TCGA-BB-4225-10A-01D-1434-08_HNSC	101	1	2	85	102	92	87	101	65	19	37	1	58	68	31	1	122
TCGA-BB-4227-10A-01D-1870-08_HNSC	118	67	70	62	77	78	104	132	118	0	0	1	0	0	33	74	130
TCGA-BB-4228-10A-01D-1434-08_HNSC	100	75	81	45	84	80	101	136	101	20	1	0	0	1	41	76	97
TCGA-BB-7861-10A-01D-2229-08_HNSC	105	0	0	61	114	96	104	75	129	0	0	0	0	0	0	78	117
TCGA-BB-7862-10A-01D-2229-08_HNSC	96	73	58	46	109	93	101	79	122	0	45	69	0	0	0	89	126
TCGA-BB-7863-10A-01D-2229-08_HNSC	103	86	83	0	105	120	99	111	86	22	97	110	60	88	30	0	134
TCGA-BB-7864-10A-01D-2229-08_HNSC	100	0	0	80	114	105	107	99	61	20	40	0	62	82	0	59	112
TCGA-BB-7866-10A-01D-2229-08_HNSC	105	0	0	100	119	107	105	111	130	0	0	0	0	1	36	57	129
TCGA-BB-7870-10A-01D-2229-08_HNSC	111	0	1	79	102	102	99	109	124	0	0	0	0	0	29	56	122
TCGA-BB-7871-10A-01D-2229-08_HNSC	113	64	73	49	68	72	95	95	105	0	0	0	0	1	26	61	123
TCGA-BB-7872-10A-01D-2229-08_HNSC	104	54	55	47	75	78	58	47	67	0	35	1	56	74	0	53	109
TCGA-BB-8596-10A-01D-2394-08_HNSC	82	58	0	39	65	60	63	60	51	0	48	0	53	53	0	60	90
TCGA-BB-8601-10A-01D-2394-08_HNSC	82	55	67	36	104	74	79	91	99	0	55	64	0	0	28	56	92
TCGA-BC-4073-10A-01D-A12Z-10_LIHC	58	36	40	22	67	70	90	50	87	0	16	36	0	0	8	0	65
TCGA-BC-A217-10A-01D-A152-10_LIHC	87	73	74	0	0	0	81	63	64	18	52	0	44	48	0	42	96
TCGA-BC-A3KF-10A-01D-A20W-10_LIHC	62	37	48	21	34	37	82	58	42	8	28	0	33	44	0	35	78
TCGA-BC-A3KG-10A-01D-A20W-10_LIHC	70	0	0	42	65	66	84	64	89	0	0	0	0	0	0	71	81
TCGA-BC-A5W4-10A-01D-A28X-10_LIHC	97	0	0	76	96	111	117	130	100	0	0	0	0	0	0	109	88
TCGA-BC-A69H-10A-01D-A30V-10_LIHC	53	70	71	1	1	1	69	67	45	5	20	0	31	40	14	0	65
TCGA-BC-A69I-10A-01D-A30V-10_LIHC	43	1	0	31	57	58	66	57	69	0	1	0	0	0	11	34	58
TCGA-BF-A1PU-10A-01D-A19A-08_SKCM	91	61	55	42	65	62	75	90	72	10	43	0	43	67	0	50	96
TCGA-BF-A1PV-10A-01D-A19A-08_SKCM	80	0	0	67	47	43	65	55	33	8	18	0	18	27	14	1	86
TCGA-BF-A1PX-10A-01D-A19A-08_SKCM	93	0	1	64	76	75	73	68	35	10	21	0	32	48	0	47	101
TCGA-BF-A1PZ-10A-01D-A19A-08_SKCM	94	77	88	2	44	39	63	73	68	0	21	34	0	2	15	44	113
TCGA-BF-A1Q0-10A-01D-A19A-08_SKCM	107	1	0	65	107	93	90	125	108	0	0	0	0	1	0	132	124
TCGA-BF-A3DJ-10A-02D-A20D-08_SKCM	84	60	57	47	113	89	72	84	93	0	31	58	0	0	27	58	129
TCGA-BF-A3DL-10A-02D-A20D-08_SKCM	92	62	65	45	73	74	84	94	90	0	0	1	0	0	28	62	111
TCGA-BF-A3DM-10A-02D-A20D-08_SKCM	76	0	0	69	89	84	80	87	94	0	0	1	0	2	0	87	95
TCGA-BF-A3DN-10A-01D-A20D-08_SKCM	83	57	63	40	116	85	76	85	88	0	52	66	0	0	0	122	108
TCGA-BF-A5EO-10A-01D-A27N-08_SKCM	83	0	0	69	84	76	80	85	76	11	43	0	64	72	0	53	97
TCGA-BF-A5EP-10A-01D-A27N-08_SKCM	83	0	1	54	76	81	87	91	106	0	0	0	0	2	0	73	92
TCGA-BF-A5EQ-10A-01D-A27N-08_SKCM	79	0	0	82	87	79	81	70	87	0	0	0	0	0	0	70	86
TCGA-BF-A5ER-10A-01D-A27N-08_SKCM	115	77	76	0	73	67	82	73	75	0	52	68	0	0	0	74	90
TCGA-BF-A5ES-10A-01D-A27N-08_SKCM	84	1	1	47	82	76	80	92	101	0	0	0	0	0	0	101	96
TCGA-BG-A0M0-10A-01D-A10B-09_UCEC	73	102	110	45	160	116	122	135	0	26	162	145	100	133	0	0	89
TCGA-BG-A0M3-10A-01D-A127-09_UCEC	41	0	0	64	95	66	65	38	72	0	0	0	0	60	0	40	47
TCGA-BG-A0M8-10A-01D-A10O-09_UCEC	64	0	0	85	112	125	147	173	205	0	0	0	0	0	46	87	91
TCGA-BG-A0M9-10A-01D-A10B-09_UCEC	48	91	92	43	148	102	112	91	117	0	64	85	1	0	0	115	88
TCGA-BG-A0MG-10A-01D-A10B-09_UCEC	51	74	65	38	70	67	102	85	99	0	0	0	0	0	30	61	74
TCGA-BG-A0MK-10A-01D-A19Y-09_UCEC	47	0	0	27	99	85	80	94	105	0	0	0	0	0	31	0	59
TCGA-BG-A0MQ-10A-02D-A10B-09_UCEC	77	0	0	48	140	134	157	109	106	21	79	0	112	97	0	76	105
TCGA-BG-A0MU-10A-02D-A10B-09_UCEC	58	0	1	66	135	136	149	122	147	0	0	0	0	0	0	117	104
TCGA-BG-A0RY-10A-02D-A10B-09_UCEC	65	119	115	0	0	0	118	126	125	0	0	0	0	0	47	74	91
TCGA-BG-A0VV-10A-01D-A122-09_UCEC	116	134	136	60	270	216	206	246	260	0	122	148	0	0	64	146	155
TCGA-BG-A0VW-10A-01D-A122-09_UCEC	103	143	134	56	228	175	177	180	181	0	102	130	0	0	0	150	121
TCGA-BG-A0VX-10A-01D-A122-09_UCEC	82	0	1	106	157	147	160	134	171	0	0	0	0	0	84	0	130
TCGA-BG-A0VZ-10A-02D-A117-09_UCEC	70	118	102	58	178	142	203	157	172	44	48	107	0	0	0	112	125
TCGA-BG-A0W1-10A-01D-A117-09_UCEC	117	145	152	59	147	152	229	222	148	29	156	0	150	153	0	152	154
TCGA-BG-A0YU-10A-01D-A10M-09_UCEC	73	2	0	92	134	138	165	135	0	26	141	108	108	136	0	0	107
TCGA-BG-A0YV-10A-01D-A10M-09_UCEC	87	122	113	55	112	110	117	95	110	0	85	0	111	110	0	105	125
TCGA-BG-A186-10A-01D-A12J-09_UCEC	79	118	165	1	0	1	185	150	201	1	1	1	0	0	87	1	124
TCGA-BG-A187-10A-01D-A12J-09_UCEC	83	0	0	111	241	188	230	185	109	34	163	101	113	114	44	0	116
TCGA-BG-A18A-10A-01D-A12J-09_UCEC	85	0	0	80	166	186	184	197	130	28	117	136	1	120	0	106	138
TCGA-BG-A18B-10A-01D-A12J-09_UCEC	79	0	1	72	171	169	193	147	147	28	108	1	125	109	0	120	123
TCGA-BG-A18C-10A-01D-A12J-09_UCEC	100	128	122	59	137	139	188	199	228	1	0	0	0	1	98	0	136
TCGA-BG-A220-10A-01D-A159-09_UCEC	53	0	0	23	100	94	85	77	85	0	0	0	0	0	27	41	71
TCGA-BG-A221-10A-01D-A159-09_UCEC	53	65	60	17	63	64	89	85	72	10	56	2	59	54	28	0	65
TCGA-BG-A222-10A-01D-A159-09_UCEC	56	1	1	34	81	87	99	80	95	0	1	2	0	1	0	108	69
TCGA-BG-A2AE-10A-01D-A16D-09_UCEC	66	105	89	46	85	102	165	125	107	32	71	0	98	94	0	79	109
TCGA-BG-A2L7-10A-01D-A18P-09_UCEC	54	94	93	0	83	90	98	87	120	0	72	82	6	2	51	1	88
TCGA-BG-A3PP-10A-01D-A22A-09_UCEC	51	55	63	17	114	90	91	96	117	0	36	55	0	1	0	98	76
TCGA-BH-A0AV-10A-01D-A110-09_BRCA	80	127	174	1	121	119	183	188	244	0	103	0	118	0	48	89	141
TCGA-BH-A0B0-10A-01D-A110-09_BRCA	67	143	111	53	116	108	128	90	134	0	93	1	107	111	0	105	130
TCGA-BH-A0B6-10A-01D-A19Y-09_BRCA	44	50	30	16	45	38	77	95	55	9	29	0	40	44	0	34	76
TCGA-BH-A0B7-10A-01D-A110-09_BRCA	110	0	1	122	182	153	167	213	201	0	0	2	0	1	0	244	105
TCGA-BH-A0BC-10A-01D-A099-09_BRCA	74	113	122	48	121	111	166	138	170	0	0	0	0	0	57	90	103
TCGA-BH-A0BG-10A-01D-A110-09_BRCA	54	11	8	60	10	89	108	94	89	0	5	0	2	5	0	53	79
TCGA-BH-A0BL-10A-01D-A110-09_BRCA	122	122	127	58	125	128	188	235	127	23	134	0	132	125	0	121	129
TCGA-BH-A0BO-10A-01D-A12B-09_BRCA	126	172	173	64	333	262	295	234	298	0	115	197	0	1	82	142	190
TCGA-BH-A0BP-10A-01D-A110-09_BRCA	112	138	138	59	262	255	246	246	248	0	139	172	0	0	70	165	164
TCGA-BH-A0BQ-10A-01D-A110-09_BRCA	68	100	132	49	111	94	156	182	112	24	121	1	130	96	0	90	110
TCGA-BH-A0BR-10A-01D-A110-09_BRCA	66	1	0	56	126	123	133	114	135	0	2	0	1	1	0	125	87
TCGA-BH-A0BW-10A-01D-A110-09_BRCA	92	9	7	137	276	209	229	160	246	0	1	9	0	0	46	82	152
TCGA-BH-A0C1-10A-01D-A12B-09_BRCA	102	146	136	61	142	152	200	164	145	33	125	0	144	139	0	123	160
TCGA-BH-A0C7-10A-01D-A110-09_BRCA	71	117	120	40	204	173	166	132	104	27	112	167	0	121	52	0	115
TCGA-BH-A0DE-10A-02D-A110-09_BRCA	55	0	0	68	112	101	110	80	123	0	1	0	0	0	0	81	86
TCGA-BH-A0DH-10A-01D-A099-09_BRCA	57	97	96	41	89	81	136	153	117	0	0	0	0	0	48	79	85
TCGA-BH-A0DL-10A-01D-A110-09_BRCA	91	145	144	53	150	140	225	192	130	29	128	1	128	140	62	0	137
TCGA-BH-A0DQ-10A-01D-A099-09_BRCA	60	76	91	48	79	73	118	94	112	0	0	0	0	0	0	112	92
TCGA-BH-A0DX-10A-02D-A110-09_BRCA	114	152	150	57	290	257	241	169	239	0	129	170	1	0	0	238	147
TCGA-BH-A0E9-10A-01D-A110-09_BRCA	75	0	0	44	123	136	159	101	146	0	0	0	0	0	0	117	101
TCGA-BH-A0EA-10A-01D-A110-09_BRCA	97	170	179	68	274	225	243	190	241	1	130	166	0	2	107	6	185
TCGA-BH-A0EI-10A-01D-A110-09_BRCA	69	0	0	64	138	132	146	183	189	0	0	0	0	0	47	91	118
TCGA-BH-A0H5-10A-01D-A110-09_BRCA	66	23	24	79	138	131	176	114	176	0	0	0	0	0	0	114	118
TCGA-BH-A0HI-10A-01D-A099-09_BRCA	59	102	115	44	198	141	170	143	105	26	157	117	106	98	0	92	102
TCGA-BH-A0HN-10A-01D-A099-09_BRCA	67	0	0	82	118	115	135	129	102	20	72	0	109	92	47	0	97
TCGA-BH-A0HP-10A-01D-A099-09_BRCA	61	0	0	87	113	115	116	135	143	0	0	0	0	0	0	143	81

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BH-A0RX-10A-01D-A099-09_BRCA	52	83	77	36	68	82	133	119	87	21	78	1	89	79	0	58	91
TCGA-BH-A0W4-10A-01D-A10G-09_BRCA	37	81	92	26	103	90	123	64	67	25	58	62	71	68	0	37	82
TCGA-BH-A0W5-10A-01D-A117-09_BRCA	69	0	0	51	110	105	125	118	93	18	88	0	92	82	0	76	87
TCGA-BH-A0W7-10A-01D-A110-09_BRCA	75	125	122	40	224	158	187	152	174	0	71	122	0	0	36	87	115
TCGA-BH-A0WA-10A-01D-A117-09_BRCA	73	113	113	46	104	106	132	123	108	21	85	0	107	104	0	102	98
TCGA-BH-A18G-10A-01D-A12B-09_BRCA	115	228	222	1	248	245	257	245	167	34	285	325	1	163	0	134	182
TCGA-BH-A18H-10A-01D-A12B-09_BRCA	96	128	127	53	220	152	184	180	166	0	94	118	0	0	59	100	117
TCGA-BH-A18I-10A-01D-A12B-09_BRCA	70	1	0	91	205	151	180	151	118	21	95	104	0	117	0	90	123
TCGA-BH-A201-10A-01D-A14K-09_BRCA	89	137	176	71	145	138	232	174	125	44	170	0	190	154	0	109	125
TCGA-BH-A202-10A-01D-A14K-09_BRCA	70	0	2	89	141	136	150	139	138	0	0	0	0	1	0	180	86
TCGA-BH-A28O-10A-01D-A22A-09_BRCA	47	5	3	23	111	99	109	119	96	9	35	46	1	1	0	87	72
TCGA-BH-A28Q-10A-01D-A16D-09_BRCA	57	0	0	56	121	108	110	87	103	1	0	1	0	0	0	87	100
TCGA-BH-A2L8-10A-01D-A18P-09_BRCA	48	2	0	60	105	92	97	94	123	0	0	0	0	0	0	96	70
TCGA-BH-A42T-10A-01D-A243-09_BRCA	35	39	28	10	83	67	65	65	79	0	28	38	0	0	35	1	52
TCGA-BH-A42U-10A-01D-A243-09_BRCA	53	3	3	29	110	95	82	90	120	1	4	0	1	1	41	42	77
TCGA-BH-A42V-10A-01D-A243-09_BRCA	39	3	3	19	58	68	70	59	89	0	2	4	0	3	18	33	59
TCGA-BH-A5IZ-10A-01D-A27P-09_BRCA	39	56	49	13	85	52	78	66	107	0	30	55	1	0	21	44	68
TCGA-BH-A5J0-10A-01D-A27P-09_BRCA	56	58	47	14	62	102	75	79	88	0	1	3	0	1	48	2	73
TCGA-BI-A0VR-10A-01D-A10S-08_CESC	92	0	0	82	93	83	83	116	90	0	1	0	0	1	31	64	107
TCGA-BI-A0VS-10A-01D-A10S-08_CESC	109	73	68	42	129	96	89	100	110	0	44	80	0	1	0	128	115
TCGA-BI-A20A-10A-01D-A14W-08_CESC	89	0	0	61	86	94	90	113	95	0	1	2	0	2	25	51	111
TCGA-BJ-A0YZ-10A-01D-A10S-08_THCA	108	0	1	83	105	100	91	119	86	0	0	0	2	2	0	146	119
TCGA-BJ-A0Z0-10A-01D-A10S-08_THCA	96	70	72	44	133	95	84	98	80	18	73	77	67	81	0	76	116
TCGA-BJ-A0Z2-10A-01D-A10S-08_THCA	140	0	0	80	92	91	85	118	109	0	0	0	1	1	35	81	113
TCGA-BJ-A0Z3-10A-01D-A13W-08_THCA	163	113	109	67	205	174	136	160	109	26	95	176	0	122	0	82	214
TCGA-BJ-A0Z9-10A-01D-A10S-08_THCA	101	68	75	42	127	89	94	114	94	0	57	74	1	1	0	142	117
TCGA-BJ-A0ZA-10A-02D-A10S-08_THCA	139	0	1	52	100	100	81	90	77	13	46	3	70	79	0	72	112
TCGA-BJ-A0ZB-10A-01D-A10S-08_THCA	103	72	78	43	77	77	63	62	83	0	59	0	69	78	0	66	99
TCGA-BJ-A0ZC-10A-01D-A13W-08_THCA	173	2	3	98	193	169	170	146	195	0	1	1	1	0	48	88	224
TCGA-BJ-A0ZE-10A-01D-A10S-08_THCA	103	0	2	76	104	90	100	94	115	0	0	0	0	0	0	94	105
TCGA-BJ-A0ZF-10A-01D-A10S-08_THCA	97	90	92	0	2	0	87	111	96	0	0	1	0	1	32	78	105
TCGA-BJ-A0ZG-10A-01D-A10S-08_THCA	116	0	3	83	102	88	93	90	82	19	54	0	66	79	0	80	127
TCGA-BJ-A0ZH-10A-01D-A10S-08_THCA	101	0	1	74	129	96	82	122	71	17	49	0	61	75	0	79	107
TCGA-BJ-A0ZJ-10A-01D-A10S-08_THCA	136	1	0	60	92	90	88	128	79	20	55	0	73	71	0	72	121
TCGA-BJ-A18Y-10A-01D-A13W-08_THCA	171	99	114	61	105	106	144	142	199	0	0	0	0	1	43	80	203
TCGA-BJ-A18Z-10A-01D-A13W-08_THCA	166	101	99	68	127	114	113	96	120	0	51	0	102	131	0	98	245
TCGA-BJ-A190-10A-01D-A13W-08_THCA	197	97	103	68	101	98	173	151	173	0	1	0	0	3	35	80	208
TCGA-BJ-A191-10A-01D-A13W-08_THCA	209	146	165	0	200	191	162	131	2	39	152	221	84	194	0	3	220
TCGA-BJ-A192-10A-01D-A13W-08_THCA	167	0	1	108	160	148	133	132	162	0	0	0	0	0	0	131	191
TCGA-BJ-A28R-10A-01D-A16O-08_THCA	113	0	1	62	88	100	106	126	72	21	63	0	68	85	0	73	127
TCGA-BJ-A28S-10A-01D-A19M-08_THCA	84	62	59	43	68	57	82	73	0	16	67	1	69	97	0	0	101
TCGA-BJ-A28T-10A-01D-A16O-08_THCA	116	79	80	57	82	71	96	141	128	0	0	0	0	0	33	78	121
TCGA-BJ-A28V-10A-01D-A19M-08_THCA	105	59	74	48	159	130	130	152	120	13	68	98	0	1	27	54	117
TCGA-BJ-A28W-10A-01D-A17V-08_THCA	93	59	62	49	114	84	86	101	76	15	75	73	58	68	0	69	89
TCGA-BJ-A28X-10A-01D-A22D-08_THCA	89	71	72	0	75	69	83	108	76	11	43	64	0	0	0	128	89
TCGA-BJ-A28Z-10A-01D-A16O-08_THCA	106	76	80	54	127	94	90	126	75	18	79	74	68	76	0	72	95
TCGA-BJ-A290-10A-01D-A17V-08_THCA	98	86	96	3	77	64	78	94	67	13	80	62	63	81	0	57	107
TCGA-BJ-A2N7-10A-01D-A18F-08_THCA	95	0	0	55	84	95	86	101	109	0	0	0	0	1	0	106	106
TCGA-BJ-A2N8-10A-01D-A18F-08_THCA	87	0	0	89	94	84	82	105	69	18	44	0	60	69	24	0	113
TCGA-BJ-A2N9-10A-01D-A18F-08_THCA	93	55	66	37	62	62	81	75	78	0	0	0	0	0	0	82	98
TCGA-BJ-A2NA-10A-01D-A19M-08_THCA	113	101	103	8	129	108	132	107	65	23	90	103	60	84	0	63	132
TCGA-BJ-A2P4-10A-01D-A18F-08_THCA	97	0	0	85	94	97	79	89	79	10	44	0	67	69	0	60	107
TCGA-BJ-A3EZ-10A-01D-A202-08_THCA	89	0	0	80	91	81	71	109	109	0	0	0	0	0	0	80	101
TCGA-BJ-A3F0-10A-01D-A202-08_THCA	81	58	68	48	70	56	79	96	103	0	0	0	0	1	33	56	96
TCGA-BJ-A3PR-10A-01D-A21Z-08_THCA	127	64	67	55	78	73	87	97	97	0	1	0	0	0	27	64	107
TCGA-BJ-A3PT-10A-01D-A21Z-08_THCA	94	65	69	49	74	73	93	97	95	0	0	0	0	0	28	70	99
TCGA-BJ-A3PU-10A-01D-A21Z-08_THCA	88	69	71	49	77	75	86	110	95	0	0	2	0	1	34	67	106
TCGA-BJ-A45C-10A-01D-A23U-08_THCA	141	80	75	49	126	119	132	101	136	0	46	0	70	0	0	62	117
TCGA-BJ-A45D-10A-01D-A23U-08_THCA	72	45	58	38	93	65	72	77	68	0	38	50	0	0	0	70	74
TCGA-BJ-A45E-10A-01D-A23U-08_THCA	61	43	42	29	72	70	69	71	8	21	74	45	57	65	0	3	75
TCGA-BJ-A45F-10A-01D-A23U-08_THCA	149	147	149	0	122	98	138	148	171	1	58	88	0	0	44	80	187
TCGA-BJ-A45G-10A-01D-A23U-08_THCA	84	61	67	37	110	83	72	82	64	15	69	81	1	68	0	67	86
TCGA-BJ-A45H-10A-01D-A23U-08_THCA	213	88	107	78	114	103	157	135	102	21	74	0	80	113	0	85	209
TCGA-BJ-A45I-10A-01D-A23U-08_THCA	94	3	2	51	89	76	77	99	88	0	0	0	0	1	0	80	95
TCGA-BJ-A45J-10A-01D-A23U-08_THCA	75	53	58	32	61	60	73	89	82	1	0	5	0	4	0	87	80
TCGA-BJ-A45K-10A-01D-A23U-08_THCA	69	0	0	42	63	70	58	84	66	0	0	0	0	0	0	95	79
TCGA-BJ-A4O8-10A-01D-A25A-08_THCA	67	56	60	41	57	49	68	82	81	0	1	3	0	0	25	50	75
TCGA-BJ-A4O9-10A-01D-A25A-08_THCA	65	0	1	38	47	61	52	79	45	9	41	1	39	35	0	53	70
TCGA-BK-A0CA-10A-02D-A272-09_UCEC	82	1	4	49	121	130	150	155	117	15	91	0	93	93	0	83	107
TCGA-BK-A0CC-10A-02D-A272-09_UCEC	28	4	3	18	70	73	80	105	86	0	0	0	1	1	24	37	69
TCGA-BK-A139-10A-01D-A272-09_UCEC	76	0	0	65	122	124	148	211	185	0	3	0	2	0	63	98	121
TCGA-BK-A13B-10A-01D-A22A-09_UCEC	44	0	63	17	94	90	91	90	114	0	33	0	66	0	33	44	88
TCGA-BK-A13C-10A-01D-A122-09_UCEC	109	0	1	117	249	255	247	255	305	0	0	0	0	1	58	140	174
TCGA-BK-A26L-10A-01D-A16D-09_UCEC	73	112	107	0	0	0	114	132	112	0	0	0	0	0	40	60	93
TCGA-BK-A4ZD-10A-01D-A27P-09_UCEC	60	60	1	13	60	59	50	64	56	0	40	0	63	52	0	51	66
TCGA-BK-A56F-10A-01D-A27P-09_UCEC	66	0	0	34	93	104	89	101	110	0	1	0	0	0	43	58	77
TCGA-BL-A0C8-10A-01D-A10S-08_BLCA	97	0	1	89	110	92	95	124	97	1	0	0	0	0	0	150	108
TCGA-BL-A13I-10A-01D-A271-08_BLCA	82	0	0	42	72	74	72	103	93	0	0	0	0	2	0	94	81
TCGA-BL-A13J-10A-01D-A271-08_BLCA	80	0	0	68	73	77	71	92	69	0	0	0	0	1	0	102	88
TCGA-BL-A5ZZ-10A-01D-A30H-08_BLCA	181	107	109	75	117	129	154	142	185	0	0	0	0	0	71	0	196
TCGA-BM-6198-10A-01D-1733-10_READ	81	73	40	1	75	81	96	59	2	21	63	35	67	64	0	0	97
TCGA-BR-6452-10A-01D-1800-08_STAD	120	1	1	83	107	64	73	50	65	0	1	0	0	67	0	61	102
TCGA-BR-6455-10A-01D-1800-08_STAD	98	70	88	50	74	73	100	93	84	27	80	2	84	81	0	64	109
TCGA-BR-6456-10A-01D-1800-08_STAD	99	71	66	47	85	68	96	101	106	1	1	5	3	1	0	122	107
TCGA-BR-6457-10A-01D-1800-08_STAD	102	73	73	51	116	86	86	112	89	1	54	75	0	0	0	124	103
TCGA-BR-6458-10A-01D-1800-08_STAD	96	0	3	68	86	89	87	118	74	14	51	0	65	71	0	66	110
TCGA-BR-6563-10A-01D-2053-08_STAD	85	56	62	44	116	84	88	85	69	17	56	77	0	64	28	0	89
TCGA-BR-6564-10A-01D-1882-08_STAD	127	0	0	93	112	96	105	111	115	0	0	0	0	0	35	81	149
TCGA-BR-6565-10A-01D-1800-08_STAD	130	61	76	49	77	72	92	110	98	0	0	0	1	2	30	62	107
TCGA-BR-6566-10A-01D-1800-08_STAD	85	69	93	50	79	69	94	113	101	13	58	0	68	0	0	91	105
TCGA-BR-6705-10A-01D-1882-08_STAD	108	1	0	93	112	99	107	101	125	2	0	1	2	4	0	89	142
TCGA-BR-6706-10A-01D-1882-08_STAD	101	73	89	55	86	86	103	103	92	0	0	0	0	0	0	105	132
TCGA-BR-6707-10A-01D-1882-08_STAD	119	107	97	0	82	85	77	63	74	0	85	82	64	83	0	79	120
TCGA-BR-6709-10A-01D-1882-08_STAD	133	68	76	57	77	84	89	125	125	0	0	0	0	0	0	98	133
TCGA-BR-6710-10A-01D-1882-08_STAD	106	70	72	47	127	103	96	120	111	0	52	85	0	0	0	141	120
TCGA-BR-6801-10A-01D-1882-08_STAD	127	77	92	51	89	85	109	151	127	0	0	3	0	1	38	69	132

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BR-6802-10A-01D-1882-08_STAD	100	67	82	51	76	0	73	80	2	17	59	0	63	101	0	1	86
TCGA-BR-6803-10A-01D-1882-08_STAD	112	0	0	100	112	102	102	106	82	17	55	0	66	81	0	62	135
TCGA-BR-6852-10A-01D-1882-08_STAD	124	72	89	57	156	105	101	105	74	22	82	113	0	91	0	73	146
TCGA-BR-7196-10A-01D-2053-08_STAD	92	75	83	0	67	63	84	65	85	0	40	57	0	0	0	72	93
TCGA-BR-7197-10A-01D-2201-08_STAD	121	91	79	54	86	80	118	91	79	21	61	98	0	84	0	77	130
TCGA-BR-7703-10A-01D-2053-08_STAD	104	59	54	44	65	61	76	78	97	1	0	2	0	2	0	70	89
TCGA-BR-7704-10A-01D-2053-08_STAD	80	65	58	39	68	67	78	85	68	11	34	63	0	71	0	60	97
TCGA-BR-7707-10A-01D-2053-08_STAD	86	76	75	1	6	6	73	82	106	0	1	1	0	0	26	61	89
TCGA-BR-7715-10A-01D-2053-08_STAD	81	59	53	46	122	87	79	68	77	0	37	65	0	1	0	117	99
TCGA-BR-7716-10A-01D-2053-08_STAD	77	56	52	45	63	72	85	71	92	0	0	0	0	0	0	67	101
TCGA-BR-7717-10A-01D-2053-08_STAD	79	0	0	79	87	84	79	78	58	16	39	0	48	54	0	52	99
TCGA-BR-7722-10A-01D-2201-08_STAD	92	66	58	57	80	74	100	90	115	0	0	1	0	1	0	89	127
TCGA-BR-7723-10A-01D-2053-08_STAD	84	61	71	45	66	59	98	76	63	22	61	0	62	76	0	60	102
TCGA-BR-7851-10A-01D-2201-08_STAD	113	65	66	59	134	104	96	104	125	0	43	63	0	1	28	59	134
TCGA-BR-7901-10A-01D-2201-08_STAD	130	62	64	60	80	76	77	57	90	0	46	1	53	82	0	60	151
TCGA-BR-7957-10A-01D-2201-08_STAD	116	52	68	55	120	102	97	91	94	0	35	74	0	0	30	68	121
TCGA-BR-7958-10A-01D-2340-08_STAD	102	79	78	57	99	0	84	71	0	24	55	0	73	104	0	0	94
TCGA-BR-7959-10A-01D-2340-08_STAD	134	1	0	115	135	105	125	114	136	0	0	0	0	2	0	96	133
TCGA-BR-8058-10A-01D-2340-08_STAD	67	44	43	38	77	64	62	57	77	0	25	40	0	0	0	60	72
TCGA-BR-8059-10A-01D-2340-08_STAD	120	0	0	67	115	107	93	122	136	0	0	0	0	0	0	133	115
TCGA-BR-8060-10A-01D-2340-08_STAD	111	0	0	100	111	103	94	126	80	19	51	0	80	81	0	71	120
TCGA-BR-8077-10A-01D-2340-08_STAD	113	0	0	61	132	99	101	92	83	18	64	78	0	88	0	66	129
TCGA-BR-8078-10A-01D-2340-08_STAD	114	0	0	96	105	74	70	69	70	0	0	0	0	88	0	70	94
TCGA-BR-8080-10A-01D-2340-08_STAD	132	0	1	90	105	101	101	97	85	14	33	0	64	69	26	0	117
TCGA-BR-8081-10A-01D-2340-08_STAD	112	1	0	68	115	99	97	126	117	0	0	1	0	0	0	146	122
TCGA-BR-8284-10A-01D-2340-08_STAD	107	0	1	101	127	107	108	120	83	21	52	0	79	92	0	77	116
TCGA-BR-8285-10A-01D-2340-08_STAD	90	85	85	1	0	0	84	107	74	16	57	0	59	75	38	0	107
TCGA-BR-8286-10A-01D-2340-08_STAD	162	74	83	58	138	104	103	133	126	0	60	83	0	2	41	70	121
TCGA-BR-8289-10A-01D-2340-08_STAD	90	13	7	77	86	70	64	59	78	0	7	11	0	63	0	41	81
TCGA-BR-8291-10A-01D-2340-08_STAD	58	41	36	25	45	43	52	67	52	7	21	0	33	42	0	21	71
TCGA-BR-8295-10A-01D-2340-08_STAD	156	0	0	66	116	76	98	102	123	0	0	1	0	0	0	97	122
TCGA-BR-8296-10A-01D-2340-08_STAD	122	0	1	69	113	106	109	120	135	0	0	0	0	0	32	78	125
TCGA-BR-8297-10A-01D-2340-08_STAD	64	0	0	58	67	40	40	32	38	0	0	0	0	45	0	40	55
TCGA-BR-8360-10A-01D-2340-08_STAD	110	93	95	0	110	116	112	149	142	0	88	119	0	0	38	77	115
TCGA-BR-8361-10A-01D-2340-08_STAD	112	78	0	54	91	77	113	85	92	22	53	0	71	90	0	75	124
TCGA-BR-8362-10A-01D-2340-08_STAD	78	58	55	44	107	74	76	93	93	0	30	61	1	2	25	58	89
TCGA-BR-8363-10A-01D-2341-08_STAD	127	70	69	39	121	82	81	112	103	0	52	57	0	0	29	63	100
TCGA-BR-8364-10A-01D-2341-08_STAD	61	53	62	0	74	64	58	62	0	16	69	69	28	69	0	0	78
TCGA-BR-8365-10A-01D-2341-08_STAD	108	98	113	0	113	101	97	107	83	22	89	123	5	86	0	68	121
TCGA-BR-8366-10A-01D-2341-08_STAD	119	78	93	59	89	83	94	96	82	19	64	0	69	81	0	79	121
TCGA-BR-8367-10A-01D-2341-08_STAD	98	75	80	55	120	104	97	95	116	0	50	78	0	1	0	141	117
TCGA-BR-8368-10A-01D-2341-08_STAD	113	0	0	69	103	112	90	128	136	0	0	0	0	0	0	102	123
TCGA-BR-8369-10A-01D-2341-08_STAD	84	0	0	76	92	84	77	72	112	0	0	0	0	0	0	80	97
TCGA-BR-8370-10A-01D-2341-08_STAD	111	77	77	58	136	78	80	67	84	0	56	80	0	95	37	0	103
TCGA-BR-8371-10A-01D-2341-08_STAD	125	77	78	65	163	107	109	125	136	0	63	85	0	0	34	80	130
TCGA-BR-8372-10A-01D-2341-08_STAD	119	0	1	96	134	100	104	117	107	0	0	0	1	1	0	146	123
TCGA-BR-8373-10A-01D-2341-08_STAD	110	0	0	89	109	107	96	98	102	0	0	0	0	0	0	92	181
TCGA-BR-8380-10A-01D-2341-08_STAD	75	0	1	40	67	51	52	51	43	11	25	0	33	41	0	42	71
TCGA-BR-8381-10A-01D-2394-08_STAD	82	0	0	82	96	69	61	64	71	1	0	0	0	71	0	59	82
TCGA-BR-8382-10A-01D-2394-08_STAD	84	70	69	42	112	79	80	113	102	0	47	61	2	4	0	101	95
TCGA-BR-8384-10A-01D-2394-08_STAD	79	69	71	46	113	84	78	79	62	17	62	78	1	62	0	63	90
TCGA-BR-8483-10A-01D-2394-08_STAD	94	71	73	45	121	89	86	147	113	18	46	65	0	4	34	64	102
TCGA-BR-8484-10A-01D-2394-08_STAD	96	5	0	77	85	79	86	92	84	0	1	0	2	4	0	88	100
TCGA-BR-8485-10A-01D-2394-08_STAD	90	67	74	55	112	87	87	107	65	19	78	80	1	79	0	61	92
TCGA-BR-8486-10A-01D-2394-08_STAD	79	73	72	47	120	77	57	64	81	0	45	69	0	77	28	4	75
TCGA-BR-8487-10A-01D-2394-08_STAD	88	87	85	3	7	4	84	81	83	0	4	3	0	1	35	3	96
TCGA-BR-8588-10A-01D-2394-08_STAD	87	58	73	41	98	71	74	80	81	0	48	61	0	0	0	117	90
TCGA-BR-8589-10A-01D-2394-08_STAD	92	81	88	0	74	72	86	107	111	0	59	81	2	3	0	118	88
TCGA-BR-8590-10A-01D-2394-08_STAD	89	65	71	50	69	68	86	94	108	0	1	0	1	3	0	121	100
TCGA-BR-8591-10A-01D-2394-08_STAD	80	6	5	51	87	90	79	128	111	1	9	6	1	5	39	72	114
TCGA-BR-8592-10A-01D-2394-08_STAD	59	31	33	26	40	45	59	43	31	10	28	0	32	37	0	31	71
TCGA-BR-8676-10A-01D-2394-08_STAD	88	72	71	44	109	81	84	100	108	0	54	66	0	2	29	55	98
TCGA-BR-8677-10A-01D-2394-08_STAD	89	68	74	55	78	69	83	95	71	21	51	1	64	74	31	3	100
TCGA-BR-8678-10A-01D-2394-08_STAD	94	3	2	85	86	87	78	89	88	0	4	8	1	5	29	63	103
TCGA-BR-8679-10A-01D-2394-08_STAD	84	66	70	53	78	72	85	98	89	0	1	0	0	0	26	69	93
TCGA-BR-8680-10A-01D-2394-08_STAD	92	66	76	58	120	94	95	135	83	21	53	74	9	16	32	62	89
TCGA-BR-8682-10A-01D-2394-08_STAD	93	73	77	44	78	77	81	90	12	27	65	6	80	87	0	8	104
TCGA-BR-8683-10A-01D-2394-08_STAD	93	73	73	43	75	75	141	82	110	0	0	0	1	0	0	83	101
TCGA-BR-8686-10A-01D-2394-08_STAD	67	57	56	1	0	0	63	52	71	0	0	0	0	0	0	53	81
TCGA-BR-8687-10A-01D-2394-08_STAD	90	0	0	54	86	88	89	121	110	17	1	0	0	0	33	67	91
TCGA-BR-8690-10A-01D-2394-08_STAD	79	72	76	44	71	64	80	90	62	22	49	0	61	72	0	77	101
TCGA-BR-A44T-10A-01D-A24F-08_STAD	89	49	50	40	58	49	63	74	73	0	0	0	0	1	28	54	83
TCGA-BR-A44U-10A-01D-A24F-08_STAD	146	67	70	46	75	75	86	84	101	0	0	0	0	0	40	0	95
TCGA-BR-A452-10A-01D-A25E-08_STAD	92	0	0	49	84	88	85	97	110	0	0	0	0	1	29	54	99
TCGA-BR-A453-10A-01D-A24F-08_STAD	75	0	3	75	84	76	71	83	97	0	0	0	0	0	0	113	93
TCGA-BR-A4CQ-10A-01D-A25E-08_STAD	89	66	65	44	111	88	83	75	73	14	72	87	0	69	0	69	87
TCGA-BR-A4CR-10A-01D-A24F-08_STAD	88	62	65	38	113	81	79	100	65	14	68	80	0	69	0	60	97
TCGA-BR-A4CS-10A-01D-A24F-08_STAD	84	63	67	38	62	0	62	64	68	0	0	0	0	67	33	1	79
TCGA-BR-A4IU-10A-01D-A25E-08_STAD	62	49	46	34	53	42	63	65	67	0	0	0	0	0	19	46	76
TCGA-BR-A4IV-10A-01D-A25E-08_STAD	88	65	88	42	78	72	84	123	70	33	66	0	70	58	33	5	115
TCGA-BR-A4IY-10A-01D-A25E-08_STAD	120	0	0	63	95	86	90	92	80	16	42	0	51	66	29	5	95
TCGA-BR-A4IZ-10A-01D-A25E-08_STAD	96	62	64	47	65	70	85	117	120	0	0	0	0	0	27	65	109
TCGA-BR-A4J1-10A-01D-A25E-08_STAD	97	61	59	43	70	61	80	97	73	15	48	0	58	70	28	2	103
TCGA-BR-A4J2-10A-01D-A25E-08_STAD	82	84	77	0	74	75	90	122	86	19	53	69	0	1	38	0	103
TCGA-BR-A4J4-10A-01D-A25E-08_STAD	95	0	1	49	88	87	84	109	77	17	62	68	0	78	36	0	87
TCGA-BR-A4J5-10A-01D-A25E-08_STAD	120	0	0	75	84	77	83	103	101	0	0	0	0	1	23	61	98
TCGA-BR-A4J6-10A-01D-A25E-08_STAD	86	58	63	44	67	73	83	78	95	0	3	0	1	0	0	73	114
TCGA-BR-A4J7-10A-01D-A25E-08_STAD	89	60	65	41	71	62	66	65	1	17	63	1	77	80	0	0	99
TCGA-BR-A4J8-10A-01D-A25E-08_STAD	93	4	8	48	93	84	91	82	111	0	0	0	0	0	0	82	103
TCGA-BR-A4J9-10A-01D-A25E-08_STAD	91	67	67	48	110	93	93	88	70	19	72	85	8	69	29	7	106
TCGA-BR-A4PD-10A-01D-A25E-08_STAD	79	81	85	1	79	87	82	97	71	11	83	93	0	62	32	0	100
TCGA-BR-A4PE-10A-01D-A25E-08_STAD	114	77	77	53	75	83	105	98	102	0	0	0	0	1	45	0	125
TCGA-BR-A4PF-10A-01D-A25E-08_STAD	85	0	0	56	83	75	78	82	54	14	55	60	0	65	0	65	84
TCGA-BR-A4QI-10A-01D-A25E-08_STAD	95	95	86	5	6	9	88	104	119	0	0	0	0	1	0	134	108
TCGA-BR-A4QL-10A-01D-A25E-08_STAD	80	74	79	2	70	71	62	58	8	15	86	82	51	86	0	7	104
TCGA-BR-A4QM-10A-01D-A25E-08_STAD	73	49	46	39	70	46	74	81	80	0	0	0	0	0	0	87	71

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BS-A0T9-10C-01D-A12J-09_UCEC	96	0	1	72	209	184	190	169	222	0	0	0	0	3	93	0	145
TCGA-BS-A0TA-10A-01D-A10B-09_UCEC	21	66	57	22	42	49	83	39	47	18	28	0	43	45	0	24	53
TCGA-BS-A0TC-10A-01D-A10B-09_UCEC	27	41	36	32	52	55	54	43	72	0	24	41	0	0	10	25	40
TCGA-BS-A0TD-10A-01D-A10B-09_UCEC	32	0	0	62	87	75	97	65	102	0	0	0	0	0	19	28	64
TCGA-BS-A0TE-10A-01D-A10B-09_UCEC	57	0	0	51	111	104	102	75	112	0	0	0	0	0	0	84	73
TCGA-BS-A0TG-10A-01D-A14K-09_UCEC	92	0	1	84	214	188	176	176	223	0	0	0	0	0	0	175	129
TCGA-BS-A0TI-10A-01D-A10B-09_UCEC	73	157	146	63	117	128	125	74	1	33	177	0	220	237	0	0	170
TCGA-BS-A0TJ-10A-01D-A10B-09_UCEC	97	1	0	111	214	212	245	170	229	0	1	0	0	0	0	180	184
TCGA-BS-A0U5-10A-01D-A10G-09_UCEC	71	0	1	61	155	149	161	127	0	30	131	1	150	144	0	0	114
TCGA-BS-A0U7-10A-01D-A10B-09_UCEC	64	92	109	40	161	128	114	153	156	0	61	87	0	0	0	151	94
TCGA-BS-A0U8-10A-01D-A10B-09_UCEC	81	87	84	36	152	120	122	139	94	18	138	92	85	94	0	81	82
TCGA-BS-A0U9-10A-01D-A10M-09_UCEC	65	129	124	52	198	157	168	147	130	0	86	127	1	0	48	100	124
TCGA-BS-A0UA-10A-01D-A122-09_UCEC	98	130	133	61	127	134	176	165	200	0	0	0	0	0	64	125	123
TCGA-BS-A0UF-10A-01D-A10B-09_UCEC	60	0	0	51	108	110	119	107	0	22	89	107	0	103	0	0	76
TCGA-BS-A0UJ-10A-01D-A127-09_UCEC	39	0	0	56	71	75	94	45	98	0	0	0	0	0	16	32	63
TCGA-BS-A0UL-10A-01D-A10G-09_UCEC	87	0	0	71	168	160	154	130	117	23	93	105	0	105	0	90	114
TCGA-BS-A0UM-10A-01D-A10B-09_UCEC	114	189	204	0	235	218	204	202	0	49	357	297	141	199	0	0	146
TCGA-BS-A0UT-10A-01D-A10B-09_UCEC	48	0	1	55	120	107	120	68	127	0	0	0	0	0	35	0	87
TCGA-BS-A0UV-10A-01D-A10B-09_UCEC	100	0	0	74	282	223	219	279	200	26	143	136	1	0	0	247	130
TCGA-BS-A0V4-10A-01D-A14G-09_UCEC	36	3	0	21	92	73	81	79	63	9	41	0	59	64	0	34	68
TCGA-BS-A0V6-10A-01D-A122-09_UCEC	111	0	0	122	192	169	210	220	221	0	0	0	0	1	69	115	153
TCGA-BS-A0V7-10A-01D-A122-09_UCEC	96	7	4	119	198	182	199	202	214	0	2	0	2	3	70	130	140
TCGA-BS-A0V8-10A-01D-A122-09_UCEC	107	0	1	82	182	171	181	239	211	0	0	0	0	1	73	125	132
TCGA-BS-A0VI-10A-01D-A14G-09_UCEC	52	86	84	1	5	2	97	98	69	13	46	54	0	66	32	0	64
TCGA-BS-A0WQ-10A-01D-A10G-09_UCEC	75	132	133	52	124	111	166	144	177	0	0	0	0	0	45	85	126
TCGA-BT-A0S7-10A-01D-A10S-08_BLCA	114	75	0	42	122	99	79	93	88	21	51	0	65	80	0	77	119
TCGA-BT-A0YX-10A-01D-A10S-08_BLCA	116	0	0	88	120	92	90	134	125	0	0	0	0	2	0	129	109
TCGA-BT-A2LB-10A-01D-A18F-08_BLCA	114	1	1	89	87	84	98	117	117	0	0	0	0	0	28	73	112
TCGA-BT-A2LD-10A-01D-A20D-08_BLCA	101	0	1	61	88	89	83	91	79	15	44	0	61	77	31	0	109
TCGA-BT-A3PH-10A-01D-A21Z-08_BLCA	94	84	86	2	91	75	85	78	109	0	64	85	0	0	0	85	113
TCGA-BT-A3PJ-10A-01D-A21Z-08_BLCA	99	84	83	1	87	95	86	112	72	16	83	86	62	83	0	70	105
TCGA-BT-A3PK-10A-01D-A21Z-08_BLCA	90	62	64	43	110	92	80	97	101	0	43	65	0	0	0	109	98
TCGA-BT-A42B-10A-01D-A23K-08_BLCA	152	136	166	2	119	110	152	143	170	3	87	111	1	2	44	100	185
TCGA-BT-A42C-10A-01D-A23K-08_BLCA	149	135	137	0	0	0	142	160	93	17	49	0	75	119	37	0	163
TCGA-BT-A42E-10A-01D-A23U-08_BLCA	70	70	65	1	70	55	71	76	89	0	38	50	0	0	28	50	91
TCGA-BT-A42F-10A-01D-A23U-08_BLCA	131	69	72	63	84	85	112	113	142	0	1	0	0	1	0	106	138
TCGA-BW-A5NO-10A-01D-A27I-10_LIHC	105	0	0	71	42	81	83	54	67	0	17	0	56	79	31	0	96
TCGA-BW-A5NP-10A-01D-A27I-10_LIHC	77	0	0	58	86	106	124	87	53	7	29	71	0	66	28	0	96
TCGA-BW-A5NQ-10A-01D-A27I-10_LIHC	65	1	0	75	96	98	101	104	98	0	0	0	0	0	23	45	77
TCGA-C4-A0EZ-10A-01D-A10S-08_BLCA	140	1	0	78	105	96	89	130	72	12	56	0	69	87	0	69	116
TCGA-C4-A0F0-10A-01D-A10S-08_BLCA	115	67	78	44	130	93	87	124	120	0	51	74	1	3	37	76	105
TCGA-C4-A0F1-10A-01D-A10S-08_BLCA	97	88	90	1	0	2	84	127	102	0	0	0	1	0	35	74	116
TCGA-C4-A0F6-10A-01D-A10S-08_BLCA	105	72	73	49	83	77	98	117	100	0	0	0	0	1	34	68	103
TCGA-C4-A0F7-10A-01D-A10S-08_BLCA	99	1	1	55	104	103	87	115	103	1	0	1	0	2	0	92	108
TCGA-C5-A0TN-10B-01D-A14W-08_CESC	88	1	1	59	90	83	92	83	95	0	1	1	0	1	28	1	114
TCGA-C5-A1BE-10A-01D-A13W-08_CESC	166	96	111	69	117	115	159	137	2	41	105	108	94	177	0	1	196
TCGA-C5-A1BF-10A-01D-A13W-08_CESC	182	1	1	98	184	167	168	160	195	0	0	3	0	2	29	81	221
TCGA-C5-A1BI-10A-01D-A13W-08_CESC	174	97	92	64	114	108	156	141	105	28	44	1	80	125	49	0	212
TCGA-C5-A1BJ-10A-01D-A13W-08_CESC	179	147	164	1	130	134	168	162	143	23	93	123	89	123	42	0	252
TCGA-C5-A1BK-10A-01D-A13W-08_CESC	186	98	100	68	217	159	182	143	176	0	42	116	0	0	57	0	207
TCGA-C5-A1BL-10A-01D-A13W-08_CESC	172	0	1	131	160	158	148	145	179	0	1	0	0	3	43	95	224
TCGA-C5-A1BM-10A-01D-A13W-08_CESC	166	102	103	59	115	123	146	134	190	0	0	1	0	1	54	1	192
TCGA-C5-A1BN-10A-01D-A14W-08_CESC	94	69	62	38	69	65	91	74	60	15	34	1	52	74	0	51	105
TCGA-C5-A1BQ-10A-01D-A20U-09_CESC	44	56	62	18	105	90	88	104	104	0	54	63	1	1	0	125	77
TCGA-C5-A1M5-10A-01D-A13W-08_CESC	166	142	148	2	1	1	161	165	184	1	0	1	0	0	32	72	191
TCGA-C5-A1M6-10A-01D-A13W-08_CESC	175	0	0	88	164	153	140	110	146	0	0	0	0	1	0	138	199
TCGA-C5-A1M7-10A-01D-A13W-08_CESC	153	80	82	57	93	96	142	110	143	0	0	1	0	1	61	0	196
TCGA-C5-A1M8-10A-01D-A13W-08_CESC	150	79	90	58	108	103	150	142	115	11	43	90	2	110	29	0	177
TCGA-C5-A1M9-10A-01D-A13W-08_CESC	157	0	3	92	158	160	149	122	134	0	0	0	0	1	0	183	198
TCGA-C5-A1ME-10A-01D-A13W-08_CESC	167	2	0	113	172	163	137	145	124	17	60	0	73	103	37	2	206
TCGA-C5-A1MF-10A-01D-A13W-08_CESC	183	2	1	136	186	176	151	184	204	0	0	0	0	2	0	161	231
TCGA-C5-A1MH-10A-01D-A14W-08_CESC	103	1	0	59	92	93	89	84	109	0	0	0	1	0	0	76	111
TCGA-C5-A1MI-10A-01D-A14W-08_CESC	96	61	58	42	71	63	84	91	64	19	42	0	59	70	0	48	103
TCGA-C5-A1MJ-10A-01D-A14W-08_CESC	85	64	68	43	121	92	99	120	111	15	47	55	0	0	25	64	94
TCGA-C5-A1MK-10A-01D-A14W-08_CESC	116	1	0	71	97	87	82	108	98	0	0	1	2	2	26	61	97
TCGA-C5-A1ML-10A-01D-A14W-08_CESC	82	0	0	67	100	88	87	96	69	17	39	0	49	76	0	61	96
TCGA-C5-A1MN-10A-01D-A14W-08_CESC	120	0	1	70	97	91	85	80	72	15	41	0	63	76	0	51	108
TCGA-C5-A1MP-10A-01D-A14W-08_CESC	92	67	65	40	109	89	78	70	100	0	31	62	0	1	32	0	102
TCGA-C5-A1MQ-10A-01D-A14W-08_CESC	80	58	51	46	103	85	82	78	0	18	71	89	53	93	0	0	114
TCGA-C5-A2LS-10A-01D-A22X-09_CESC	64	0	1	37	109	111	97	111	130	0	1	1	0	0	0	124	94
TCGA-C5-A2LT-10A-01D-A18J-09_CESC	41	41	39	5	46	42	72	65	86	0	0	0	0	0	0	67	72
TCGA-C5-A2LV-10A-01D-A18J-09_CESC	44	0	0	28	91	103	97	70	104	0	0	0	0	1	46	3	77
TCGA-C5-A2LX-10A-01D-A18J-09_CESC	51	0	0	31	78	92	93	76	96	0	0	0	0	1	0	88	73
TCGA-C5-A2LY-10A-01D-A18J-09_CESC	46	1	0	50	92	101	121	105	117	0	0	0	0	0	0	121	77
TCGA-C5-A2LZ-10B-01D-A20U-09_CESC	58	86	98	0	75	69	104	124	79	22	96	63	80	68	33	6	68
TCGA-C5-A2M1-10A-01D-A18J-09_CESC	34	0	2	24	69	72	71	51	55	7	27	0	45	35	0	33	54
TCGA-C5-A2M2-10A-01D-A18J-09_CESC	52	62	54	22	106	78	79	76	2	16	90	91	52	85	0	1	73
TCGA-C5-A3HD-10A-01D-A20U-09_CESC	57	5	2	37	93	83	94	80	97	0	4	0	0	6	34	51	81
TCGA-C5-A3HF-10A-01D-A20U-09_CESC	72	64	67	20	66	65	110	113	156	1	1	6	7	2	38	72	82
TCGA-C5-A3HL-10A-01D-A20U-09_CESC	58	5	11	44	112	105	107	122	98	13	51	1	63	76	0	59	91
TCGA-C8-A12K-10A-01D-A110-09_BRCA	63	0	0	60	119	120	123	129	160	0	0	0	0	0	41	77	94
TCGA-C8-A12L-10A-01D-A110-09_BRCA	78	0	2	80	207	189	208	151	229	0	0	0	0	1	79	0	130
TCGA-C8-A12M-10A-01D-A110-09_BRCA	63	234	213	0	0	1	233	127	0	54	115	220	0	207	0	0	156
TCGA-C8-A12N-10A-01D-A110-09_BRCA	81	0	0	67	145	148	163	148	205	0	0	0	0	1	56	97	96
TCGA-C8-A12O-10A-01D-A110-09_BRCA	62	0	0	53	120	130	125	103	128	0	0	1	0	0	63	0	85
TCGA-C8-A12P-10A-01D-A110-09_BRCA	97	0	0	143	241	277	285	198	183	37	136	0	172	148	66	0	196
TCGA-C8-A12Q-10A-01D-A110-09_BRCA	72	0	3	64	166	146	154	143	112	28	93	0	112	114	45	0	110
TCGA-C8-A12T-10A-01D-A110-09_BRCA	84	0	0	62	148	148	150	139	172	0	0	0	0	0	67	1	97
TCGA-C8-A12U-10A-01D-A110-09_BRCA	73	107	119	42	206	158	148	94	151	0	68	126	0	0	42	74	105
TCGA-C8-A12V-10A-01D-A110-09_BRCA	63	0	0	56	121	135	126	123	135	0	0	0	0	0	63	0	87
TCGA-C8-A12W-10A-01D-A110-09_BRCA	71	93	87	43	85	70	115	105	145	0	0	0	0	0	53	0	94
TCGA-C8-A12X-10A-01D-A110-09_BRCA	40	0	0	39	45	78	73	60	96	0	0	0	0	0	19	41	68
TCGA-C8-A12Y-10A-01D-A12B-09_BRCA	112	0	2	90	222	250	281	209	258	0	0	0	0	2	0	271	138
TCGA-C8-A12Z-10A-01D-A110-09_BRCA	74	0	0	66	133	139	158	140	212	0	0	1	0	0	0	173	115
TCGA-C8-A130-10A-01D-A110-09_BRCA	57	0	0	88	136	124	134	107	143	0	0	0	0	0	56	0	98
TCGA-C8-A131-10A-01D-A110-09_BRCA	77	0	0	81	183	157	176	167	175	0	0	0	0	0	62	103	126

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-C8-A132-10A-01D-A110-09_BRCA	97	0	0	71	171	177	184	184	184	0	0	0	0	1	63	102	133
TCGA-C8-A133-10A-01D-A12B-09_BRCA	126	1	2	140	347	312	348	311	215	49	177	1	184	206	0	176	237
TCGA-C8-A134-10A-01D-A110-09_BRCA	85	103	114	53	197	152	151	132	152	0	106	109	1	1	78	0	101
TCGA-C8-A135-10A-02D-A110-09_BRCA	126	0	2	92	206	230	206	190	189	1	0	0	0	1	137	0	145
TCGA-C8-A137-10A-02D-A110-09_BRCA	70	0	1	54	118	126	126	114	131	0	0	1	0	0	71	0	90
TCGA-C8-A138-10A-01D-A110-09_BRCA	36	75	69	28	90	80	79	83	55	17	83	59	61	44	19	0	66
TCGA-C8-A1HE-10A-01D-A13O-09_BRCA	29	0	0	39	72	76	90	63	69	0	0	0	0	0	0	66	52
TCGA-C8-A1HF-10A-01D-A135-09_BRCA	130	1	0	69	239	246	246	245	289	0	0	1	0	0	0	307	181
TCGA-C8-A1HG-10A-01D-A135-09_BRCA	120	148	149	78	172	158	259	262	260	0	0	1	0	1	80	155	176
TCGA-C8-A1HI-10A-01D-A135-09_BRCA	138	0	1	114	252	272	269	255	249	0	0	0	0	1	92	158	172
TCGA-C8-A1HJ-10A-01D-A13O-09_BRCA	30	0	0	39	86	73	91	72	52	17	31	66	0	53	0	33	62
TCGA-C8-A1HK-10A-01D-A13O-09_BRCA	34	45	36	20	41	43	81	59	73	0	0	0	0	0	0	49	58
TCGA-C8-A1HL-10A-01D-A135-09_BRCA	153	0	1	144	267	227	296	244	167	30	160	0	170	159	74	0	181
TCGA-C8-A1HM-10A-01D-A135-09_BRCA	117	0	0	154	221	235	240	256	151	24	139	172	0	161	91	0	172
TCGA-C8-A1HN-10A-01D-A135-09_BRCA	95	0	1	70	172	163	207	169	214	1	0	0	1	0	98	0	112
TCGA-C8-A1HO-10A-01D-A188-09_BRCA	53	0	1	54	109	118	135	143	120	0	0	1	0	0	40	73	79
TCGA-C8-A26V-10A-01D-A16D-09_BRCA	45	0	0	62	147	115	137	145	95	16	39	58	0	1	47	1	67
TCGA-C8-A26W-10A-01D-A16D-09_BRCA	82	1	0	85	113	125	121	125	105	26	70	0	92	81	42	3	96
TCGA-C8-A26X-10A-01D-A16D-09_BRCA	36	63	66	34	106	85	97	80	80	18	42	65	0	0	44	0	70
TCGA-C8-A26Y-10A-01D-A16D-09_BRCA	45	0	0	42	74	68	74	71	80	0	0	0	0	1	24	50	52
TCGA-C8-A26Z-10A-01D-A16D-09_BRCA	47	70	67	32	68	71	94	81	97	0	0	0	1	0	28	51	66
TCGA-C8-A273-10A-01D-A16D-09_BRCA	42	73	54	33	106	92	102	100	52	18	66	90	0	56	26	0	67
TCGA-C8-A274-10A-01D-A16D-09_BRCA	38	0	0	40	80	64	83	75	57	11	44	0	41	49	0	44	60
TCGA-C8-A275-10A-01D-A16D-09_BRCA	56	66	69	34	66	60	107	98	72	17	42	60	0	74	0	56	83
TCGA-C8-A278-10A-01D-A167-09_BRCA	46	0	0	32	78	78	85	69	46	17	50	0	54	53	0	37	70
TCGA-C8-A27A-10B-01D-A167-09_BRCA	42	1	0	32	67	64	72	68	52	17	31	0	37	42	21	0	50
TCGA-C8-A27B-10A-01D-A167-09_BRCA	34	1	0	15	47	43	66	62	57	1	0	1	0	0	34	1	44
TCGA-C8-A3M7-10A-01D-A21Q-09_BRCA	39	8	12	20	61	72	73	51	68	10	27	47	0	41	0	33	60
TCGA-C8-A3M8-10A-01D-A20S-09_BRCA	39	5	0	26	66	75	80	59	55	9	35	3	27	36	0	35	56
TCGA-C9-A47Z-10A-01D-A24F-08_HNSC	123	1	0	71	81	86	84	82	67	22	54	0	66	73	0	53	89
TCGA-C9-A480-10A-01D-A24F-08_HNSC	80	0	1	48	75	69	71	65	71	0	0	0	0	0	34	1	78
TCGA-CA-5796-10A-01D-1650-10_COAD	76	0	0	63	112	88	132	43	71	13	29	46	0	80	12	0	103
TCGA-CA-5797-10A-01D-1650-10_COAD	93	0	1	46	97	102	127	76	71	22	35	45	0	50	14	0	128
TCGA-CA-6716-10A-01D-1835-10_COAD	38	17	24	22	46	52	55	39	57	0	12	17	0	0	14	0	67
TCGA-CA-6719-10A-01D-1835-10_COAD	37	0	0	21	39	43	51	22	47	0	0	0	0	0	10	1	47
TCGA-CC-5258-10A-01D-A12Z-10_LIHC	71	0	0	52	93	71	131	63	107	0	0	0	0	1	18	0	127
TCGA-CC-5259-10A-01D-A20W-10_LIHC	82	0	0	43	83	84	109	74	96	0	1	1	0	0	39	0	90
TCGA-CC-5260-10B-01D-A12Z-10_LIHC	94	0	2	60	101	118	133	61	137	0	0	0	0	1	8	35	149
TCGA-CC-5261-10A-01D-A12Z-10_LIHC	76	0	0	55	83	102	112	68	73	16	36	2	41	52	0	21	124
TCGA-CC-5262-10B-01D-A12Z-10_LIHC	97	0	2	51	103	83	104	60	0	18	58	56	46	98	0	0	104
TCGA-CC-5263-10B-01D-A12Z-10_LIHC	84	0	0	49	92	80	115	57	136	0	0	0	0	0	8	33	123
TCGA-CC-5264-10A-01D-A12Z-10_LIHC	75	0	0	34	85	104	115	52	67	15	18	0	26	53	0	23	113
TCGA-CC-A123-10A-01D-A12Z-10_LIHC	91	0	0	49	92	85	112	53	59	13	28	0	38	42	0	32	127
TCGA-CC-A1HT-10A-01D-A12Z-10_LIHC	95	0	0	47	102	91	110	69	112	0	0	0	0	0	32	0	134
TCGA-CC-A3M9-10A-01D-A20W-10_LIHC	93	0	0	48	80	102	133	80	136	0	0	2	0	0	19	39	103
TCGA-CC-A3MA-10A-01D-A20W-10_LIHC	86	0	2	48	79	91	109	69	61	8	24	0	49	55	0	43	77
TCGA-CC-A3MB-10A-01D-A20W-10_LIHC	80	0	0	34	91	89	94	65	110	0	0	0	0	0	33	0	89
TCGA-CC-A3MC-10A-01D-A22F-10_LIHC	53	38	29	18	30	23	38	22	48	0	17	0	29	30	12	0	64
TCGA-CC-A5UC-10A-01D-A28X-10_LIHC	72	0	0	44	73	93	96	74	77	0	0	0	0	2	18	44	67
TCGA-CC-A5UD-10A-01D-A28X-10_LIHC	68	0	0	52	62	85	89	88	56	4	32	51	0	51	30	1	59
TCGA-CC-A5UE-10A-01D-A28X-10_LIHC	62	0	0	42	82	103	89	80	71	0	0	0	0	0	28	43	69
TCGA-CD-5798-10A-01D-1600-08_STAD	138	81	81	45	98	99	125	106	92	26	45	89	1	99	0	75	139
TCGA-CD-5799-10A-01D-1600-08_STAD	124	1	4	98	121	121	108	104	109	0	0	0	1	0	46	0	118
TCGA-CD-5800-10A-01D-1600-08_STAD	148	0	0	68	124	116	103	95	114	0	0	0	1	1	42	1	127
TCGA-CD-5801-10A-01D-1600-08_STAD	125	79	83	52	94	87	117	130	129	0	0	0	0	0	36	79	128
TCGA-CD-5802-10A-01D-1600-08_STAD	126	0	2	66	128	132	98	145	143	0	1	1	0	3	36	86	144
TCGA-CD-5803-10A-01D-1600-08_STAD	133	0	2	63	137	122	106	133	147	0	0	3	1	0	33	75	133
TCGA-CD-5804-10A-01D-2053-08_STAD	75	56	54	39	72	66	78	74	100	0	0	0	0	0	33	60	97
TCGA-CD-5813-10A-01D-1600-08_STAD	128	0	0	58	129	128	103	124	117	0	0	0	1	1	35	62	127
TCGA-CD-8524-10A-01D-2341-08_STAD	112	0	0	95	98	108	89	110	87	20	54	0	73	86	38	0	138
TCGA-CD-8525-10A-01D-2341-08_STAD	150	0	1	104	110	102	104	124	128	0	0	0	0	1	36	76	129
TCGA-CD-8526-10A-01D-2341-08_STAD	108	71	73	58	83	76	99	101	88	24	44	0	73	85	0	70	115
TCGA-CD-8527-10A-01D-2341-08_STAD	101	0	1	62	104	95	98	89	72	20	55	0	66	86	0	67	113
TCGA-CD-8528-10A-01D-2341-08_STAD	117	0	0	96	106	111	93	107	87	19	59	0	62	80	41	0	127
TCGA-CD-8529-10A-01D-2341-08_STAD	113	71	85	53	84	80	99	90	121	0	0	0	0	1	32	84	128
TCGA-CD-8530-10A-01D-2341-08_STAD	107	0	2	71	106	112	97	108	85	21	59	75	0	92	40	0	109
TCGA-CD-8531-10A-01D-2341-08_STAD	112	0	0	68	95	103	106	115	90	22	58	78	0	86	28	0	148
TCGA-CD-8532-10A-01D-2341-08_STAD	100	0	2	69	107	96	97	84	113	0	0	0	0	1	41	0	119
TCGA-CD-8533-10A-01D-2341-08_STAD	65	40	45	30	50	44	40	43	5	13	52	64	4	69	0	1	82
TCGA-CD-8534-10A-01D-2341-08_STAD	128	0	0	78	89	87	89	99	70	15	37	0	53	68	0	38	113
TCGA-CD-8535-10A-01D-2341-08_STAD	85	52	54	48	93	93	70	77	93	0	38	54	1	16	0	12	99
TCGA-CD-8536-10A-01D-2341-08_STAD	101	0	0	64	102	102	104	112	108	0	0	0	0	0	30	69	125
TCGA-CD-A486-10A-01D-A24F-08_STAD	73	54	50	38	96	72	75	81	62	17	66	62	52	64	0	53	84
TCGA-CD-A487-10A-01D-A24F-08_STAD	89	1	0	46	92	74	82	78	94	0	3	6	0	2	36	1	98
TCGA-CD-A489-10A-01D-A24F-08_STAD	71	0	0	43	79	69	73	80	70	14	41	56	0	60	27	2	77
TCGA-CD-A48A-10A-01D-A24F-08_STAD	81	1	1	46	80	72	73	87	76	0	0	0	0	1	31	64	89
TCGA-CD-A48C-10A-01D-A24F-08_STAD	88	0	0	49	83	89	77	109	81	0	2	4	0	5	29	60	82
TCGA-CD-A4MG-10A-01D-A25E-08_STAD	91	0	0	58	99	83	80	99	87	0	0	0	0	0	29	57	92
TCGA-CD-A4MH-10A-01D-A25E-08_STAD	91	59	57	38	102	78	83	85	70	11	66	61	47	70	25	3	95
TCGA-CD-A4MI-10A-01D-A25E-08_STAD	111	1	0	57	89	85	88	90	92	1	3	0	1	2	38	0	96
TCGA-CD-A4MJ-10A-01D-A25E-08_STAD	116	5	3	52	93	87	83	103	111	0	1	0	4	4	35	63	104
TCGA-CE-A13K-10A-01D-A10S-08_THCA	98	68	74	45	76	78	85	109	1	22	70	0	87	99	0	0	110
TCGA-CE-A27D-10A-01D-A17V-08_THCA	99	0	0	56	91	92	93	85	98	0	0	0	0	0	33	0	96
TCGA-CE-A3MD-10A-01D-A20C-08_THCA	92	79	87	1	74	73	93	107	100	18	41	66	1	0	32	68	104
TCGA-CE-A3ME-10A-01D-A20C-08_THCA	136	2	2	90	87	99	85	102	81	23	55	0	57	78	29	0	109
TCGA-CE-A481-10A-01D-A23U-08_THCA	70	54	55	30	52	53	54	50	5	11	53	51	34	64	0	3	86
TCGA-CE-A482-10A-01D-A23U-08_THCA	75	1	0	49	77	77	87	90	98	0	0	0	0	1	28	57	83
TCGA-CE-A483-10A-01D-A23U-08_THCA	185	82	82	60	97	117	137	105	94	16	61	104	2	106	0	71	175
TCGA-CE-A484-10A-01D-A23U-08_THCA	70	0	2	42	73	70	64	65	69	0	2	5	1	2	30	0	82
TCGA-CE-A485-10A-01D-A23U-08_THCA	72	43	44	32	69	63	73	90	54	17	55	65	0	48	25	0	80
TCGA-CF-A1HR-10A-01D-A13W-08_BLCA	156	0	2	105	169	173	136	130	174	0	0	1	2	0	52	0	196
TCGA-CF-A1HS-10A-01D-A13W-08_BLCA	149	149	160	1	2	1	160	142	197	0	0	0	0	1	36	84	215
TCGA-CF-A27C-10A-01D-A16O-08_BLCA	104	0	1	67	115	97	99	86	112	0	0	0	0	1	43	0	124
TCGA-CF-A3MF-10A-01D-A21A-08_BLCA	91	0	1	62	82	74	78	86	74	16	43	56	0	64	0	62	93
TCGA-CF-A3MG-10A-01D-A20D-08_BLCA	124	2	3	83	91	89	96	101	119	0	0	1	0	1	31	71	91
TCGA-CF-A3MH-10A-01D-A20D-08_BLCA	125	0	0	71	91	89	79	92	68	19	50	67	0	68	29	0	121

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CF-A3MI-10A-01D-A20D-08_BLCA	116	0	1	84	83	94	84	71	67	17	42	0	38	70	0	58	99
TCGA-CF-A47S-10A-01D-A23U-08_BLCA	73	52	63	35	55	62	73	75	67	14	37	3	54	56	26	1	76
TCGA-CF-A47T-10A-01D-A23U-08_BLCA	77	0	0	49	76	71	75	86	84	0	0	1	0	1	27	54	80
TCGA-CF-A47V-10A-01D-A23U-08_BLCA	82	57	64	42	64	64	68	85	66	13	44	0	57	74	28	2	88
TCGA-CF-A47W-10A-01D-A23U-08_BLCA	152	96	90	69	98	92	133	155	141	0	0	0	0	0	39	68	160
TCGA-CF-A47X-10A-01D-A23U-08_BLCA	69	66	55	35	91	70	80	92	95	12	39	47	3	4	23	49	76
TCGA-CF-A47Y-10A-01D-A23U-08_BLCA	156	0	1	99	153	153	142	130	158	0	0	0	0	0	64	0	174
TCGA-CF-A5U8-10A-01D-A289-08_BLCA	113	76	71	59	79	70	116	99	122	0	0	0	0	0	0	141	130
TCGA-CF-A5UA-10A-01D-A289-08_BLCA	111	0	1	82	112	125	97	105	125	0	0	0	0	0	45	0	152
TCGA-CG-4300-10A-01D-1158-08_STAD	144	75	89	48	109	90	125	115	142	0	0	2	0	0	0	119	148
TCGA-CG-4301-10A-01D-1158-08_STAD	163	88	100	54	164	151	140	125	148	1	60	111	0	2	34	73	171
TCGA-CG-4304-10A-01D-1158-08_STAD	176	0	2	87	177	141	131	132	153	0	0	0	0	0	0	159	179
TCGA-CG-4305-10A-01D-1158-08_STAD	127	84	90	53	169	130	120	127	84	21	76	75	75	87	0	69	150
TCGA-CG-4306-10A-01D-1158-08_STAD	121	1	0	58	143	136	114	107	83	23	48	0	67	91	0	74	144
TCGA-CG-4436-10A-01D-1158-08_STAD	153	0	4	78	166	143	133	148	92	19	62	1	83	98	0	85	174
TCGA-CG-4437-10A-01D-1800-08_STAD	103	1	0	64	93	75	74	63	80	0	0	0	0	73	0	57	88
TCGA-CG-4438-10A-01D-1158-08_STAD	151	2	1	115	176	157	131	146	137	0	0	1	0	4	0	171	170
TCGA-CG-4440-10A-01D-1158-08_STAD	128	0	1	67	140	140	108	103	145	0	0	2	0	1	0	110	159
TCGA-CG-4441-10A-01D-1800-08_STAD	103	3	1	82	97	96	90	78	76	16	49	1	52	73	0	73	130
TCGA-CG-4442-10A-01D-1158-08_STAD	125	76	75	53	156	138	103	139	147	0	53	100	2	1	30	70	146
TCGA-CG-4443-10A-01D-1158-08_STAD	122	0	0	92	139	142	104	101	135	0	0	0	1	1	0	126	151
TCGA-CG-4444-10A-01D-1158-08_STAD	152	99	121	2	98	105	112	108	129	0	65	98	0	1	50	1	145
TCGA-CG-4449-10A-01D-1158-08_STAD	163	96	100	60	208	169	122	159	133	0	67	134	0	0	0	169	190
TCGA-CG-4455-10A-01D-1158-08_STAD	160	2	4	116	172	129	139	175	119	0	0	0	2	2	0	159	154
TCGA-CG-4460-10A-01D-1158-08_STAD	126	1	1	65	138	125	110	129	132	0	0	0	0	0	0	132	137
TCGA-CG-4462-10A-01D-1158-08_STAD	152	0	0	71	151	138	126	147	144	0	1	0	0	0	0	126	172
TCGA-CG-4465-10A-01D-1158-08_STAD	126	104	112	1	5	2	106	123	102	20	62	0	77	94	36	1	151
TCGA-CG-4466-10A-01D-1158-08_STAD	140	1	1	70	152	124	144	142	171	0	0	0	0	2	0	141	161
TCGA-CG-4469-10A-01D-1158-08_STAD	121	2	1	89	145	138	117	137	97	19	55	0	74	95	0	88	153
TCGA-CG-4472-10A-01D-1158-08_STAD	158	2	4	65	137	139	111	120	86	16	44	0	79	93	0	71	136
TCGA-CG-4474-10A-01D-1158-08_STAD	139	85	89	49	105	84	109	151	151	0	1	3	1	6	0	168	138
TCGA-CG-4475-10A-01D-1158-08_STAD	177	105	129	1	143	155	140	146	105	15	113	241	0	106	36	0	182
TCGA-CG-4476-10A-01D-1158-08_STAD	188	0	1	92	158	136	111	130	142	0	0	0	0	0	33	88	148
TCGA-CG-4477-10A-01D-1158-08_STAD	161	116	127	0	6	1	131	151	133	0	0	0	1	0	0	114	173
TCGA-CG-5716-10A-01D-1800-08_STAD	103	0	1	89	94	96	90	139	163	0	0	0	1	2	28	73	104
TCGA-CG-5717-10A-01D-1600-08_STAD	118	1	1	67	135	127	111	132	133	0	0	0	0	0	33	70	122
TCGA-CG-5718-10A-01D-1600-08_STAD	135	1	2	98	147	126	105	148	97	20	68	2	84	100	0	91	139
TCGA-CG-5719-10A-01D-1600-08_STAD	131	68	85	48	94	0	86	77	94	0	0	0	0	99	0	73	97
TCGA-CH-5737-10A-01D-1576-08_PRAD	138	3	1	73	158	138	113	140	106	23	60	0	73	98	0	75	171
TCGA-CH-5738-10A-01D-1576-08_PRAD	181	108	111	1	142	138	111	154	88	19	90	181	0	103	0	79	147
TCGA-CH-5739-10A-01D-1576-08_PRAD	148	1	3	67	125	127	110	122	124	0	0	1	1	1	0	103	145
TCGA-CH-5740-10A-01D-1576-08_PRAD	114	83	78	46	96	86	99	113	107	28	51	0	73	92	0	88	122
TCGA-CH-5741-10A-01D-1576-08_PRAD	118	1	1	91	121	111	105	131	145	0	0	1	0	1	0	107	118
TCGA-CH-5743-10A-01D-1576-08_PRAD	136	0	0	65	124	123	109	136	127	0	0	0	0	1	0	116	125
TCGA-CH-5744-10A-01D-1576-08_PRAD	128	0	0	64	155	115	105	110	86	22	57	0	70	88	0	78	123
TCGA-CH-5745-10A-01D-1576-08_PRAD	136	1	0	99	139	119	110	110	131	0	2	0	0	1	44	3	140
TCGA-CH-5746-10A-01D-1576-08_PRAD	104	68	78	45	77	72	96	96	75	19	53	0	58	73	0	73	113
TCGA-CH-5748-10A-01D-1576-08_PRAD	135	88	85	56	176	127	116	119	2	28	101	135	81	129	0	4	133
TCGA-CH-5750-10A-01D-1576-08_PRAD	124	2	1	93	112	118	101	127	146	0	0	0	0	1	0	137	128
TCGA-CH-5751-10A-01D-1576-08_PRAD	129	0	1	104	135	131	110	151	151	0	0	0	0	3	0	166	154
TCGA-CH-5752-10A-01D-1576-08_PRAD	144	108	132	1	98	98	118	141	87	22	88	135	0	99	0	87	138
TCGA-CH-5753-10A-01D-1576-08_PRAD	128	0	2	64	116	127	112	156	135	0	0	1	1	0	0	178	141
TCGA-CH-5754-10A-01D-1576-08_PRAD	133	1	1	56	119	102	113	112	101	0	0	0	0	4	0	118	126
TCGA-CH-5788-10A-01D-1576-08_PRAD	129	2	1	72	124	123	115	153	137	1	0	0	2	3	0	157	138
TCGA-CH-5789-10A-01D-1576-08_PRAD	103	75	87	51	132	109	96	146	136	0	48	89	0	3	33	75	121
TCGA-CH-5790-10A-01D-1576-08_PRAD	114	81	79	58	94	93	106	112	122	0	1	0	0	6	0	110	140
TCGA-CH-5791-10A-01D-1576-08_PRAD	152	2	0	71	128	119	116	121	114	0	0	0	0	1	0	116	146
TCGA-CH-5792-10A-01D-1576-08_PRAD	107	2	0	82	124	119	88	132	134	0	0	1	0	0	30	74	128
TCGA-CH-5794-10A-01D-1577-08_PRAD	105	1	1	77	112	95	87	90	83	21	48	2	78	85	0	75	124
TCGA-CI-6621-10A-01D-1826-10_READ	61	0	0	52	43	52	72	50	79	0	0	0	0	0	13	29	67
TCGA-CI-6622-10A-01D-1826-10_READ	55	0	0	43	68	69	75	68	33	21	19	28	22	41	0	23	68
TCGA-CI-6624-10A-01D-1826-10_READ	55	0	0	34	51	48	69	53	66	0	0	0	0	0	0	66	59
TCGA-CK-4947-10A-01D-1650-10_COAD	96	0	1	60	116	92	122	82	74	19	40	0	57	65	0	39	131
TCGA-CK-4952-10A-01D-1719-10_COAD	57	35	29	17	38	28	85	49	45	6	14	0	33	38	0	14	78
TCGA-CK-5912-10A-01D-1650-10_COAD	98	123	118	0	0	0	59	42	76	0	30	0	62	70	0	34	109
TCGA-CK-5913-10A-01D-1650-10_COAD	88	58	62	24	61	50	105	69	114	0	0	0	0	0	11	25	107
TCGA-CK-5915-10A-01D-1650-10_COAD	68	0	1	46	80	79	90	43	50	15	14	0	35	54	0	32	95
TCGA-CK-5916-10A-01D-1650-10_COAD	70	0	0	40	51	43	72	31	89	0	0	0	0	0	0	44	77
TCGA-CL-5917-10A-01D-1657-10_READ	82	73	81	0	45	39	114	41	109	0	21	32	0	0	0	45	92
TCGA-CL-5918-10A-01D-1657-10_READ	79	49	64	26	46	51	73	32	72	0	23	0	35	58	0	28	127
TCGA-CM-4743-10A-01D-1719-10_COAD	106	107	90	44	87	84	98	74	110	0	61	0	90	110	0	54	169
TCGA-CM-4746-10A-01D-1408-10_COAD	34	0	0	34	35	34	36	37	38	0	0	0	0	0	7	19	34
TCGA-CM-4747-10A-01D-1408-10_COAD	49	0	0	25	21	37	49	31	49	0	0	0	0	0	0	30	45
TCGA-CM-4748-10A-01D-1408-10_COAD	34	0	0	22	34	29	44	28	29	7	16	0	13	19	0	20	39
TCGA-CM-4752-10A-01D-1408-10_COAD	38	0	0	31	39	37	37	31	27	9	15	0	19	24	0	29	47
TCGA-CM-5341-10A-01D-1408-10_COAD	43	0	0	22	18	30	32	28	17	3	8	0	15	10	6	0	48
TCGA-CM-5344-10A-01D-1719-10_COAD	125	93	97	45	96	69	199	133	185	0	0	0	1	0	35	47	166
TCGA-CM-5348-10A-01D-1719-10_COAD	109	0	0	82	153	146	157	124	207	0	0	0	0	0	23	55	158
TCGA-CM-5349-10A-01D-1719-10_COAD	121	91	117	60	182	128	176	134	119	18	90	90	78	94	0	49	153
TCGA-CM-5860-10A-01D-1650-10_COAD	91	0	0	65	92	83	116	53	0	23	64	0	81	110	0	0	107
TCGA-CM-5861-10A-01D-1650-10_COAD	76	100	85	0	0	0	105	72	99	0	0	0	0	0	17	39	101
TCGA-CM-5862-10A-01D-1650-10_COAD	57	82	69	0	34	32	82	54	77	0	29	48	0	0	32	0	93
TCGA-CM-5864-10A-01D-1650-10_COAD	60	34	33	14	68	68	83	45	69	0	19	31	0	0	0	49	81
TCGA-CM-5868-10A-01D-1650-10_COAD	48	52	39	0	17	20	49	31	69	0	12	18	0	0	7	13	77
TCGA-CM-6161-10A-01D-1650-10_COAD	76	76	57	39	109	96	97	65	135	0	19	63	0	0	0	58	107
TCGA-CM-6163-10A-01D-1650-10_COAD	71	0	0	20	69	65	80	50	59	11	30	0	41	29	0	24	85
TCGA-CM-6164-10A-01D-1650-10_COAD	88	67	79	36	71	75	122	60	145	0	0	1	0	0	0	60	132
TCGA-CM-6165-10A-01D-1650-10_COAD	81	100	107	0	0	0	106	81	137	0	0	0	0	0	26	0	87
TCGA-CM-6166-10A-01D-1650-10_COAD	93	0	0	47	77	83	95	65	56	12	13	0	43	46	0	26	80
TCGA-CM-6168-10A-01D-1650-10_COAD	73	29	62	23	40	38	41	33	48	0	22	0	26	38	0	24	82
TCGA-CM-6169-10A-01D-1650-10_COAD	80	0	1	35	61	61	86	44	90	0	0	0	0	0	9	26	94
TCGA-CM-6170-10A-01D-1650-10_COAD	101	0	0	61	86	72	107	70	104	0	0	0	0	0	13	23	118
TCGA-CM-6171-10A-01D-1650-10_COAD	86	119	122	0	0	0	116	59	119	0	0	0	0	1	34	0	122
TCGA-CM-6172-10A-01D-1650-10_COAD	82	47	50	34	54	56	105	68	60	21	26	0	40	60	0	25	129
TCGA-CM-6674-10A-01D-1835-10_COAD	57	0	0	41	52	56	65	49	68	0	0	0	0	0	0	49	72
TCGA-CM-6675-10A-01D-1835-10_COAD	62	0	32	26	64	57	63	50	73	0	24	0	29	0	17	23	69

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CM-6676-10A-01D-1835-10_COAD	60	31	36	15	54	65	58	40	69	0	13	32	0	1	0	44	55
TCGA-CM-6677-10A-01D-1835-10_COAD	69	64	75	1	0	0	61	84	72	0	0	0	0	0	0	70	80
TCGA-CM-6678-10A-01D-1835-10_COAD	65	0	1	26	53	57	67	46	44	13	25	0	32	36	0	29	82
TCGA-CM-6679-10A-01D-1835-10_COAD	77	39	50	30	48	49	53	34	66	0	24	0	35	57	0	33	89
TCGA-CN-4723-10A-01D-1434-08_HNSC	99	83	90	1	85	81	94	116	125	0	51	86	1	0	0	137	120
TCGA-CN-4725-10A-01D-1434-08_HNSC	105	0	0	58	115	100	87	90	110	0	0	1	1	1	0	100	116
TCGA-CN-4726-10A-01D-1434-08_HNSC	99	0	0	54	102	97	90	111	114	0	0	0	2	0	0	96	121
TCGA-CN-4727-10A-01D-1434-08_HNSC	95	0	1	88	102	99	94	119	101	0	0	2	1	0	38	86	104
TCGA-CN-4728-10A-01D-1434-08_HNSC	112	75	76	54	147	92	109	122	99	0	62	77	0	2	36	77	120
TCGA-CN-4729-10A-01D-1434-08_HNSC	113	0	0	57	109	106	90	122	87	0	0	1	0	0	0	144	106
TCGA-CN-4730-10A-01D-1434-08_HNSC	110	77	77	46	87	85	99	132	107	0	0	0	0	0	41	78	119
TCGA-CN-4731-10A-01D-1434-08_HNSC	115	77	75	52	137	99	83	129	108	0	44	84	0	0	0	138	109
TCGA-CN-4733-10A-01D-1870-08_HNSC	137	114	116	50	102	78	78	79	88	0	84	113	0	94	35	1	136
TCGA-CN-4734-10A-01D-1434-08_HNSC	124	76	80	49	126	108	93	128	126	0	53	78	0	0	37	79	115
TCGA-CN-4735-10A-01D-1434-08_HNSC	111	70	78	44	141	95	95	87	79	17	69	105	0	76	0	81	130
TCGA-CN-4736-10A-01D-1434-08_HNSC	152	93	105	62	97	97	141	137	169	0	0	0	0	0	42	87	190
TCGA-CN-4737-10A-01D-1434-08_HNSC	110	0	1	92	105	105	95	101	82	21	52	89	1	90	0	81	123
TCGA-CN-4738-10A-01D-1512-08_HNSC	109	69	78	47	79	77	90	114	109	0	0	0	0	0	31	77	106
TCGA-CN-4739-10A-01D-1512-08_HNSC	107	76	75	44	133	93	85	120	105	0	42	77	0	3	37	59	102
TCGA-CN-4740-10A-01D-1434-08_HNSC	101	69	78	43	134	103	83	115	137	0	57	81	0	2	38	71	114
TCGA-CN-4741-10A-01D-1434-08_HNSC	102	90	88	0	1	2	90	118	80	21	63	0	62	84	36	4	127
TCGA-CN-4742-10A-01D-1512-08_HNSC	110	0	0	55	104	103	96	115	85	18	55	1	71	77	26	3	112
TCGA-CN-5355-10A-01D-1434-08_HNSC	108	1	0	56	166	117	134	148	96	0	68	0	93	1	0	66	86
TCGA-CN-5356-10A-01D-1434-08_HNSC	91	0	0	58	96	105	84	107	112	0	0	1	0	0	0	119	107
TCGA-CN-5358-10A-01D-1512-08_HNSC	96	75	74	44	85	71	87	89	105	1	0	1	0	1	0	91	101
TCGA-CN-5359-10A-01D-1434-08_HNSC	113	0	1	88	109	100	101	133	104	23	0	0	0	0	48	3	103
TCGA-CN-5360-10A-01D-1434-08_HNSC	99	72	71	44	78	75	87	102	123	0	0	1	0	0	0	92	106
TCGA-CN-5361-10A-01D-1434-08_HNSC	106	79	80	51	129	96	94	130	132	0	54	90	0	0	0	147	124
TCGA-CN-5363-10A-01D-1434-08_HNSC	94	0	0	50	112	102	94	82	95	0	0	2	0	1	44	1	104
TCGA-CN-5364-10A-01D-1434-08_HNSC	117	2	0	55	111	114	87	97	98	0	0	0	0	0	0	104	104
TCGA-CN-5365-10A-01D-1434-08_HNSC	91	1	3	56	96	90	93	90	4	26	65	0	84	98	0	1	111
TCGA-CN-5366-10A-01D-1434-08_HNSC	105	2	1	79	100	97	91	112	75	21	53	85	1	78	0	72	106
TCGA-CN-5367-10A-01D-1434-08_HNSC	95	2	0	68	96	87	86	93	112	0	1	0	0	0	0	89	111
TCGA-CN-5369-10A-01D-1434-08_HNSC	109	0	2	57	109	86	94	100	90	0	0	0	0	0	0	99	115
TCGA-CN-5370-10A-01D-2013-08_HNSC	95	1	0	62	87	83	89	112	116	0	0	1	0	0	35	57	92
TCGA-CN-5373-10A-01D-1434-08_HNSC	104	0	1	89	103	104	85	93	103	0	0	0	0	0	48	0	99
TCGA-CN-5374-10A-01D-1434-08_HNSC	109	82	84	59	84	80	96	136	121	0	0	0	0	1	39	85	115
TCGA-CN-6010-10A-01D-1683-08_HNSC	91	69	68	43	70	63	96	103	105	0	1	0	0	0	0	79	115
TCGA-CN-6011-10A-01D-1683-08_HNSC	77	62	68	38	65	65	80	94	107	0	1	1	0	0	24	42	108
TCGA-CN-6012-10A-01D-1683-08_HNSC	117	65	68	44	122	102	99	115	122	0	39	68	0	1	23	59	122
TCGA-CN-6013-10A-01D-1683-08_HNSC	95	0	1	54	93	89	85	112	107	0	1	0	1	0	25	52	112
TCGA-CN-6016-10A-01D-1683-08_HNSC	94	58	70	47	111	90	77	93	65	12	50	61	54	70	27	0	111
TCGA-CN-6017-10A-01D-1683-08_HNSC	79	61	74	43	129	98	85	84	116	0	37	68	1	1	0	89	120
TCGA-CN-6018-10A-01D-1683-08_HNSC	94	0	1	57	106	94	83	88	102	1	1	2	0	0	23	51	113
TCGA-CN-6019-10A-01D-1683-08_HNSC	107	1	0	68	92	88	78	91	86	0	0	1	0	0	0	66	116
TCGA-CN-6020-10A-01D-1683-08_HNSC	98	59	77	40	94	94	87	87	117	0	34	61	0	1	28	53	108
TCGA-CN-6021-10A-01D-1683-08_HNSC	115	1	0	63	92	102	80	90	62	18	29	56	0	79	0	45	109
TCGA-CN-6022-10A-01D-1683-08_HNSC	142	0	1	74	106	91	91	96	63	17	45	0	51	83	0	64	130
TCGA-CN-6023-10A-01D-1683-08_HNSC	94	63	59	41	128	84	90	78	91	0	42	62	0	0	19	52	110
TCGA-CN-6024-10A-01D-1683-08_HNSC	92	0	2	66	103	95	91	80	48	17	36	0	61	58	0	53	122
TCGA-CN-6988-10A-01D-1912-08_HNSC	132	1	1	96	107	92	103	91	110	0	0	1	0	0	0	91	121
TCGA-CN-6989-10A-01D-1912-08_HNSC	119	76	92	59	77	89	107	127	131	0	0	0	0	0	30	67	142
TCGA-CN-6992-10A-01D-1912-08_HNSC	148	0	0	73	116	118	110	90	107	0	0	0	0	1	0	97	131
TCGA-CN-6994-10A-01D-1912-08_HNSC	111	72	77	51	134	114	88	91	75	11	75	92	0	88	0	65	135
TCGA-CN-6995-10A-01D-2013-08_HNSC	146	72	79	56	81	93	110	111	116	0	0	0	0	0	38	1	141
TCGA-CN-6996-10A-01D-1912-08_HNSC	111	71	81	52	89	1	77	68	68	0	55	77	1	69	0	57	132
TCGA-CN-6997-10A-01D-2013-08_HNSC	128	75	79	48	77	80	101	108	125	0	0	0	1	1	0	109	125
TCGA-CN-6998-10A-01D-2013-08_HNSC	115	83	92	56	148	111	112	128	123	0	56	82	0	1	29	76	144
TCGA-CN-A497-10A-01D-A24F-08_HNSC	109	58	71	41	63	61	74	109	96	0	1	0	1	3	30	55	82
TCGA-CN-A498-10A-01D-A24F-08_HNSC	72	2	2	44	70	69	68	103	86	0	0	1	0	0	0	114	90
TCGA-CN-A499-10A-01D-A24F-08_HNSC	73	1	1	71	77	79	76	72	50	16	48	6	52	64	0	55	77
TCGA-CN-A49A-10A-01D-A24F-08_HNSC	72	49	65	32	92	76	66	58	43	13	56	65	1	64	0	51	83
TCGA-CN-A49B-10A-01D-A24F-08_HNSC	100	0	0	73	84	82	73	68	80	0	0	0	1	1	32	3	90
TCGA-CN-A49C-10B-01D-A24F-08_HNSC	113	4	1	51	78	79	73	86	99	1	3	1	2	4	0	110	89
TCGA-CN-A63U-10A-01D-A30H-08_HNSC	121	87	92	61	91	95	116	104	138	0	0	0	0	0	0	98	138
TCGA-CN-A63W-10A-01D-A30H-08_HNSC	162	0	0	110	155	160	147	152	180	0	0	0	0	0	0	177	206
TCGA-CN-A63Y-10A-01D-A30H-08_HNSC	165	104	95	67	212	159	159	132	0	37	131	164	82	176	0	0	190
TCGA-CN-A640-10A-01D-A30H-08_HNSC	152	106	98	74	176	142	133	146	160	0	51	100	0	1	42	75	168
TCGA-CN-A641-10A-01D-A30H-08_HNSC	171	0	0	106	169	144	143	118	123	21	49	0	82	110	0	82	185
TCGA-CN-A642-10A-01D-A30H-08_HNSC	173	101	86	63	173	151	138	126	0	28	139	93	122	159	0	1	194
TCGA-CQ-5323-10A-01D-1683-08_HNSC	98	63	66	37	115	103	77	80	108	0	39	58	0	1	0	78	124
TCGA-CQ-5324-10A-01D-1683-08_HNSC	119	62	63	34	128	114	97	103	67	22	78	80	57	70	0	56	100
TCGA-CQ-5325-10A-01D-1683-08_HNSC	90	67	74	44	70	65	90	72	111	0	0	0	0	0	36	2	102
TCGA-CQ-5326-10A-01D-1870-08_HNSC	154	0	1	81	123	136	120	115	101	23	53	0	73	86	0	78	154
TCGA-CQ-5327-10A-01D-1683-08_HNSC	91	2	2	50	100	106	89	93	88	0	0	0	0	0	23	57	115
TCGA-CQ-5329-10A-01D-1683-08_HNSC	93	56	64	34	67	0	52	47	74	0	0	0	0	61	0	49	87
TCGA-CQ-5330-10A-01D-1683-08_HNSC	92	51	65	39	69	63	90	84	92	0	0	0	0	1	0	84	108
TCGA-CQ-5331-10A-01D-1870-08_HNSC	151	0	0	103	109	95	93	113	124	0	0	1	0	1	33	66	137
TCGA-CQ-5332-10A-01D-1683-08_HNSC	104	68	61	0	116	94	83	114	110	0	44	76	1	0	26	61	127
TCGA-CQ-5333-10A-01D-2394-08_HNSC	78	58	51	34	94	74	76	80	69	12	61	63	50	66	0	61	90
TCGA-CQ-5334-10A-01D-1683-08_HNSC	109	3	2	35	57	65	62	41	54	0	1	2	0	1	0	49	105
TCGA-CQ-6218-10A-01D-1912-08_HNSC	90	70	74	51	73	62	83	85	81	13	59	3	68	73	0	62	105
TCGA-CQ-6219-10A-01D-1912-08_HNSC	179	0	0	88	138	143	129	138	137	0	0	0	0	0	22	69	174
TCGA-CQ-6220-10A-01D-1912-08_HNSC	97	0	0	84	122	98	84	109	66	17	52	1	61	74	0	63	97
TCGA-CQ-6221-10A-01D-2078-08_HNSC	81	0	0	64	78	72	78	81	104	0	2	0	0	2	21	55	93
TCGA-CQ-6222-10A-01D-1912-08_HNSC	101	71	71	50	83	72	92	108	123	0	0	0	0	0	0	73	102
TCGA-CQ-6223-10A-01D-1912-08_HNSC	86	68	71	45	120	82	77	80	64	19	76	71	58	74	0	65	96
TCGA-CQ-6224-10A-01D-1912-08_HNSC	95	0	1	83	94	80	80	107	115	0	0	0	1	0	0	117	106
TCGA-CQ-6225-10A-01D-1912-08_HNSC	101	0	1	94	97	88	96	75	74	19	48	70	0	75	0	56	107
TCGA-CQ-6227-10A-01D-1912-08_HNSC	101	0	1	86	99	92	90	81	64	22	53	67	0	81	0	64	103
TCGA-CQ-6228-10A-01D-1912-08_HNSC	126	78	74	45	71	64	97	104	83	18	56	71	0	70	28	0	109
TCGA-CQ-6229-10A-01D-1912-08_HNSC	94	89	94	1	72	66	67	73	0	20	98	71	85	91	0	0	117
TCGA-CQ-7063-10A-01D-2394-08_HNSC	84	1	0	69	87	90	75	77	70	14	43	0	58	67	0	59	90
TCGA-CQ-7064-10A-01D-2394-08_HNSC	86	60	67	48	112	77	76	79	69	19	81	62	59	72	0	71	88
TCGA-CQ-7065-10A-01D-2078-08_HNSC	85	50	46	42	68	52	94	67	66	14	26	1	42	47	0	41	108
TCGA-CQ-7067-10A-01D-2229-08_HNSC	104	67	68	45	117	99	96	79	73	14	64	77	56	73	0	43	118

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CQ-7068-10A-01D-2078-08_HNSC	117	70	59	49	125	89	85	78	73	18	71	66	57	65	0	64	97
TCGA-CQ-7069-10A-01D-2394-08_HNSC	91	73	75	46	112	80	87	84	4	28	86	84	79	100	0	2	97
TCGA-CQ-7071-10A-01D-A30H-08_HNSC	152	0	0	89	141	145	138	124	163	0	0	0	0	0	0	143	173
TCGA-CQ-7072-10A-01D-A30H-08_HNSC	129	95	92	47	109	100	74	79	86	0	64	90	0	98	0	69	171
TCGA-CQ-A4C6-10A-01D-A25E-08_HNSC	101	0	0	63	110	83	82	84	3	23	66	50	71	75	0	1	82
TCGA-CQ-A4C7-10A-01D-A25E-08_HNSC	79	77	79	2	93	76	70	82	92	2	51	73	0	0	20	60	89
TCGA-CQ-A4C9-10A-01D-A25E-08_HNSC	79	59	65	43	101	73	81	68	64	15	55	76	2	68	0	50	89
TCGA-CQ-A4CA-10A-01D-A25E-08_HNSC	87	60	57	39	100	77	71	85	52	11	61	58	51	60	0	57	89
TCGA-CQ-A4CB-10A-01D-A25E-08_HNSC	68	5	4	46	82	69	73	83	97	0	1	6	0	0	0	99	92
TCGA-CQ-A4CD-10A-01D-A25E-08_HNSC	74	56	63	34	57	56	68	88	98	0	1	1	1	1	0	106	95
TCGA-CQ-A4CE-10A-01D-A25Y-08_HNSC	79	61	54	28	93	68	67	66	67	13	59	73	1	54	0	36	88
TCGA-CQ-A4CG-10A-01D-A25Y-08_HNSC	109	1	0	81	93	85	78	78	75	16	47	65	0	65	0	71	106
TCGA-CQ-A4CH-10A-01D-A25Y-08_HNSC	102	60	80	40	123	82	82	80	103	0	42	62	2	2	37	2	93
TCGA-CQ-A4CI-10A-01D-A25Y-08_HNSC	103	94	95	4	77	66	84	109	73	20	73	71	62	74	38	3	102
TCGA-CR-5243-10A-01D-1512-08_HNSC	91	46	57	36	54	56	80	71	62	12	36	0	43	53	0	44	79
TCGA-CR-5247-10A-01D-2013-08_HNSC	107	0	67	49	70	72	88	132	120	0	0	0	0	2	34	72	102
TCGA-CR-5248-10A-01D-2013-08_HNSC	105	0	0	89	99	97	71	73	84	0	1	0	0	0	0	85	106
TCGA-CR-5249-10A-01D-1512-08_HNSC	99	65	76	44	128	102	89	115	128	0	49	74	0	2	27	66	95
TCGA-CR-5250-10A-01D-1512-08_HNSC	139	102	91	64	163	139	139	137	149	0	58	86	0	0	69	0	169
TCGA-CR-6467-10A-01D-1870-08_HNSC	135	72	75	51	127	104	104	99	100	0	56	79	1	0	0	95	129
TCGA-CR-6470-10A-01D-1870-08_HNSC	150	0	0	67	108	102	100	116	89	12	50	0	66	80	31	0	127
TCGA-CR-6471-10A-01D-1870-08_HNSC	128	65	68	45	118	85	92	83	63	11	73	66	49	73	0	57	138
TCGA-CR-6472-10A-01D-1870-08_HNSC	116	0	1	75	100	87	114	129	72	26	50	0	60	91	0	65	114
TCGA-CR-6473-10A-01D-1870-08_HNSC	141	70	77	44	129	95	95	88	101	0	49	76	1	2	0	84	112
TCGA-CR-6474-10A-01D-1870-08_HNSC	150	81	74	52	78	74	78	64	72	0	50	0	69	74	0	67	136
TCGA-CR-6477-10A-01D-1870-08_HNSC	115	67	80	56	82	74	121	110	137	15	0	0	0	0	0	95	133
TCGA-CR-6478-10A-01D-1870-08_HNSC	117	0	1	100	108	105	88	83	75	18	46	0	64	79	0	63	124
TCGA-CR-6480-10A-01D-1870-08_HNSC	126	0	0	68	99	101	102	112	130	0	2	2	0	0	0	96	127
TCGA-CR-6481-10A-01D-1870-08_HNSC	127	72	79	53	73	88	105	103	117	0	1	0	0	2	48	0	133
TCGA-CR-6482-10A-01D-1870-08_HNSC	112	0	2	73	103	96	73	70	79	0	54	1	71	82	31	1	123
TCGA-CR-6484-10A-01D-1870-08_HNSC	115	0	1	101	107	110	95	112	110	0	0	0	0	0	38	63	120
TCGA-CR-6487-10A-01D-1870-08_HNSC	122	0	0	91	110	100	98	112	114	0	0	0	0	1	29	65	128
TCGA-CR-6488-10A-01D-2078-08_HNSC	69	49	51	40	97	72	70	76	88	0	31	54	0	5	19	47	85
TCGA-CR-6491-10A-01D-1870-08_HNSC	150	0	2	82	152	123	106	144	132	0	57	77	1	0	39	80	161
TCGA-CR-6492-10A-01D-2078-08_HNSC	72	59	54	38	60	50	71	77	78	0	1	0	0	0	20	37	87
TCGA-CR-6493-10A-01D-1870-08_HNSC	165	0	0	79	115	103	107	101	98	26	61	0	79	81	0	81	143
TCGA-CR-7364-10A-01D-2013-08_HNSC	110	0	1	95	97	99	99	134	121	0	0	0	0	1	34	72	115
TCGA-CR-7365-10A-01D-2013-08_HNSC	109	0	0	57	104	95	88	117	108	0	0	0	0	0	32	77	111
TCGA-CR-7367-10A-01D-2013-08_HNSC	102	99	99	1	0	2	96	92	96	0	0	1	0	0	45	0	119
TCGA-CR-7368-10A-01D-2129-08_HNSC	84	1	0	79	90	89	83	93	80	0	0	1	0	0	0	109	100
TCGA-CR-7369-10A-01D-2129-08_HNSC	91	53	60	41	78	62	77	82	104	0	0	0	0	1	0	124	92
TCGA-CR-7370-10A-01D-2129-08_HNSC	121	72	73	47	78	66	75	74	4	24	71	6	74	99	0	2	94
TCGA-CR-7371-10A-01D-2013-08_HNSC	102	2	1	83	95	95	84	116	71	21	59	0	69	78	0	74	104
TCGA-CR-7372-10A-01D-2013-08_HNSC	106	96	104	1	80	71	93	87	87	16	86	71	68	85	0	72	110
TCGA-CR-7373-10A-01D-2013-08_HNSC	107	73	81	45	82	72	69	76	69	0	66	0	69	83	0	72	126
TCGA-CR-7374-10A-01D-2013-08_HNSC	107	74	78	50	131	97	91	105	97	0	62	68	2	0	0	93	99
TCGA-CR-7376-10A-01D-2129-08_HNSC	86	78	83	2	0	2	73	100	96	0	1	0	2	5	26	55	90
TCGA-CR-7377-10A-01D-2013-08_HNSC	116	74	81	53	120	98	91	130	109	0	60	76	0	0	29	66	102
TCGA-CR-7379-10A-01D-2013-08_HNSC	109	82	78	56	82	70	90	103	83	17	54	0	68	75	24	0	108
TCGA-CR-7380-10A-01D-2013-08_HNSC	140	0	1	91	101	89	93	95	99	0	0	1	0	3	31	77	108
TCGA-CR-7382-10A-01D-2129-08_HNSC	87	2	2	53	93	83	82	85	102	2	2	1	2	0	29	51	92
TCGA-CR-7383-10A-01D-2129-08_HNSC	99	11	4	76	91	79	61	51	8	19	39	67	1	71	0	3	94
TCGA-CR-7385-10A-01D-2013-08_HNSC	109	77	76	50	70	77	91	99	112	0	1	0	1	0	0	132	124
TCGA-CR-7386-10A-01D-2013-08_HNSC	106	0	0	65	101	106	93	129	114	0	1	0	0	1	0	131	116
TCGA-CR-7388-10A-01D-2013-08_HNSC	96	72	77	53	112	95	85	95	67	15	78	95	0	80	0	69	106
TCGA-CR-7389-10A-01D-2013-08_HNSC	107	1	2	91	151	98	93	85	102	0	0	2	0	4	34	1	120
TCGA-CR-7390-10A-01D-2013-08_HNSC	97	0	0	80	102	93	94	125	117	0	0	0	0	0	28	79	101
TCGA-CR-7391-10A-01D-2013-08_HNSC	96	0	3	70	102	101	95	121	126	0	1	0	1	2	0	143	110
TCGA-CR-7392-10A-01D-2013-08_HNSC	114	0	2	58	100	98	95	91	91	0	0	0	0	0	0	93	114
TCGA-CR-7393-10A-01D-2013-08_HNSC	100	3	1	60	111	104	95	102	79	19	65	0	74	84	0	76	124
TCGA-CR-7394-10A-01D-2013-08_HNSC	105	0	0	52	95	92	87	107	111	0	1	0	0	2	0	127	111
TCGA-CR-7395-10A-01D-2013-08_HNSC	112	72	77	56	80	84	86	112	96	0	0	1	0	0	32	66	97
TCGA-CR-7397-10A-01D-2013-08_HNSC	115	68	89	52	134	96	90	130	79	16	82	102	0	79	32	0	112
TCGA-CR-7398-10A-01D-2013-08_HNSC	117	1	2	76	105	88	103	103	122	0	0	0	0	2	0	149	113
TCGA-CR-7399-10A-01D-2013-08_HNSC	115	1	0	91	101	102	82	115	96	0	1	1	0	1	0	133	101
TCGA-CR-7401-10A-01D-2013-08_HNSC	131	1	0	83	105	102	96	114	117	0	1	0	0	0	38	74	122
TCGA-CR-7402-10A-01D-2013-08_HNSC	105	76	82	53	131	91	99	126	76	24	86	77	68	79	29	0	110
TCGA-CR-7404-10A-01D-2129-08_HNSC	85	0	3	47	81	85	81	101	81	0	0	1	0	1	0	111	99
TCGA-CS-4938-10A-01D-1893-08_LGG	106	0	0	95	98	100	93	102	114	0	1	0	0	0	0	88	123
TCGA-CS-4941-10A-01D-1468-08_LGG	98	71	80	47	131	89	85	121	106	0	57	78	1	0	35	71	98
TCGA-CS-4942-10A-01D-1468-08_LGG	113	0	1	78	104	127	83	126	86	21	46	1	67	78	33	1	121
TCGA-CS-4943-10A-01D-1468-08_LGG	95	1	1	53	100	72	64	57	79	0	0	0	0	57	0	65	82
TCGA-CS-4944-10A-01D-1468-08_LGG	124	95	87	0	111	108	84	99	0	24	107	96	78	98	0	0	116
TCGA-CS-5390-10A-01D-1468-08_LGG	114	0	0	56	105	98	95	135	120	0	1	1	0	1	0	141	112
TCGA-CS-5393-10A-01D-1468-08_LGG	103	65	65	39	144	106	102	109	65	19	89	118	2	82	0	71	98
TCGA-CS-5394-10A-01D-1468-08_LGG	109	82	84	0	98	90	80	101	78	15	88	89	61	75	0	75	115
TCGA-CS-5395-10A-01D-1468-08_LGG	107	62	65	40	112	84	83	122	112	14	53	66	0	1	25	71	101
TCGA-CS-5396-10A-01D-1468-08_LGG	105	66	69	46	82	76	90	93	96	0	0	0	2	1	0	98	110
TCGA-CS-5397-10A-03D-1893-08_LGG	157	0	0	64	99	76	90	84	94	0	1	0	1	1	0	98	118
TCGA-CS-6186-10A-01D-2024-08_LGG	101	75	80	3	91	86	88	71	0	22	85	84	77	98	0	0	102
TCGA-CS-6188-10A-01D-1893-08_LGG	146	0	3	77	113	94	91	122	90	22	70	1	77	83	34	1	112
TCGA-CS-6290-10A-01D-1705-08_LGG	94	0	2	58	97	90	75	85	122	0	0	1	0	1	0	93	101
TCGA-CS-6665-10A-01D-1893-08_LGG	113	2	1	77	104	106	91	123	114	0	0	0	0	2	31	58	124
TCGA-CS-6666-10A-01D-1893-08_LGG	147	74	73	59	87	75	91	103	115	0	0	0	1	3	45	0	114
TCGA-CS-6667-10A-01D-2024-08_LGG	88	75	82	0	72	65	86	115	105	16	39	63	0	2	0	109	105
TCGA-CS-6668-10A-01D-1893-08_LGG	118	77	85	58	89	84	104	139	127	0	0	0	0	0	31	83	111
TCGA-CS-6669-10A-01D-1893-08_LGG	123	77	87	57	97	80	116	124	140	0	0	0	2	3	0	154	135
TCGA-CS-6670-10A-01D-1893-08_LGG	144	76	72	55	144	107	98	109	101	0	67	83	0	0	0	150	138
TCGA-CU-A0YO-10A-01D-A10S-08_BLCA	107	74	67	42	123	96	88	107	76	15	67	94	0	79	0	79	115
TCGA-CU-A0YR-10A-01D-A10S-08_BLCA	106	84	97	2	82	86	87	112	110	0	54	67	0	0	0	105	115
TCGA-CU-A3KJ-10A-01D-A21A-08_BLCA	103	52	51	49	108	103	82	67	102	0	24	58	0	1	0	80	129
TCGA-CU-A3QU-10B-01D-A22Z-08_BLCA	142	0	0	110	126	132	123	132	144	0	0	0	0	0	35	79	154
TCGA-CU-A3YL-10A-01D-A22Z-08_BLCA	155	87	76	69	81	94	130	112	183	0	0	0	0	0	0	127	181
TCGA-CU-A5W6-10A-01D-A289-08_BLCA	110	0	0	93	112	102	99	106	128	0	0	0	0	0	0	92	126
TCGA-CU-A72E-10A-01D-A339-08_BLCA	123	79	90	0	72	77	84	83	60	13	67	85	0	71	28	0	107
TCGA-CV-5430-10A-01D-1870-08_HNSC	131	0	2	107	101	101	97	93	1	25	76	1	86	113	0	0	136

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CV-5432-10A-01D-1870-08_HNSC	122	86	79	52	129	101	120	124	98	0	60	83	0	0	0	129	141
TCGA-CV-5434-10A-01D-1870-08_HNSC	123	106	110	2	82	82	87	73	84	0	87	83	60	88	42	0	130
TCGA-CV-5435-10A-01D-1870-08_HNSC	132	103	98	0	107	106	111	100	0	27	104	148	1	115	0	0	132
TCGA-CV-5436-10A-01D-1870-08_HNSC	163	72	0	44	140	104	105	110	86	13	46	0	69	88	31	0	128
TCGA-CV-5966-10A-01D-1870-08_HNSC	161	67	85	49	138	98	104	83	70	9	77	76	67	82	0	70	139
TCGA-CV-5970-10A-01D-1870-08_HNSC	124	72	73	47	136	113	92	114	121	0	47	80	0	1	31	63	135
TCGA-CV-6933-10A-01D-1912-08_HNSC	104	74	70	40	109	90	89	131	114	0	54	71	0	0	34	67	117
TCGA-CV-6934-10A-01D-1912-08_HNSC	86	0	2	58	87	81	85	102	122	0	0	0	0	1	0	127	100
TCGA-CV-6935-10A-01D-1912-08_HNSC	92	69	73	44	118	92	85	133	119	0	51	72	0	1	25	58	104
TCGA-CV-6936-10A-01D-1912-08_HNSC	98	1	0	53	96	92	86	112	78	22	52	1	71	74	27	0	111
TCGA-CV-6937-10A-01D-2013-08_HNSC	95	0	0	79	84	93	91	109	101	0	0	0	0	0	30	71	97
TCGA-CV-6938-10A-01D-1912-08_HNSC	98	69	71	44	113	85	83	103	76	21	73	67	71	77	0	55	112
TCGA-CV-6939-10A-01D-1912-08_HNSC	97	0	2	64	96	90	77	75	61	14	45	1	58	66	0	69	96
TCGA-CV-6940-10A-01D-1912-08_HNSC	102	67	71	49	120	90	85	91	80	13	83	71	69	76	0	60	104
TCGA-CV-6941-10A-01D-1912-08_HNSC	96	73	66	49	131	93	80	118	110	0	48	61	0	0	28	66	98
TCGA-CV-6942-10A-01D-2013-08_HNSC	93	0	0	56	90	94	95	112	76	19	56	0	65	76	33	1	101
TCGA-CV-6943-10A-01D-1912-08_HNSC	128	1	0	63	87	91	81	108	92	0	0	0	0	0	0	123	105
TCGA-CV-6945-10A-01D-1912-08_HNSC	95	92	88	1	75	70	92	80	73	16	75	83	1	83	0	65	114
TCGA-CV-6948-10A-01D-1912-08_HNSC	102	0	2	63	93	87	89	114	127	0	0	0	0	1	0	117	105
TCGA-CV-6950-10A-01D-1912-08_HNSC	118	67	72	43	126	94	92	108	77	16	71	87	0	80	0	71	108
TCGA-CV-6951-10A-01D-1912-08_HNSC	100	0	1	62	98	89	81	111	107	0	1	0	1	0	0	124	106
TCGA-CV-6952-10A-01D-1912-08_HNSC	97	60	73	45	113	90	74	108	65	16	74	86	0	63	0	59	99
TCGA-CV-6953-10A-01D-1912-08_HNSC	94	69	67	49	67	76	85	100	89	0	0	0	0	0	0	133	89
TCGA-CV-6954-10A-01D-1912-08_HNSC	103	1	0	63	98	89	85	98	95	0	1	0	0	0	0	133	100
TCGA-CV-6955-10A-01D-2013-08_HNSC	110	0	0	60	91	96	98	147	113	0	0	0	0	0	36	80	111
TCGA-CV-6956-10A-01D-2013-08_HNSC	94	0	0	58	104	94	89	94	92	0	0	0	0	0	29	68	123
TCGA-CV-6959-10A-01D-1912-08_HNSC	104	1	1	86	89	88	78	74	92	0	0	0	0	0	0	81	105
TCGA-CV-6960-10A-01D-2013-08_HNSC	103	1	1	63	91	91	87	102	111	0	0	0	0	2	36	62	99
TCGA-CV-6961-10A-01D-1912-08_HNSC	97	1	0	88	95	94	80	89	93	0	0	0	0	1	29	66	109
TCGA-CV-6962-10A-01D-1912-08_HNSC	89	0	70	47	126	86	85	110	112	0	50	0	66	0	29	64	103
TCGA-CV-7089-10A-01D-2013-08_HNSC	99	0	0	60	88	79	80	84	84	0	0	0	0	0	0	83	109
TCGA-CV-7090-10A-01D-2013-08_HNSC	96	83	91	1	0	1	72	57	59	0	54	63	0	75	0	70	101
TCGA-CV-7091-10A-01D-2013-08_HNSC	96	0	1	90	147	96	97	91	71	23	76	72	70	71	0	62	96
TCGA-CV-7095-10A-01D-2013-08_HNSC	101	1	1	89	102	85	88	96	96	0	0	0	1	0	0	116	108
TCGA-CV-7097-10A-01D-2013-08_HNSC	138	0	0	77	123	120	98	116	122	0	0	0	0	1	0	125	154
TCGA-CV-7099-10A-01D-2013-08_HNSC	140	70	78	51	151	138	116	136	77	21	84	71	70	86	0	57	149
TCGA-CV-7100-10A-01D-2013-08_HNSC	103	0	2	66	107	108	98	142	116	0	0	0	1	0	30	71	119
TCGA-CV-7101-10A-01D-2013-08_HNSC	105	78	80	52	140	111	98	122	74	19	86	76	70	83	33	2	119
TCGA-CV-7102-10A-01D-2013-08_HNSC	103	0	1	59	103	90	105	109	103	0	0	0	0	1	30	69	107
TCGA-CV-7103-10A-01D-2013-08_HNSC	100	80	91	0	0	2	96	113	73	14	58	0	78	78	0	64	120
TCGA-CV-7104-10A-01D-2013-08_HNSC	106	84	74	51	135	101	92	117	73	16	83	74	67	84	0	82	123
TCGA-CV-7177-10A-01D-2013-08_HNSC	106	74	82	47	129	89	68	62	2	13	85	74	75	83	0	1	88
TCGA-CV-7178-10A-01D-2013-08_HNSC	98	0	0	62	90	99	97	111	137	0	1	2	0	1	32	70	109
TCGA-CV-7180-10A-01D-2013-08_HNSC	111	0	0	92	99	91	90	118	97	0	0	0	0	0	39	76	114
TCGA-CV-7183-10A-01D-2013-08_HNSC	154	0	0	100	106	107	103	122	97	0	0	0	0	0	0	129	143
TCGA-CV-7235-10A-01D-2013-08_HNSC	135	88	89	54	141	116	135	135	134	0	62	95	0	3	0	105	148
TCGA-CV-7236-10A-01D-2013-08_HNSC	118	1	2	72	109	117	92	115	117	0	0	0	0	0	35	64	119
TCGA-CV-7238-10A-01D-2013-08_HNSC	134	0	1	90	95	99	91	119	99	0	0	0	1	0	35	77	117
TCGA-CV-7242-10A-01D-2013-08_HNSC	103	0	0	92	103	90	98	120	117	0	0	0	1	0	0	118	109
TCGA-CV-7243-10A-01D-2013-08_HNSC	95	88	72	42	77	76	91	134	100	0	0	0	0	0	30	71	121
TCGA-CV-7245-10A-01D-2013-08_HNSC	93	82	78	50	85	79	86	88	75	18	54	0	73	87	0	67	110
TCGA-CV-7247-10A-01D-2013-08_HNSC	106	0	1	87	99	96	85	125	110	0	0	0	0	0	0	129	108
TCGA-CV-7248-10A-01D-2013-08_HNSC	110	72	77	51	98	96	91	121	107	0	55	0	69	2	38	76	116
TCGA-CV-7250-10A-01D-2013-08_HNSC	132	0	2	67	96	114	109	120	105	0	1	0	0	1	0	137	115
TCGA-CV-7252-10A-01D-2013-08_HNSC	101	74	81	47	103	84	90	109	85	18	85	68	75	75	0	64	107
TCGA-CV-7253-10A-01D-2013-08_HNSC	99	161	114	2	84	77	92	96	103	0	56	74	0	3	0	77	109
TCGA-CV-7254-10A-01D-2013-08_HNSC	106	1	1	87	117	96	86	84	73	21	56	0	78	78	0	66	108
TCGA-CV-7255-10A-01D-2013-08_HNSC	103	72	71	46	76	70	87	125	110	0	0	0	0	1	33	61	108
TCGA-CV-7261-10A-01D-2013-08_HNSC	121	0	3	97	105	91	95	121	103	0	0	0	0	2	0	83	106
TCGA-CV-7263-10A-01D-2013-08_HNSC	109	75	77	52	123	94	92	87	75	18	86	71	68	80	0	71	113
TCGA-CV-7406-10A-01D-2078-08_HNSC	80	3	0	73	84	80	77	64	64	14	34	0	54	70	0	52	91
TCGA-CV-7407-10A-01D-2078-08_HNSC	82	1	0	49	83	85	66	71	62	14	40	0	46	63	0	43	95
TCGA-CV-7409-10A-01D-2229-08_HNSC	108	0	68	53	100	96	97	76	102	0	46	0	53	0	23	59	136
TCGA-CV-7410-10A-01D-2078-08_HNSC	116	57	56	40	59	68	73	109	106	1	0	0	2	6	29	54	91
TCGA-CV-7411-10A-01D-2078-08_HNSC	81	0	0	47	80	72	69	70	55	14	38	0	58	72	0	46	94
TCGA-CV-7413-10A-01D-2078-08_HNSC	75	0	3	74	75	72	69	87	49	13	33	0	52	64	0	52	89
TCGA-CV-7414-10A-01D-2078-08_HNSC	78	0	1	51	80	75	81	79	55	14	42	0	57	69	0	52	91
TCGA-CV-7415-10A-01D-2078-08_HNSC	78	72	80	1	2	4	71	82	57	18	31	1	47	59	20	2	87
TCGA-CV-7416-10A-01D-2078-08_HNSC	84	60	61	38	112	77	73	78	57	20	58	72	2	64	0	53	89
TCGA-CV-7418-10A-01D-2078-08_HNSC	87	0	61	39	103	73	79	68	83	0	37	0	51	1	24	55	92
TCGA-CV-7421-10A-01D-2078-08_HNSC	85	0	0	81	85	83	74	90	85	0	0	2	0	1	24	45	86
TCGA-CV-7422-10A-01D-2078-08_HNSC	89	0	0	52	96	79	84	74	92	0	1	0	2	3	0	83	105
TCGA-CV-7423-10A-01D-2078-08_HNSC	78	0	0	74	82	78	71	68	83	0	0	0	0	0	0	83	90
TCGA-CV-7424-10A-01D-2078-08_HNSC	99	0	1	48	79	72	78	77	74	17	30	0	52	62	27	1	98
TCGA-CV-7425-10A-01D-2078-08_HNSC	75	0	0	66	79	74	74	88	75	0	1	0	0	2	0	103	82
TCGA-CV-7427-10A-01D-2078-08_HNSC	74	47	50	41	64	52	72	85	71	0	0	0	2	6	0	92	83
TCGA-CV-7429-10A-01D-2129-08_HNSC	92	2	0	75	94	82	83	89	108	0	0	0	0	0	23	59	93
TCGA-CV-7430-10A-01D-2129-08_HNSC	90	2	2	79	82	80	80	93	82	0	1	0	5	2	0	107	95
TCGA-CV-7432-10A-01D-2129-08_HNSC	86	63	63	49	138	89	79	109	101	11	60	82	0	2	0	108	101
TCGA-CV-7433-10A-01D-2129-08_HNSC	90	69	59	48	71	67	85	115	103	0	0	0	0	0	28	61	106
TCGA-CV-7434-10A-01D-2129-08_HNSC	156	126	145	3	149	142	129	119	150	0	89	128	0	1	39	71	169
TCGA-CV-7435-10A-01D-2129-08_HNSC	113	81	78	5	89	86	80	71	75	17	67	77	52	69	0	53	90
TCGA-CV-7437-10A-01D-2129-08_HNSC	82	82	64	2	71	74	80	80	10	28	67	0	74	87	0	8	95
TCGA-CV-7438-10A-01D-2129-08_HNSC	83	5	4	74	91	83	84	74	60	17	44	4	53	70	0	56	98
TCGA-CV-7440-10A-01D-2129-08_HNSC	90	1	0	54	90	93	70	101	98	0	4	7	0	6	0	100	107
TCGA-CV-7446-10A-01D-2229-08_HNSC	94	56	61	38	86	55	79	76	71	20	35	0	60	72	0	64	100
TCGA-CV-7568-10A-01D-2229-08_HNSC	113	54	57	56	61	68	80	81	64	17	39	0	42	65	0	55	100
TCGA-CV-A45O-10A-01D-A24F-08_HNSC	77	67	64	38	67	60	73	69	97	1	2	2	0	3	0	82	85
TCGA-CV-A45P-10A-01D-A24F-08_HNSC	79	65	52	37	61	65	72	67	89	0	1	0	1	1	0	79	88
TCGA-CV-A45Q-10A-01D-A24F-08_HNSC	80	62	67	35	103	76	84	96	70	18	67	60	59	68	0	69	93
TCGA-CV-A45R-10A-01D-A24F-08_HNSC	154	0	0	118	149	154	142	129	154	0	0	0	0	0	64	1	178
TCGA-CV-A45T-10A-01D-A24F-08_HNSC	90	3	5	78	91	89	83	87	89	0	3	3	1	6	0	81	103
TCGA-CV-A45U-10A-01D-A24F-08_HNSC	91	63	71	46	80	72	85	85	118	0	1	0	4	4	0	75	108
TCGA-CV-A45V-10A-01D-A25E-08_HNSC	82	0	0	55	76	82	78	61	63	19	34	57	5	66	0	55	86
TCGA-CV-A45W-10A-01D-A25E-08_HNSC	82	58	71	46	70	61	78	94	82	0	2	0	2	2	32	60	92
TCGA-CV-A45X-10A-01D-A25E-08_HNSC	85	1	2	64	71	77	66	88	57	14	1	0	56	58	0	59	89

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CV-A45Y-10A-01D-A25E-08_HNSC	82	0	0	55	82	81	70	88	66	14	39	0	58	65	31	3	83
TCGA-CV-A45Z-10A-01D-A25E-08_HNSC	77	0	0	49	78	80	69	102	108	0	0	0	1	1	28	60	85
TCGA-CV-A460-10A-01D-A25E-08_HNSC	77	56	56	35	59	46	68	84	57	14	45	0	39	55	0	58	83
TCGA-CV-A461-10A-01D-A25Y-08_HNSC	81	9	3	75	91	79	83	105	85	0	1	3	1	5	0	83	101
TCGA-CV-A463-10A-01D-A25Y-08_HNSC	86	83	92	3	83	73	85	107	108	0	58	5	68	2	29	70	116
TCGA-CV-A464-10A-01D-A25Y-08_HNSC	125	73	73	44	119	86	86	88	115	0	47	63	1	4	0	85	111
TCGA-CV-A465-10A-01D-A25Y-08_HNSC	91	1	0	54	99	97	91	125	78	21	52	0	65	81	0	68	103
TCGA-CV-A468-10A-01D-A25Y-08_HNSC	82	52	63	36	105	79	74	101	99	0	40	57	1	0	27	61	80
TCGA-CV-A6JD-10A-01D-A31J-08_HNSC	93	0	0	84	90	86	73	67	72	10	34	1	60	62	0	59	102
TCGA-CV-A6JE-10A-01D-A31J-08_HNSC	95	56	64	40	63	71	76	83	86	0	0	0	0	0	24	49	106
TCGA-CV-A6JM-10A-01D-A31J-08_HNSC	93	55	57	42	58	67	83	69	107	0	1	0	0	0	0	73	87
TCGA-CV-A6JN-10A-01D-A31J-08_HNSC	94	80	82	0	87	79	74	92	71	15	68	93	0	61	29	0	91
TCGA-CV-A6JT-10A-01D-A31J-08_HNSC	116	61	61	46	69	56	78	84	80	0	0	0	0	0	27	49	94
TCGA-CV-A6JU-10A-01D-A31J-08_HNSC	79	52	59	37	101	80	71	64	65	13	61	53	57	67	0	58	91
TCGA-CV-A6JY-10A-01D-A31J-08_HNSC	98	56	62	38	114	83	84	70	79	0	33	66	0	0	0	82	95
TCGA-CV-A6JZ-10A-01D-A31J-08_HNSC	94	57	58	37	65	63	60	51	54	0	42	0	53	72	0	51	88
TCGA-CV-A6K0-10A-01D-A31J-08_HNSC	87	0	0	69	90	90	80	104	108	0	0	0	0	0	31	53	106
TCGA-CV-A6K1-10A-01D-A31J-08_HNSC	88	0	1	56	83	78	79	82	68	19	50	0	60	73	30	1	88
TCGA-CV-A6K2-10A-01D-A31J-08_HNSC	86	0	0	56	84	80	73	95	82	0	0	0	0	0	0	74	101
TCGA-CX-7082-10A-01D-2013-08_HNSC	115	1	0	74	146	121	117	125	145	0	0	0	0	1	0	129	144
TCGA-CX-7085-10A-01D-2013-08_HNSC	88	0	0	65	98	90	88	106	73	18	50	1	63	83	31	0	107
TCGA-CX-7086-10D-01D-2078-08_HNSC	74	5	5	75	84	72	70	99	76	0	0	0	2	3	0	48	71
TCGA-CX-7219-10A-01D-2013-08_HNSC	151	1	3	110	172	140	124	120	134	0	0	0	0	1	42	0	169
TCGA-CX-A4AQ-10A-01D-A25E-08_HNSC	89	0	2	48	83	71	72	78	92	0	1	0	2	4	0	73	94
TCGA-D1-A0ZN-10A-01D-A122-09_UCEC	76	0	2	66	145	143	160	168	132	22	102	0	112	110	63	0	108
TCGA-D1-A0ZO-10A-01D-A122-09_UCEC	98	0	0	85	189	194	200	187	214	0	0	0	0	0	0	177	155
TCGA-D1-A0ZP-10A-01D-A10M-09_UCEC	71	102	113	39	187	113	128	91	110	25	108	98	103	101	0	62	105
TCGA-D1-A0ZQ-10A-01D-A122-09_UCEC	112	131	133	70	267	223	220	220	149	23	183	227	0	148	65	0	157
TCGA-D1-A0ZR-10A-01D-A10M-09_UCEC	81	115	117	51	211	173	191	189	122	25	155	180	0	123	0	105	142
TCGA-D1-A0ZS-10A-01D-A122-09_UCEC	107	135	135	59	247	189	217	180	4	40	259	206	143	178	0	0	145
TCGA-D1-A0ZU-10A-01D-A10M-09_UCEC	99	134	143	65	216	180	190	160	244	1	96	132	1	1	0	161	155
TCGA-D1-A0ZV-10A-01D-A10M-09_UCEC	89	119	115	45	216	165	189	149	118	21	141	153	0	109	0	98	114
TCGA-D1-A0ZZ-10A-01D-A10M-09_UCEC	90	110	119	42	114	108	170	176	123	25	105	1	113	119	57	0	103
TCGA-D1-A101-10A-01D-A10M-09_UCEC	86	0	0	113	164	153	172	131	187	0	0	0	0	1	0	158	118
TCGA-D1-A102-10A-01D-A10M-09_UCEC	88	144	139	0	0	0	154	168	187	0	0	0	0	0	0	199	116
TCGA-D1-A103-10A-01D-A10M-09_UCEC	92	119	118	68	225	187	211	136	1	46	250	121	179	185	0	0	144
TCGA-D1-A15V-10A-01D-A122-09_UCEC	116	137	139	72	287	205	215	230	150	32	247	139	148	146	0	141	153
TCGA-D1-A15W-10A-01D-A122-09_UCEC	63	0	0	61	147	121	136	111	112	19	76	0	91	99	0	68	97
TCGA-D1-A15X-10A-01D-A122-09_UCEC	102	0	0	115	175	171	191	171	127	26	116	1	125	117	0	116	126
TCGA-D1-A15Z-10A-01D-A122-09_UCEC	106	0	1	66	167	157	175	191	216	0	0	0	1	0	0	144	131
TCGA-D1-A160-10A-01D-A122-09_UCEC	88	3	1	137	183	192	233	202	148	33	116	0	151	148	0	115	150
TCGA-D1-A161-10A-01D-A122-09_UCEC	100	118	122	52	143	130	187	171	131	25	113	0	120	134	0	126	131
TCGA-D1-A163-10A-01D-A12J-09_UCEC	115	0	2	82	179	155	192	186	222	0	0	0	0	1	0	210	142
TCGA-D1-A165-10A-01D-A12J-09_UCEC	85	0	1	109	189	150	199	187	121	45	98	0	117	120	0	95	120
TCGA-D1-A167-10A-01D-A12J-09_UCEC	102	165	148	62	158	169	241	206	274	0	0	0	0	0	67	169	157
TCGA-D1-A168-10A-01D-A12J-09_UCEC	79	0	0	87	186	160	180	129	108	31	85	0	123	126	0	91	135
TCGA-D1-A169-10A-01D-A12J-09_UCEC	99	146	158	0	173	186	173	215	133	25	237	245	0	127	0	134	121
TCGA-D1-A16B-10A-01D-A12J-09_UCEC	87	0	0	70	174	182	186	181	167	0	0	0	0	0	0	185	135
TCGA-D1-A16D-10A-01D-A12J-09_UCEC	109	1	0	121	214	208	209	224	209	0	0	1	0	0	69	150	172
TCGA-D1-A16E-10A-01D-A12J-09_UCEC	132	0	0	110	172	184	186	177	129	26	113	0	124	129	0	119	129
TCGA-D1-A16F-10A-01D-A12J-09_UCEC	104	0	1	83	208	173	179	236	247	0	0	1	0	1	0	263	146
TCGA-D1-A16G-10A-01D-A12J-09_UCEC	69	0	1	112	153	151	162	162	197	0	0	0	0	0	0	158	118
TCGA-D1-A16I-10A-01D-A12J-09_UCEC	96	111	93	55	197	161	154	136	183	1	79	118	0	0	0	143	113
TCGA-D1-A16J-10A-01D-A12J-09_UCEC	68	146	160	0	118	114	156	136	206	0	112	132	0	0	0	148	117
TCGA-D1-A16N-10A-01D-A12J-09_UCEC	100	0	1	107	282	221	227	233	166	37	131	0	154	166	0	141	157
TCGA-D1-A16O-10A-01D-A12J-09_UCEC	102	0	1	63	224	204	209	142	0	56	201	1	202	185	0	0	143
TCGA-D1-A16Q-10A-01D-A12J-09_UCEC	95	108	127	54	125	127	178	225	211	0	0	1	0	0	70	126	121
TCGA-D1-A16R-10A-01D-A12J-09_UCEC	146	1	2	127	302	290	278	262	308	0	0	1	0	2	0	309	226
TCGA-D1-A16S-10A-01D-A12J-09_UCEC	94	1	1	58	180	161	166	191	256	0	0	0	0	1	0	221	128
TCGA-D1-A16V-10A-01D-A12J-09_UCEC	74	104	109	44	103	96	143	151	146	0	0	0	0	0	0	175	100
TCGA-D1-A16X-10A-01D-A12J-09_UCEC	88	134	132	59	129	125	182	160	191	0	0	0	0	0	0	143	120
TCGA-D1-A16Y-10A-01D-A12J-09_UCEC	55	99	91	49	163	124	158	118	145	0	56	84	0	0	30	65	100
TCGA-D1-A174-10A-01D-A12J-09_UCEC	83	128	139	61	121	108	217	167	212	0	0	0	0	1	42	98	139
TCGA-D1-A175-10A-01D-A12J-09_UCEC	86	138	139	56	126	147	234	226	248	0	1	0	1	1	0	186	161
TCGA-D1-A176-10A-01D-A12J-09_UCEC	77	124	181	61	109	127	225	215	135	45	192	0	178	126	0	111	126
TCGA-D1-A177-10A-01D-A12J-09_UCEC	70	111	112	59	177	148	164	145	161	6	101	108	12	21	0	127	122
TCGA-D1-A179-10A-01D-A12J-09_UCEC	98	137	163	22	196	164	185	180	227	11	178	196	20	16	0	193	120
TCGA-D1-A17A-10A-01D-A12J-09_UCEC	78	0	1	89	141	145	144	94	133	0	0	0	0	120	0	77	95
TCGA-D1-A17B-10A-01D-A12J-09_UCEC	96	137	143	64	190	171	246	191	238	30	100	143	0	0	0	130	134
TCGA-D1-A17C-10A-01D-A12J-09_UCEC	109	136	155	70	137	129	223	174	152	35	127	0	139	137	0	116	152
TCGA-D1-A17D-10A-01D-A12J-09_UCEC	82	125	133	59	101	119	227	192	234	0	0	0	0	0	0	154	134
TCGA-D1-A17F-10A-01D-A12J-09_UCEC	72	0	0	102	175	170	179	158	118	28	113	0	107	119	0	89	124
TCGA-D1-A17H-10A-01D-A12J-09_UCEC	81	146	140	61	134	130	256	191	219	0	0	0	0	0	50	89	165
TCGA-D1-A17K-10A-01D-A12J-09_UCEC	83	140	156	65	135	134	237	166	162	34	118	0	145	143	0	124	143
TCGA-D1-A17L-10A-01D-A12J-09_UCEC	94	0	1	74	207	198	192	177	194	0	0	0	0	0	69	131	123
TCGA-D1-A17M-10A-01D-A12J-09_UCEC	112	0	1	120	258	208	207	220	250	0	0	0	0	0	58	122	133
TCGA-D1-A17N-10A-01D-A12J-09_UCEC	102	1	0	122	213	213	213	179	220	0	0	0	0	0	0	223	133
TCGA-D1-A17Q-10A-01D-A12J-09_UCEC	74	0	0	112	166	158	175	189	202	0	0	0	0	1	45	118	126
TCGA-D1-A17R-10A-01D-A12J-09_UCEC	117	0	3	127	199	222	227	231	220	0	0	0	0	0	69	126	179
TCGA-D1-A17S-10A-01D-A12J-09_UCEC	104	0	0	93	204	278	222	223	153	24	144	0	150	141	0	130	163
TCGA-D1-A17T-10A-01D-A12J-09_UCEC	115	137	142	57	290	240	286	243	233	0	125	182	0	2	0	266	201
TCGA-D1-A17U-10A-01D-A12J-09_UCEC	132	129	159	64	321	249	285	226	178	28	229	193	149	148	0	149	180
TCGA-D1-A1NS-10A-01D-A14G-09_UCEC	48	73	68	19	111	100	107	134	108	11	48	62	2	3	57	1	66
TCGA-D1-A1NU-10A-01D-A14G-09_UCEC	50	61	55	26	46	49	102	73	94	0	0	0	0	0	29	41	70
TCGA-D1-A1NX-10A-01D-A16D-09_UCEC	54	0	0	70	115	129	143	110	129	0	0	0	0	0	39	75	94
TCGA-D1-A1NY-10A-01D-A16D-09_UCEC	48	1	0	23	92	90	82	82	74	10	46	1	55	56	0	46	69
TCGA-D1-A1NZ-10A-01D-A14G-09_UCEC	43	1	0	28	82	73	94	79	104	0	0	0	0	0	0	74	73
TCGA-D1-A1O0-10A-01D-A17D-09_UCEC	60	0	0	28	88	88	80	90	112	0	0	0	0	0	30	52	78
TCGA-D1-A1O5-10A-01D-A14G-09_UCEC	43	53	53	12	53	51	83	88	98	0	0	2	0	0	0	74	73
TCGA-D1-A1O7-10A-01D-A14G-09_UCEC	53	1	2	27	76	73	81	94	102	0	1	1	0	1	36	45	70
TCGA-D1-A1O8-10A-01D-A14G-09_UCEC	37	0	2	18	71	69	68	65	54	9	37	0	42	45	0	41	62
TCGA-D1-A2G0-10A-01D-A17D-09_UCEC	63	0	1	28	99	97	98	129	134	0	0	0	0	2	41	64	83
TCGA-D1-A2G5-10A-01D-A17D-09_UCEC	63	0	4	27	90	95	95	96	81	10	56	0	60	67	0	60	75
TCGA-D1-A2G6-10A-01D-A17D-09_UCEC	41	78	80	0	54	58	78	83	66	10	54	80	0	56	35	0	60
TCGA-D1-A2G7-10A-01D-A17W-09_UCEC	51	55	52	16	55	53	84	95	86	0	0	0	1	1	33	44	71
TCGA-D1-A3DA-10A-01D-A20S-09_UCEC	73	65	58	22	69	62	103	104	135	0	0	0	3	4	30	66	70

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-D1-A3DG-10A-01D-A19Y-09_UCEC	67	1	4	56	108	66	97	87	109	0	1	0	0	60	0	51	61
TCGA-D1-A3DH-10A-01D-A19Y-09_UCEC	52	72	68	24	68	69	103	54	76	9	35	1	72	68	0	35	75
TCGA-D1-A3JP-10B-01D-A22A-09_UCEC	62	54	59	18	54	58	113	108	104	0	0	2	0	1	37	51	76
TCGA-D1-A3JQ-10B-01D-A22A-09_UCEC	63	2	0	33	93	87	105	91	130	1	0	0	0	2	36	48	84
TCGA-D3-A1Q1-10A-01D-A198-08_SKCM	108	0	0	59	104	95	82	90	0	24	69	0	80	98	0	1	110
TCGA-D3-A1Q3-10A-01D-A198-08_SKCM	84	0	0	82	87	74	75	77	86	0	0	0	0	1	35	0	101
TCGA-D3-A1Q4-10A-01D-A198-08_SKCM	95	0	0	49	79	81	75	113	103	0	0	0	0	0	33	56	93
TCGA-D3-A1Q5-10A-01D-A198-08_SKCM	121	0	0	67	83	81	77	82	82	0	0	0	0	0	34	0	104
TCGA-D3-A1Q6-10A-01D-A198-08_SKCM	99	51	61	44	61	62	70	80	61	9	43	0	51	59	0	58	93
TCGA-D3-A1Q7-10A-01D-A19A-08_SKCM	96	80	87	1	0	0	77	76	93	0	0	0	0	0	0	79	98
TCGA-D3-A1Q8-10A-01D-A19A-08_SKCM	97	64	66	43	105	77	80	81	64	13	64	81	0	68	0	58	112
TCGA-D3-A1Q9-10A-01D-A19A-08_SKCM	94	0	1	62	88	77	79	87	101	0	0	0	0	1	0	101	94
TCGA-D3-A1QA-10A-01D-A198-08_SKCM	103	70	74	52	78	69	89	87	95	0	0	0	0	2	0	89	107
TCGA-D3-A1QB-10A-01D-A19A-08_SKCM	98	0	0	79	104	78	73	78	0	17	71	0	71	87	0	3	106
TCGA-D3-A2J6-10A-01D-A19A-08_SKCM	100	0	0	62	83	63	55	67	0	12	43	0	54	93	0	0	82
TCGA-D3-A2J7-10A-01D-A198-08_SKCM	91	54	59	40	108	79	77	96	61	14	56	51	47	65	27	0	93
TCGA-D3-A2J8-10A-01D-A198-08_SKCM	91	59	61	46	69	67	89	103	113	0	0	0	0	0	0	121	106
TCGA-D3-A2J9-10A-01D-A198-08_SKCM	104	0	3	85	96	84	75	87	77	20	41	0	58	63	0	68	111
TCGA-D3-A2JA-10A-01D-A198-08_SKCM	102	53	56	49	66	53	73	87	74	0	0	0	0	0	0	76	98
TCGA-D3-A2JB-10A-01D-A198-08_SKCM	109	67	66	44	60	67	81	108	62	22	49	0	55	69	0	61	92
TCGA-D3-A2JC-10A-01D-A19A-08_SKCM	89	0	1	74	86	76	75	128	111	1	0	1	0	0	0	130	103
TCGA-D3-A2JD-10A-01D-A19A-08_SKCM	103	66	67	1	123	100	94	128	109	0	59	0	56	1	30	70	107
TCGA-D3-A2JF-10A-01D-A198-08_SKCM	94	1	1	53	85	77	78	78	81	0	0	0	0	0	26	53	91
TCGA-D3-A2JG-10A-01D-A198-08_SKCM	95	0	0	54	86	89	83	99	95	0	0	1	0	0	34	67	108
TCGA-D3-A2JH-10A-01D-A198-08_SKCM	88	61	70	46	64	70	83	89	91	1	0	0	0	0	31	61	102
TCGA-D3-A2JK-10A-01D-A198-08_SKCM	86	59	69	43	65	61	82	81	75	9	38	0	54	64	0	54	103
TCGA-D3-A2JL-10A-01D-A198-08_SKCM	92	76	76	0	62	59	81	81	68	13	57	80	0	56	0	52	99
TCGA-D3-A2JN-10A-01D-A198-08_SKCM	84	62	0	42	102	75	78	96	62	12	41	0	48	59	28	0	86
TCGA-D3-A2JO-10A-01D-A198-08_SKCM	101	88	88	0	70	57	81	80	0	21	88	89	57	87	0	1	107
TCGA-D3-A2JP-10A-01D-A19A-08_SKCM	99	73	67	50	126	98	84	124	73	20	79	62	61	80	30	0	117
TCGA-D3-A3BZ-10A-01D-A198-08_SKCM	104	60	66	38	76	69	91	91	1	21	72	1	85	100	0	1	114
TCGA-D3-A3C1-10A-01D-A198-08_SKCM	93	62	65	36	106	86	75	97	77	0	48	60	0	1	0	113	89
TCGA-D3-A3C3-10A-01D-A19A-08_SKCM	122	57	55	47	108	79	78	78	62	10	57	79	0	56	0	39	119
TCGA-D3-A3C6-10A-01D-A198-08_SKCM	90	0	0	55	89	84	81	94	105	0	0	0	0	2	25	67	111
TCGA-D3-A3C7-10A-01D-A198-08_SKCM	111	48	58	39	46	54	72	80	62	10	38	0	50	69	25	1	93
TCGA-D3-A3C8-10A-01D-A19A-08_SKCM	122	59	52	52	59	49	92	98	106	0	1	0	0	0	17	54	110
TCGA-D3-A3CB-10A-01D-A198-08_SKCM	85	0	3	78	65	61	59	66	69	0	0	0	0	0	0	68	90
TCGA-D3-A3CC-10A-01D-A19A-08_SKCM	111	91	94	1	2	0	79	84	111	0	0	0	0	0	0	90	113
TCGA-D3-A3CE-10A-01D-A19A-08_SKCM	105	76	80	0	0	0	74	114	104	0	0	1	0	0	35	72	105
TCGA-D3-A3CF-10A-01D-A198-08_SKCM	85	82	84	1	1	1	70	86	89	0	0	0	0	1	25	50	88
TCGA-D3-A3ML-10A-01D-A21A-08_SKCM	87	55	49	35	93	76	86	92	78	10	42	48	1	0	34	1	89
TCGA-D3-A3MO-10A-01D-A21A-08_SKCM	86	58	49	55	122	89	79	84	72	16	75	83	0	70	0	70	115
TCGA-D3-A3MR-10A-01D-A21A-08_SKCM	95	1	2	58	95	94	91	84	87	0	0	0	0	2	0	133	117
TCGA-D3-A3MU-10A-01D-A21A-08_SKCM	85	68	70	51	128	88	98	93	113	0	54	64	1	3	28	66	102
TCGA-D3-A3MV-10A-01D-A21A-08_SKCM	93	0	0	60	86	90	84	102	70	19	44	0	51	81	0	81	105
TCGA-D3-A51E-10A-01D-A25O-08_SKCM	70	0	0	46	72	70	73	70	86	0	0	0	0	0	0	68	83
TCGA-D3-A51F-10A-01D-A25O-08_SKCM	70	48	56	31	59	50	64	56	70	0	0	0	0	2	0	57	88
TCGA-D3-A51G-10A-01D-A25O-08_SKCM	68	0	0	40	77	74	74	87	51	13	38	0	46	59	0	59	93
TCGA-D3-A51H-10A-01D-A25O-08_SKCM	103	0	0	44	98	80	91	93	54	15	57	52	51	66	0	48	87
TCGA-D3-A51J-10A-01D-A25O-08_SKCM	102	46	49	36	60	49	68	63	79	0	0	0	0	2	35	0	78
TCGA-D3-A51K-10A-01D-A25O-08_SKCM	84	0	0	43	77	68	69	79	96	0	0	0	0	0	23	47	91
TCGA-D3-A51N-10A-01D-A25O-08_SKCM	74	0	0	27	79	70	70	81	87	0	0	0	0	0	0	86	81
TCGA-D3-A51R-10A-01D-A25O-08_SKCM	75	32	43	27	84	70	60	64	45	11	45	49	36	59	0	37	82
TCGA-D3-A51T-10A-01D-A25O-08_SKCM	76	54	53	31	61	56	72	88	83	0	0	0	0	1	0	88	84
TCGA-D3-A5GL-10A-01D-A27N-08_SKCM	80	0	0	47	79	76	73	83	73	0	0	0	0	0	0	99	86
TCGA-D3-A5GN-10A-01D-A27N-08_SKCM	88	58	62	46	104	83	92	114	101	19	50	62	0	1	23	53	101
TCGA-D3-A5GO-10A-01D-A27N-08_SKCM	82	55	61	47	69	65	73	107	74	19	44	0	63	65	30	0	97
TCGA-D3-A5GR-10A-01D-A27N-08_SKCM	85	53	61	42	61	65	74	87	57	0	0	0	0	0	0	71	86
TCGA-D3-A5GS-10A-01D-A27N-08_SKCM	92	0	0	60	90	93	82	105	108	0	0	0	0	0	0	114	96
TCGA-D3-A5GT-10A-01D-A30X-08_SKCM	79	63	67	46	110	85	78	77	87	0	37	65	0	0	0	99	85
TCGA-D3-A5GU-10A-01D-A27N-08_SKCM	94	0	1	87	84	83	76	106	90	0	0	0	0	0	0	114	104
TCGA-D5-5537-10A-01D-1924-10_COAD	34	0	0	31	26	29	47	34	30	0	0	0	0	0	0	26	52
TCGA-D5-5538-10A-02D-1650-10_COAD	89	0	0	60	112	104	115	86	84	10	36	0	57	65	16	0	127
TCGA-D5-6529-10A-01D-1771-10_COAD	56	22	20	35	45	19	65	56	78	0	0	0	0	0	8	28	60
TCGA-D5-6531-10A-01D-1719-10_COAD	74	29	32	24	53	67	84	53	48	7	26	28	26	42	0	37	94
TCGA-D5-6532-10A-01D-1719-10_COAD	96	133	126	0	0	0	151	86	140	0	0	0	0	0	0	90	164
TCGA-D5-6533-10A-01D-1719-10_COAD	109	0	1	77	143	128	171	121	209	0	0	0	0	0	0	84	158
TCGA-D5-6534-10A-01D-1924-10_COAD	64	32	27	31	65	62	77	51	36	5	29	56	0	35	0	25	65
TCGA-D5-6535-10A-01D-1719-10_COAD	104	0	0	67	135	125	161	112	177	0	0	0	0	0	30	54	149
TCGA-D5-6536-10A-01D-1719-10_COAD	114	0	0	93	140	140	180	140	194	0	0	0	0	1	0	113	173
TCGA-D5-6538-10A-01D-1719-10_COAD	84	62	55	34	48	54	110	69	114	0	0	0	0	2	0	60	116
TCGA-D5-6539-10A-01D-1719-10_COAD	96	3	1	65	102	91	115	78	58	13	42	1	42	44	0	26	127
TCGA-D5-6540-10A-01D-1719-10_COAD	115	0	2	46	100	109	132	96	135	0	0	0	0	1	0	61	145
TCGA-D5-6541-10A-01D-1719-10_COAD	128	1	0	91	125	130	169	148	168	0	0	1	0	0	32	50	137
TCGA-D5-6898-10A-01D-1924-10_COAD	53	0	0	47	41	57	69	54	67	0	0	0	0	0	23	26	81
TCGA-D5-6920-10A-01D-1924-10_COAD	64	0	0	58	73	63	80	64	75	0	0	0	0	0	0	73	94
TCGA-D5-6922-10A-01D-1924-10_COAD	52	0	0	40	50	54	69	45	44	10	14	0	25	26	0	23	63
TCGA-D5-6924-10A-01D-1924-10_COAD	44	18	0	22	40	45	39	32	34	9	23	0	18	20	0	26	57
TCGA-D5-6926-10A-01D-1924-10_COAD	35	0	0	38	42	26	60	50	48	0	0	0	0	0	0	30	56
TCGA-D5-6927-10A-01D-1924-10_COAD	56	0	0	44	49	44	71	51	64	0	0	0	0	1	0	32	63
TCGA-D5-6928-10A-01D-1924-10_COAD	50	48	41	0	19	22	41	40	34	7	42	23	25	33	0	16	54
TCGA-D5-6929-10A-01D-1924-10_COAD	42	29	23	22	44	43	62	29	27	11	32	26	0	26	0	21	53
TCGA-D5-6930-10A-01D-1924-10_COAD	33	0	0	26	35	29	34	31	42	0	0	0	0	0	5	11	45
TCGA-D5-6931-10A-01D-1924-10_COAD	27	22	32	0	33	29	37	20	21	9	23	31	0	18	0	0	34
TCGA-D5-6932-10A-01D-1924-10_COAD	50	18	23	14	21	18	45	37	57	0	0	1	0	1	0	42	60
TCGA-D5-7000-10A-01D-1924-10_COAD	29	17	16	14	18	19	44	25	0	12	13	0	27	46	0	0	46
TCGA-D6-6515-10A-01D-1870-08_HNSC	120	92	98	1	109	114	90	112	129	1	89	107	0	1	25	71	122
TCGA-D6-6516-10A-01D-1870-08_HNSC	125	0	0	92	114	103	97	103	111	0	0	1	0	1	0	129	129
TCGA-D6-6517-10A-01D-1870-08_HNSC	117	0	1	93	106	106	104	85	104	0	0	0	0	1	26	59	140
TCGA-D6-6823-10A-01D-1912-08_HNSC	123	0	0	90	108	100	105	111	125	0	0	0	0	0	0	110	139
TCGA-D6-6824-10A-01D-1912-08_HNSC	125	0	1	86	116	109	93	101	96	0	0	0	0	0	0	94	134
TCGA-D6-6825-10A-01D-1912-08_HNSC	122	67	71	45	71	78	110	100	120	0	1	0	0	0	0	116	130
TCGA-D6-6826-10A-01D-1912-08_HNSC	129	0	0	79	129	112	116	127	109	15	49	0	65	86	0	62	127
TCGA-D6-6827-10A-01D-1912-08_HNSC	141	0	1	73	115	117	120	130	129	0	0	0	0	0	0	121	147
TCGA-D6-8568-10A-01D-2394-08_HNSC	122	70	66	63	151	74	68	69	0	20	83	78	56	125	0	0	109
TCGA-D6-8569-10A-01D-2394-08_HNSC	88	68	65	50	69	60	80	109	80	0	0	0	0	1	0	124	83

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-D6-A4Z9-10A-01D-A25E-08_HNSC	85	5	3	76	83	85	84	79	93	0	2	0	3	6	0	76	83
TCGA-D6-A4ZB-10A-01D-A25E-08_HNSC	82	3	1	78	83	75	68	93	76	15	46	3	49	64	30	4	87
TCGA-D6-A6EK-10A-01D-A31J-08_HNSC	93	0	0	52	92	84	85	101	69	13	40	63	0	71	29	1	105
TCGA-D6-A6EM-10A-01D-A31J-08_HNSC	86	49	0	43	103	80	75	74	61	12	40	0	58	64	0	53	93
TCGA-D6-A6EN-10A-01D-A31J-08_HNSC	80	70	81	1	1	2	76	86	80	0	0	1	0	0	23	52	93
TCGA-D6-A6EO-10A-01D-A31J-08_HNSC	85	59	68	35	67	61	59	48	57	0	39	0	43	60	0	58	92
TCGA-D6-A6EP-10A-01D-A31J-08_HNSC	86	0	0	62	90	86	77	82	70	14	42	0	56	72	27	1	87
TCGA-D6-A6EQ-10A-01D-A31J-08_HNSC	84	58	66	45	65	64	80	103	104	0	0	0	0	0	27	60	87
TCGA-D6-A6ES-10A-01D-A31J-08_HNSC	85	0	0	50	89	78	77	75	0	20	58	63	56	89	0	1	96
TCGA-D7-5577-10A-01D-1600-08_STAD	130	1	0	68	129	120	110	142	142	0	0	2	0	1	0	148	136
TCGA-D7-5578-10A-01D-1600-08_STAD	124	79	82	46	148	105	98	92	132	0	59	88	0	1	0	104	124
TCGA-D7-5579-10A-01D-1600-08_STAD	144	100	75	0	109	96	98	133	91	26	50	0	72	96	27	0	132
TCGA-D7-6518-10A-01D-1800-08_STAD	111	2	3	60	95	93	97	108	79	14	47	1	62	75	34	0	105
TCGA-D7-6519-10A-01D-1800-08_STAD	93	86	89	2	96	89	103	96	0	26	100	102	81	89	0	1	115
TCGA-D7-6520-10A-01D-1800-08_STAD	101	0	2	90	109	97	99	95	81	17	46	0	69	91	0	51	112
TCGA-D7-6521-10A-01D-1800-08_STAD	123	0	0	70	96	97	81	86	75	16	53	0	77	84	0	69	106
TCGA-D7-6522-10A-01D-1800-08_STAD	97	0	1	98	111	94	99	83	116	0	0	2	1	1	0	92	103
TCGA-D7-6524-10A-01D-1800-08_STAD	99	1	1	90	96	90	96	121	115	0	1	0	0	0	0	121	94
TCGA-D7-6525-10A-01D-1800-08_STAD	95	0	0	84	96	95	105	117	118	0	1	1	0	2	29	67	120
TCGA-D7-6526-10A-01D-1800-08_STAD	102	70	74	48	137	101	100	134	115	0	47	76	0	1	31	72	113
TCGA-D7-6527-10A-01D-1800-08_STAD	104	1	2	59	96	94	86	90	121	0	1	1	0	2	0	98	108
TCGA-D7-6528-10A-01D-1800-08_STAD	107	0	1	75	99	103	83	84	84	18	54	0	64	76	0	78	109
TCGA-D7-6815-10A-01D-1882-08_STAD	141	1	0	69	102	132	117	88	94	0	0	1	0	0	0	97	125
TCGA-D7-6817-10A-01D-1882-08_STAD	130	77	88	60	154	115	102	109	79	21	84	85	72	85	0	74	144
TCGA-D7-6818-10A-01D-1882-08_STAD	125	0	0	97	108	103	107	92	136	0	0	0	0	2	0	102	143
TCGA-D7-6820-10A-01D-1882-08_STAD	111	0	2	91	112	102	100	111	125	0	0	1	0	1	0	155	132
TCGA-D7-6822-10A-01D-1882-08_STAD	107	0	1	60	123	91	98	108	89	19	58	0	72	87	30	0	130
TCGA-D7-8570-10A-01D-2341-08_STAD	117	0	1	80	99	101	108	90	119	0	0	0	0	0	34	71	125
TCGA-D7-8572-10A-01D-2341-08_STAD	101	73	75	50	142	98	98	99	113	0	48	72	0	2	45	0	114
TCGA-D7-8573-10A-01D-2341-08_STAD	111	70	74	47	124	104	107	94	0	24	94	90	63	106	0	0	136
TCGA-D7-8574-10A-01D-2341-08_STAD	101	0	1	100	106	115	112	111	133	0	0	1	0	0	0	93	113
TCGA-D7-8575-10A-01D-2341-08_STAD	134	0	0	68	143	101	117	143	82	32	78	78	82	83	33	0	136
TCGA-D7-8576-10A-01D-2341-08_STAD	96	16	17	56	93	68	76	63	83	0	12	15	0	68	0	66	83
TCGA-D7-8578-10A-01D-2341-08_STAD	106	74	79	48	140	111	96	124	128	0	51	81	0	0	0	139	118
TCGA-D7-8579-10A-01D-2341-08_STAD	105	69	70	47	77	84	89	111	87	0	0	0	0	1	0	127	122
TCGA-D7-A4YT-10A-01D-A25E-08_STAD	96	4	1	64	94	87	88	88	75	18	45	1	64	72	0	68	110
TCGA-D7-A4YU-10A-01D-A25E-08_STAD	89	54	64	36	59	62	65	57	80	0	42	0	53	65	0	60	94
TCGA-D7-A4YV-10A-01D-A25E-08_STAD	89	0	1	60	93	87	91	107	106	0	0	1	1	1	0	125	105
TCGA-D7-A4YX-10A-01D-A25E-08_STAD	72	88	91	0	71	71	82	99	112	0	50	66	0	0	33	64	103
TCGA-D7-A4YY-10A-01D-A25E-08_STAD	92	63	69	46	67	64	78	99	81	0	0	0	0	0	0	114	93
TCGA-D7-A4Z0-10A-01D-A25E-08_STAD	120	0	1	85	86	89	74	121	101	0	0	0	1	3	33	66	105
TCGA-D7-A6ET-10A-01D-A32N-08_STAD	103	0	0	89	111	107	108	127	103	0	0	0	0	1	34	67	109
TCGA-D7-A6EV-10A-01D-A31J-08_STAD	80	61	72	35	73	66	75	101	100	0	0	0	0	1	24	60	92
TCGA-D7-A6EX-10A-01D-A31J-08_STAD	104	0	0	51	81	78	74	91	75	0	0	0	0	1	0	72	87
TCGA-D7-A6EY-10A-01D-A31J-08_STAD	83	65	2	48	111	77	78	100	62	17	41	0	66	66	0	56	87
TCGA-D7-A6EZ-10A-01D-A31J-08_STAD	88	64	68	48	109	86	72	75	62	20	71	69	61	76	0	52	89
TCGA-D7-A6F0-10A-01D-A31J-08_STAD	85	61	64	42	114	81	74	70	70	15	58	55	57	64	0	47	86
TCGA-D7-A6F2-10A-01D-A31J-08_STAD	78	76	77	0	75	65	83	88	70	14	59	71	1	71	29	0	92
TCGA-D7-A747-10A-21D-A33W-08_STAD	95	60	67	46	122	91	81	82	68	11	77	70	59	62	0	67	107
TCGA-D7-A748-10A-21D-A32N-08_STAD	115	2	3	64	95	104	111	121	75	14	61	0	74	86	0	71	116
TCGA-D7-A74A-10A-21D-A32N-08_STAD	101	99	96	0	99	108	95	89	105	0	81	100	1	1	38	0	127
TCGA-D7-A74B-10A-01D-A33W-08_STAD	84	68	66	47	97	82	86	119	94	15	44	61	0	0	24	56	100
TCGA-D8-A13Y-10A-01D-A110-09_BRCA	71	115	103	51	122	126	179	133	102	26	90	0	103	97	0	86	113
TCGA-D8-A13Z-10A-01D-A110-09_BRCA	48	59	64	33	15	53	116	109	92	0	0	0	0	0	0	53	69
TCGA-D8-A140-10A-01D-A110-09_BRCA	95	123	134	51	224	194	200	158	137	33	169	202	0	129	0	117	152
TCGA-D8-A141-10A-01D-A110-09_BRCA	79	0	0	69	141	149	176	166	214	0	0	0	0	0	0	188	124
TCGA-D8-A142-10A-01D-A110-09_BRCA	105	0	0	93	153	145	156	156	160	0	0	0	0	0	42	84	105
TCGA-D8-A143-10A-01D-A110-09_BRCA	54	114	121	39	103	78	161	103	110	27	72	0	101	110	0	66	129
TCGA-D8-A145-10A-01D-A110-09_BRCA	95	0	0	78	179	145	196	171	225	0	0	0	0	0	0	127	109
TCGA-D8-A146-10A-01D-A110-09_BRCA	75	122	111	44	71	92	168	106	143	0	0	0	0	0	0	109	135
TCGA-D8-A147-10A-01D-A110-09_BRCA	69	1	1	90	187	137	151	148	107	21	101	0	97	107	0	104	107
TCGA-D8-A1J8-10A-01D-A13O-09_BRCA	55	0	1	81	126	119	145	129	129	0	0	0	0	0	0	150	103
TCGA-D8-A1J9-10A-01D-A13O-09_BRCA	36	0	1	41	91	91	90	88	109	0	0	0	0	0	0	104	73
TCGA-D8-A1JB-10A-01D-A13O-09_BRCA	38	53	48	21	42	48	81	67	75	0	0	0	0	0	0	63	67
TCGA-D8-A1JC-10A-01D-A13O-09_BRCA	48	0	0	50	116	105	111	102	109	0	0	0	0	0	0	123	79
TCGA-D8-A1JD-10A-01D-A13O-09_BRCA	60	0	0	63	110	105	105	129	119	0	0	0	0	0	0	162	81
TCGA-D8-A1JE-10A-01D-A188-09_BRCA	31	85	80	0	31	41	85	65	50	16	50	79	0	43	0	27	57
TCGA-D8-A1JF-10A-01D-A17G-09_BRCA	57	113	114	1	74	79	108	123	77	21	87	106	0	86	0	68	82
TCGA-D8-A1JG-10A-01D-A13O-09_BRCA	37	67	59	26	92	92	109	107	91	15	37	53	0	2	29	40	74
TCGA-D8-A1JH-10A-01D-A13O-09_BRCA	47	60	58	34	72	52	104	109	102	0	0	0	0	0	0	99	75
TCGA-D8-A1JI-10A-01D-A13O-09_BRCA	53	105	98	0	104	103	104	107	76	17	97	124	0	77	36	0	75
TCGA-D8-A1JJ-10A-01D-A14K-09_BRCA	72	121	122	50	213	146	161	162	163	0	98	133	0	0	54	116	116
TCGA-D8-A1JK-10A-01D-A13O-09_BRCA	23	53	58	24	87	84	94	75	44	14	60	77	0	47	0	34	59
TCGA-D8-A1JL-10A-01D-A188-09_BRCA	69	0	0	56	111	116	107	149	146	0	0	0	0	0	0	169	90
TCGA-D8-A1JM-10A-01D-A188-09_BRCA	55	1	0	76	118	111	124	108	139	0	0	1	0	0	0	107	102
TCGA-D8-A1JN-10A-01D-A13O-09_BRCA	29	0	0	45	88	77	82	65	81	0	0	0	0	0	19	46	59
TCGA-D8-A1JP-10A-01D-A13O-09_BRCA	58	1	0	89	128	116	126	106	77	24	79	0	85	82	0	72	101
TCGA-D8-A1JS-10A-01D-A13O-09_BRCA	48	0	0	62	99	102	108	107	102	0	0	0	0	0	0	112	79
TCGA-D8-A1JT-10A-01D-A13O-09_BRCA	33	0	1	43	83	91	105	87	95	1	0	0	0	1	19	33	59
TCGA-D8-A1JU-10A-01D-A188-09_BRCA	21	59	52	0	24	31	59	54	39	8	50	29	18	33	9	1	44
TCGA-D8-A1X5-10A-01D-A14G-09_BRCA	32	1	0	46	67	82	86	58	86	0	0	0	0	0	0	59	55
TCGA-D8-A1X6-10A-01D-A14K-09_BRCA	45	74	64	32	124	111	98	69	80	24	87	74	69	73	0	54	74
TCGA-D8-A1X7-10A-01D-A14K-09_BRCA	44	0	1	43	72	34	58	38	50	0	0	0	0	52	0	40	54
TCGA-D8-A1X9-10A-01D-A17G-09_BRCA	33	57	54	23	84	74	93	51	80	0	33	44	0	2	26	25	68
TCGA-D8-A1XA-10A-01D-A14G-09_BRCA	49	0	0	39	103	104	97	98	69	14	64	0	70	67	37	0	78
TCGA-D8-A1XB-10A-01D-A14G-09_BRCA	52	0	0	62	99	95	107	107	104	1	0	0	0	0	0	120	76
TCGA-D8-A1XC-10A-01D-A14G-09_BRCA	37	0	0	31	62	67	71	55	95	0	0	0	0	0	11	29	44
TCGA-D8-A1XF-10A-01D-A14G-09_BRCA	62	0	0	54	90	70	97	84	104	0	1	0	1	0	19	35	57
TCGA-D8-A1XG-10A-01D-A14G-09_BRCA	61	58	64	29	115	90	103	81	98	0	45	71	0	1	39	61	82
TCGA-D8-A1XK-10A-01D-A14K-09_BRCA	49	126	114	0	87	95	90	57	81	0	107	137	0	89	37	0	97
TCGA-D8-A1XL-10A-01D-A14K-09_BRCA	59	0	2	63	138	134	155	102	95	26	85	0	105	107	0	93	94
TCGA-D8-A1XM-10A-01D-A14K-09_BRCA	44	0	0	62	133	113	124	106	85	20	60	0	94	98	0	77	89
TCGA-D8-A1XO-10A-01D-A14K-09_BRCA	50	108	110	0	70	84	84	59	69	0	119	77	88	86	0	71	81
TCGA-D8-A1XQ-10A-01D-A14K-09_BRCA	54	0	0	93	142	145	150	127	143	1	0	0	0	0	0	165	110
TCGA-D8-A1XR-10A-01D-A14K-09_BRCA	59	117	106	57	207	134	156	115	167	0	77	109	1	0	0	152	96
TCGA-D8-A1XS-10A-01D-A14K-09_BRCA	27	2	2	45	74	73	95	71	79	0	0	0	0	0	32	1	59

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-D8-A1XT-10A-01D-A14K-09_BRCA	70	134	156	0	0	0	139	152	180	0	0	0	0	0	0	188	105
TCGA-D8-A1XU-10A-01D-A14K-09_BRCA	57	1	0	49	110	127	126	120	140	0	0	0	0	0	0	173	85
TCGA-D8-A1XV-10A-01D-A14K-09_BRCA	61	93	96	44	167	135	116	111	91	22	147	101	96	98	0	90	91
TCGA-D8-A1XW-10A-01D-A14K-09_BRCA	68	134	136	0	0	0	145	117	168	0	0	0	0	0	0	130	101
TCGA-D8-A1XY-10A-01D-A14K-09_BRCA	63	3	2	81	133	123	136	127	146	0	0	0	0	0	0	114	83
TCGA-D8-A1XZ-10A-01D-A14K-09_BRCA	73	99	88	46	167	124	135	153	153	0	82	98	0	0	51	86	85
TCGA-D8-A1Y0-10A-01D-A14K-09_BRCA	46	64	60	27	59	56	92	87	103	0	0	0	0	0	0	71	77
TCGA-D8-A1Y1-10A-01D-A14K-09_BRCA	31	65	48	20	62	51	91	76	90	0	0	1	1	0	0	75	62
TCGA-D8-A1Y2-10A-01D-A159-09_BRCA	41	0	1	38	57	87	93	82	74	0	0	1	0	0	0	17	66
TCGA-D8-A1Y3-10A-01D-A159-09_BRCA	39	86	73	42	70	73	108	104	86	0	0	1	0	0	34	50	78
TCGA-D8-A27E-10A-01D-A16D-09_BRCA	39	50	67	36	117	78	111	98	102	16	36	62	0	0	0	76	67
TCGA-D8-A27F-10A-01D-A16D-09_BRCA	31	0	0	36	108	81	100	64	56	20	52	0	55	67	0	40	66
TCGA-D8-A27G-10A-01D-A16D-09_BRCA	64	68	64	43	138	85	110	102	91	17	78	62	62	56	0	52	73
TCGA-D8-A27H-10A-01D-A16D-09_BRCA	55	66	71	33	67	64	97	103	114	0	0	0	0	0	0	105	73
TCGA-D8-A27I-10A-02D-A16D-09_BRCA	36	46	38	30	101	78	97	76	88	0	36	47	0	0	0	76	62
TCGA-D8-A27K-10A-01D-A16D-09_BRCA	60	1	0	79	117	112	129	131	115	0	0	1	1	0	0	124	90
TCGA-D8-A27L-10A-01D-A16D-09_BRCA	59	79	98	33	82	76	123	111	77	22	95	0	91	75	0	68	80
TCGA-D8-A27M-10A-01D-A16D-09_BRCA	31	0	0	54	71	66	83	58	47	14	36	49	0	48	0	36	58
TCGA-D8-A27N-10A-01D-A16D-09_BRCA	39	94	90	0	58	48	110	70	54	18	64	93	0	44	23	0	68
TCGA-D8-A27P-10A-01D-A16D-09_BRCA	45	0	0	39	99	57	69	53	69	0	0	0	0	74	0	57	47
TCGA-D8-A27R-10A-01D-A16D-09_BRCA	54	1	0	66	91	95	117	92	115	0	0	0	0	0	0	96	74
TCGA-D8-A27T-10A-01D-A16D-09_BRCA	47	71	75	28	56	58	124	69	125	0	0	0	0	0	0	86	74
TCGA-D8-A27V-10A-01D-A17D-09_BRCA	30	55	36	20	49	44	78	47	70	0	0	0	0	0	20	19	60
TCGA-D8-A27W-10A-01D-A16D-09_BRCA	51	0	1	61	113	104	131	85	110	0	1	0	0	0	0	96	73
TCGA-D8-A3Z5-10A-01D-A243-09_BRCA	36	55	48	18	51	53	82	74	112	2	2	1	0	1	0	83	70
TCGA-D8-A3Z6-10A-01D-A23C-09_BRCA	47	54	40	13	54	48	98	69	86	0	1	0	1	2	0	77	73
TCGA-D8-A4Z1-10A-01D-A25Q-09_BRCA	56	0	3	27	76	85	83	78	112	0	1	0	0	0	0	68	75
TCGA-D9-A148-10A-01D-A19A-08_SKCM	108	0	1	76	94	92	85	79	97	0	0	0	0	0	0	97	115
TCGA-D9-A149-10A-01D-A198-08_SKCM	101	0	0	57	81	71	88	77	88	0	0	0	0	2	36	61	123
TCGA-D9-A1JW-10A-01D-A19A-08_SKCM	100	53	56	45	56	65	78	78	94	0	0	2	0	1	0	104	105
TCGA-D9-A1JX-10A-01D-A19A-08_SKCM	123	59	78	58	80	73	110	93	125	0	0	0	0	0	0	97	159
TCGA-D9-A1X3-10A-01D-A199-08_SKCM	92	2	0	58	97	68	71	93	65	13	44	0	54	74	0	62	105
TCGA-D9-A3Z1-10A-01D-A23B-08_SKCM	92	77	63	45	66	76	88	106	66	16	43	1	61	67	0	66	100
TCGA-D9-A3Z3-10A-01D-A23B-08_SKCM	118	2	2	74	93	79	81	112	102	0	5	4	4	3	0	116	97
TCGA-D9-A3Z4-10A-01D-A23B-08_SKCM	92	73	72	45	124	79	85	112	74	19	79	74	65	79	0	73	107
TCGA-D9-A4Z2-10A-01D-A24R-08_SKCM	73	71	78	7	65	62	79	91	88	0	36	59	1	5	0	53	92
TCGA-D9-A4Z3-10A-01D-A25O-08_SKCM	76	0	0	43	71	65	59	88	64	0	0	0	0	0	0	83	82
TCGA-D9-A4Z5-10A-01D-A25O-08_SKCM	72	53	54	34	85	69	73	64	55	9	47	70	0	58	0	43	84
TCGA-D9-A4Z6-10A-01D-A25O-08_SKCM	78	52	62	39	62	51	74	63	88	0	0	0	0	0	35	0	87
TCGA-D9-A6E9-10A-01D-A30X-08_SKCM	89	61	75	48	64	64	74	75	100	0	0	0	0	0	0	67	98
TCGA-D9-A6EA-10A-01D-A30X-08_SKCM	81	63	62	35	131	83	74	91	97	0	38	65	0	0	27	55	99
TCGA-D9-A6EC-10A-01D-A30X-08_SKCM	91	64	65	50	66	60	82	106	114	0	0	0	0	0	0	71	103
TCGA-D9-A6EG-10A-01D-A32N-08_SKCM	104	68	80	46	123	77	70	58	80	0	50	71	0	73	31	0	85
TCGA-DA-A1HV-10A-01D-A198-08_SKCM	120	0	0	68	78	71	73	92	85	0	0	0	0	0	22	56	102
TCGA-DA-A1HW-10A-01D-A19A-08_SKCM	98	66	67	0	73	68	79	96	98	0	1	0	0	0	0	106	102
TCGA-DA-A1HY-10A-01D-A19A-08_SKCM	105	0	0	68	78	93	67	78	94	0	0	0	0	0	0	91	110
TCGA-DA-A1I0-10B-01D-A20D-08_SKCM	100	59	58	44	114	96	74	89	101	0	44	69	0	1	28	67	123
TCGA-DA-A1I1-10A-01D-A198-08_SKCM	86	76	76	0	0	0	72	82	62	15	32	0	54	66	0	49	97
TCGA-DA-A1I2-10A-01D-A19A-08_SKCM	95	40	61	44	83	84	77	77	47	13	57	71	0	58	0	35	107
TCGA-DA-A1I4-10A-01D-A198-08_SKCM	129	64	64	51	79	61	64	67	64	0	38	1	49	69	0	74	110
TCGA-DA-A1I5-10A-01D-A199-08_SKCM	133	61	55	45	107	82	86	85	84	0	34	59	0	0	0	98	110
TCGA-DA-A1I7-10A-01D-A199-08_SKCM	136	0	0	82	107	93	88	88	0	26	57	1	91	107	0	0	146
TCGA-DA-A1I8-10A-01D-A199-08_SKCM	89	0	0	72	111	107	83	98	99	12	18	40	0	0	0	71	114
TCGA-DA-A1IA-10A-01D-A198-08_SKCM	97	0	1	75	87	65	93	90	87	0	1	0	0	2	26	48	117
TCGA-DA-A1IB-10A-01D-A198-08_SKCM	100	52	62	37	57	52	75	73	80	0	38	38	0	0	30	0	102
TCGA-DA-A1IC-10A-01D-A199-08_SKCM	126	55	68	51	72	76	96	105	77	22	41	1	42	72	27	0	138
TCGA-DA-A3F2-10A-01D-A20D-08_SKCM	92	0	0	55	98	95	84	91	73	14	42	1	50	74	0	54	117
TCGA-DA-A3F3-10A-01D-A20D-08_SKCM	94	1	1	89	91	90	85	79	66	23	50	0	48	74	0	63	105
TCGA-DA-A3F5-10A-01D-A20D-08_SKCM	127	67	67	48	82	81	96	88	83	22	52	0	58	80	0	65	116
TCGA-DA-A3F8-10A-01D-A20D-08_SKCM	89	0	0	84	88	80	79	87	107	0	0	1	0	0	0	78	108
TCGA-DB-5270-10A-01D-1468-08_LGG	108	68	70	41	69	66	85	124	95	0	0	0	0	0	33	75	99
TCGA-DB-5273-10A-01D-1468-08_LGG	114	0	0	47	104	96	93	122	123	1	0	0	0	0	38	78	109
TCGA-DB-5274-10A-01D-1468-08_LGG	149	0	0	85	114	103	86	100	131	0	1	0	1	1	0	115	112
TCGA-DB-5275-10A-01D-1468-08_LGG	107	0	0	83	106	104	91	87	86	17	49	1	68	77	0	76	127
TCGA-DB-5276-10A-01D-1468-08_LGG	99	71	68	45	67	71	87	107	101	0	0	0	0	0	32	77	101
TCGA-DB-5277-10A-01D-1468-08_LGG	108	65	64	43	122	100	93	93	99	0	36	61	0	0	50	1	98
TCGA-DB-5278-10A-01D-1468-08_LGG	103	0	0	53	94	106	88	103	74	20	52	0	59	76	0	75	105
TCGA-DB-5279-10A-01D-1468-08_LGG	144	0	0	59	93	98	86	122	122	1	0	1	0	1	0	139	106
TCGA-DB-5280-10A-01D-1468-08_LGG	102	0	0	79	115	105	94	90	88	0	0	0	0	0	0	104	111
TCGA-DB-5281-10A-01D-1468-08_LGG	110	65	73	47	117	99	95	90	90	0	56	76	0	0	0	91	133
TCGA-DB-A4X9-10A-01D-A26K-08_LGG	148	1	1	90	130	129	120	110	132	0	0	0	0	0	0	150	168
TCGA-DB-A4XA-10A-01D-A26K-08_LGG	83	52	55	47	77	73	93	100	98	1	0	0	1	6	35	2	103
TCGA-DB-A4XB-10A-01D-A26K-08_LGG	86	59	56	42	107	86	85	74	57	13	56	58	48	71	0	57	96
TCGA-DB-A4XC-10A-01D-A26K-08_LGG	93	80	79	4	81	64	93	95	72	25	63	80	0	68	0	43	104
TCGA-DB-A4XD-10A-01D-A27N-08_LGG	123	0	0	99	112	112	107	95	137	0	0	0	0	1	0	95	132
TCGA-DB-A4XE-10A-01D-A27N-08_LGG	123	0	0	69	116	104	111	127	124	0	0	0	0	0	0	144	132
TCGA-DB-A4XF-10A-01D-A27N-08_LGG	130	71	70	56	76	80	104	101	107	0	0	0	0	0	0	99	143
TCGA-DB-A4XG-10A-01D-A27N-08_LGG	115	87	80	54	69	79	96	127	123	0	0	0	0	0	30	69	137
TCGA-DB-A4XH-10A-01D-A27N-08_LGG	107	63	76	48	86	76	98	107	123	1	0	0	0	0	0	146	141
TCGA-DB-A64L-10A-01D-A29Q-08_LGG	98	50	63	42	118	102	76	114	63	14	66	68	50	67	30	0	115
TCGA-DB-A64O-10A-01D-A29Q-08_LGG	111	0	0	89	102	92	91	119	136	0	0	0	0	0	0	146	145
TCGA-DB-A64P-10A-01D-A29Q-08_LGG	106	65	79	48	80	81	98	107	125	0	1	0	1	0	0	152	135
TCGA-DB-A64Q-10A-01D-A29Q-08_LGG	123	0	0	56	121	113	99	103	126	0	0	0	0	1	0	141	135
TCGA-DB-A64R-10A-01D-A29Q-08_LGG	142	0	0	78	101	107	92	99	116	0	0	0	0	0	0	101	134
TCGA-DB-A64S-10A-01D-A29Q-08_LGG	148	0	0	86	107	105	89	112	111	0	0	0	0	0	34	59	125
TCGA-DB-A64U-10A-01D-A29Q-08_LGG	119	69	82	46	85	79	103	101	73	17	47	0	65	84	0	71	121
TCGA-DB-A64V-10A-01D-A29Q-08_LGG	119	79	77	52	87	77	110	124	135	0	0	0	0	0	41	76	134
TCGA-DB-A64W-10A-01D-A29Q-08_LGG	125	0	0	81	119	123	113	120	150	0	0	0	0	2	0	114	160
TCGA-DB-A64X-10A-01D-A29Q-08_LGG	135	83	76	60	157	125	109	99	135	0	53	76	0	0	0	117	163
TCGA-DB-A75K-10A-01D-A329-08_LGG	79	0	0	73	79	76	76	82	83	0	0	0	0	1	0	98	100
TCGA-DB-A75L-10A-01D-A329-08_LGG	81	0	1	65	80	77	93	94	97	0	0	0	0	0	23	54	99
TCGA-DB-A75M-10A-01D-A329-08_LGG	79	56	60	44	68	60	77	83	73	0	0	0	0	0	0	90	91
TCGA-DB-A75O-10A-01D-A329-08_LGG	104	55	55	35	104	80	74	73	71	19	48	71	0	59	19	0	86
TCGA-DB-A75P-10A-01D-A329-08_LGG	87	49	61	40	64	62	106	74	0	22	54	0	79	101	0	0	94
TCGA-DC-4745-10A-01D-1733-10_READ	63	1	1	50	81	73	98	68	105	0	0	0	0	2	0	70	98
TCGA-DC-4749-10A-01D-1733-10_READ	77	0	2	42	92	76	105	88	63	9	31	0	31	66	14	0	128

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DC-5337-10A-01D-1657-10_READ	80	53	64	34	62	58	113	52	78	16	22	0	48	52	0	21	111
TCGA-DC-5869-10A-01D-1657-10_READ	92	62	61	27	87	94	118	58	66	11	37	43	57	62	0	20	109
TCGA-DC-6154-10A-01D-1924-10_READ	32	0	0	31	37	66	72	33	46	0	0	0	0	0	0	48	61
TCGA-DC-6155-10A-01D-1657-10_READ	89	0	0	71	129	105	133	81	4	18	51	51	64	114	0	0	119
TCGA-DC-6157-10A-01D-1657-10_READ	58	91	92	0	61	45	105	43	112	0	20	38	0	0	0	50	115
TCGA-DC-6158-10A-01D-1657-10_READ	79	54	68	29	84	86	129	51	133	0	20	48	0	2	0	38	131
TCGA-DC-6681-10A-01D-1826-10_READ	47	0	0	37	49	41	59	38	38	8	23	0	20	25	0	25	70
TCGA-DC-6682-10A-01D-1826-10_READ	61	25	30	20	41	56	62	51	68	0	23	22	0	0	0	45	70
TCGA-DC-6683-10A-01D-1826-10_READ	47	0	0	39	53	58	65	52	35	10	15	0	41	24	0	37	65
TCGA-DD-A113-10A-01D-A12Z-10_LIHC	89	70	59	30	126	96	113	83	139	0	32	56	0	0	24	36	111
TCGA-DD-A114-10A-01D-A12Z-10_LIHC	95	0	0	60	123	105	106	83	133	0	0	0	0	0	0	44	84
TCGA-DD-A115-10A-01D-A12Z-10_LIHC	91	0	0	69	117	100	115	65	120	0	0	0	0	0	0	79	104
TCGA-DD-A116-10A-01D-A12Z-10_LIHC	63	0	0	29	62	54	56	44	59	0	0	0	0	0	14	20	73
TCGA-DD-A119-10A-01D-A12Z-10_LIHC	80	64	58	27	61	54	106	64	127	0	0	0	0	0	15	41	105
TCGA-DD-A11A-10A-01D-A12Z-10_LIHC	50	0	0	16	65	55	85	52	68	9	14	27	0	1	14	0	69
TCGA-DD-A11B-10A-01D-A12Z-10_LIHC	84	101	96	0	0	1	66	40	0	11	80	55	60	102	0	0	94
TCGA-DD-A1EA-10A-01D-A12Z-10_LIHC	58	30	44	18	39	37	71	34	62	0	0	0	0	0	18	0	65
TCGA-DD-A1EB-10A-01D-A12Z-10_LIHC	51	0	0	27	55	55	61	35	34	15	16	0	19	32	0	12	67
TCGA-DD-A1ED-10A-01D-A152-10_LIHC	76	50	43	30	65	62	79	74	49	15	43	67	0	39	0	38	90
TCGA-DD-A1EE-10A-01D-A12Z-10_LIHC	55	0	0	27	52	39	67	39	66	0	2	0	0	0	8	15	68
TCGA-DD-A1EF-10A-01D-A12Z-10_LIHC	48	33	32	16	33	28	61	33	66	0	0	0	0	0	0	29	60
TCGA-DD-A1EG-10A-01D-A20W-10_LIHC	68	75	70	0	63	76	96	75	50	11	59	79	45	45	18	0	83
TCGA-DD-A1EH-10A-01D-A12Z-10_LIHC	51	57	59	0	24	30	34	23	0	11	46	37	27	46	0	0	66
TCGA-DD-A1EJ-10A-01D-A152-10_LIHC	94	5	8	5	9	10	28	157	41	0	0	0	0	0	0	80	32
TCGA-DD-A1EK-10A-01D-A20W-10_LIHC	79	1	0	46	93	115	108	110	126	0	0	0	0	0	19	37	93
TCGA-DD-A1EL-10A-01D-A152-10_LIHC	71	52	58	36	104	80	104	78	98	0	32	48	0	1	26	43	95
TCGA-DD-A4NF-10A-01D-A27I-10_LIHC	82	75	74	47	104	107	117	101	101	1	50	0	62	1	0	80	68
TCGA-DD-A4NG-10A-01D-A27I-10_LIHC	71	0	1	45	84	101	79	74	61	8	30	0	56	68	0	69	93
TCGA-DD-A4NH-10A-01D-A27I-10_LIHC	90	56	49	39	104	117	113	94	99	0	13	61	0	0	47	0	88
TCGA-DD-A4NI-10A-01D-A27I-10_LIHC	83	1	1	66	71	96	86	70	104	0	0	2	0	0	27	58	79
TCGA-DD-A4NJ-10A-01D-A27I-10_LIHC	76	58	62	36	43	85	98	77	103	0	0	0	0	0	0	87	86
TCGA-DD-A4NK-10A-01D-A28X-10_LIHC	89	60	58	25	61	66	107	115	90	0	0	1	0	0	0	117	75
TCGA-DD-A4NN-10A-01D-A28X-10_LIHC	67	1	1	45	70	84	90	90	46	4	41	0	57	71	0	59	70
TCGA-DD-A4NO-10A-01D-A28X-10_LIHC	59	54	41	24	86	86	85	58	54	2	56	70	0	47	0	34	58
TCGA-DD-A4NP-10A-01D-A28X-10_LIHC	60	2	1	38	59	83	74	59	28	5	31	45	0	46	0	35	54
TCGA-DD-A4NQ-10A-01D-A28X-10_LIHC	83	79	86	0	47	56	81	84	65	0	44	56	0	0	26	56	57
TCGA-DD-A4NR-10A-01D-A30V-10_LIHC	43	19	51	14	23	36	77	56	23	9	21	0	39	31	0	21	52
TCGA-DD-A4NS-10A-01D-A30V-10_LIHC	41	38	21	18	25	27	41	28	38	0	18	0	18	27	0	25	45
TCGA-DD-A4NV-10A-01D-A30V-10_LIHC	39	32	40	0	28	32	70	59	54	0	0	0	0	0	15	30	58
TCGA-DE-A0XZ-10A-01D-A17V-08_THCA	121	78	79	60	81	71	82	126	84	18	58	81	0	93	30	0	126
TCGA-DE-A0Y2-10A-01D-A10S-08_THCA	90	74	71	46	74	77	92	108	122	0	0	0	0	2	34	84	98
TCGA-DE-A0Y3-10A-01D-A10S-08_THCA	95	70	67	44	81	75	85	92	104	0	0	0	0	0	40	1	101
TCGA-DE-A2OL-10A-01D-A18F-08_THCA	92	82	89	1	71	65	91	72	99	0	53	70	0	0	35	0	110
TCGA-DE-A3KN-10A-01D-A20C-08_THCA	89	0	0	96	96	91	87	76	94	0	0	1	0	1	40	1	114
TCGA-DE-A4M8-10A-01D-A25A-08_THCA	73	0	0	44	76	72	67	97	73	0	0	0	0	0	0	111	77
TCGA-DE-A4M9-10A-01D-A25A-08_THCA	64	0	0	49	67	68	62	67	69	0	0	0	0	0	21	38	72
TCGA-DE-A4MA-10A-01D-A25A-08_THCA	71	1	2	59	69	65	62	85	56	9	34	2	51	44	0	50	94
TCGA-DE-A4MB-10A-01D-A25A-08_THCA	156	88	94	61	193	136	144	126	171	0	46	98	0	0	37	72	171
TCGA-DE-A4MC-10A-01D-A25A-08_THCA	159	64	79	92	126	130	134	128	144	5	9	0	15	45	31	63	178
TCGA-DF-A2KN-10A-01D-A17W-09_UCEC	52	0	2	31	98	80	92	111	133	0	0	1	2	0	0	117	83
TCGA-DF-A2KR-10A-01D-A17W-09_UCEC	47	2	1	32	68	62	77	80	105	0	0	0	0	0	33	44	56
TCGA-DF-A2KS-10A-01D-A18P-09_UCEC	56	66	64	21	130	105	103	101	112	0	54	72	1	0	39	67	74
TCGA-DF-A2KU-10A-01D-A17W-09_UCEC	35	43	49	12	49	55	90	58	92	0	1	0	0	0	21	45	63
TCGA-DF-A2KV-10A-01D-A17W-09_UCEC	46	0	0	28	80	76	92	66	64	10	37	0	55	62	0	53	68
TCGA-DF-A2KY-10A-01D-A20S-09_UCEC	43	61	45	14	55	46	96	90	60	14	41	64	1	61	0	45	71
TCGA-DF-A2KZ-10A-01D-A20S-09_UCEC	40	65	58	14	57	71	101	81	120	0	0	0	0	0	0	79	68
TCGA-DF-A2L0-10A-01D-A17W-09_UCEC	34	2	0	26	79	47	63	46	61	0	0	0	0	54	0	41	44
TCGA-DG-A2KH-10A-01D-A22X-09_CESC	47	70	62	14	103	86	95	101	74	17	77	80	0	71	0	52	80
TCGA-DG-A2KJ-10A-01D-A18J-09_CESC	38	51	47	22	66	54	87	85	92	0	2	1	0	1	34	49	68
TCGA-DG-A2KK-10A-01D-A17W-09_CESC	65	0	1	44	106	116	113	102	99	11	55	0	74	81	0	66	84
TCGA-DG-A2KL-10A-01D-A17W-09_CESC	57	0	0	35	140	122	131	109	7	18	125	70	101	100	0	1	78
TCGA-DG-A2KM-10A-01D-A17W-09_CESC	53	0	0	27	93	93	109	98	135	0	0	0	0	0	0	92	91
TCGA-DH-5140-10A-01D-1468-08_LGG	152	77	85	51	87	81	99	110	126	0	1	0	0	0	0	104	135
TCGA-DH-5141-10A-01D-1468-08_LGG	114	1	1	72	114	113	127	153	84	23	61	0	77	93	41	1	153
TCGA-DH-5142-10A-01D-1468-08_LGG	107	93	89	1	87	85	87	119	97	0	50	83	0	1	36	64	112
TCGA-DH-5143-10A-01D-1468-08_LGG	148	79	84	45	143	112	92	129	129	0	57	0	1	1	39	89	128
TCGA-DH-5144-10A-01D-1468-08_LGG	118	0	0	67	101	110	107	136	113	0	1	1	1	3	44	84	116
TCGA-DH-A669-10A-01D-A31J-08_LGG	83	0	0	50	83	81	75	94	73	0	0	0	0	0	0	114	93
TCGA-DH-A66B-10A-01D-A29Q-08_LGG	151	0	0	69	146	150	134	142	164	0	0	0	0	0	0	155	173
TCGA-DH-A66D-10A-01D-A31J-08_LGG	86	0	1	59	109	85	76	73	0	26	70	0	81	88	0	0	95
TCGA-DH-A66F-10A-01D-A29Q-08_LGG	118	0	1	101	125	133	111	133	99	17	53	0	84	81	0	84	135
TCGA-DH-A66G-10A-01D-A31J-08_LGG	79	0	0	83	81	80	84	112	77	0	0	0	0	0	0	116	96
TCGA-DI-A0WH-10B-01D-A12J-09_UCEC	117	0	0	115	193	194	192	195	193	0	0	0	0	0	0	222	150
TCGA-DI-A1BU-10A-01D-A135-09_UCEC	41	32	32	10	78	65	58	60	75	0	29	34	0	1	20	29	48
TCGA-DI-A1BY-10A-01D-A135-09_UCEC	49	65	49	12	57	54	97	74	68	13	50	1	58	57	0	55	72
TCGA-DI-A1C3-10A-01D-A135-09_UCEC	50	3	2	20	80	96	91	79	122	0	0	0	1	1	0	83	74
TCGA-DI-A2QT-10A-01D-A19Y-09_UCEC	51	71	62	21	70	70	97	65	109	0	0	1	0	1	44	1	84
TCGA-DJ-A13L-10A-01D-A21Z-08_THCA	96	62	67	49	70	73	80	79	74	21	54	0	65	78	0	60	105
TCGA-DJ-A13M-10A-01D-A10S-08_THCA	116	87	74	45	135	100	94	103	89	18	77	84	70	75	0	83	126
TCGA-DJ-A13O-10A-01D-A10S-08_THCA	116	76	73	43	92	82	100	112	83	18	45	0	70	90	0	69	124
TCGA-DJ-A13P-10A-01D-A10S-08_THCA	145	80	82	44	89	71	87	123	111	0	0	0	0	1	37	83	124
TCGA-DJ-A13R-10A-01D-A10S-08_THCA	134	62	68	47	126	102	89	102	93	0	52	76	0	1	0	138	113
TCGA-DJ-A13S-10A-01D-A10S-08_THCA	96	0	0	80	104	111	77	124	130	0	0	1	0	2	34	78	120
TCGA-DJ-A13T-10A-01D-A10S-08_THCA	97	71	76	48	80	72	86	122	78	15	55	0	65	77	0	73	118
TCGA-DJ-A13U-10A-01D-A10S-08_THCA	97	68	78	43	76	70	100	116	82	23	47	0	68	83	32	0	121
TCGA-DJ-A13V-10A-01D-A10S-08_THCA	129	0	1	88	109	112	94	128	122	0	0	0	0	0	0	140	130
TCGA-DJ-A13W-10A-01D-A10S-08_THCA	115	73	76	48	131	105	108	95	106	0	54	84	0	0	0	106	120
TCGA-DJ-A13X-10A-01D-A10S-08_THCA	119	106	97	1	85	90	105	120	88	17	76	88	63	90	35	0	127
TCGA-DJ-A1QD-10A-01D-A14W-08_THCA	92	67	63	45	68	70	55	58	0	16	69	0	78	88	0	0	100
TCGA-DJ-A1QE-10A-01D-A14W-08_THCA	107	59	69	41	77	72	97	84	73	19	41	0	64	78	0	61	128
TCGA-DJ-A1QF-10A-01D-A14W-08_THCA	100	91	112	0	63	67	123	112	80	24	80	69	95	76	30	0	143
TCGA-DJ-A1QG-10A-01D-A14W-08_THCA	86	91	88	2	72	67	67	60	72	0	71	66	57	82	0	54	117
TCGA-DJ-A1QH-10A-01D-A14W-08_THCA	90	1	3	64	102	105	105	81	105	0	0	0	0	0	0	72	141
TCGA-DJ-A1QI-10A-01D-A14W-08_THCA	97	82	112	0	0	0	98	90	77	19	36	0	48	82	21	0	135
TCGA-DJ-A1QL-10A-01D-A14W-08_THCA	127	59	64	39	119	91	96	82	74	22	71	86	0	73	24	1	133
TCGA-DJ-A1QM-10A-01D-A14W-08_THCA	119	0	0	85	116	107	102	83	56	20	39	0	57	60	0	52	130

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DJ-A1QN-10A-01D-A14W-08_THCA	92	63	69	39	106	89	86	73	71	13	63	65	62	65	0	52	114
TCGA-DJ-A1QO-10A-01D-A14W-08_THCA	91	0	1	57	101	96	95	85	110	0	0	0	0	2	24	49	115
TCGA-DJ-A1QQ-10A-01D-A14W-08_THCA	104	57	64	43	122	101	97	104	101	0	36	85	0	1	0	72	143
TCGA-DJ-A2PN-10A-01D-A19M-08_THCA	136	0	1	68	118	113	95	113	137	0	0	1	0	0	29	71	149
TCGA-DJ-A2PO-10A-01D-A19M-08_THCA	118	2	3	79	127	129	130	117	131	0	1	1	0	0	0	109	154
TCGA-DJ-A2PP-10A-01D-A19M-08_THCA	118	69	69	54	88	70	106	109	85	18	61	0	65	91	34	2	144
TCGA-DJ-A2PQ-10A-01D-A18F-08_THCA	94	64	66	48	119	91	86	109	64	16	71	96	1	73	0	60	103
TCGA-DJ-A2PR-10A-01D-A19M-08_THCA	104	71	69	59	84	77	80	56	90	0	56	0	56	71	0	62	149
TCGA-DJ-A2PS-10A-01D-A18F-08_THCA	107	70	72	58	84	86	82	71	84	0	55	0	68	84	34	0	116
TCGA-DJ-A2PT-10A-01D-A18F-08_THCA	96	0	2	88	98	99	89	108	71	18	53	2	63	81	0	62	124
TCGA-DJ-A2PU-10A-01D-A19M-08_THCA	91	51	69	44	66	61	78	99	115	0	0	0	0	0	0	110	104
TCGA-DJ-A2PV-10A-01D-A19M-08_THCA	115	3	0	77	122	119	111	95	114	0	1	1	2	3	0	96	147
TCGA-DJ-A2PW-10A-01D-A19M-08_THCA	110	2	3	106	123	125	101	92	118	0	0	0	1	1	0	95	170
TCGA-DJ-A2PX-10A-01D-A18F-08_THCA	100	0	1	65	107	91	97	113	107	0	0	0	0	0	0	125	127
TCGA-DJ-A2PY-10A-01D-A18F-08_THCA	105	0	0	87	98	101	92	79	118	0	1	0	0	1	0	91	104
TCGA-DJ-A2PZ-10A-01D-A18F-08_THCA	102	0	0	70	119	107	93	109	77	19	38	0	62	78	0	71	112
TCGA-DJ-A2Q0-10A-01D-A202-08_THCA	92	62	62	38	58	65	71	67	79	0	0	0	0	0	0	75	86
TCGA-DJ-A2Q1-10A-01D-A19M-08_THCA	102	55	67	49	141	99	112	103	122	0	37	76	0	0	0	104	136
TCGA-DJ-A2Q2-10A-01D-A19M-08_THCA	108	65	76	56	117	109	111	74	108	0	32	68	0	0	17	44	150
TCGA-DJ-A2Q3-10A-01D-A18F-08_THCA	140	69	71	90	112	102	103	92	123	0	1	0	0	0	0	89	131
TCGA-DJ-A2Q4-10A-01D-A18F-08_THCA	95	62	63	47	74	74	92	84	83	13	55	0	59	73	0	73	105
TCGA-DJ-A2Q5-10A-01D-A18F-08_THCA	100	0	0	60	95	90	95	113	93	0	0	0	0	0	33	59	104
TCGA-DJ-A2Q6-10A-01D-A18F-08_THCA	134	0	0	89	99	84	84	122	107	0	0	0	1	0	29	58	113
TCGA-DJ-A2Q7-10A-01D-A18F-08_THCA	119	0	5	97	105	101	82	85	74	15	45	0	60	70	0	72	102
TCGA-DJ-A2Q8-10A-01D-A18F-08_THCA	110	65	63	52	78	67	92	101	82	0	0	0	0	0	30	64	110
TCGA-DJ-A2Q9-10A-01D-A18F-08_THCA	91	0	0	77	97	87	83	95	76	12	42	0	63	68	34	0	106
TCGA-DJ-A2QA-10A-01D-A18F-08_THCA	112	0	0	62	95	94	89	73	104	0	0	0	0	0	38	0	112
TCGA-DJ-A2QB-10A-01D-A19M-08_THCA	104	70	71	53	73	80	105	106	131	0	0	0	0	0	34	65	126
TCGA-DJ-A2QC-10A-01D-A18F-08_THCA	98	62	67	50	69	67	85	82	113	0	0	0	0	2	0	86	111
TCGA-DJ-A3UK-10A-01D-A22D-08_THCA	90	87	88	1	80	69	95	103	76	23	70	83	0	72	22	0	100
TCGA-DJ-A3UM-10A-01D-A22D-08_THCA	100	0	0	63	87	91	90	90	97	0	0	0	0	0	32	66	109
TCGA-DJ-A3UN-10A-01D-A22D-08_THCA	97	0	0	60	103	106	81	97	80	17	47	0	59	73	28	0	104
TCGA-DJ-A3UO-10A-01D-A22D-08_THCA	90	64	54	47	74	1	60	53	63	0	1	1	0	73	0	61	86
TCGA-DJ-A3UP-10A-01D-A22D-08_THCA	90	0	1	52	98	82	91	94	1	31	65	0	74	99	0	0	105
TCGA-DJ-A3UQ-10A-01D-A22D-08_THCA	92	4	0	61	84	106	88	83	92	0	0	0	0	1	29	62	108
TCGA-DJ-A3UR-10A-01D-A22D-08_THCA	101	0	2	80	95	86	89	100	80	18	55	0	63	80	33	0	108
TCGA-DJ-A3US-10A-01D-A22D-08_THCA	94	0	0	54	94	84	71	88	67	12	30	0	52	70	29	0	103
TCGA-DJ-A3UT-10A-01D-A22D-08_THCA	95	1	0	76	79	91	65	70	67	17	37	0	58	62	0	55	101
TCGA-DJ-A3UU-10A-01D-A22D-08_THCA	106	73	66	46	77	68	95	72	78	19	55	74	0	83	0	68	122
TCGA-DJ-A3UV-10A-01D-A22D-08_THCA	87	0	0	54	94	82	87	76	84	0	0	2	0	0	27	64	91
TCGA-DJ-A3UW-10A-01D-A22D-08_THCA	98	65	68	52	73	68	83	83	79	13	47	72	0	73	29	0	107
TCGA-DJ-A3UX-10A-01D-A22D-08_THCA	123	1	2	61	102	90	82	97	77	18	54	70	0	87	0	74	116
TCGA-DJ-A3UY-10A-01D-A22D-08_THCA	88	0	0	66	91	99	86	73	87	0	0	1	0	1	37	1	113
TCGA-DJ-A3UZ-10A-01D-A22Z-08_THCA	95	0	2	62	112	95	94	87	98	1	2	1	0	2	26	63	134
TCGA-DJ-A3V0-10A-01D-A22Z-08_THCA	159	113	93	73	193	171	188	128	131	22	114	119	92	130	0	68	197
TCGA-DJ-A3V2-10A-01D-A22Z-08_THCA	77	56	47	28	56	53	71	68	52	7	39	0	56	57	0	49	83
TCGA-DJ-A3V3-10A-01D-A22Z-08_THCA	76	66	55	0	71	71	62	70	57	12	59	53	47	60	23	0	79
TCGA-DJ-A3V4-10A-01D-A22Z-08_THCA	102	70	76	49	72	81	97	96	107	0	0	1	0	0	0	125	136
TCGA-DJ-A3V5-10A-01D-A22Z-08_THCA	77	60	63	37	94	79	76	63	57	18	57	58	52	61	0	43	96
TCGA-DJ-A3V6-10A-01D-A22Z-08_THCA	150	0	0	97	157	154	146	115	163	0	0	0	0	0	66	0	192
TCGA-DJ-A3V7-10A-01D-A23K-08_THCA	86	66	63	44	73	65	76	88	105	0	0	1	0	1	0	81	99
TCGA-DJ-A3V8-10A-01D-A23K-08_THCA	86	6	8	78	96	80	75	101	72	17	42	1	61	64	29	4	88
TCGA-DJ-A3V9-10A-01D-A23K-08_THCA	129	5	3	55	83	93	85	139	113	3	6	1	5	4	33	69	110
TCGA-DJ-A3VA-10A-01D-A23K-08_THCA	98	65	68	46	113	83	79	94	73	20	70	74	72	70	0	75	89
TCGA-DJ-A3VB-10A-01D-A23K-08_THCA	79	0	2	59	82	74	121	75	90	0	0	1	0	1	0	127	88
TCGA-DJ-A3VD-10A-01D-A23K-08_THCA	136	69	95	61	207	165	155	147	106	31	100	164	0	84	29	0	175
TCGA-DJ-A3VE-10A-01D-A23K-08_THCA	79	71	66	44	71	69	83	83	68	23	53	1	62	71	0	65	84
TCGA-DJ-A3VF-10A-01D-A23K-08_THCA	85	66	65	48	74	67	79	113	96	0	3	4	3	6	0	118	95
TCGA-DJ-A3VG-10A-01D-A23K-08_THCA	93	69	78	48	121	86	89	123	106	0	49	76	1	0	36	73	107
TCGA-DJ-A3VI-10A-01D-A23K-08_THCA	84	65	63	45	81	71	71	61	69	1	49	8	62	70	27	2	90
TCGA-DJ-A3VJ-10A-01D-A23K-08_THCA	95	83	84	2	8	5	102	88	90	1	1	9	3	5	0	84	107
TCGA-DJ-A3VK-10A-01D-A23K-08_THCA	84	82	76	6	93	82	79	77	90	0	65	80	0	2	0	75	91
TCGA-DJ-A3VL-10A-01D-A23K-08_THCA	104	62	63	41	102	74	79	95	74	16	64	61	61	65	21	1	91
TCGA-DJ-A3VM-10A-01D-A23K-08_THCA	84	4	6	81	95	80	80	71	106	0	0	1	0	1	0	84	100
TCGA-DJ-A4UL-10A-01D-A25A-08_THCA	55	47	49	29	77	57	64	59	59	0	35	40	2	1	0	83	67
TCGA-DJ-A4UP-10A-01D-A25A-08_THCA	74	62	58	42	59	52	51	47	59	0	38	0	57	55	0	48	87
TCGA-DJ-A4UQ-10A-01D-A25A-08_THCA	189	0	1	108	144	145	145	112	171	0	0	0	0	0	48	0	187
TCGA-DJ-A4UR-10A-01D-A25A-08_THCA	163	95	95	72	181	158	144	119	204	0	54	111	0	1	0	174	184
TCGA-DJ-A4UT-10A-01D-A25A-08_THCA	62	47	48	30	77	66	64	61	51	9	47	42	41	41	0	49	68
TCGA-DJ-A4UW-10A-01D-A25A-08_THCA	59	1	1	44	85	68	61	60	69	0	0	0	0	0	31	4	72
TCGA-DJ-A4V0-10A-01D-A25A-08_THCA	74	1	4	46	69	68	65	68	75	0	4	1	0	0	29	3	73
TCGA-DJ-A4V2-10A-01D-A25A-08_THCA	77	0	0	44	70	69	61	75	84	0	0	0	0	0	23	54	80
TCGA-DJ-A4V4-10A-01D-A25A-08_THCA	63	53	46	33	88	65	64	87	80	1	29	44	1	3	25	42	71
TCGA-DJ-A4V5-10A-01D-A25A-08_THCA	76	51	60	29	51	50	59	68	50	14	34	2	56	54	0	50	70
TCGA-DK-A1A3-10A-01D-A13W-08_BLCA	194	110	99	77	136	108	91	87	93	0	50	1	87	120	0	75	221
TCGA-DK-A1A5-10A-01D-A13W-08_BLCA	158	0	0	86	154	144	131	127	178	0	0	0	0	0	0	116	186
TCGA-DK-A1A6-10A-01D-A13W-08_BLCA	143	92	95	60	110	101	144	135	168	0	1	0	0	2	46	0	207
TCGA-DK-A1A7-10A-01D-A13W-08_BLCA	166	106	100	74	232	165	158	148	186	0	32	122	0	3	42	79	222
TCGA-DK-A1AA-10A-01D-A13W-08_BLCA	162	84	88	89	119	98	156	104	182	0	1	0	0	1	59	0	187
TCGA-DK-A1AB-10A-01D-A13W-08_BLCA	180	82	91	70	231	187	187	149	152	17	84	158	0	0	0	122	186
TCGA-DK-A1AC-10A-01D-A13W-08_BLCA	104	96	123	0	128	73	131	96	140	0	43	71	1	1	21	67	201
TCGA-DK-A1AD-10A-01D-A13W-08_BLCA	157	1	1	148	205	169	173	130	161	2	1	1	1	1	0	164	239
TCGA-DK-A1AE-10A-01D-A13W-08_BLCA	126	97	3	81	206	144	143	116	100	16	34	1	75	116	0	85	199
TCGA-DK-A1AF-10A-01D-A13W-08_BLCA	104	94	99	1	1	2	0	1	2	0	78	0	88	175	0	1	183
TCGA-DK-A1AG-10A-01D-A13W-08_BLCA	86	12	12	82	106	92	90	96	119	1	5	11	0	3	0	99	117
TCGA-DK-A2HX-10A-01D-A18F-08_BLCA	90	0	0	81	77	83	82	95	91	0	1	0	0	2	0	83	98
TCGA-DK-A2I1-10A-01D-A17V-08_BLCA	146	69	79	56	92	71	109	114	129	0	0	0	2	3	23	56	166
TCGA-DK-A2I2-10A-01D-A17V-08_BLCA	124	71	76	60	89	86	116	110	104	0	0	1	0	0	23	67	148
TCGA-DK-A2I4-10A-01D-A21A-08_BLCA	126	38	58	44	97	73	75	86	58	12	61	85	0	57	26	0	93
TCGA-DK-A2I6-10A-01D-A18F-08_BLCA	106	0	2	76	87	72	84	90	101	0	1	0	0	0	26	53	96
TCGA-DK-A3IK-10A-01D-A21A-08_BLCA	85	1	1	65	89	97	83	53	85	0	0	0	0	0	0	125	111
TCGA-DK-A3IL-10A-01D-A20D-08_BLCA	89	60	56	48	66	68	68	59	72	0	45	65	0	65	0	66	98
TCGA-DK-A3IM-10A-01D-A20D-08_BLCA	104	0	0	83	89	94	77	84	104	0	0	0	0	0	29	65	124
TCGA-DK-A3IN-10A-01D-A20D-08_BLCA	94	67	71	61	132	94	94	82	73	20	79	70	54	78	0	70	108
TCGA-DK-A3IQ-10A-01D-A20D-08_BLCA	91	44	47	48	98	86	75	61	52	19	52	50	38	64	0	46	107
TCGA-DK-A3IS-10A-01D-A21A-08_BLCA	92	61	55	45	69	60	76	68	100	0	0	0	0	0	27	75	93

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DK-A3IT-10A-01D-A20D-08_BLCA	86	1	1	84	101	90	94	107	126	0	0	0	0	1	36	73	114
TCGA-DK-A3IU-10A-01D-A20D-08_BLCA	95	1	0	55	86	93	82	100	124	0	0	0	0	0	25	68	120
TCGA-DK-A3IV-10A-01D-A21A-08_BLCA	122	0	1	56	90	86	81	121	73	16	55	0	67	72	0	75	106
TCGA-DK-A3WW-10A-01D-A23K-08_BLCA	101	70	65	46	108	84	87	120	77	22	77	66	64	70	0	57	105
TCGA-DK-A3WX-10A-01D-A22Z-08_BLCA	154	0	0	113	138	155	137	129	78	20	54	0	77	96	0	76	170
TCGA-DK-A3WY-10A-01D-A22Z-08_BLCA	147	91	115	64	102	94	150	158	107	22	59	0	89	111	47	0	185
TCGA-DK-A3X1-10A-01D-A22Z-08_BLCA	150	100	116	68	105	105	137	133	108	22	57	0	88	96	0	84	178
TCGA-DK-A3X2-10A-01D-A22Z-08_BLCA	156	91	103	68	188	155	141	139	158	11	59	107	0	0	46	98	186
TCGA-DK-A6AV-10A-01D-A30H-08_BLCA	147	0	2	122	146	143	133	128	143	0	0	0	0	2	33	66	174
TCGA-DK-A6AW-10A-01D-A30H-08_BLCA	175	106	104	78	179	160	139	135	2	32	128	141	92	173	0	0	215
TCGA-DK-A6B0-10A-01D-A31J-08_BLCA	88	60	62	44	59	62	74	79	87	0	0	0	0	0	0	82	101
TCGA-DK-A6B1-10A-01D-A30H-08_BLCA	162	0	0	60	147	146	139	142	169	0	0	0	0	0	0	163	190
TCGA-DK-A6B2-10A-01D-A30H-08_BLCA	158	174	156	0	170	151	159	137	119	29	150	150	83	122	0	102	194
TCGA-DK-A6B5-10A-01D-A31J-08_BLCA	90	57	65	45	110	79	68	71	58	12	62	61	51	65	0	55	96
TCGA-DK-A6B6-10A-01D-A30H-08_BLCA	156	88	106	60	170	155	146	123	97	18	101	97	91	113	0	81	197
TCGA-DM-A0X9-10A-01D-A152-10_COAD	51	0	0	34	47	62	70	53	66	0	0	0	0	1	0	41	77
TCGA-DM-A0XD-10A-01D-A152-10_COAD	66	34	44	29	64	63	71	66	83	0	25	38	0	0	0	65	81
TCGA-DM-A0XF-10A-01D-A152-10_COAD	47	25	26	17	17	15	50	26	0	15	14	0	39	41	0	0	46
TCGA-DM-A1D0-10A-01D-A152-10_COAD	53	34	32	27	35	32	41	23	39	0	26	0	30	36	0	26	65
TCGA-DM-A1D4-10A-01D-A152-10_COAD	57	0	0	62	62	52	80	68	49	9	28	0	44	44	0	25	79
TCGA-DM-A1D6-10A-01D-A152-10_COAD	69	0	0	47	63	63	74	63	75	0	0	0	0	0	0	56	94
TCGA-DM-A1D7-10A-01D-A152-10_COAD	45	0	0	36	41	63	63	41	72	0	0	0	0	0	0	42	56
TCGA-DM-A1D8-10A-01D-A152-10_COAD	59	33	39	38	84	65	83	92	66	12	26	52	0	0	13	33	66
TCGA-DM-A1D9-10A-01D-A152-10_COAD	70	0	0	54	56	61	56	59	47	13	18	0	27	33	15	0	75
TCGA-DM-A1DA-10A-01D-A152-10_COAD	63	0	1	39	58	62	61	60	73	0	0	0	0	0	28	0	67
TCGA-DM-A1DB-10A-01D-A152-10_COAD	60	0	0	44	59	47	67	64	83	0	0	0	0	0	13	24	70
TCGA-DM-A1HA-10A-01D-A152-10_COAD	60	0	0	62	30	44	56	34	59	0	0	0	0	0	16	0	56
TCGA-DM-A285-10A-01D-A16V-10_COAD	43	35	37	0	0	0	64	39	52	0	0	0	0	0	23	0	73
TCGA-DM-A28C-10A-01D-A16V-10_COAD	59	29	20	21	27	27	59	36	67	0	0	0	0	0	11	26	64
TCGA-DM-A28E-10A-01D-A16V-10_COAD	47	23	29	18	34	44	48	47	69	0	17	23	0	0	11	28	75
TCGA-DM-A28F-10A-01D-A16V-10_COAD	43	0	3	45	48	41	65	52	57	0	0	0	0	0	0	39	65
TCGA-DM-A28G-10A-01D-A16V-10_COAD	65	61	52	0	27	26	55	47	55	0	15	28	0	0	16	23	84
TCGA-DM-A28H-10A-01D-A16V-10_COAD	46	0	0	23	40	37	36	38	34	8	18	1	9	17	10	0	43
TCGA-DM-A28K-10A-01D-A16V-10_COAD	43	23	26	14	26	27	44	39	34	1	0	0	0	0	0	36	48
TCGA-DO-A1JZ-10A-01D-A13W-08_THCA	197	115	136	75	216	175	171	158	111	26	94	114	84	120	42	0	221
TCGA-DO-A1K0-10A-01D-A13W-08_THCA	168	0	0	91	179	165	142	139	177	0	0	1	1	2	29	80	198
TCGA-DO-A2HM-10B-01D-A22D-08_THCA	96	64	71	43	124	98	84	107	81	18	71	73	62	74	33	0	112
TCGA-DQ-5624-10A-01D-1870-08_HNSC	104	0	3	90	101	98	95	90	94	0	0	0	1	0	30	57	117
TCGA-DQ-5625-10A-01D-1870-08_HNSC	120	0	1	79	115	102	105	96	97	1	0	0	0	2	0	101	131
TCGA-DQ-5629-10A-01D-1870-08_HNSC	117	0	0	69	127	116	114	98	139	0	1	0	0	1	0	104	136
TCGA-DQ-5630-10A-01D-1870-08_HNSC	139	86	89	55	141	110	120	142	86	20	94	88	71	86	0	75	131
TCGA-DQ-5631-10A-01D-1870-08_HNSC	157	1	0	81	111	117	97	108	90	25	59	0	76	96	38	1	131
TCGA-DQ-7588-10B-01D-2078-08_HNSC	84	54	53	37	56	60	77	87	73	0	1	1	1	1	24	52	93
TCGA-DQ-7589-10C-01D-2229-08_HNSC	104	0	0	94	168	126	121	140	135	14	47	72	0	1	0	110	128
TCGA-DQ-7590-10D-01D-2229-08_HNSC	130	0	1	93	103	102	109	97	95	0	0	0	0	0	0	96	128
TCGA-DQ-7591-10A-01D-2078-08_HNSC	78	0	0	66	75	72	69	63	7	25	54	0	60	73	0	1	99
TCGA-DQ-7592-10A-01D-2078-08_HNSC	73	53	56	38	64	63	77	86	72	0	0	1	0	0	0	116	83
TCGA-DQ-7593-10D-01D-2229-08_HNSC	104	64	80	54	135	106	102	92	119	0	42	83	0	0	0	93	127
TCGA-DQ-7594-10D-01D-2229-08_HNSC	112	72	78	48	126	109	87	77	67	18	68	97	0	78	0	60	122
TCGA-DQ-7595-10D-01D-2229-08_HNSC	92	0	0	62	109	93	96	104	131	0	0	0	0	0	0	108	114
TCGA-DQ-7596-10D-01D-2229-08_HNSC	103	0	0	69	110	103	100	80	109	0	0	0	0	0	0	85	114
TCGA-DR-A0ZL-10A-01D-A10S-08_CESC	87	0	1	51	96	96	88	92	111	0	0	0	0	1	49	1	98
TCGA-DR-A0ZM-10A-01D-A10S-08_CESC	105	0	0	57	105	92	93	83	97	0	0	0	1	1	0	98	118
TCGA-DS-A0VK-10A-01D-A10S-08_CESC	102	71	69	42	77	73	89	128	118	0	0	0	0	0	0	150	112
TCGA-DS-A0VL-10A-01D-A10S-08_CESC	96	1	3	60	107	88	79	111	104	1	0	1	7	8	0	149	111
TCGA-DS-A0VM-10A-01D-A10S-08_CESC	100	1	1	83	98	99	83	112	105	0	1	0	0	2	29	66	96
TCGA-DS-A0VN-10A-01D-A10S-08_CESC	95	69	69	2	78	76	67	79	0	16	74	76	73	96	0	1	101
TCGA-DS-A1OA-10A-01D-A16Y-08_CESC	82	0	0	82	83	84	87	118	108	0	0	1	0	2	31	58	91
TCGA-DS-A1OB-10A-01D-A14W-08_CESC	100	0	0	64	93	83	83	88	82	0	0	0	1	0	0	94	108
TCGA-DS-A1OC-10A-01D-A14W-08_CESC	94	9	9	62	93	88	88	87	99	0	1	3	0	0	0	13	106
TCGA-DS-A1OD-10A-01D-A14W-08_CESC	92	0	0	91	103	87	84	88	85	0	1	0	0	0	33	70	114
TCGA-DS-A3LQ-10A-01D-A21Q-09_CESC	45	0	0	37	113	100	95	85	108	0	0	0	0	1	38	42	82
TCGA-DS-A5RQ-10A-01D-A28E-09_CESC	54	77	61	19	56	65	152	111	149	0	0	0	0	0	0	128	90
TCGA-DT-5265-10A-01D-1826-10_READ	61	27	24	36	36	31	76	43	73	0	0	0	0	0	13	29	74
TCGA-DU-5847-10A-01D-1705-08_LGG	86	79	79	0	58	57	75	64	69	16	42	77	0	59	0	47	109
TCGA-DU-5849-10A-01D-1705-08_LGG	89	69	59	39	108	85	79	78	87	0	36	54	0	1	34	1	91
TCGA-DU-5851-10A-01D-1893-08_LGG	110	0	1	69	103	102	108	127	124	0	0	1	1	0	0	142	117
TCGA-DU-5852-10A-01D-1705-08_LGG	91	0	0	50	97	99	78	83	114	0	0	0	0	2	22	49	111
TCGA-DU-5853-10A-01D-1893-08_LGG	129	1	0	72	103	91	92	110	120	0	1	0	0	4	31	79	110
TCGA-DU-5854-10A-01D-1705-08_LGG	92	1	2	49	82	92	86	72	100	0	0	0	1	0	36	1	105
TCGA-DU-5855-10A-01D-1705-08_LGG	93	88	92	2	93	86	86	77	66	15	69	99	1	70	20	0	109
TCGA-DU-5870-10A-01D-1705-08_LGG	112	0	2	61	89	85	90	83	110	0	0	0	2	1	20	41	101
TCGA-DU-5871-10A-01D-1705-08_LGG	95	77	88	1	73	63	73	68	2	23	76	66	75	82	0	0	102
TCGA-DU-5872-10A-01D-1705-08_LGG	94	58	65	37	72	64	79	95	74	18	38	0	44	73	22	0	104
TCGA-DU-5874-10A-01D-1705-08_LGG	88	1	0	70	80	65	61	38	63	0	0	0	1	72	0	51	75
TCGA-DU-6392-10A-01D-1705-08_LGG	84	68	65	40	116	90	88	94	86	0	31	73	0	2	22	45	106
TCGA-DU-6393-10A-01D-1705-08_LGG	94	54	63	40	65	66	76	84	122	0	0	0	1	1	21	55	116
TCGA-DU-6394-10A-01D-1705-08_LGG	99	66	68	43	78	64	90	81	103	0	0	1	0	1	0	80	111
TCGA-DU-6395-10A-01D-1705-08_LGG	105	90	87	0	98	101	83	98	49	15	65	107	0	70	0	54	101
TCGA-DU-6396-10A-01D-1705-08_LGG	100	2	0	59	84	101	87	77	62	13	27	2	48	76	0	46	104
TCGA-DU-6397-10A-01D-1705-08_LGG	93	74	85	1	71	67	79	78	74	12	55	60	54	65	0	55	99
TCGA-DU-6399-10A-01D-1705-08_LGG	94	0	2	55	86	90	80	97	71	14	36	62	0	70	24	0	104
TCGA-DU-6400-10A-01D-1705-08_LGG	100	0	0	77	86	80	81	75	101	0	0	2	0	2	0	68	99
TCGA-DU-6401-10A-01D-1705-08_LGG	88	57	68	37	112	88	81	87	61	20	49	49	55	74	18	0	94
TCGA-DU-6402-10A-01D-1705-08_LGG	104	58	62	35	66	65	71	72	94	0	0	2	1	1	32	0	106
TCGA-DU-6403-10A-01D-1705-08_LGG	97	56	62	40	95	80	85	82	94	0	32	66	0	0	20	36	107
TCGA-DU-6404-10A-01D-1705-08_LGG	87	0	1	70	98	83	83	82	66	16	30	0	49	68	0	55	108
TCGA-DU-6405-10A-01D-1705-08_LGG	109	62	60	41	67	62	81	91	62	16	32	62	0	67	0	51	111
TCGA-DU-6406-10A-01D-1705-08_LGG	119	0	3	54	86	82	78	82	39	18	40	0	49	61	0	45	119
TCGA-DU-6407-10A-01D-1705-08_LGG	92	58	68	33	58	52	75	90	101	0	0	0	0	2	32	52	99
TCGA-DU-6408-10A-01D-1705-08_LGG	95	0	0	52	92	84	78	82	77	0	1	1	0	0	0	104	109
TCGA-DU-6410-10A-01D-1893-08_LGG	140	69	82	59	157	126	114	121	2	39	107	155	1	105	0	0	124
TCGA-DU-6542-10A-01D-1893-08_LGG	114	81	75	52	83	80	92	116	85	17	62	0	67	87	33	0	106
TCGA-DU-7006-10A-01D-2024-08_LGG	87	3	2	58	89	88	82	78	66	12	32	0	49	71	0	60	99
TCGA-DU-7007-10A-01D-2024-08_LGG	94	64	63	44	114	88	84	84	74	10	68	99	0	70	0	63	103
TCGA-DU-7008-10A-01D-2024-08_LGG	85	61	69	46	64	70	67	44	60	0	45	1	62	72	0	59	98

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DU-7009-10A-01D-2024-08_LGG	96	61	71	47	120	96	96	120	69	22	64	75	49	70	17	2	104
TCGA-DU-7010-10A-01D-2024-08_LGG	117	1	2	50	85	76	91	94	98	0	0	0	0	0	33	53	98
TCGA-DU-7011-10A-01D-2024-08_LGG	87	58	62	41	62	64	78	70	95	0	1	0	1	3	0	77	92
TCGA-DU-7012-10A-01D-2024-08_LGG	81	0	0	68	115	85	78	72	91	0	0	0	1	4	33	2	99
TCGA-DU-7013-10A-01D-2024-08_LGG	99	67	74	47	85	83	88	109	113	0	5	9	0	4	0	119	108
TCGA-DU-7014-10A-01D-2024-08_LGG	89	1	6	82	90	79	91	106	106	1	6	3	3	1	22	57	96
TCGA-DU-7015-10B-01D-2024-08_LGG	113	3	1	58	120	84	90	112	83	19	51	57	0	1	36	4	101
TCGA-DU-7018-10A-01D-2024-08_LGG	83	59	71	41	72	63	86	82	87	0	1	1	0	0	23	62	93
TCGA-DU-7019-10A-01D-2024-08_LGG	87	53	62	42	59	62	72	90	95	0	0	0	1	0	22	70	95
TCGA-DU-7290-10A-01D-2024-08_LGG	99	0	2	50	80	74	86	98	99	0	0	0	0	0	0	109	103
TCGA-DU-7292-10A-01D-2024-08_LGG	98	80	82	3	79	69	83	84	78	0	45	68	0	2	0	79	101
TCGA-DU-7294-10A-01D-2024-08_LGG	86	0	0	76	93	88	79	92	76	0	3	0	4	4	0	108	92
TCGA-DU-7298-10A-01D-2024-08_LGG	92	67	76	40	129	84	86	108	110	0	40	61	0	0	0	105	94
TCGA-DU-7299-10A-01D-2024-08_LGG	90	0	0	54	96	87	85	74	68	12	48	0	51	62	0	59	96
TCGA-DU-7300-10A-01D-2086-08_LGG	80	46	56	41	63	55	76	68	88	0	0	1	0	2	0	79	90
TCGA-DU-7301-10A-01D-2086-08_LGG	90	0	1	74	91	85	82	94	99	0	0	1	0	0	0	118	96
TCGA-DU-7302-10A-01D-2086-08_LGG	88	65	57	50	69	77	80	93	90	0	1	0	0	0	26	65	100
TCGA-DU-7304-10A-01D-2086-08_LGG	86	0	1	73	89	85	83	70	2	23	64	54	50	91	0	0	97
TCGA-DU-7306-10A-01D-2086-08_LGG	107	0	1	84	88	87	74	82	97	0	0	0	0	1	0	117	96
TCGA-DU-7309-10A-01D-2086-08_LGG	98	83	82	0	2	4	97	103	92	0	1	1	0	1	30	65	107
TCGA-DU-8158-10A-01D-2253-08_LGG	89	0	1	93	92	99	87	83	80	20	44	0	56	81	0	79	121
TCGA-DU-8161-10A-01D-2253-08_LGG	100	70	65	45	72	67	84	98	75	19	55	0	56	73	0	69	107
TCGA-DU-8162-10A-01D-2253-08_LGG	141	0	0	75	104	106	101	91	108	0	0	0	0	1	0	122	137
TCGA-DU-8163-10A-01D-2253-08_LGG	96	56	45	39	107	83	69	69	65	15	64	80	0	63	0	62	77
TCGA-DU-8164-10A-01D-2253-08_LGG	90	0	2	56	97	90	87	87	78	9	40	62	0	71	0	59	101
TCGA-DU-8165-10A-01D-2253-08_LGG	121	0	0	62	106	83	83	81	64	16	38	0	43	62	0	70	105
TCGA-DU-8166-10A-01D-2253-08_LGG	86	2	1	65	94	88	70	76	90	0	0	0	0	2	39	0	101
TCGA-DU-8167-10A-01D-2253-08_LGG	87	65	59	53	134	92	80	103	92	0	43	72	1	1	34	76	95
TCGA-DU-8168-10A-01D-2253-08_LGG	95	65	68	49	79	72	101	73	77	17	47	0	58	76	0	75	115
TCGA-DU-A5TP-10A-01D-A289-08_LGG	115	77	79	47	84	79	110	98	100	0	0	0	0	0	0	110	137
TCGA-DU-A5TR-10A-01D-A289-08_LGG	125	0	1	80	118	103	132	118	88	21	45	0	69	86	0	74	140
TCGA-DU-A5TS-10A-01D-A289-08_LGG	120	0	1	96	112	132	99	125	108	0	0	0	0	1	43	61	135
TCGA-DU-A5TT-10A-01D-A289-08_LGG	119	0	0	66	106	124	104	92	2	25	83	0	102	125	0	0	136
TCGA-DU-A5TU-10A-01D-A289-08_LGG	111	63	77	44	122	100	110	87	83	18	79	74	67	67	0	65	126
TCGA-DU-A5TW-10A-01D-A289-08_LGG	118	65	69	42	116	75	154	113	128	0	51	0	68	1	0	129	127
TCGA-DU-A5TY-10A-01D-A289-08_LGG	105	86	94	0	84	71	99	99	77	21	71	70	54	86	0	74	118
TCGA-DU-A6S2-10A-01D-A329-08_LGG	79	0	2	44	91	70	70	78	96	0	0	0	0	0	25	48	94
TCGA-DU-A6S3-10A-01D-A329-08_LGG	79	0	0	66	82	76	78	90	70	9	33	0	50	68	17	0	94
TCGA-DU-A6S6-10A-01D-A329-08_LGG	80	76	78	0	0	1	80	72	63	10	33	0	49	65	0	37	102
TCGA-DU-A6S7-10A-01D-A329-08_LGG	82	0	0	72	82	76	75	95	101	0	0	0	0	0	16	52	92
TCGA-DU-A6S8-10A-01D-A329-08_LGG	96	66	77	0	80	67	91	79	0	21	84	106	52	99	0	0	106
TCGA-DU-A76L-10A-01D-A329-08_LGG	77	49	44	32	99	76	72	80	50	13	50	68	0	66	0	44	86
TCGA-DU-A76O-10A-01D-A329-08_LGG	109	92	96	0	2	2	93	91	89	0	0	2	0	1	37	0	131
TCGA-DU-A76R-10A-01D-A329-08_LGG	77	55	57	34	57	60	69	77	81	0	0	0	0	0	26	42	74
TCGA-DV-5565-10A-01D-1535-10_KIRC	81	0	0	143	174	167	190	162	0	59	95	0	136	122	0	0	133
TCGA-DV-5566-10A-01D-1535-10_KIRC	74	0	0	137	161	166	194	124	120	49	76	0	123	106	0	70	146
TCGA-DV-5568-10A-01D-1535-10_KIRC	85	174	144	63	121	130	195	166	137	74	103	0	143	124	23	0	140
TCGA-DV-5569-10A-01D-1535-10_KIRC	41	0	1	52	88	88	151	96	70	22	47	0	77	74	14	0	82
TCGA-DV-5573-10A-01D-1535-10_KIRC	44	0	0	53	82	80	91	85	91	0	0	0	0	0	15	43	78
TCGA-DV-5574-10A-01D-1535-10_KIRC	47	0	0	47	80	88	98	93	95	0	0	0	0	0	20	45	79
TCGA-DV-5575-10A-01D-1535-10_KIRC	47	98	82	38	65	71	96	84	100	0	0	0	0	0	0	72	68
TCGA-DV-5576-10A-01D-1535-10_KIRC	52	0	1	43	98	92	111	86	96	0	0	0	0	0	15	45	98
TCGA-DV-A4VX-10A-01D-A25V-10_KIRC	66	0	2	37	69	88	78	92	83	0	0	0	0	0	29	49	72
TCGA-DV-A4VZ-10A-01D-A25V-10_KIRC	84	0	51	0	59	110	100	88	120	0	34	0	63	0	26	48	100
TCGA-DV-A4W0-10A-01D-A25V-10_KIRC	85	69	56	36	123	105	112	89	108	0	39	4	59	0	30	65	79
TCGA-DW-5560-10A-01D-1589-08_KIRP	87	1	3	40	95	82	81	89	97	0	2	2	1	1	29	63	98
TCGA-DW-5561-10A-01D-1589-08_KIRP	111	2	1	62	105	99	100	93	108	0	0	0	0	1	0	97	118
TCGA-DW-7834-10A-01D-2136-08_KIRP	103	61	67	41	73	83	89	103	91	0	3	0	2	7	33	63	106
TCGA-DW-7836-10A-01D-2136-08_KIRP	108	1	0	66	101	90	103	109	122	0	0	1	0	0	0	134	134
TCGA-DW-7837-10A-01D-2136-08_KIRP	100	2	3	85	112	90	91	88	90	0	1	4	0	2	39	66	106
TCGA-DW-7838-10A-01D-2136-08_KIRP	89	1	0	82	103	86	93	116	113	1	0	2	2	3	0	132	107
TCGA-DW-7839-10A-01D-2136-08_KIRP	98	2	4	58	93	97	96	130	95	0	0	0	0	0	0	151	105
TCGA-DW-7840-10A-01D-2136-08_KIRP	84	57	81	1	84	82	82	80	94	0	69	69	54	3	43	2	103
TCGA-DW-7841-10A-01D-2136-08_KIRP	103	66	62	48	121	94	85	102	107	0	45	68	0	0	29	64	109
TCGA-DW-7842-10A-01D-2136-08_KIRP	89	3	1	53	105	80	81	79	65	14	44	0	66	74	0	71	106
TCGA-DW-7963-10C-01D-A28G-10_KIRP	69	65	46	22	73	94	95	70	81	0	31	49	0	0	31	0	76
TCGA-DX-A1KU-10A-01D-A24N-09_SARC	51	64	52	21	63	55	99	84	107	2	0	1	1	0	0	75	68
TCGA-DX-A1KW-10A-01D-A24N-09_SARC	40	1	0	19	65	71	69	62	69	1	0	3	0	5	17	25	61
TCGA-DX-A1KX-10A-01D-A24N-09_SARC	44	1	0	26	78	74	94	82	56	11	39	0	50	69	33	1	61
TCGA-DX-A1KY-10A-01D-A24N-09_SARC	51	12	7	36	107	104	110	140	141	0	0	4	3	1	0	104	88
TCGA-DX-A1KZ-10A-01D-A24N-09_SARC	47	51	45	17	90	86	85	71	87	0	41	46	4	3	0	70	73
TCGA-DX-A1L0-10A-01D-A24N-09_SARC	54	3	5	30	95	97	91	83	122	0	0	1	0	0	0	106	89
TCGA-DX-A1L1-10A-01D-A24N-09_SARC	40	61	46	14	46	58	101	76	74	15	30	1	45	65	35	2	79
TCGA-DX-A1L2-10A-01D-A24N-09_SARC	38	57	47	14	55	61	86	94	113	0	0	2	3	0	0	86	78
TCGA-DX-A1L3-10A-01D-A24N-09_SARC	43	0	0	29	89	84	90	99	65	11	51	0	37	58	0	41	70
TCGA-DX-A1L4-10A-01D-A26G-09_SARC	37	4	3	20	62	70	88	76	50	16	26	0	32	40	0	33	55
TCGA-DX-A23R-10A-01D-A26G-09_SARC	55	60	49	21	55	57	57	54	69	1	39	0	42	58	0	39	79
TCGA-DX-A23T-10A-01D-A26G-09_SARC	30	41	37	9	43	36	79	66	45	6	23	0	37	48	0	38	54
TCGA-DX-A23U-10A-01D-A26G-09_SARC	37	78	63	3	10	4	86	82	59	11	40	0	53	46	29	4	62
TCGA-DX-A23V-10A-01D-A29N-09_SARC	45	48	41	14	80	75	78	79	95	0	31	28	1	1	0	73	61
TCGA-DX-A23Y-10A-01D-A27P-09_SARC	53	56	58	13	51	51	89	104	55	14	45	0	53	62	0	48	87
TCGA-DX-A240-10A-01D-A27P-09_SARC	43	1	0	35	81	86	80	72	70	14	36	2	59	53	0	43	70
TCGA-DX-A2IZ-10A-01D-A21Q-09_SARC	50	64	55	24	47	78	104	90	132	1	0	1	0	0	36	66	75
TCGA-DX-A2J0-10A-01D-A21Q-09_SARC	45	0	1	21	84	88	78	90	109	2	1	1	1	0	0	93	73
TCGA-DX-A2J1-10A-01D-A21Q-09_SARC	59	1	0	29	99	115	106	101	114	0	0	4	2	0	44	64	91
TCGA-DX-A2J4-10A-01D-A21Q-09_SARC	60	75	57	17	109	122	104	105	82	14	90	65	68	79	0	58	80
TCGA-DX-A3LS-10A-01D-A21Q-09_SARC	52	0	0	31	100	78	99	103	82	14	37	1	51	46	0	50	65
TCGA-DX-A3LT-10A-01D-A21Q-09_SARC	52	70	49	20	59	71	94	88	102	0	0	0	0	0	34	53	75
TCGA-DX-A3LU-10A-01D-A21Q-09_SARC	34	41	37	17	49	44	63	37	51	0	45	0	46	50	0	42	60
TCGA-DX-A3LW-10A-01D-A21Q-09_SARC	49	96	92	0	0	0	99	114	124	0	0	0	2	1	0	101	81
TCGA-DX-A3LY-10B-01D-A27P-09_SARC	45	89	83	0	43	56	77	81	59	13	67	76	0	54	0	39	63
TCGA-DX-A3M1-10A-01D-A22A-09_SARC	61	0	0	33	94	106	165	99	6	21	80	0	91	100	0	1	82
TCGA-DX-A3M2-10A-01D-A22A-09_SARC	50	0	0	34	89	86	101	86	125	1	0	0	1	0	0	111	81
TCGA-DX-A3U5-10A-01D-A22A-09_SARC	38	47	43	13	54	60	83	74	113	0	0	0	0	0	0	75	74
TCGA-DX-A3U6-10A-01D-A29N-09_SARC	58	55	52	13	52	44	90	73	124	0	1	0	0	0	0	80	76
TCGA-DX-A3U7-10A-01D-A29N-09_SARC	44	3	1	19	67	62	69	63	61	11	30	0	54	49	0	37	57

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DX-A3U8-10A-01D-A29N-09_SARC	38	1	2	20	81	73	89	84	112	0	0	0	1	0	0	97	65
TCGA-DX-A3U9-10A-01D-A307-09_SARC	37	48	50	19	60	53	101	83	74	16	43	0	54	62	28	0	87
TCGA-DX-A3UA-10A-01D-A307-09_SARC	29	56	47	16	46	45	84	81	62	12	31	0	51	57	0	54	72
TCGA-DX-A3UB-10A-01D-A307-09_SARC	29	0	0	16	76	63	65	58	74	0	0	0	0	0	0	87	59
TCGA-DX-A3UC-10A-01D-A307-09_SARC	18	74	58	0	42	38	67	75	86	0	25	42	0	0	22	32	63
TCGA-DX-A3UD-10A-01D-A307-09_SARC	53	81	68	19	65	65	98	121	122	0	0	0	0	0	40	60	88
TCGA-DX-A3UE-10A-01D-A307-09_SARC	30	45	43	11	41	41	43	28	57	0	20	31	0	55	0	43	69
TCGA-DX-A3UF-10A-01D-A307-09_SARC	46	0	0	46	108	106	127	107	185	0	0	0	0	0	52	63	83
TCGA-DX-A48J-10A-01D-A307-09_SARC	48	79	80	0	123	96	103	93	80	11	82	60	77	70	34	0	80
TCGA-DX-A48K-10A-01D-A307-09_SARC	36	0	0	24	78	71	89	78	115	0	0	0	0	0	38	41	75
TCGA-DX-A48L-10A-01D-A307-09_SARC	31	0	0	22	90	62	71	58	0	18	38	0	62	77	0	0	63
TCGA-DX-A48O-10A-01D-A307-09_SARC	46	70	59	26	110	81	91	84	106	0	41	63	0	0	38	50	75
TCGA-DX-A48P-10A-01D-A307-09_SARC	52	98	88	0	86	105	98	93	82	14	93	85	63	66	0	49	87
TCGA-DX-A48R-10A-01D-A307-09_SARC	68	95	90	28	167	134	148	170	193	0	71	85	0	0	62	81	110
TCGA-DX-A48U-10A-01D-A307-09_SARC	62	82	71	29	66	78	125	112	129	0	0	1	0	0	50	66	89
TCGA-DX-A48V-10A-01D-A307-09_SARC	82	95	96	31	100	99	150	161	162	0	0	0	0	0	0	165	113
TCGA-DX-A6B7-10A-01D-A307-09_SARC	41	94	75	0	74	60	101	90	108	0	38	53	0	0	0	88	83
TCGA-DX-A6B8-10A-01D-A307-09_SARC	68	92	79	31	164	125	131	134	137	0	66	73	0	0	0	153	113
TCGA-DX-A6BA-10A-01D-A307-09_SARC	71	0	0	65	133	121	122	122	149	0	0	1	1	0	0	125	92
TCGA-DX-A6BF-10A-01D-A307-09_SARC	64	0	1	47	117	115	128	169	145	0	0	0	0	0	0	165	105
TCGA-DX-A6BG-10A-01D-A307-09_SARC	66	0	0	48	116	116	137	136	135	0	0	0	0	0	0	147	96
TCGA-DX-A6BH-10A-01D-A307-09_SARC	64	94	75	24	156	121	152	182	177	22	76	88	0	0	56	73	108
TCGA-DX-A6BK-10A-01D-A307-09_SARC	72	97	87	25	170	133	123	123	185	0	61	91	0	0	0	120	101
TCGA-DY-A0XA-10A-01D-A152-10_READ	82	34	36	38	78	81	85	68	51	14	55	50	41	43	0	47	88
TCGA-DY-A1DC-10A-01D-A152-10_READ	69	48	53	24	82	69	86	80	60	14	67	79	0	42	0	34	81
TCGA-DY-A1DD-10A-01D-A152-10_READ	62	45	47	31	45	37	52	29	0	13	55	0	64	72	0	0	84
TCGA-DY-A1DF-10A-01D-A152-10_READ	79	35	38	24	69	66	76	71	83	0	24	40	0	0	0	82	84
TCGA-DY-A1DG-10A-01D-A152-10_READ	47	49	46	1	23	27	80	57	30	12	43	57	0	41	0	28	66
TCGA-DY-A1H8-10A-01D-A152-10_READ	38	21	17	20	11	14	51	43	18	6	15	0	16	25	0	17	47
TCGA-DZ-6133-10A-01D-1962-08_KIRP	121	2	1	77	121	110	113	129	122	0	0	0	0	0	38	84	141
TCGA-DZ-6134-10A-01D-1962-08_KIRP	126	1	3	123	124	111	110	116	98	0	0	0	1	1	0	108	129
TCGA-DZ-6135-10A-01D-1962-08_KIRP	116	75	87	49	88	79	101	113	86	21	64	0	72	82	0	81	141
TCGA-E1-5302-10A-01D-1468-08_LGG	126	81	77	48	155	115	104	134	126	0	52	94	0	0	44	92	118
TCGA-E1-5303-10A-01D-1468-08_LGG	148	1	2	62	173	124	126	173	90	32	87	76	81	83	0	87	130
TCGA-E1-5304-10A-01D-1468-08_LGG	116	1	1	56	126	109	98	106	78	25	58	0	72	92	0	74	131
TCGA-E1-5305-10A-01D-1893-08_LGG	141	1	2	74	97	100	91	126	130	0	0	0	0	0	29	70	128
TCGA-E1-5307-10A-01D-1893-08_LGG	125	103	83	1	104	79	94	144	94	17	53	0	73	79	30	0	167
TCGA-E1-5311-10A-01D-1468-08_LGG	127	2	3	69	118	101	93	143	141	0	0	3	0	3	0	160	125
TCGA-E1-5318-10A-01D-1468-08_LGG	117	1	1	94	127	115	95	105	89	19	61	1	74	89	0	74	132
TCGA-E1-5319-10A-01D-1893-08_LGG	127	0	0	104	104	114	112	127	100	0	0	0	0	1	0	158	133
TCGA-E1-5322-10A-01D-1468-08_LGG	117	3	2	63	108	136	105	127	81	20	63	0	68	82	0	94	148
TCGA-E2-A105-10A-01D-A10M-09_BRCA	40	0	0	49	120	110	119	78	141	0	0	0	0	0	22	48	89
TCGA-E2-A107-10A-01D-A10M-09_BRCA	83	0	0	126	251	222	278	178	231	0	0	0	0	1	0	216	192
TCGA-E2-A108-10A-01D-A10M-09_BRCA	83	0	0	72	164	158	173	168	189	0	0	1	0	0	0	150	112
TCGA-E2-A109-10A-01D-A10M-09_BRCA	95	120	131	55	143	120	189	176	213	0	0	0	0	0	0	230	125
TCGA-E2-A10A-10A-01D-A110-09_BRCA	105	3	2	143	279	204	230	220	221	0	0	0	1	1	0	112	110
TCGA-E2-A10B-10A-01D-A10M-09_BRCA	71	0	1	108	204	217	256	158	233	1	0	0	0	0	41	105	145
TCGA-E2-A10C-10A-01D-A10M-09_BRCA	67	0	0	94	155	136	157	111	160	0	0	0	0	2	0	133	106
TCGA-E2-A10F-10A-01D-A10M-09_BRCA	60	151	160	0	132	133	167	75	98	28	100	168	1	101	29	0	97
TCGA-E2-A14N-10A-01D-A135-09_BRCA	135	0	1	130	297	272	284	247	192	39	154	0	174	181	0	178	204
TCGA-E2-A14O-10A-01D-A110-09_BRCA	63	1	0	87	141	128	125	144	128	0	0	0	0	0	51	93	83
TCGA-E2-A14P-10A-01D-A12B-09_BRCA	106	0	3	146	245	213	268	221	151	31	114	0	149	141	76	0	148
TCGA-E2-A14Q-10A-01D-A12B-09_BRCA	45	0	1	46	102	100	105	92	119	0	0	0	0	1	0	87	65
TCGA-E2-A14R-10A-01D-A110-09_BRCA	93	0	1	96	192	217	203	178	152	31	101	0	139	128	0	91	160
TCGA-E2-A14S-10A-01D-A12B-09_BRCA	101	146	143	69	241	189	202	192	200	0	122	132	0	1	0	196	151
TCGA-E2-A14T-10A-01D-A110-09_BRCA	125	0	0	143	255	232	271	246	184	35	161	0	176	161	0	173	207
TCGA-E2-A14U-10A-01D-A22A-09_BRCA	49	84	72	3	41	51	92	74	62	8	66	39	46	58	24	0	68
TCGA-E2-A14V-10A-01D-A12B-09_BRCA	106	151	161	63	303	229	231	245	285	0	118	141	0	0	0	248	165
TCGA-E2-A14W-10A-01D-A12B-09_BRCA	131	0	2	115	253	249	255	232	270	0	0	0	0	1	109	135	198
TCGA-E2-A14X-10A-01D-A110-09_BRCA	133	153	149	3	162	145	177	157	168	1	222	0	223	155	75	1	160
TCGA-E2-A14Y-10A-01D-A12B-09_BRCA	130	138	125	59	282	228	234	261	247	0	118	170	0	0	0	235	177
TCGA-E2-A14Z-10A-01D-A110-09_BRCA	55	104	100	40	157	113	131	88	166	0	52	95	1	0	0	112	102
TCGA-E2-A150-10A-01D-A12B-09_BRCA	104	0	1	145	222	202	230	235	144	41	140	0	161	160	77	0	171
TCGA-E2-A152-10A-01D-A12B-09_BRCA	89	108	114	58	149	143	155	130	2	34	184	155	116	157	0	0	132
TCGA-E2-A153-10A-01D-A12B-09_BRCA	109	137	128	57	167	132	217	223	272	0	0	0	0	0	0	203	149
TCGA-E2-A154-10A-01D-A110-09_BRCA	72	0	0	66	136	138	145	140	157	0	0	0	0	0	50	92	108
TCGA-E2-A155-10A-01D-A12B-09_BRCA	90	159	178	0	0	0	179	179	185	0	0	1	0	0	82	0	144
TCGA-E2-A156-10A-01D-A12B-09_BRCA	97	132	136	66	250	224	195	213	139	22	185	145	133	137	0	105	156
TCGA-E2-A158-10A-01D-A12B-09_BRCA	125	148	141	64	162	176	259	280	232	0	0	0	0	0	76	136	163
TCGA-E2-A159-10A-01D-A110-09_BRCA	123	144	148	69	260	233	310	294	248	21	136	166	0	0	99	0	171
TCGA-E2-A15A-10A-01D-A12B-09_BRCA	97	0	0	95	211	223	249	274	290	0	0	0	0	0	0	200	167
TCGA-E2-A15C-10A-01D-A12B-09_BRCA	114	0	2	124	199	175	167	209	122	21	133	0	133	130	56	0	125
TCGA-E2-A15D-10A-01D-A110-09_BRCA	139	0	0	83	241	259	250	294	298	0	0	0	1	1	77	160	205
TCGA-E2-A15E-10A-01D-A12B-09_BRCA	92	122	118	53	231	165	169	175	203	0	119	122	1	1	61	101	114
TCGA-E2-A15F-10A-01D-A110-09_BRCA	68	116	125	45	101	116	165	142	128	26	83	1	115	115	0	101	115
TCGA-E2-A15G-10A-01D-A12B-09_BRCA	106	0	4	88	232	230	227	190	223	0	0	0	0	1	0	212	163
TCGA-E2-A15H-10A-01D-A12B-09_BRCA	94	0	1	121	241	213	207	215	263	0	0	0	0	0	61	127	153
TCGA-E2-A15I-10A-01D-A135-09_BRCA	134	0	1	134	249	236	271	239	159	28	157	0	158	164	0	151	196
TCGA-E2-A15J-10A-01D-A12Q-09_BRCA	73	98	113	52	74	95	148	119	127	0	0	0	0	0	0	90	101
TCGA-E2-A15K-10A-01D-A12Q-09_BRCA	91	0	0	113	182	205	220	198	139	29	99	0	137	138	65	0	125
TCGA-E2-A15L-10A-01D-A12B-09_BRCA	111	166	154	70	163	170	248	279	298	0	0	0	0	1	71	171	174
TCGA-E2-A15M-10A-01D-A12B-09_BRCA	102	0	1	68	239	240	247	245	276	0	0	0	0	2	0	308	171
TCGA-E2-A15O-10A-01D-A110-09_BRCA	79	165	171	0	1	1	130	105	124	0	110	0	120	133	0	100	129
TCGA-E2-A15P-10A-01D-A110-09_BRCA	102	109	103	49	181	121	148	142	135	0	90	96	0	0	53	78	89
TCGA-E2-A15R-10A-01D-A110-09_BRCA	99	1	2	67	194	170	192	213	125	26	125	4	123	135	0	132	132
TCGA-E2-A15S-10A-01D-A110-09_BRCA	122	132	129	58	128	133	208	195	149	29	136	0	153	135	0	126	126
TCGA-E2-A15T-10A-01D-A110-09_BRCA	125	141	147	58	150	140	244	260	229	0	0	1	0	1	73	144	164
TCGA-E2-A1AZ-10A-01D-A12Q-09_BRCA	102	0	3	71	156	159	166	193	162	0	1	1	0	1	0	169	109
TCGA-E2-A1B0-10A-01D-A12Q-09_BRCA	100	120	112	49	135	126	146	142	121	22	133	0	123	117	0	117	131
TCGA-E2-A1B1-10A-01D-A12Q-09_BRCA	77	89	93	56	171	116	123	121	102	19	112	120	0	101	0	82	93
TCGA-E2-A1B4-10A-01D-A12Q-09_BRCA	106	0	0	113	196	199	178	192	186	0	0	0	0	0	0	215	132
TCGA-E2-A1B5-10A-01D-A12Q-09_BRCA	77	0	0	101	144	127	149	112	138	0	0	0	0	0	0	130	112
TCGA-E2-A1B6-10A-01D-A12Q-09_BRCA	77	128	129	57	269	206	219	198	235	0	87	147	0	1	54	94	153
TCGA-E2-A1BC-10A-01D-A12Q-09_BRCA	94	151	161	0	177	176	182	193	118	26	182	222	0	126	0	113	141
TCGA-E2-A1BD-10A-01D-A12Q-09_BRCA	88	0	2	111	178	194	209	178	182	0	0	0	0	0	0	173	134
TCGA-E2-A1IE-10A-01D-A13O-09_BRCA	44	0	85	37	81	85	105	105	125	0	0	0	0	0	0	113	75

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-E2-A1IF-10A-01D-A142-09_BRCA	37	59	48	26	82	70	93	83	86	0	34	46	0	0	24	45	68
TCGA-E2-A1IG-10A-01D-A142-09_BRCA	40	0	0	47	85	80	83	71	52	10	39	54	0	56	0	55	57
TCGA-E2-A1IH-10A-01D-A13O-09_BRCA	58	96	105	42	90	90	132	137	147	0	0	0	0	0	42	93	96
TCGA-E2-A1II-10A-01D-A142-09_BRCA	42	72	65	2	46	32	73	82	85	0	31	43	0	0	25	35	60
TCGA-E2-A1IJ-10A-01D-A142-09_BRCA	35	0	0	44	81	74	79	73	51	17	39	0	50	52	0	34	57
TCGA-E2-A1IK-10A-01D-A142-09_BRCA	43	75	67	33	109	91	100	93	121	0	51	69	0	0	0	104	71
TCGA-E2-A1IL-10A-01D-A14G-09_BRCA	36	66	66	31	76	70	96	86	74	17	68	0	67	75	0	52	81
TCGA-E2-A1IN-10A-01D-A188-09_BRCA	50	111	110	0	108	113	112	87	1	25	125	147	0	109	0	0	82
TCGA-E2-A1IO-10A-01D-A142-09_BRCA	40	60	55	19	61	50	93	76	69	1	0	0	0	1	27	43	70
TCGA-E2-A1L6-10A-01D-A13O-09_BRCA	23	2	2	33	70	72	88	66	73	0	1	0	0	0	11	39	68
TCGA-E2-A1L7-10A-01D-A142-09_BRCA	37	0	0	48	71	79	80	60	49	16	47	0	43	53	0	46	63
TCGA-E2-A1L8-10A-01D-A13O-09_BRCA	45	0	0	51	111	104	113	93	106	0	0	0	2	1	49	0	87
TCGA-E2-A1L9-10A-01D-A188-09_BRCA	64	95	83	40	154	144	137	119	105	22	126	142	0	91	0	96	109
TCGA-E2-A1LA-10A-01D-A142-09_BRCA	41	0	0	44	78	76	85	76	84	0	0	0	0	0	22	43	56
TCGA-E2-A2P5-10B-01D-A19Y-09_BRCA	36	0	0	32	80	78	68	74	65	14	31	0	42	49	0	41	73
TCGA-E2-A2P6-10B-01D-A19Y-09_BRCA	31	3	2	21	80	54	67	55	54	8	29	3	43	40	0	41	56
TCGA-E2-A3DX-10A-01D-A20S-09_BRCA	26	8	6	21	58	68	70	63	11	11	48	2	59	50	0	8	63
TCGA-E2-A56Z-10A-01D-A29N-09_BRCA	63	66	71	21	126	106	109	115	98	0	43	51	0	1	41	56	83
TCGA-E2-A570-10A-01D-A29N-09_BRCA	58	66	62	22	68	108	101	136	126	1	0	1	2	1	47	56	78
TCGA-E2-A572-10B-01D-A31U-09_BRCA	29	58	79	0	0	0	98	103	126	0	0	0	0	0	32	46	87
TCGA-E2-A573-10A-01D-A29N-09_BRCA	36	2	2	25	79	108	88	81	85	0	0	0	0	0	36	53	61
TCGA-E2-A574-10A-01D-A29N-09_BRCA	58	2	0	22	95	90	84	75	105	0	0	0	1	1	36	49	73
TCGA-E2-A576-10B-01D-A31U-09_BRCA	43	0	0	27	92	87	88	91	111	0	0	0	0	0	48	0	49
TCGA-E3-A3DY-10A-01D-A20C-08_THCA	104	0	0	83	93	85	82	80	111	0	0	1	0	1	0	120	111
TCGA-E3-A3DZ-10A-01D-A20C-08_THCA	112	71	74	51	89	85	80	64	68	0	0	0	1	0	0	74	98
TCGA-E3-A3E0-10A-01D-A20C-08_THCA	100	74	78	50	80	73	102	107	81	24	54	2	60	82	33	0	132
TCGA-E3-A3E1-10A-01D-A20C-08_THCA	124	66	74	52	78	79	135	93	78	16	43	1	59	77	34	1	131
TCGA-E3-A3E2-10A-01D-A20C-08_THCA	92	0	0	60	92	89	82	70	72	16	42	0	54	73	0	62	102
TCGA-E3-A3E3-10A-01D-A20C-08_THCA	89	1	0	63	97	90	84	96	69	24	50	0	57	73	0	71	104
TCGA-E3-A3E5-10A-01D-A20C-08_THCA	97	73	79	2	65	66	83	85	96	0	43	66	0	0	30	61	110
TCGA-E5-A2PC-10B-01D-A202-08_BLCA	83	1	1	74	76	73	66	77	84	1	2	0	0	3	0	91	89
TCGA-E5-A4TZ-10B-01D-A31J-08_BLCA	131	0	0	59	105	99	84	95	78	16	48	0	63	76	30	0	122
TCGA-E5-A4U1-10B-01D-A31J-08_BLCA	97	71	80	50	79	77	95	80	119	0	0	1	0	0	0	88	125
TCGA-E6-A1LX-10A-01D-A14G-09_UCEC	38	2	0	30	79	83	93	77	107	0	0	2	0	1	26	44	67
TCGA-E6-A1LZ-10A-01D-A142-09_UCEC	45	0	0	39	120	134	130	100	74	19	100	76	60	72	34	0	98
TCGA-E6-A1M0-10A-01D-A142-09_UCEC	49	72	50	20	66	60	104	115	132	1	2	0	2	1	37	52	87
TCGA-E6-A2P8-10B-01D-A19Y-09_UCEC	43	56	56	20	119	105	111	81	121	0	49	59	0	0	37	52	84
TCGA-E6-A2P9-10B-01D-A19Y-09_UCEC	37	5	1	29	80	96	85	80	98	0	1	0	2	1	0	70	61
TCGA-E7-A3X6-10A-01D-A22Z-08_BLCA	132	1	3	99	144	136	120	108	125	1	3	1	0	2	0	111	161
TCGA-E7-A3Y1-10A-01D-A22Z-08_BLCA	145	0	1	126	147	139	122	119	0	28	87	0	112	148	0	0	171
TCGA-E7-A4IJ-10A-01D-A26K-08_BLCA	88	61	46	33	108	92	86	109	86	11	40	50	4	2	32	2	91
TCGA-E7-A4XJ-10A-01D-A26K-08_BLCA	86	0	0	59	81	98	77	78	84	0	0	0	0	0	37	1	108
TCGA-E7-A519-10A-01D-A26K-08_BLCA	90	0	1	68	87	82	70	77	99	0	1	0	1	3	0	78	102
TCGA-E7-A541-10A-01D-A26K-08_BLCA	83	0	0	54	90	81	72	65	75	12	43	0	60	63	0	52	110
TCGA-E7-A5KE-10A-01D-A289-08_BLCA	115	1	0	58	112	68	117	128	86	19	46	0	54	78	27	0	123
TCGA-E7-A5KF-10A-01D-A289-08_BLCA	119	0	0	90	104	109	101	109	65	20	58	0	62	84	0	87	128
TCGA-E7-A677-10A-01D-A30H-08_BLCA	170	0	1	112	158	158	167	168	116	25	60	0	84	128	38	0	190
TCGA-E7-A678-10A-01D-A30H-08_BLCA	152	0	0	96	157	157	150	146	202	0	0	0	0	1	44	99	178
TCGA-E7-A6ME-10B-01D-A329-08_BLCA	121	1	1	59	99	93	106	83	108	0	0	0	0	0	25	46	118
TCGA-E7-A6MF-10B-01D-A329-08_BLCA	84	0	1	63	110	86	84	66	72	15	32	0	49	64	0	37	110
TCGA-E7-A7DU-10A-01D-A329-08_BLCA	100	54	60	40	58	67	84	80	102	0	0	0	0	0	19	44	108
TCGA-E7-A7DV-10A-01D-A339-08_BLCA	75	85	89	0	0	0	80	69	67	14	40	0	61	67	0	51	95
TCGA-E8-A242-10A-01D-A16O-08_THCA	117	78	83	52	143	103	106	132	106	0	60	85	0	1	36	80	118
TCGA-E8-A2EA-10A-01D-A17V-08_THCA	117	75	1	53	92	83	80	68	84	0	55	0	74	87	0	71	128
TCGA-E8-A2JQ-10A-01D-A19M-08_THCA	82	6	3	73	93	90	71	90	109	0	0	0	0	1	0	105	95
TCGA-E8-A3X7-10A-01D-A22Z-08_THCA	69	73	70	0	74	65	71	74	83	0	52	73	0	0	24	44	85
TCGA-E8-A413-10A-01D-A23K-08_THCA	96	84	92	1	1	5	89	79	5	25	69	0	78	91	0	0	100
TCGA-E8-A414-10A-01D-A23K-08_THCA	92	1	0	56	81	89	77	119	67	19	54	69	4	73	26	0	103
TCGA-E8-A415-10A-01D-A23K-08_THCA	90	6	11	49	84	81	72	99	105	0	2	5	0	3	32	65	93
TCGA-E8-A416-10A-01D-A23K-08_THCA	89	3	4	61	76	72	77	104	89	1	6	3	4	2	28	52	95
TCGA-E8-A417-10A-01D-A23K-08_THCA	115	5	2	89	98	77	81	75	107	0	2	2	3	5	0	112	90
TCGA-E8-A418-10A-01D-A23K-08_THCA	117	71	69	88	95	72	102	144	96	0	0	0	0	0	32	68	99
TCGA-E8-A419-10A-01D-A23K-08_THCA	94	6	11	81	96	97	89	86	81	18	56	10	71	84	0	65	108
TCGA-E8-A432-10A-01D-A23K-08_THCA	158	72	79	69	97	91	131	129	105	19	49	0	71	92	33	0	166
TCGA-E8-A433-10A-01D-A23K-08_THCA	89	69	76	47	70	69	83	88	76	23	52	0	67	78	0	64	95
TCGA-E8-A434-10A-01D-A23K-08_THCA	102	79	77	48	79	85	89	111	92	1	0	1	7	6	34	69	112
TCGA-E8-A436-10A-01D-A23U-08_THCA	68	65	70	6	9	3	48	45	7	13	52	0	63	74	0	1	81
TCGA-E8-A437-10A-01D-A23U-08_THCA	70	47	39	32	83	76	65	113	88	0	40	54	0	1	26	59	82
TCGA-E8-A438-10B-01D-A23U-08_THCA	74	44	46	32	81	66	67	78	55	11	80	51	47	63	0	65	79
TCGA-E8-A44K-10A-01D-A23U-08_THCA	79	56	52	39	62	63	68	92	80	0	1	1	0	0	32	55	83
TCGA-E8-A44M-10A-01D-A23U-08_THCA	90	0	1	43	71	72	78	81	80	0	4	0	1	2	27	55	82
TCGA-E9-A1N3-10A-01D-A159-09_BRCA	36	40	38	19	34	42	70	56	62	0	0	0	0	0	0	43	51
TCGA-E9-A1N4-10A-01D-A14K-09_BRCA	93	111	2	51	196	163	159	169	183	1	0	0	2	0	54	97	112
TCGA-E9-A1N5-10A-01D-A14G-09_BRCA	42	36	42	20	44	51	90	71	49	12	34	6	36	61	0	30	50
TCGA-E9-A1N8-10A-01D-A142-09_BRCA	42	0	0	28	66	40	53	35	38	0	0	0	0	47	0	34	41
TCGA-E9-A1N9-10A-01D-A14G-09_BRCA	36	56	57	23	95	75	80	66	0	17	104	54	79	93	0	0	65
TCGA-E9-A1NA-10A-01D-A142-09_BRCA	31	52	36	23	71	46	57	49	1	6	59	52	43	73	0	1	28
TCGA-E9-A1NC-10A-01D-A159-09_BRCA	43	0	1	43	88	87	91	74	98	0	0	0	0	0	18	46	77
TCGA-E9-A1NE-10A-01D-A14K-09_BRCA	65	117	133	1	103	107	133	137	108	23	147	98	100	99	46	0	91
TCGA-E9-A1NF-10A-01D-A14G-09_BRCA	51	92	89	42	67	76	128	80	136	0	0	0	0	1	0	101	87
TCGA-E9-A1NG-10A-01D-A14K-09_BRCA	47	1	0	38	90	92	97	84	92	0	1	0	0	0	27	45	68
TCGA-E9-A1NI-10A-01D-A17G-09_BRCA	49	75	0	39	74	73	81	62	70	0	55	0	75	86	37	0	97
TCGA-E9-A1QZ-10A-01D-A167-09_BRCA	36	50	45	29	49	44	83	61	72	0	0	0	0	0	20	37	61
TCGA-E9-A1R0-10A-01D-A16D-09_BRCA	51	102	100	37	88	96	111	147	80	18	76	0	98	89	0	66	98
TCGA-E9-A1R2-10A-01D-A14G-09_BRCA	36	63	68	31	66	66	98	86	56	17	40	59	0	65	0	51	70
TCGA-E9-A1R3-10A-01D-A14K-09_BRCA	47	140	145	0	90	84	157	107	148	0	58	91	0	0	32	69	109
TCGA-E9-A1R4-10A-01D-A14G-09_BRCA	62	0	0	46	107	94	101	90	81	15	56	73	0	71	43	0	80
TCGA-E9-A1R5-10A-01D-A14K-09_BRCA	75	0	1	52	188	167	146	151	3	24	150	0	159	137	0	1	115
TCGA-E9-A1R6-10A-01D-A14G-09_BRCA	56	0	0	45	99	90	109	114	102	0	0	0	0	0	34	68	77
TCGA-E9-A1R7-10A-01D-A14K-09_BRCA	36	51	49	20	31	44	69	52	77	0	1	0	0	0	17	38	66
TCGA-E9-A1RA-10A-01D-A14G-09_BRCA	41	0	0	45	83	86	85	77	72	0	0	0	0	0	19	32	67
TCGA-E9-A1RB-10A-01D-A159-09_BRCA	40	103	99	0	59	69	101	86	66	15	76	87	0	75	32	0	68
TCGA-E9-A1RC-10A-01D-A159-09_BRCA	46	80	77	32	111	100	98	77	67	14	75	102	0	75	0	56	68
TCGA-E9-A1RD-10A-01D-A159-09_BRCA	53	0	0	71	97	94	113	119	115	0	0	0	0	1	0	128	73
TCGA-E9-A1RE-10A-01D-A159-09_BRCA	42	44	42	25	25	40	93	64	67	0	0	0	1	0	0	15	64
TCGA-E9-A1RF-10A-01D-A159-09_BRCA	71	112	134	0	86	85	131	139	143	0	73	97	0	0	37	64	95

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-E9-A1RG-10A-01D-A14G-09_BRCA	31	40	44	20	24	36	67	51	59	0	0	0	0	0	33	0	41
TCGA-E9-A1RH-10A-01D-A167-09_BRCA	49	0	1	44	99	94	93	88	104	0	0	0	0	0	0	107	70
TCGA-E9-A1RI-10A-01D-A167-09_BRCA	35	96	87	0	0	1	89	80	92	1	1	1	0	0	21	49	67
TCGA-E9-A226-10A-01D-A159-09_BRCA	62	66	69	32	112	94	90	104	77	13	95	67	60	66	0	44	61
TCGA-E9-A227-10A-01D-A159-09_BRCA	28	77	65	0	60	72	64	47	36	16	69	62	49	49	0	29	53
TCGA-E9-A228-10A-01D-A159-09_BRCA	42	0	0	33	43	76	72	67	47	13	25	0	38	47	0	19	67
TCGA-E9-A229-10B-01D-A159-09_BRCA	49	96	101	0	74	70	102	91	112	0	57	64	0	0	30	71	70
TCGA-E9-A22A-10A-01D-A159-09_BRCA	47	0	0	51	55	60	104	93	99	0	0	0	0	0	0	30	45
TCGA-E9-A22B-10A-01D-A159-09_BRCA	49	78	68	38	77	68	103	83	2	20	88	69	61	99	0	1	64
TCGA-E9-A22D-10A-01D-A159-09_BRCA	55	75	67	38	83	82	107	85	94	0	0	0	1	1	0	99	73
TCGA-E9-A22E-10A-01D-A159-09_BRCA	43	0	2	31	59	34	31	19	35	0	1	0	0	38	0	29	27
TCGA-E9-A22G-10A-01D-A159-09_BRCA	29	0	0	42	73	56	82	70	72	0	0	0	0	0	0	52	54
TCGA-E9-A22H-10A-01D-A17G-09_BRCA	19	0	0	35	42	56	67	47	48	1	0	0	0	0	10	14	45
TCGA-E9-A243-10A-01D-A17G-09_BRCA	58	0	0	76	119	115	120	113	138	0	0	0	0	0	34	69	100
TCGA-E9-A244-10A-01D-A167-09_BRCA	28	0	0	37	89	72	91	82	39	12	53	45	30	36	0	29	58
TCGA-E9-A245-10A-01D-A16D-09_BRCA	38	0	0	49	99	116	114	89	72	13	47	0	72	61	0	40	87
TCGA-E9-A247-10A-01D-A167-09_BRCA	30	49	46	0	21	21	63	48	23	6	42	29	34	34	0	25	41
TCGA-E9-A248-10A-01D-A167-09_BRCA	33	34	29	10	27	40	73	54	63	0	0	0	0	0	0	48	62
TCGA-E9-A249-10A-01D-A167-09_BRCA	36	5	8	32	59	70	77	68	66	1	0	1	0	1	0	71	55
TCGA-E9-A24A-10A-01D-A167-09_BRCA	33	0	0	64	88	86	90	84	105	0	0	0	0	0	0	72	58
TCGA-E9-A295-10A-01D-A16D-09_BRCA	49	57	53	27	103	81	91	82	96	0	48	61	0	0	27	36	75
TCGA-E9-A2JS-10A-01D-A17W-09_BRCA	58	102	97	0	0	0	97	96	96	0	0	0	1	0	30	69	69
TCGA-E9-A2JT-10A-01D-A18P-09_BRCA	41	69	66	33	47	50	108	74	121	1	0	0	1	0	20	47	86
TCGA-E9-A3HO-10A-02D-A20S-09_BRCA	27	71	68	3	6	9	64	59	82	1	2	4	2	2	0	33	62
TCGA-E9-A3Q9-10A-01D-A21Q-09_BRCA	64	111	110	2	74	76	112	124	85	19	85	99	4	81	0	60	88
TCGA-E9-A3QA-10A-01D-A22A-09_BRCA	39	44	43	0	47	47	74	82	90	0	0	0	0	0	33	40	65
TCGA-E9-A3X8-10B-01D-A22X-09_BRCA	43	97	42	1	78	76	77	94	97	0	64	76	1	1	0	84	75
TCGA-E9-A54X-10A-01D-A25Q-09_BRCA	37	57	37	16	52	42	77	73	97	0	2	0	1	1	0	67	72
TCGA-E9-A54Y-10A-01D-A25Q-09_BRCA	45	99	93	1	57	68	100	108	82	14	90	82	2	65	0	65	86
TCGA-E9-A5FK-10A-01D-A27P-09_BRCA	50	52	56	17	95	69	84	79	86	0	46	53	0	1	46	1	67
TCGA-E9-A5FL-10A-01D-A27P-09_BRCA	57	62	71	20	74	69	102	86	145	0	2	0	0	0	0	93	76
TCGA-E9-A5UO-10A-01D-A28E-09_BRCA	52	82	79	19	62	74	103	100	146	0	1	0	0	1	0	113	85
TCGA-E9-A5UP-10A-01D-A28E-09_BRCA	61	1	0	44	114	90	125	99	133	9	54	71	0	66	0	68	87
TCGA-E9-A6HE-10A-01D-A31U-09_BRCA	45	66	64	19	63	69	105	87	115	0	0	0	0	0	0	84	92
TCGA-EA-A1QS-10A-01D-A22X-09_CESC	64	0	3	37	106	77	69	80	95	0	0	1	0	75	0	64	65
TCGA-EA-A1QT-10A-01D-A14W-08_CESC	92	0	1	67	115	94	100	80	85	12	32	0	61	67	0	44	108
TCGA-EA-A3HQ-10A-01D-A20U-09_CESC	61	72	65	19	65	71	92	118	104	0	1	1	0	0	0	124	77
TCGA-EA-A3HR-10A-01D-A20U-09_CESC	67	3	5	46	94	90	111	109	123	0	2	2	0	1	41	63	70
TCGA-EA-A3HS-10B-01D-A20U-09_CESC	53	101	100	0	64	68	101	115	85	6	67	88	0	63	0	60	73
TCGA-EA-A3HT-10A-01D-A21Q-09_CESC	51	63	56	18	107	95	99	111	70	13	79	58	52	65	0	57	76
TCGA-EA-A3HU-10B-01D-A20U-09_CESC	62	114	107	0	71	78	111	125	144	1	59	1	0	2	46	59	85
TCGA-EA-A3QD-10A-01D-A22X-09_CESC	52	70	64	23	120	104	121	95	74	12	85	105	0	67	0	57	82
TCGA-EA-A3QE-10A-01D-A21Q-09_CESC	48	59	55	22	78	63	123	92	124	0	0	6	0	2	0	95	88
TCGA-EA-A3Y4-10A-01D-A243-09_CESC	56	1	2	45	94	89	106	88	112	0	0	0	0	0	0	101	75
TCGA-EA-A410-10A-01D-A243-09_CESC	47	2	1	26	94	77	89	86	102	0	0	1	0	0	0	108	76
TCGA-EA-A411-10A-01D-A243-09_CESC	47	91	83	1	4	2	101	104	131	0	0	0	1	0	0	96	77
TCGA-EA-A439-10A-01D-A243-09_CESC	47	2	6	29	99	95	99	93	88	10	46	0	58	64	0	45	70
TCGA-EA-A43B-10A-01D-A243-09_CESC	57	63	54	14	65	60	94	73	67	9	48	0	69	62	0	55	81
TCGA-EA-A44S-10A-01D-A26G-09_CESC	59	90	89	4	17	13	94	96	95	1	1	9	1	3	0	85	73
TCGA-EA-A4BA-10A-01D-A26G-09_CESC	57	67	67	22	106	86	103	93	114	1	48	56	5	6	0	81	82
TCGA-EA-A50E-10A-01D-A26G-09_CESC	43	5	4	21	71	69	74	78	92	2	6	3	2	5	32	5	68
TCGA-EA-A556-10A-01D-A26G-09_CESC	58	10	8	32	94	91	94	78	113	1	7	4	2	4	0	77	75
TCGA-EA-A5FO-10A-01D-A28E-09_CESC	51	0	1	19	84	93	90	93	115	0	0	0	0	0	0	119	86
TCGA-EA-A5O9-10A-01D-A28E-09_CESC	75	78	72	12	79	66	119	97	93	12	55	0	70	69	39	0	107
TCGA-EA-A5ZD-10A-01D-A28E-09_CESC	50	1	0	26	93	89	100	78	117	0	0	0	0	0	57	0	78
TCGA-EA-A5ZE-10A-01D-A28E-09_CESC	46	0	0	29	90	97	112	81	104	0	0	0	0	0	59	1	71
TCGA-EA-A5ZF-10A-01D-A28E-09_CESC	68	1	0	42	123	71	132	110	80	14	59	81	0	70	43	0	109
TCGA-EB-A1NK-10A-01D-A198-08_SKCM	128	45	56	36	41	40	82	99	88	0	0	0	0	0	17	43	109
TCGA-EB-A24C-10A-01D-A199-08_SKCM	91	86	65	0	56	53	79	98	92	0	34	46	0	0	16	54	112
TCGA-EB-A24D-10A-01D-A199-08_SKCM	96	81	73	0	88	72	84	70	84	0	49	79	0	0	26	49	116
TCGA-EB-A299-10A-01D-A199-08_SKCM	96	53	45	43	59	51	82	94	98	0	0	0	1	0	0	79	101
TCGA-EB-A3HV-10B-01D-A21A-08_SKCM	89	64	61	51	71	72	75	73	96	1	1	0	0	1	0	80	99
TCGA-EB-A3XB-10B-01D-A23B-08_SKCM	82	0	3	48	122	82	76	82	71	20	48	66	5	74	0	59	93
TCGA-EB-A3XC-10A-01D-A23B-08_SKCM	96	77	76	54	131	106	93	141	116	0	56	89	2	0	33	74	110
TCGA-EB-A3XD-10A-01D-A23B-08_SKCM	72	71	70	2	4	3	74	95	73	0	0	1	0	0	24	60	85
TCGA-EB-A3XE-10A-01D-A23B-08_SKCM	92	0	0	58	79	80	78	82	101	0	5	7	0	5	0	78	89
TCGA-EB-A3XF-10A-01D-A23B-08_SKCM	81	0	3	86	82	84	82	87	60	19	34	59	1	74	0	56	94
TCGA-EB-A3Y6-10A-01D-A23B-08_SKCM	90	71	73	48	121	75	73	79	79	2	59	78	0	76	33	5	87
TCGA-EB-A3Y7-10A-01D-A23B-08_SKCM	89	63	67	42	79	68	79	76	104	0	3	6	0	8	0	75	89
TCGA-EB-A41A-10A-01D-A24R-08_SKCM	70	74	79	2	75	71	68	77	93	0	66	70	2	3	0	88	84
TCGA-EB-A41B-10A-01D-A24R-08_SKCM	81	61	60	40	100	79	78	101	66	12	73	75	1	71	28	1	94
TCGA-EB-A42Y-10A-01D-A24R-08_SKCM	123	70	68	39	73	65	73	95	100	0	0	0	0	1	31	63	92
TCGA-EB-A42Z-10A-01D-A24R-08_SKCM	81	63	68	44	108	88	80	79	100	0	54	65	1	0	0	73	92
TCGA-EB-A430-10A-01D-A24R-08_SKCM	85	63	74	46	73	66	77	62	77	0	1	0	0	0	0	74	87
TCGA-EB-A431-10A-01D-A25O-08_SKCM	74	47	42	32	58	42	64	72	59	0	0	0	0	1	0	82	81
TCGA-EB-A44N-10A-01D-A25O-08_SKCM	80	57	61	32	62	57	71	71	91	0	0	0	0	0	0	69	83
TCGA-EB-A44O-10A-01D-A25O-08_SKCM	66	51	52	37	79	73	66	66	86	0	32	60	0	0	0	65	90
TCGA-EB-A44P-10A-01D-A25O-08_SKCM	204	109	141	91	125	124	193	189	152	27	91	0	119	140	0	124	229
TCGA-EB-A44Q-10A-01D-A25O-08_SKCM	72	0	0	43	72	68	70	67	71	0	0	0	0	0	28	0	78
TCGA-EB-A44R-10A-01D-A25O-08_SKCM	72	36	42	31	88	68	66	75	56	11	64	38	41	46	23	0	74
TCGA-EB-A4IQ-10A-01D-A25O-08_SKCM	78	0	0	45	77	75	71	77	74	0	0	0	0	0	18	41	84
TCGA-EB-A4IS-10A-01D-A25O-08_SKCM	75	64	68	0	0	0	63	75	74	0	0	0	0	0	22	46	76
TCGA-EB-A4OY-10A-01D-A25O-08_SKCM	70	35	50	32	78	73	66	70	68	0	37	51	0	0	0	59	80
TCGA-EB-A4OZ-10A-01D-A25O-08_SKCM	66	67	70	0	55	44	67	66	50	14	56	49	43	64	23	0	90
TCGA-EB-A4P0-10A-01D-A25O-08_SKCM	74	59	64	0	54	55	62	77	85	0	31	55	0	0	16	34	77
TCGA-EB-A4XL-10A-01D-A27N-08_SKCM	82	0	1	74	87	79	85	94	101	0	0	0	0	0	0	101	96
TCGA-EB-A51B-10A-01D-A27N-08_SKCM	87	58	70	45	106	78	77	87	63	14	62	80	0	67	0	55	81
TCGA-EB-A550-10A-01D-A27N-08_SKCM	85	65	66	42	74	66	83	105	106	0	0	0	0	0	0	125	95
TCGA-EB-A551-10A-01D-A27N-08_SKCM	85	0	1	71	76	76	74	71	48	10	42	57	0	58	0	48	86
TCGA-EB-A553-10A-01D-A27N-08_SKCM	89	89	84	0	71	66	77	104	77	21	68	83	0	75	30	0	101
TCGA-EB-A57M-10A-01D-A30X-08_SKCM	95	0	0	53	92	86	85	85	86	0	0	0	0	0	27	39	101
TCGA-EB-A5FP-10A-01D-A27N-08_SKCM	86	66	71	44	72	76	86	93	63	16	53	1	60	74	0	61	96
TCGA-EB-A5KH-10A-01D-A27N-08_SKCM	81	0	0	44	80	80	79	74	69	14	40	0	59	61	0	50	88
TCGA-EB-A5SE-10A-01D-A30X-08_SKCM	91	1	1	53	87	86	84	91	87	0	0	0	1	0	0	109	103
TCGA-EB-A5SF-10A-01D-A30X-08_SKCM	82	0	0	52	78	88	77	74	86	0	0	0	0	1	0	71	88
TCGA-EB-A5SG-10A-01D-A30X-08_SKCM	87	55	68	40	76	56	81	64	67	12	44	0	49	73	0	56	103

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EB-A5SH-10A-01D-A30X-08_SKCM	115	0	0	71	84	74	80	70	99	0	0	0	0	1	0	90	104
TCGA-EB-A5UL-10A-01D-A30X-08_SKCM	91	69	68	46	70	0	0	1	0	0	42	0	62	104	0	0	82
TCGA-EB-A5UM-10A-01D-A30X-08_SKCM	87	53	52	32	73	66	81	87	96	0	0	0	0	0	23	59	93
TCGA-EB-A5UN-10A-01D-A30X-08_SKCM	91	0	0	50	84	83	79	65	65	12	21	0	52	63	0	45	93
TCGA-EB-A5VU-10A-01D-A32N-08_SKCM	117	0	1	108	100	108	94	87	113	0	0	1	0	2	0	95	120
TCGA-EB-A5VV-10A-01D-A32N-08_SKCM	135	78	78	45	128	93	114	138	84	26	91	80	71	96	38	0	123
TCGA-EB-A6L9-10A-01D-A32N-08_SKCM	103	0	0	70	100	96	105	99	82	19	55	1	70	83	31	0	125
TCGA-EB-A6QY-10B-01D-A32N-08_SKCM	106	77	82	51	142	99	96	129	87	17	82	75	71	82	34	0	121
TCGA-EB-A6QZ-10B-01D-A32N-08_SKCM	103	0	1	87	111	96	93	115	98	0	0	0	0	0	0	139	126
TCGA-EB-A6R0-10B-01D-A32N-08_SKCM	107	72	76	48	123	87	92	109	118	0	51	71	0	0	28	75	112
TCGA-EC-A1NJ-10A-01D-A14G-09_UCEC	46	51	44	15	96	87	96	67	99	0	49	59	1	0	44	0	67
TCGA-EC-A1QX-10A-01D-A16D-09_UCEC	51	44	50	20	45	57	84	66	89	0	0	0	0	1	0	83	72
TCGA-EC-A24G-10A-01D-A16D-09_UCEC	58	61	68	18	117	101	108	105	75	16	81	90	1	84	38	0	77
TCGA-ED-A459-10A-01D-A25V-10_LIHC	90	81	73	45	64	90	99	108	113	0	0	0	0	0	33	73	85
TCGA-ED-A4XI-10A-01D-A25V-10_LIHC	90	76	74	34	48	78	114	91	107	0	0	0	0	0	43	1	95
TCGA-ED-A5KG-10A-01D-A27I-10_LIHC	73	0	0	46	68	89	90	65	85	0	0	0	0	0	22	56	74
TCGA-ED-A627-10B-01D-A30V-10_LIHC	51	31	25	21	21	34	62	55	37	4	17	0	21	40	0	15	52
TCGA-ED-A66X-10A-01D-A30V-10_LIHC	55	1	0	32	43	41	47	43	51	0	0	0	2	0	0	51	46
TCGA-ED-A66Y-10A-01D-A30V-10_LIHC	33	37	22	23	50	48	66	33	54	0	19	28	0	0	22	0	48
TCGA-EE-A17X-10A-01D-A199-08_SKCM	137	52	73	65	82	67	94	93	131	0	0	0	0	1	33	0	144
TCGA-EE-A17Y-10B-01D-A198-08_SKCM	125	0	0	76	105	79	86	84	108	0	0	0	0	1	34	0	113
TCGA-EE-A17Z-10A-01D-A198-08_SKCM	102	25	34	40	77	68	64	48	81	0	28	33	0	0	0	60	109
TCGA-EE-A180-10B-01D-A21A-08_SKCM	92	58	68	48	75	65	89	99	109	1	0	0	0	0	27	70	110
TCGA-EE-A181-10A-01D-A198-08_SKCM	129	1	0	67	106	94	90	117	132	0	0	0	0	1	0	110	133
TCGA-EE-A182-10A-01D-A198-08_SKCM	120	67	70	58	79	76	106	101	77	12	49	0	49	74	0	60	127
TCGA-EE-A183-10A-01D-A198-08_SKCM	95	0	1	78	85	83	81	75	56	15	42	0	56	70	0	55	85
TCGA-EE-A184-10B-01D-A198-08_SKCM	136	0	0	85	113	93	93	101	100	0	1	0	1	1	0	100	131
TCGA-EE-A185-10A-01D-A198-08_SKCM	136	51	61	50	78	74	105	102	112	0	0	0	0	0	36	0	146
TCGA-EE-A20B-10A-01D-A198-08_SKCM	122	53	69	41	111	91	85	117	108	0	43	48	0	0	28	59	129
TCGA-EE-A20C-10A-01D-A198-08_SKCM	119	1	1	85	111	102	96	103	129	0	0	0	0	0	0	89	106
TCGA-EE-A20F-10A-01D-A198-08_SKCM	116	3	2	69	114	103	99	124	126	0	0	0	0	1	31	66	141
TCGA-EE-A20H-10A-01D-A199-08_SKCM	127	51	64	44	81	93	76	66	97	0	21	45	0	0	20	32	122
TCGA-EE-A20I-10A-01D-A198-08_SKCM	113	48	55	50	55	54	92	92	94	0	0	0	0	0	21	46	124
TCGA-EE-A29A-10A-01D-A198-08_SKCM	119	74	67	52	111	102	90	105	121	0	40	63	0	2	0	107	120
TCGA-EE-A29B-10A-01D-A199-08_SKCM	130	0	0	89	96	99	95	103	98	0	0	0	0	1	0	121	126
TCGA-EE-A29C-10A-01D-A199-08_SKCM	116	1	0	72	99	96	102	95	66	23	59	70	4	78	0	83	132
TCGA-EE-A29D-10A-01D-A199-08_SKCM	120	56	77	54	81	63	97	118	77	11	47	0	56	80	25	2	162
TCGA-EE-A29E-10A-01D-A199-08_SKCM	104	0	2	58	102	86	89	92	70	13	34	0	57	64	0	63	120
TCGA-EE-A29G-10A-01D-A198-08_SKCM	121	0	1	82	106	119	93	110	107	0	0	0	0	1	0	105	127
TCGA-EE-A29H-10A-01D-A199-08_SKCM	102	51	57	48	69	49	87	95	67	13	35	0	39	66	0	51	125
TCGA-EE-A29L-10A-01D-A198-08_SKCM	97	0	0	70	93	75	87	79	100	0	0	0	0	0	0	102	106
TCGA-EE-A29M-10A-01D-A198-08_SKCM	140	0	1	69	108	102	88	116	120	0	0	0	0	0	0	131	141
TCGA-EE-A29N-10A-01D-A199-08_SKCM	129	1	0	113	111	101	111	98	92	0	0	0	0	1	0	96	149
TCGA-EE-A29P-10A-01D-A199-08_SKCM	118	56	59	45	63	55	87	107	126	0	0	2	0	0	23	59	135
TCGA-EE-A29Q-10A-01D-A199-08_SKCM	91	71	76	0	64	48	76	81	61	16	50	55	42	63	0	49	109
TCGA-EE-A29R-10A-01D-A199-08_SKCM	117	0	0	80	98	96	103	105	122	0	0	2	1	0	0	94	129
TCGA-EE-A29S-10A-01D-A199-08_SKCM	103	0	0	73	96	91	86	90	101	0	0	0	1	2	16	43	135
TCGA-EE-A29T-10A-01D-A199-08_SKCM	130	70	69	50	80	79	87	109	128	0	0	0	1	0	0	129	121
TCGA-EE-A29V-10A-01D-A199-08_SKCM	93	61	60	48	59	55	80	74	46	12	34	0	29	58	0	34	118
TCGA-EE-A29W-10A-01D-A198-08_SKCM	128	0	0	93	117	74	95	97	63	8	35	0	45	72	0	56	119
TCGA-EE-A29X-10A-01D-A198-08_SKCM	155	62	77	59	130	91	93	99	65	21	84	60	55	81	0	57	140
TCGA-EE-A2A0-10A-01D-A198-08_SKCM	101	0	0	71	79	74	69	77	87	0	0	0	0	0	20	36	102
TCGA-EE-A2A1-10A-01D-A199-08_SKCM	93	1	0	76	103	71	72	75	58	14	32	0	40	71	0	56	98
TCGA-EE-A2A2-10A-01D-A198-08_SKCM	118	89	99	0	68	66	116	138	72	24	65	59	62	75	0	59	128
TCGA-EE-A2A5-10A-01D-A199-08_SKCM	138	1	0	83	108	95	89	121	119	0	0	1	0	1	0	105	130
TCGA-EE-A2A6-10A-01D-A199-08_SKCM	166	0	0	61	92	98	95	112	81	0	0	0	0	1	0	113	125
TCGA-EE-A2GB-10A-01D-A199-08_SKCM	110	0	0	89	99	95	79	88	94	0	0	0	0	1	0	76	149
TCGA-EE-A2GC-10A-01D-A199-08_SKCM	115	68	63	49	68	72	98	106	79	16	56	0	66	82	0	73	104
TCGA-EE-A2GD-10A-01D-A198-08_SKCM	115	0	0	93	109	79	92	98	105	0	0	0	0	3	0	110	118
TCGA-EE-A2GE-10A-01D-A198-08_SKCM	109	0	1	85	106	98	81	79	106	0	0	0	0	0	35	0	112
TCGA-EE-A2GH-10A-01D-A198-08_SKCM	80	64	59	40	69	58	81	67	77	0	2	0	0	1	0	69	93
TCGA-EE-A2GI-10A-01D-A198-08_SKCM	128	93	96	1	0	0	96	91	90	0	1	0	0	1	39	0	110
TCGA-EE-A2GJ-10A-01D-A198-08_SKCM	102	1	0	66	77	80	73	77	31	13	27	1	32	47	0	34	118
TCGA-EE-A2GK-10A-01D-A198-08_SKCM	111	0	1	62	100	100	86	116	65	18	44	0	57	71	0	69	126
TCGA-EE-A2GL-10A-01D-A198-08_SKCM	98	50	55	43	105	80	96	124	89	14	31	63	0	0	23	51	115
TCGA-EE-A2GM-10A-01D-A198-08_SKCM	133	1	0	86	100	98	92	83	104	0	0	0	0	8	22	52	130
TCGA-EE-A2GN-10A-01D-A198-08_SKCM	148	61	64	49	116	94	89	105	112	0	33	46	0	0	24	53	142
TCGA-EE-A2GO-10A-01D-A198-08_SKCM	95	48	56	55	67	58	92	77	59	9	31	0	38	69	22	2	122
TCGA-EE-A2GP-10A-01D-A199-08_SKCM	111	0	0	48	72	76	80	124	71	13	35	0	34	56	22	0	89
TCGA-EE-A2GR-10A-01D-A199-08_SKCM	90	38	44	41	88	66	59	83	39	17	35	37	23	41	0	34	109
TCGA-EE-A2GS-10A-01D-A199-08_SKCM	77	0	0	36	57	59	58	59	75	0	0	0	1	2	0	58	85
TCGA-EE-A2GT-10A-01D-A199-08_SKCM	92	1	2	66	97	82	86	95	80	18	58	1	55	77	0	63	115
TCGA-EE-A2GU-10A-01D-A198-08_SKCM	105	54	68	46	66	58	74	82	93	0	2	0	0	1	27	67	104
TCGA-EE-A2M5-10A-01D-A199-08_SKCM	87	43	48	47	77	78	69	66	52	9	36	70	0	67	0	38	116
TCGA-EE-A2M6-10A-01D-A199-08_SKCM	77	0	0	72	69	78	73	72	72	0	0	0	0	1	0	64	114
TCGA-EE-A2M7-10A-01D-A199-08_SKCM	125	0	0	90	128	101	99	115	95	0	0	0	0	1	0	120	138
TCGA-EE-A2M8-10A-01D-A198-08_SKCM	99	53	55	39	105	79	84	74	44	8	56	47	40	63	0	51	104
TCGA-EE-A2MC-10A-01D-A199-08_SKCM	113	0	0	59	83	85	80	88	80	0	0	0	0	0	15	37	127
TCGA-EE-A2MD-10A-01D-A199-08_SKCM	86	50	62	44	79	59	80	89	3	23	68	0	81	90	0	0	111
TCGA-EE-A2ME-10A-01D-A199-08_SKCM	96	0	0	58	95	86	75	89	72	17	35	0	52	69	0	54	116
TCGA-EE-A2MF-10B-01D-A21A-08_SKCM	124	0	0	57	93	88	75	67	102	0	0	0	0	1	0	77	105
TCGA-EE-A2MG-10A-01D-A199-08_SKCM	127	69	64	44	67	67	98	90	103	0	0	0	0	1	0	94	129
TCGA-EE-A2MH-10A-01D-A199-08_SKCM	65	0	0	62	64	58	47	45	53	0	1	0	0	0	11	24	86
TCGA-EE-A2MI-10A-01D-A199-08_SKCM	111	0	0	83	88	92	83	73	80	0	0	0	0	1	0	79	108
TCGA-EE-A2MJ-10A-01D-A199-08_SKCM	91	0	1	79	80	83	76	76	91	0	0	0	0	0	0	66	112
TCGA-EE-A2MK-10A-01D-A198-08_SKCM	74	45	39	39	75	54	70	57	21	8	36	68	1	38	0	37	95
TCGA-EE-A2ML-10A-01D-A199-08_SKCM	81	17	26	26	27	25	50	43	60	0	0	0	1	1	16	30	76
TCGA-EE-A2MM-10A-01D-A198-08_SKCM	127	0	0	69	117	96	96	108	67	13	38	0	54	78	21	0	148
TCGA-EE-A2MN-10A-01D-A199-08_SKCM	91	0	1	57	96	74	75	78	90	0	0	0	0	0	0	80	107
TCGA-EE-A2MP-10A-01D-A199-08_SKCM	90	46	56	37	96	92	68	98	98	0	44	56	0	0	18	48	107
TCGA-EE-A2MQ-10A-01D-A199-08_SKCM	115	0	0	101	100	109	107	112	117	0	0	0	0	2	34	68	145
TCGA-EE-A2MR-10A-01D-A198-08_SKCM	109	1	0	73	108	86	108	98	105	0	0	1	0	1	0	100	138
TCGA-EE-A2MS-10A-01D-A199-08_SKCM	101	88	96	0	99	75	86	109	69	8	79	92	0	63	31	0	109
TCGA-EE-A2MT-10A-01D-A199-08_SKCM	134	1	2	60	75	78	79	68	81	0	0	0	0	0	0	78	119
TCGA-EE-A2MU-10A-01D-A198-08_SKCM	96	0	0	82	90	82	77	85	106	0	0	0	0	0	0	75	111
TCGA-EE-A3AA-10A-01D-A198-08_SKCM	140	0	1	80	135	102	112	120	71	16	46	0	53	83	0	83	143

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EE-A3AB-10A-01D-A198-08_SKCM	113	0	0	71	111	89	94	96	113	0	1	0	0	0	0	114	142
TCGA-EE-A3AC-10A-01D-A198-08_SKCM	136	0	0	78	138	107	117	122	70	23	47	0	59	75	0	61	156
TCGA-EE-A3AD-10A-01D-A198-08_SKCM	132	2	1	73	107	91	88	118	115	0	0	0	0	0	0	105	140
TCGA-EE-A3AE-10A-01D-A198-08_SKCM	115	0	0	89	94	92	89	114	112	0	0	1	0	0	31	73	129
TCGA-EE-A3AF-10A-01D-A198-08_SKCM	129	0	0	53	83	82	78	87	99	0	0	1	0	1	34	65	96
TCGA-EE-A3AG-10A-01D-A198-08_SKCM	115	54	46	44	88	70	73	90	0	22	73	49	56	78	0	0	84
TCGA-EE-A3AH-10A-01D-A198-08_SKCM	112	74	80	1	47	50	70	68	87	0	17	51	0	0	0	78	94
TCGA-EE-A3J3-10A-01D-A20D-08_SKCM	85	71	67	47	126	83	90	93	80	20	76	70	69	83	0	65	107
TCGA-EE-A3J4-10A-01D-A20D-08_SKCM	97	1	1	79	83	81	79	97	116	0	0	0	0	1	28	60	103
TCGA-EE-A3J5-10A-01D-A20D-08_SKCM	87	0	0	81	84	88	85	118	83	13	0	1	0	0	0	118	94
TCGA-EE-A3J7-10A-01D-A20D-08_SKCM	132	0	0	66	102	87	91	101	99	0	0	0	0	1	32	68	120
TCGA-EE-A3J8-10A-01D-A20D-08_SKCM	91	68	61	51	120	84	78	81	90	0	50	68	0	1	36	62	104
TCGA-EE-A3JA-10A-01D-A20D-08_SKCM	102	0	0	87	99	88	83	81	101	1	0	0	0	1	0	115	95
TCGA-EE-A3JB-10A-01D-A21A-08_SKCM	99	1	0	67	102	106	93	107	113	1	0	0	0	1	0	105	115
TCGA-EE-A3JD-10A-01D-A20D-08_SKCM	121	1	0	60	107	68	90	79	120	0	0	0	0	1	31	59	107
TCGA-EE-A3JE-10A-01D-A20D-08_SKCM	92	0	0	56	93	82	77	90	79	0	0	1	0	1	0	106	97
TCGA-EE-A3JH-10A-01D-A21A-08_SKCM	98	0	0	57	98	84	88	75	74	17	46	0	51	73	0	61	105
TCGA-EE-A3JI-10A-01D-A21A-08_SKCM	95	67	63	43	120	94	102	113	108	21	44	68	0	0	27	67	131
TCGA-EF-5830-10A-01D-1657-10_READ	106	0	0	59	135	105	149	82	155	0	0	0	0	0	0	62	118
TCGA-EI-6506-10A-01D-1733-10_READ	73	45	50	0	53	52	89	59	71	9	31	0	43	42	9	0	123
TCGA-EI-6507-10A-01D-1733-10_READ	97	46	0	23	86	78	107	59	76	12	34	0	37	46	0	23	117
TCGA-EI-6508-10A-01D-1733-10_READ	74	84	88	0	33	53	90	71	57	8	44	38	50	46	10	0	113
TCGA-EI-6509-10A-01D-1733-10_READ	69	46	40	23	46	43	84	50	82	0	0	0	0	1	0	50	78
TCGA-EI-6510-10A-01D-1733-10_READ	62	29	37	25	62	65	62	54	44	8	28	61	0	37	0	16	73
TCGA-EI-6511-10A-01D-1733-10_READ	78	41	45	44	92	60	91	63	101	0	21	36	0	0	0	50	84
TCGA-EI-6512-10A-01D-1733-10_READ	82	47	55	24	41	43	79	56	105	0	0	0	0	1	0	55	90
TCGA-EI-6513-10A-01D-1733-10_READ	61	34	41	26	37	0	45	29	53	0	0	0	0	47	17	1	60
TCGA-EI-6514-10A-01D-1733-10_READ	54	0	0	36	66	63	83	51	104	0	0	0	0	0	0	50	88
TCGA-EI-6881-10A-01D-1924-10_READ	52	52	67	0	28	38	68	44	57	0	16	31	0	0	12	23	57
TCGA-EI-6882-10A-01D-1924-10_READ	48	40	26	24	47	56	60	44	0	20	47	48	33	58	0	0	56
TCGA-EI-6883-10A-01D-1924-10_READ	34	0	0	31	36	45	48	31	29	6	10	26	0	19	0	14	56
TCGA-EI-6884-10A-01D-1924-10_READ	38	14	0	21	28	22	50	35	19	8	10	0	16	30	0	16	60
TCGA-EI-6885-10A-01D-1924-10_READ	45	22	22	20	27	31	67	44	68	0	0	0	0	0	0	47	69
TCGA-EI-6917-10A-01D-1924-10_READ	38	0	0	25	40	42	49	24	58	0	0	0	0	0	0	29	55
TCGA-EI-7002-10A-01D-1924-10_READ	38	0	0	32	41	47	54	34	49	0	0	0	0	0	9	18	55
TCGA-EI-7004-10A-01D-1924-10_READ	34	0	0	53	48	57	67	32	33	7	19	0	34	27	0	15	68
TCGA-EJ-5494-10A-01D-1577-08_PRAD	119	79	77	48	144	113	96	147	129	0	50	82	0	0	0	142	132
TCGA-EJ-5495-10A-01D-1577-08_PRAD	136	1	1	74	150	127	101	149	105	24	73	2	83	104	47	2	185
TCGA-EJ-5496-10A-01D-1577-08_PRAD	131	1	2	73	138	126	115	153	142	0	0	0	1	2	0	157	142
TCGA-EJ-5497-10A-01D-1577-08_PRAD	125	0	0	100	128	117	107	134	78	19	51	1	79	99	0	76	150
TCGA-EJ-5498-10A-01D-1577-08_PRAD	151	1	2	63	112	129	109	135	126	0	1	0	0	1	0	116	149
TCGA-EJ-5499-10A-01D-1577-08_PRAD	141	1	1	81	130	117	109	105	108	0	0	1	0	1	0	109	147
TCGA-EJ-5501-10A-01D-1577-08_PRAD	122	96	98	0	3	3	88	116	102	0	1	0	0	2	53	2	115
TCGA-EJ-5502-10A-01D-1577-08_PRAD	113	3	0	89	113	109	93	122	129	0	1	1	1	2	31	64	106
TCGA-EJ-5503-10A-01D-1577-08_PRAD	126	91	92	3	2	2	95	110	110	0	1	0	0	0	52	3	113
TCGA-EJ-5504-10A-01D-1577-08_PRAD	132	94	116	3	88	88	98	108	118	0	54	87	0	0	37	81	125
TCGA-EJ-5505-10A-01D-1577-08_PRAD	112	0	1	91	120	119	114	124	106	0	0	1	0	1	0	135	123
TCGA-EJ-5506-10A-01D-1577-08_PRAD	130	0	1	55	109	107	102	115	116	0	0	2	0	2	34	72	128
TCGA-EJ-5507-10A-01D-1577-08_PRAD	137	3	0	62	129	137	133	156	154	0	0	1	0	1	0	169	151
TCGA-EJ-5508-10A-01D-1577-08_PRAD	142	1	2	71	127	121	104	135	114	20	61	0	84	103	0	84	135
TCGA-EJ-5509-10A-01D-1577-08_PRAD	110	69	60	52	120	89	79	100	80	0	34	72	0	1	0	112	114
TCGA-EJ-5510-10A-01D-1577-08_PRAD	106	1	1	84	93	82	61	77	77	0	0	0	1	73	0	73	107
TCGA-EJ-5511-10A-01D-1577-08_PRAD	143	75	79	46	101	94	104	131	119	0	1	0	0	2	36	2	96
TCGA-EJ-5512-10A-01D-1577-08_PRAD	135	88	88	54	165	126	115	113	3	29	112	88	106	128	0	3	147
TCGA-EJ-5514-10A-01D-1577-08_PRAD	121	81	88	51	156	123	117	164	150	0	50	117	0	4	44	86	141
TCGA-EJ-5515-10A-01D-1577-08_PRAD	144	84	89	57	166	117	124	110	128	0	59	98	1	1	34	77	139
TCGA-EJ-5516-10A-01D-1577-08_PRAD	129	0	1	65	120	113	104	137	117	0	0	0	0	1	0	158	132
TCGA-EJ-5517-10A-01D-1577-08_PRAD	129	89	79	60	160	143	113	145	82	25	72	152	0	111	0	84	162
TCGA-EJ-5518-10A-01D-1577-08_PRAD	104	78	86	44	86	82	98	106	99	0	2	0	0	1	39	74	117
TCGA-EJ-5519-10A-01D-1577-08_PRAD	121	95	105	1	123	92	98	136	89	21	100	129	73	86	0	93	119
TCGA-EJ-5521-10A-01D-1577-08_PRAD	115	82	77	49	85	78	98	107	72	18	54	91	0	89	0	76	114
TCGA-EJ-5522-10A-01D-1577-08_PRAD	168	84	87	49	168	129	120	138	91	17	81	96	79	97	0	80	160
TCGA-EJ-5524-10A-01D-1577-08_PRAD	166	1	1	77	133	117	106	167	147	0	0	0	1	2	0	167	144
TCGA-EJ-5525-10A-01D-1577-08_PRAD	138	92	87	65	167	136	100	116	124	0	66	107	1	1	50	2	146
TCGA-EJ-5526-10A-01D-1577-08_PRAD	128	0	0	98	118	114	114	150	84	22	64	0	70	93	0	82	142
TCGA-EJ-5527-10A-01D-1577-08_PRAD	130	90	81	50	181	121	102	122	8	31	107	124	82	128	0	4	138
TCGA-EJ-5530-10A-01D-1577-08_PRAD	117	0	0	55	116	101	86	106	106	0	1	0	0	0	0	105	117
TCGA-EJ-5531-10A-01D-1577-08_PRAD	109	74	74	43	141	108	100	103	102	0	45	74	0	3	0	124	129
TCGA-EJ-5532-10A-01D-1577-08_PRAD	105	90	97	0	1	2	64	82	83	0	53	1	72	93	0	64	121
TCGA-EJ-5542-10A-01D-1577-08_PRAD	124	12	9	92	130	124	126	160	154	0	0	1	1	1	39	76	143
TCGA-EJ-7115-10A-01D-2114-08_PRAD	92	1	0	54	85	83	78	89	110	0	1	0	1	1	0	122	107
TCGA-EJ-7123-10A-01D-1961-08_PRAD	128	1	2	81	128	114	106	108	130	0	0	0	1	2	0	126	162
TCGA-EJ-7125-10A-01D-1961-08_PRAD	119	0	0	107	124	172	105	102	105	0	0	0	0	0	0	114	135
TCGA-EJ-7218-10A-01D-A329-08_PRAD	101	55	68	48	75	75	99	84	107	0	0	1	0	0	0	104	131
TCGA-EJ-7312-10A-01D-A329-08_PRAD	85	58	56	38	119	89	80	59	101	0	32	66	0	0	0	58	97
TCGA-EJ-7314-10A-01D-2114-08_PRAD	99	87	93	1	1	2	85	93	90	2	1	3	1	6	0	82	104
TCGA-EJ-7315-10A-01D-2114-08_PRAD	126	61	90	43	123	95	91	94	1	30	94	114	59	99	0	1	107
TCGA-EJ-7317-10A-01D-2114-08_PRAD	90	0	3	67	101	96	90	79	107	0	0	0	0	2	0	107	106
TCGA-EJ-7318-10A-01D-A329-08_PRAD	92	54	63	44	67	72	108	65	91	0	0	0	0	1	0	75	114
TCGA-EJ-7321-10A-01D-2260-08_PRAD	92	62	63	47	98	90	88	87	82	0	42	1	50	1	0	60	91
TCGA-EJ-7325-10A-01D-A329-08_PRAD	92	69	75	51	80	68	90	107	109	0	0	1	0	0	0	99	109
TCGA-EJ-7327-10A-01D-2114-08_PRAD	121	3	7	58	86	85	81	88	92	0	0	0	0	2	33	62	98
TCGA-EJ-7328-10A-01D-2114-08_PRAD	87	0	1	80	91	80	82	71	72	16	35	0	53	73	0	56	98
TCGA-EJ-7330-10A-01D-2114-08_PRAD	132	80	90	4	84	71	87	101	81	16	74	86	9	75	31	6	108
TCGA-EJ-7331-10A-01D-2114-08_PRAD	96	71	65	6	119	93	96	108	126	0	51	70	0	5	28	72	117
TCGA-EJ-7781-10A-01D-2114-08_PRAD	101	89	88	3	84	74	85	105	76	15	78	68	59	73	31	4	116
TCGA-EJ-7782-10A-01D-2114-08_PRAD	92	72	66	47	105	87	79	90	88	0	49	71	4	2	36	0	113
TCGA-EJ-7783-10A-01D-2114-08_PRAD	128	62	60	39	78	0	92	78	104	0	1	0	0	0	0	93	112
TCGA-EJ-7784-10A-01D-2114-08_PRAD	118	0	0	62	108	88	79	65	111	0	0	0	0	2	0	92	112
TCGA-EJ-7785-10A-01D-2114-08_PRAD	86	5	1	78	90	89	75	95	63	13	40	0	48	60	0	52	107
TCGA-EJ-7786-10A-01D-2114-08_PRAD	99	0	0	69	105	93	97	80	79	17	36	0	33	86	0	57	107
TCGA-EJ-7788-10A-01D-2114-08_PRAD	95	58	54	51	111	97	84	86	74	15	58	89	0	67	32	0	124
TCGA-EJ-7789-10A-01D-2114-08_PRAD	93	68	66	54	78	76	85	100	112	0	0	0	1	0	34	62	121
TCGA-EJ-7791-10A-01D-2115-08_PRAD	95	4	4	59	97	88	86	103	98	0	0	0	0	1	0	151	109
TCGA-EJ-7792-10A-01D-2115-08_PRAD	91	3	2	51	93	88	80	105	71	14	44	0	60	72	37	0	96
TCGA-EJ-7793-10A-01D-2260-08_PRAD	96	1	2	85	102	92	93	97	79	19	44	2	62	69	0	69	101

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EJ-7794-10A-01D-2115-08_PRAD	85	53	51	45	60	56	66	53	63	0	44	0	44	62	0	60	95
TCGA-EJ-7797-10A-01D-2260-08_PRAD	85	67	59	48	120	88	94	88	73	18	60	84	1	69	0	57	113
TCGA-EJ-8468-10A-01D-2395-08_PRAD	85	71	68	51	116	87	79	96	77	14	70	110	2	79	0	64	109
TCGA-EJ-8469-10A-01D-2395-08_PRAD	93	2	1	78	85	83	84	128	113	0	1	2	0	0	0	128	100
TCGA-EJ-8470-10A-01D-2395-08_PRAD	123	0	0	101	110	116	120	124	84	20	52	0	81	90	37	1	131
TCGA-EJ-8472-10A-01D-2395-08_PRAD	96	0	3	55	86	85	87	80	99	0	2	2	0	0	33	65	103
TCGA-EJ-8474-10A-01D-2395-08_PRAD	96	7	5	61	86	90	85	102	84	17	50	0	69	80	30	0	102
TCGA-EJ-A46B-10A-01D-A25A-08_PRAD	95	64	68	49	115	79	74	95	89	1	34	62	3	3	26	63	104
TCGA-EJ-A46D-10A-01D-A25A-08_PRAD	131	0	0	93	85	96	82	112	119	0	0	0	0	2	32	67	116
TCGA-EJ-A46E-10A-01D-A25A-08_PRAD	88	69	70	51	123	92	85	104	119	0	46	71	0	0	27	68	123
TCGA-EJ-A46F-10A-01D-A25A-08_PRAD	92	67	70	54	72	70	82	88	113	1	3	1	2	4	0	95	114
TCGA-EJ-A46G-10A-01D-A26K-08_PRAD	73	52	49	38	63	56	82	65	88	0	0	0	0	0	32	2	104
TCGA-EJ-A46H-10A-01D-A26K-08_PRAD	80	1	4	51	89	84	82	73	88	0	2	5	1	2	25	41	103
TCGA-EJ-A46I-10A-01D-A26K-08_PRAD	74	0	0	58	67	74	69	69	88	0	1	0	0	2	0	84	82
TCGA-EJ-A65B-10A-01D-A30H-08_PRAD	180	0	0	117	175	143	157	182	175	0	0	0	0	2	44	101	192
TCGA-EJ-A65D-10A-01D-A30H-08_PRAD	181	103	104	70	110	110	149	139	170	0	0	0	0	1	0	167	183
TCGA-EJ-A65E-10A-01D-A29Q-08_PRAD	91	56	64	44	93	87	81	102	94	0	37	66	0	3	29	51	102
TCGA-EJ-A65F-10A-01D-A30X-08_PRAD	88	61	57	37	102	83	81	90	97	0	35	67	0	1	24	52	92
TCGA-EJ-A65G-10A-01D-A29Q-08_PRAD	122	80	87	49	88	91	102	110	141	0	0	0	0	1	0	109	142
TCGA-EJ-A65J-10A-01D-A30X-08_PRAD	99	0	0	89	86	79	77	86	65	12	43	0	56	72	24	0	96
TCGA-EJ-A65M-10A-01D-A29Q-08_PRAD	120	0	88	56	142	129	115	95	124	0	49	0	75	0	0	107	145
TCGA-EJ-A6RA-10A-01D-A33W-08_PRAD	97	0	0	59	78	82	71	80	62	16	41	0	48	70	0	53	92
TCGA-EJ-A6RC-10A-01D-A329-08_PRAD	99	83	93	0	69	70	75	71	106	0	28	64	0	0	0	98	107
TCGA-EJ-A7NF-10A-01D-A33W-08_PRAD	81	0	0	78	89	82	83	72	72	0	0	0	0	1	0	85	98
TCGA-EJ-A7NG-10A-01D-A33W-08_PRAD	107	48	59	44	106	77	77	68	63	15	55	81	0	68	0	56	101
TCGA-EJ-A7NH-10A-01D-A33W-08_PRAD	81	0	0	52	80	75	73	75	111	0	0	0	0	0	0	122	91
TCGA-EJ-A7NM-10A-01D-A33W-08_PRAD	84	54	59	33	63	51	73	88	67	13	33	0	41	74	25	0	97
TCGA-EJ-A7NN-10A-01D-A33W-08_PRAD	87	0	0	55	84	88	88	67	75	0	0	0	0	0	0	75	98
TCGA-EK-A2GZ-10A-01D-A17W-09_CESC	61	91	83	3	3	5	107	96	114	0	1	1	0	0	52	1	84
TCGA-EK-A2H0-10A-01D-A17W-09_CESC	58	0	0	45	129	119	139	140	119	0	0	1	0	2	39	78	102
TCGA-EK-A2H1-10A-01D-A17W-09_CESC	57	1	0	35	102	108	114	121	139	0	0	0	0	0	43	80	90
TCGA-EK-A2IP-10A-01D-A17W-09_CESC	62	3	0	40	112	110	117	90	160	0	0	0	0	1	0	101	83
TCGA-EK-A2PG-10A-01D-A18J-09_CESC	44	61	66	11	49	65	90	90	73	14	45	1	56	73	28	1	69
TCGA-EK-A2PI-10A-01D-A18J-09_CESC	48	101	86	0	3	1	92	100	98	1	2	1	1	1	43	57	72
TCGA-EK-A2PK-10A-01D-A18J-09_CESC	43	62	56	19	60	66	94	87	120	1	0	1	0	0	37	51	67
TCGA-EK-A2PL-10A-01D-A18J-09_CESC	41	76	79	1	48	61	85	72	112	0	45	49	1	1	31	47	70
TCGA-EK-A2PM-10A-01D-A18J-09_CESC	48	2	0	32	75	85	83	85	120	0	0	1	0	1	34	52	66
TCGA-EK-A2R7-10A-01D-A18J-09_CESC	42	1	0	30	77	72	79	70	61	9	37	0	50	57	39	1	55
TCGA-EK-A2R8-10A-01D-A18J-09_CESC	46	62	62	14	77	67	69	50	84	0	2	1	1	1	32	2	57
TCGA-EK-A2R9-10A-01D-A18J-09_CESC	48	77	83	0	57	59	89	84	65	13	83	55	47	55	30	0	80
TCGA-EK-A2RA-10A-01D-A18J-09_CESC	53	54	44	12	59	55	99	96	76	9	46	0	49	58	0	53	71
TCGA-EK-A2RB-10A-01D-A18J-09_CESC	57	67	64	18	100	94	101	92	84	14	83	65	58	69	0	57	80
TCGA-EK-A2RC-10A-01D-A18J-09_CESC	37	1	0	20	77	80	88	73	106	0	0	2	0	1	0	73	66
TCGA-EK-A2RD-10A-01D-A20U-09_CESC	46	1	2	21	92	81	84	78	117	1	3	1	0	2	0	80	86
TCGA-EK-A2RE-10A-01D-A18J-09_CESC	37	2	1	19	83	75	80	66	122	0	0	1	1	0	0	70	70
TCGA-EK-A2RJ-10A-01D-A18J-09_CESC	47	58	55	14	99	82	99	78	60	12	58	80	0	60	0	53	85
TCGA-EK-A2RK-10A-01D-A18J-09_CESC	47	2	1	27	77	77	77	103	109	3	0	2	0	1	0	40	70
TCGA-EK-A2RL-10A-01D-A18J-09_CESC	41	81	72	1	39	64	93	89	67	16	69	58	49	33	0	44	71
TCGA-EK-A2RN-10A-01D-A20U-09_CESC	53	0	1	24	89	87	81	105	140	0	0	0	1	0	30	51	78
TCGA-EK-A2RO-10A-01D-A18J-09_CESC	57	56	50	21	65	60	97	105	137	0	1	1	0	2	0	124	78
TCGA-EK-A3GK-10A-01D-A20U-09_CESC	40	52	54	17	68	54	92	80	75	13	46	0	50	60	36	1	74
TCGA-EK-A3GM-10A-01D-A20U-09_CESC	48	53	48	18	45	49	59	55	62	0	41	0	48	49	0	49	66
TCGA-EK-A3GN-10A-01D-A20U-09_CESC	38	55	43	16	87	86	85	76	61	13	58	41	52	50	0	44	69
TCGA-EL-A3CL-10A-01D-A19M-08_THCA	105	0	1	68	114	99	106	76	113	0	0	0	1	0	0	91	140
TCGA-EL-A3CM-10A-01D-A19M-08_THCA	81	2	0	69	86	73	74	76	79	0	1	0	0	1	0	74	95
TCGA-EL-A3CN-10A-01D-A20C-08_THCA	104	88	89	1	0	2	72	60	72	20	62	0	78	112	0	63	128
TCGA-EL-A3CO-10A-01D-A19M-08_THCA	111	77	91	56	152	110	109	116	111	0	51	69	0	2	0	139	155
TCGA-EL-A3CP-10A-01D-A19M-08_THCA	95	64	66	45	105	103	86	91	111	0	34	66	0	3	25	54	131
TCGA-EL-A3CR-10A-01D-A202-08_THCA	92	0	2	78	87	82	85	104	113	0	0	0	0	0	30	65	103
TCGA-EL-A3CS-10A-01D-A19M-08_THCA	96	1	2	89	101	95	89	97	107	0	0	0	0	1	0	91	133
TCGA-EL-A3CT-10A-01D-A202-08_THCA	93	0	0	80	94	81	114	102	81	12	52	0	53	71	0	62	104
TCGA-EL-A3CU-10A-01D-A19M-08_THCA	107	60	69	44	121	95	83	84	112	0	35	64	5	8	28	36	124
TCGA-EL-A3CV-10A-01D-A19M-08_THCA	102	66	68	51	71	74	91	80	134	0	0	0	0	0	35	5	127
TCGA-EL-A3CW-10A-01D-A19M-08_THCA	112	71	68	53	86	75	117	90	131	0	0	1	1	0	21	62	143
TCGA-EL-A3CX-10A-01D-A19M-08_THCA	84	3	4	52	87	86	80	91	88	1	1	2	4	2	26	48	86
TCGA-EL-A3CY-10A-01D-A19M-08_THCA	123	0	0	99	110	104	101	96	105	0	0	1	1	1	28	69	148
TCGA-EL-A3CZ-10A-01D-A19M-08_THCA	111	0	0	73	112	108	96	85	101	1	1	1	1	3	0	129	129
TCGA-EL-A3D0-10A-01D-A202-08_THCA	91	1	0	63	87	80	76	89	76	15	51	0	61	72	28	1	94
TCGA-EL-A3D1-10A-01D-A19M-08_THCA	121	83	78	50	78	82	87	54	5	15	80	2	89	114	0	3	124
TCGA-EL-A3D4-10A-01D-A19M-08_THCA	112	2	2	87	115	105	103	95	126	0	1	0	0	0	19	74	130
TCGA-EL-A3D5-10A-01D-A202-08_THCA	89	73	68	47	76	64	78	82	78	19	50	0	60	69	0	66	93
TCGA-EL-A3D6-10A-01D-A202-08_THCA	94	0	0	50	89	87	84	112	77	21	46	64	0	68	31	0	102
TCGA-EL-A3GO-10A-01D-A202-08_THCA	82	58	68	49	72	69	81	113	112	0	0	0	0	0	35	59	93
TCGA-EL-A3GP-10A-01D-A202-08_THCA	92	90	67	1	74	66	72	56	69	0	84	71	68	71	0	66	106
TCGA-EL-A3GQ-10A-01D-A202-08_THCA	88	66	61	46	67	67	75	94	101	0	1	0	0	2	27	57	109
TCGA-EL-A3GR-10A-01D-A202-08_THCA	88	70	69	41	81	69	81	112	107	0	0	0	0	1	33	74	101
TCGA-EL-A3GS-10A-01D-A20C-08_THCA	93	73	67	48	77	72	83	106	99	0	0	1	1	1	29	77	119
TCGA-EL-A3GV-10A-01D-A21A-08_THCA	85	1	0	53	90	81	74	84	49	14	47	0	47	70	0	56	97
TCGA-EL-A3GW-10A-01D-A202-08_THCA	89	78	63	1	65	65	77	105	59	19	43	0	59	64	0	61	100
TCGA-EL-A3GX-10A-01D-A202-08_THCA	95	61	68	49	67	70	81	81	78	17	42	0	61	74	0	63	99
TCGA-EL-A3GY-10A-01D-A202-08_THCA	89	1	0	83	102	89	82	87	75	17	51	0	69	72	0	71	92
TCGA-EL-A3H3-10A-01D-A202-08_THCA	86	59	62	43	70	63	84	102	82	0	0	0	0	0	0	113	87
TCGA-EL-A3H4-10A-01D-A202-08_THCA	87	1	0	85	95	84	88	137	120	0	58	0	64	1	30	64	100
TCGA-EL-A3H5-10A-01D-A202-08_THCA	89	88	88	1	100	86	86	105	73	17	95	88	67	71	29	1	104
TCGA-EL-A3H8-10A-01D-A20C-08_THCA	98	0	2	84	99	93	79	72	1	24	60	1	65	90	0	2	103
TCGA-EL-A4KG-10A-01D-A25A-08_THCA	62	55	51	34	48	44	69	84	83	0	0	0	0	0	20	48	76
TCGA-EL-A4KH-10A-01D-A25A-08_THCA	71	0	1	69	75	67	71	84	92	0	1	0	0	4	0	102	85
TCGA-EL-A4KI-10A-01D-A25A-08_THCA	76	0	0	57	69	72	66	93	57	10	34	0	40	59	0	53	78
TCGA-EM-A1CS-10A-01D-A13W-08_THCA	173	83	99	67	109	105	156	166	188	0	0	2	0	0	43	89	270
TCGA-EM-A1CT-10A-01D-A13W-08_THCA	199	2	0	97	172	188	144	154	118	21	61	0	80	115	46	0	234
TCGA-EM-A1CU-10A-02D-A13W-08_THCA	167	104	97	71	191	152	155	135	181	0	54	112	2	3	46	94	210
TCGA-EM-A1CV-10A-01D-A13W-08_THCA	151	124	120	1	92	91	135	137	88	20	74	127	0	98	32	1	171
TCGA-EM-A1CW-10A-01D-A13W-08_THCA	173	110	113	62	116	105	167	130	193	0	1	2	0	1	0	139	205
TCGA-EM-A1YA-10A-01D-A14W-08_THCA	109	1	0	71	99	92	82	91	81	15	43	0	56	65	25	1	112
TCGA-EM-A1YB-10A-01D-A14W-08_THCA	87	4	2	48	75	90	78	86	105	0	0	1	3	8	0	96	105
TCGA-EM-A22I-10A-01D-A17V-08_THCA	115	80	83	48	78	74	102	110	84	16	55	0	83	83	33	1	123

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EM-A22J-10A-01D-A17V-08_THCA	124	0	88	48	140	112	108	114	116	0	53	0	75	5	27	65	138
TCGA-EM-A22K-10A-01D-A17V-08_THCA	98	0	0	78	91	83	78	90	97	0	0	0	0	0	30	58	107
TCGA-EM-A22L-10A-01D-A17V-08_THCA	96	56	65	41	72	58	91	96	93	0	1	0	0	0	27	63	103
TCGA-EM-A22M-10A-01D-A17V-08_THCA	100	63	73	45	101	89	82	92	73	14	75	68	51	74	0	57	103
TCGA-EM-A22N-10A-01D-A17V-08_THCA	90	0	0	83	98	85	81	103	111	0	0	0	0	1	27	61	107
TCGA-EM-A22O-10A-01D-A17V-08_THCA	121	0	1	75	125	115	108	127	93	20	55	1	78	102	34	0	133
TCGA-EM-A22P-10A-01D-A19M-08_THCA	120	0	1	92	114	106	87	109	130	0	0	0	0	0	24	69	138
TCGA-EM-A22Q-10A-01D-A17V-08_THCA	97	77	72	57	130	107	94	90	1	25	93	72	94	112	0	0	121
TCGA-EM-A2CJ-10A-01D-A17V-08_THCA	98	88	93	0	75	74	66	58	67	0	74	91	0	82	29	0	107
TCGA-EM-A2CK-10A-01D-A17V-08_THCA	101	62	67	44	114	84	87	92	93	0	49	64	0	1	38	0	97
TCGA-EM-A2CL-10A-01D-A17V-08_THCA	127	96	119	1	1	3	115	102	85	21	69	1	72	79	0	68	140
TCGA-EM-A2CM-10A-01D-A17V-08_THCA	90	0	0	86	90	79	86	102	93	0	2	0	0	0	35	65	110
TCGA-EM-A2CN-10B-01D-A19M-08_THCA	104	2	0	93	100	106	99	87	116	0	0	0	0	1	0	102	135
TCGA-EM-A2CO-10A-01D-A19M-08_THCA	109	1	0	62	108	99	94	87	105	0	0	0	0	0	0	100	138
TCGA-EM-A2CP-10A-01D-A17V-08_THCA	86	0	1	55	91	90	84	90	89	0	0	1	0	0	20	62	88
TCGA-EM-A2CQ-10A-01D-A17V-08_THCA	101	0	0	63	98	86	93	115	112	0	0	0	0	0	32	61	119
TCGA-EM-A2CR-10A-01D-A17V-08_THCA	112	50	59	42	106	92	85	100	63	11	70	84	1	76	24	0	99
TCGA-EM-A2CS-10A-01D-A19M-08_THCA	78	53	59	35	64	58	72	92	86	0	3	1	3	3	29	57	90
TCGA-EM-A2CT-10A-01D-A17V-08_THCA	100	56	71	47	53	61	94	100	114	0	1	1	0	0	35	49	115
TCGA-EM-A2CU-10A-01D-A17V-08_THCA	102	64	71	55	72	71	87	105	103	0	0	0	0	0	0	85	110
TCGA-EM-A2OV-10A-01D-A202-08_THCA	86	0	0	58	102	85	78	87	83	0	0	0	0	0	43	2	100
TCGA-EM-A2OW-10A-01D-A202-08_THCA	90	0	0	95	96	87	113	85	84	0	0	0	0	2	0	95	114
TCGA-EM-A2OX-10A-01D-A202-08_THCA	106	85	87	0	0	0	88	101	100	0	0	0	0	0	26	63	95
TCGA-EM-A2OY-10A-01D-A202-08_THCA	126	1	0	64	96	92	75	93	76	20	59	1	59	71	0	53	105
TCGA-EM-A2OZ-10A-01D-A202-08_THCA	95	0	2	55	95	95	84	101	96	0	0	0	0	0	33	61	94
TCGA-EM-A2P0-10A-01D-A202-08_THCA	95	0	0	94	96	93	79	107	67	18	66	0	60	78	0	68	102
TCGA-EM-A2P1-10A-01D-A202-08_THCA	93	68	67	44	71	75	89	99	67	16	39	0	45	75	0	60	100
TCGA-EM-A2P2-10A-01D-A202-08_THCA	98	0	1	79	96	91	88	83	86	0	0	1	0	0	0	90	110
TCGA-EM-A2P3-10A-01D-A202-08_THCA	93	0	1	59	102	94	93	92	94	0	1	0	0	0	33	73	103
TCGA-EM-A3AI-10A-01D-A202-08_THCA	84	70	65	37	120	85	77	126	119	0	47	71	0	0	30	69	106
TCGA-EM-A3AJ-10A-01D-A202-08_THCA	105	74	71	48	79	77	79	115	109	0	0	0	0	1	0	122	100
TCGA-EM-A3AK-10A-01D-A202-08_THCA	92	65	69	48	68	77	82	77	97	0	0	0	0	0	0	90	109
TCGA-EM-A3AL-10A-01D-A202-08_THCA	81	65	64	35	63	64	77	107	86	0	0	0	0	0	0	80	98
TCGA-EM-A3AN-10A-01D-A202-08_THCA	97	0	0	82	88	95	85	84	115	0	0	0	0	0	0	90	105
TCGA-EM-A3AO-10A-01D-A202-08_THCA	88	0	0	82	91	78	76	98	101	0	0	0	0	0	31	70	97
TCGA-EM-A3AP-10A-01D-A20C-08_THCA	100	1	2	47	82	86	55	58	88	0	0	0	0	1	21	40	88
TCGA-EM-A3AQ-10A-01D-A20C-08_THCA	107	2	1	88	94	105	92	105	76	19	51	0	61	79	35	3	107
TCGA-EM-A3AR-10A-01D-A20C-08_THCA	107	1	1	89	94	94	83	97	79	0	0	0	0	1	0	153	121
TCGA-EM-A3FJ-10A-01D-A21A-08_THCA	96	58	55	48	71	66	79	91	88	0	0	1	0	0	29	60	119
TCGA-EM-A3FK-10A-01D-A21A-08_THCA	88	54	40	51	66	74	85	64	101	1	0	0	0	2	0	91	125
TCGA-EM-A3FL-10A-01D-A21A-08_THCA	127	63	64	40	81	67	81	104	59	16	51	0	54	70	31	1	105
TCGA-EM-A3FM-10A-01D-A21A-08_THCA	85	0	0	57	79	80	84	72	67	10	37	0	43	63	29	0	116
TCGA-EM-A3FN-10A-01D-A21A-08_THCA	102	60	64	50	103	96	99	92	77	20	83	78	76	63	0	77	109
TCGA-EM-A3FO-10A-01D-A21A-08_THCA	97	53	59	45	73	81	84	96	94	0	0	0	0	0	28	70	114
TCGA-EM-A3FP-10A-01D-A21A-08_THCA	101	2	0	63	95	82	83	86	73	13	46	0	52	79	32	0	102
TCGA-EM-A3FQ-10A-01D-A21A-08_THCA	96	61	57	42	71	73	92	114	107	0	0	0	0	0	35	68	115
TCGA-EM-A3FR-10A-01D-A21Z-08_THCA	92	67	62	52	80	71	89	78	101	0	1	1	0	0	35	1	94
TCGA-EM-A3O3-10A-01D-A21Z-08_THCA	91	67	64	44	81	72	84	99	74	24	51	71	0	73	32	1	107
TCGA-EM-A3O6-10A-01D-A21Z-08_THCA	89	1	0	56	90	83	81	81	87	24	48	0	54	79	0	53	108
TCGA-EM-A3O7-10A-01D-A21Z-08_THCA	96	89	83	0	78	76	89	79	96	0	49	74	0	2	36	0	110
TCGA-EM-A3O8-10A-01D-A21Z-08_THCA	108	83	88	2	79	76	92	104	78	21	81	75	73	78	35	0	101
TCGA-EM-A3O9-10A-01D-A21Z-08_THCA	86	85	77	3	87	85	80	106	69	22	78	96	0	71	0	71	112
TCGA-EM-A3OA-10A-01D-A21Z-08_THCA	95	61	66	47	74	72	91	81	89	0	0	1	0	1	35	0	104
TCGA-EM-A3OB-10A-01D-A21Z-08_THCA	94	124	86	3	91	93	85	123	115	0	59	90	0	1	32	73	114
TCGA-EM-A3SU-10A-01D-A22Z-08_THCA	71	63	72	0	56	48	71	66	0	20	69	56	62	75	0	0	70
TCGA-EM-A3SX-10A-01D-A22Z-08_THCA	77	72	64	0	0	0	70	84	81	0	0	0	0	0	21	40	74
TCGA-EM-A3SY-10A-01D-A22Z-08_THCA	72	0	0	43	77	74	72	64	88	0	0	0	0	1	0	55	60
TCGA-EM-A3SZ-10A-01D-A22Z-08_THCA	82	1	1	69	79	78	71	64	67	1	0	5	1	0	0	75	81
TCGA-EM-A4FF-10A-01D-A25A-08_THCA	164	0	0	92	149	149	134	109	161	0	0	0	0	0	51	0	184
TCGA-EM-A4FH-10A-01D-A25A-08_THCA	68	54	54	39	54	55	71	83	75	0	2	0	0	6	30	50	77
TCGA-EM-A4FK-10A-01D-A25A-08_THCA	66	68	65	6	3	3	62	72	62	0	0	0	0	0	25	36	72
TCGA-EM-A4FM-10A-01D-A25A-08_THCA	74	76	72	2	55	57	47	45	6	10	71	52	72	70	0	0	82
TCGA-EM-A4FN-10A-01D-A25A-08_THCA	75	75	81	4	55	59	68	72	61	12	57	65	2	62	0	58	72
TCGA-EM-A4FO-10A-01D-A25A-08_THCA	70	3	0	41	70	61	62	75	58	10	32	2	47	63	20	4	74
TCGA-EM-A4FQ-10A-01D-A25A-08_THCA	77	59	56	32	98	72	66	93	78	0	46	53	1	0	0	106	88
TCGA-EM-A4FR-10A-01D-A25A-08_THCA	72	2	2	60	72	70	78	93	53	10	0	0	0	0	25	61	78
TCGA-EM-A4FU-10A-01D-A25A-08_THCA	73	1	0	71	72	78	72	91	75	0	0	0	0	2	30	55	79
TCGA-EM-A4FV-10A-01D-A25A-08_THCA	68	54	50	32	86	65	68	77	63	8	57	47	36	52	15	6	75
TCGA-EM-A4G1-10A-01D-A25A-08_THCA	69	52	52	25	78	68	62	84	60	1	28	50	2	1	0	94	72
TCGA-EO-A1Y5-10A-01D-A159-09_UCEC	40	0	1	44	101	92	98	77	67	16	49	0	56	61	0	46	71
TCGA-EO-A1Y7-10A-01D-A159-09_UCEC	44	0	1	37	102	85	95	93	103	0	0	0	0	0	0	90	76
TCGA-EO-A1Y8-10A-01D-A159-09_UCEC	53	0	0	75	116	108	129	90	127	0	0	0	0	1	0	109	99
TCGA-EO-A22U-10B-01D-A17W-09_UCEC	45	55	38	16	46	55	72	89	94	0	0	0	0	0	33	40	70
TCGA-EO-A22X-10A-01D-A17W-09_UCEC	38	60	56	17	58	61	94	100	108	0	0	0	1	0	0	89	76
TCGA-EO-A22Y-10A-01D-A17W-09_UCEC	48	60	62	19	59	62	89	102	116	1	3	0	2	3	0	100	67
TCGA-EO-A2CG-10A-01D-A17W-09_UCEC	53	62	66	20	130	94	100	89	3	15	113	63	97	86	0	1	83
TCGA-EO-A2CH-10A-01D-A17W-09_UCEC	44	55	47	13	41	50	77	79	94	0	0	1	0	0	0	79	65
TCGA-EO-A3AS-10A-01D-A19Y-09_UCEC	49	97	89	0	83	96	88	114	82	14	113	96	56	70	40	3	79
TCGA-EO-A3AU-10A-01D-A19Y-09_UCEC	50	0	0	27	78	87	95	74	85	0	0	0	0	0	0	65	63
TCGA-EO-A3AV-10A-01D-A19Y-09_UCEC	58	1	2	40	106	103	113	97	134	0	0	0	0	1	27	69	82
TCGA-EO-A3AY-10A-01D-A19Y-09_UCEC	60	69	64	22	74	77	102	74	129	0	0	0	1	2	0	76	82
TCGA-EO-A3AZ-10A-01D-A19Y-09_UCEC	48	102	96	0	0	4	99	55	108	0	0	0	1	1	21	39	96
TCGA-EO-A3B0-10A-01D-A19Y-09_UCEC	46	49	49	15	103	87	87	103	58	0	44	51	0	2	36	47	69
TCGA-EO-A3B1-10A-01D-A19Y-09_UCEC	53	64	63	22	63	72	92	78	75	13	47	2	56	53	0	54	72
TCGA-EO-A3KU-10A-01D-A22A-09_UCEC	54	3	4	31	96	67	89	105	107	0	2	1	0	2	23	47	73
TCGA-EO-A3KW-10A-01D-A22A-09_UCEC	53	54	39	23	97	85	122	138	100	14	42	40	1	4	35	51	81
TCGA-EO-A3KX-10A-01D-A22A-09_UCEC	41	5	3	29	71	70	73	68	59	10	30	3	42	45	0	38	60
TCGA-EO-A3L0-10A-01D-A22A-09_UCEC	41	53	51	16	56	47	63	48	68	0	49	0	51	50	0	61	66
TCGA-EP-A12J-10A-01D-A12Z-10_LIHC	63	24	32	22	49	44	64	31	57	0	13	20	0	0	7	9	60
TCGA-EP-A26S-10A-01D-A16V-10_LIHC	49	0	0	41	56	54	62	33	19	13	16	0	21	32	0	30	70
TCGA-EP-A2KA-10A-01D-A183-10_LIHC	100	54	57	48	56	52	120	85	128	0	0	0	0	0	12	48	142
TCGA-EP-A2KB-10A-01D-A183-10_LIHC	88	56	70	35	45	78	140	78	106	0	0	0	0	0	0	98	143
TCGA-EP-A2KC-10A-01D-A20W-10_LIHC	85	71	100	1	90	108	107	86	64	0	59	61	54	0	28	39	87
TCGA-EP-A3JL-10A-01D-A20W-10_LIHC	78	0	0	40	109	93	118	86	107	0	0	0	0	0	27	37	88
TCGA-EP-A3RK-10A-01D-A22F-10_LIHC	50	37	26	13	22	35	60	38	78	0	0	0	0	0	0	52	59
TCGA-EQ-5647-10A-01D-1600-08_STAD	115	2	1	64	125	113	115	115	127	0	0	0	0	0	0	99	127

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EQ-8122-10A-01D-2341-08_STAD	103	0	1	98	108	109	99	98	131	0	0	0	0	1	0	152	118
TCGA-EQ-A4SO-10A-01D-A25E-08_STAD	78	0	0	47	86	87	76	96	61	12	55	0	64	64	34	0	93
TCGA-ER-A193-10A-01D-A199-08_SKCM	118	71	63	59	114	106	97	97	126	0	28	49	0	1	0	104	139
TCGA-ER-A194-10A-01D-A199-08_SKCM	97	0	1	77	86	81	85	87	111	0	0	0	0	2	30	60	111
TCGA-ER-A195-10A-01D-A198-08_SKCM	105	64	64	46	60	70	82	95	71	13	48	0	56	80	0	60	112
TCGA-ER-A196-10A-01D-A199-08_SKCM	116	67	70	49	79	75	103	90	116	0	0	0	1	1	27	72	118
TCGA-ER-A197-10A-01D-A199-08_SKCM	107	74	72	48	116	97	86	127	72	13	57	62	59	77	22	0	114
TCGA-ER-A198-10A-01D-A198-08_SKCM	91	0	0	58	82	81	78	86	65	12	28	0	37	60	16	0	110
TCGA-ER-A199-10A-01D-A199-08_SKCM	113	61	44	46	61	49	76	68	86	0	0	0	0	0	0	74	109
TCGA-ER-A19A-10A-01D-A199-08_SKCM	100	0	0	75	89	80	83	83	93	0	0	0	0	0	0	76	108
TCGA-ER-A19B-10A-01D-A198-08_SKCM	101	49	46	43	66	50	78	76	87	0	0	0	0	0	17	40	124
TCGA-ER-A19C-10A-01D-A198-08_SKCM	100	41	44	54	66	73	54	68	40	10	50	77	0	50	0	35	104
TCGA-ER-A19D-10A-01D-A199-08_SKCM	85	42	67	37	104	74	72	67	49	10	56	54	49	59	0	52	96
TCGA-ER-A19E-10A-01D-A199-08_SKCM	106	0	1	78	81	92	76	88	77	0	0	0	0	0	0	97	96
TCGA-ER-A19F-10A-01D-A198-08_SKCM	95	0	2	78	85	82	73	93	75	0	0	0	0	0	0	98	99
TCGA-ER-A19G-10A-01D-A198-08_SKCM	111	53	45	43	124	91	91	84	6	23	89	90	45	79	0	1	102
TCGA-ER-A19H-10A-01D-A198-08_SKCM	122	47	58	45	102	74	82	80	94	0	22	48	0	0	0	66	129
TCGA-ER-A19J-10A-01D-A198-08_SKCM	119	80	84	0	65	52	101	85	98	0	34	60	0	0	26	57	126
TCGA-ER-A19K-10A-01D-A199-08_SKCM	89	78	73	0	1	1	80	99	76	14	51	0	52	67	0	67	105
TCGA-ER-A19L-10A-01D-A199-08_SKCM	98	0	0	72	89	75	70	83	59	9	21	0	35	47	0	41	97
TCGA-ER-A19M-10A-01D-A23B-08_SKCM	92	73	74	51	126	103	94	108	84	22	87	69	65	79	32	4	102
TCGA-ER-A19N-10A-01D-A199-08_SKCM	104	0	1	84	68	87	86	79	60	8	27	0	44	64	0	43	112
TCGA-ER-A19O-10A-01D-A199-08_SKCM	117	77	83	1	1	1	77	81	103	0	0	0	0	1	12	41	128
TCGA-ER-A19P-10A-01D-A198-08_SKCM	118	0	0	87	91	90	77	94	70	12	48	0	52	68	18	0	109
TCGA-ER-A19Q-10A-01D-A199-08_SKCM	102	91	103	0	71	70	81	104	99	0	54	67	0	0	36	76	113
TCGA-ER-A19S-10A-01D-A198-08_SKCM	102	64	67	45	111	89	76	94	114	0	47	64	0	0	0	128	105
TCGA-ER-A19T-10A-01D-A19A-08_SKCM	114	62	39	49	92	72	78	100	83	0	26	37	0	1	0	80	102
TCGA-ER-A19W-10A-01D-A23B-08_SKCM	145	86	87	44	151	104	108	109	119	0	46	84	0	0	28	75	141
TCGA-ER-A1A1-10A-01D-A199-08_SKCM	124	70	77	44	70	57	98	105	110	0	0	0	0	1	36	62	153
TCGA-ER-A2NB-10A-01D-A198-08_SKCM	80	51	56	40	99	71	71	69	52	12	57	74	0	50	0	49	79
TCGA-ER-A2NC-10A-01D-A199-08_SKCM	108	61	67	42	110	86	83	83	75	12	69	79	0	72	0	62	97
TCGA-ER-A2ND-10A-01D-A198-08_SKCM	126	63	61	39	110	90	104	101	112	0	31	57	0	1	0	124	145
TCGA-ER-A2NE-10A-01D-A198-08_SKCM	131	56	67	50	103	99	75	104	102	1	22	50	0	2	0	85	136
TCGA-ER-A2NF-10A-01D-A19A-08_SKCM	134	0	2	63	100	89	79	99	67	14	44	0	56	78	30	2	107
TCGA-ER-A2NG-10A-01D-A198-08_SKCM	77	69	71	1	44	47	74	95	78	9	27	49	0	0	20	52	85
TCGA-ER-A2NH-10A-01D-A198-08_SKCM	108	62	66	52	65	57	111	89	93	0	0	0	0	0	0	81	119
TCGA-ER-A3ES-10A-01D-A20D-08_SKCM	85	0	1	69	91	86	87	79	99	0	0	3	0	0	39	1	97
TCGA-ER-A3ET-10A-01D-A20D-08_SKCM	82	57	65	48	108	92	75	100	106	0	39	65	0	0	28	54	97
TCGA-ER-A3EV-10A-01D-A20D-08_SKCM	87	0	1	61	99	90	83	84	83	0	0	1	0	1	0	85	118
TCGA-ER-A3PL-10A-01D-A23B-08_SKCM	106	1	1	71	142	113	102	87	93	22	48	0	78	89	0	67	141
TCGA-ER-A42H-10A-01D-A24R-08_SKCM	88	0	0	56	87	82	84	91	82	0	0	0	2	0	0	123	92
TCGA-ER-A42K-10A-01D-A24R-08_SKCM	106	5	3	77	82	75	80	75	66	17	49	0	53	66	0	66	84
TCGA-ER-A42L-10A-01D-A24R-08_SKCM	74	0	1	72	83	82	79	75	106	0	1	0	1	0	0	73	90
TCGA-ET-A25G-10A-01D-A16O-08_THCA	121	66	68	57	79	84	104	128	100	0	0	0	0	0	0	136	131
TCGA-ET-A25I-10A-01D-A16O-08_THCA	127	83	77	62	80	81	121	108	110	14	1	0	0	0	0	102	130
TCGA-ET-A25K-10A-01D-A16O-08_THCA	125	81	74	55	80	87	79	77	2	17	81	81	68	123	0	0	137
TCGA-ET-A25O-10A-01D-A17V-08_THCA	97	1	0	77	140	104	90	124	98	13	56	65	0	2	30	56	110
TCGA-ET-A25R-10A-01D-A16O-08_THCA	103	0	0	64	103	91	94	87	120	0	1	0	0	1	0	123	137
TCGA-ET-A2MZ-10A-01D-A19M-08_THCA	116	67	73	51	80	84	99	114	126	0	0	1	0	0	26	76	135
TCGA-ET-A2N0-10A-01D-A18F-08_THCA	116	1	1	66	119	92	99	95	61	16	35	0	47	65	0	55	145
TCGA-ET-A2N1-10A-01D-A18F-08_THCA	102	66	60	40	107	95	84	83	97	0	43	61	0	0	0	84	99
TCGA-ET-A2N3-10A-01D-A23K-08_THCA	152	0	0	102	152	141	135	113	97	14	50	0	71	118	0	73	174
TCGA-ET-A2N4-10A-01D-A19M-08_THCA	112	79	79	55	136	115	120	122	122	0	49	73	0	2	0	111	149
TCGA-ET-A39I-10A-01D-A19M-08_THCA	102	59	67	43	66	58	103	91	124	0	0	0	0	0	0	109	127
TCGA-ET-A39J-10A-01D-A19M-08_THCA	104	75	62	45	78	68	108	71	120	0	0	0	0	3	27	2	130
TCGA-ET-A39K-10A-01D-A19M-08_THCA	97	0	2	67	109	92	89	89	84	21	46	0	56	71	0	55	123
TCGA-ET-A39L-10A-01D-A19M-08_THCA	127	3	0	98	112	119	115	80	123	0	1	0	4	2	0	96	166
TCGA-ET-A39M-10A-01D-A19M-08_THCA	88	46	62	40	112	82	82	75	71	17	75	59	60	62	0	61	103
TCGA-ET-A39N-10A-01D-A19M-08_THCA	120	64	64	58	79	71	118	117	121	0	0	0	0	1	25	51	127
TCGA-ET-A39O-10A-01D-A19M-08_THCA	117	2	0	62	117	120	113	113	137	0	0	0	6	6	22	52	132
TCGA-ET-A39P-10A-01D-A19M-08_THCA	109	63	79	44	133	110	110	86	115	0	40	68	0	0	21	57	149
TCGA-ET-A39R-10A-01D-A19M-08_THCA	114	82	84	54	91	88	105	91	77	18	54	1	75	93	0	76	140
TCGA-ET-A39S-10A-01D-A19M-08_THCA	112	3	1	79	124	119	116	97	118	0	0	3	0	2	29	50	141
TCGA-ET-A39T-10A-01D-A19M-08_THCA	94	54	71	46	63	52	90	79	94	0	0	0	0	0	0	95	114
TCGA-ET-A3BN-10A-01D-A19M-08_THCA	127	1	0	73	126	129	125	81	86	25	32	0	62	85	0	47	146
TCGA-ET-A3BO-10A-01D-A19M-08_THCA	116	81	78	51	85	78	108	125	145	0	0	1	0	0	35	69	138
TCGA-ET-A3BP-10A-01D-A19M-08_THCA	141	0	0	58	111	92	95	116	77	16	53	0	60	78	0	56	140
TCGA-ET-A3BQ-10A-01D-A202-08_THCA	87	0	1	53	95	86	78	105	110	0	0	0	0	0	0	81	100
TCGA-ET-A3BS-10A-01D-A202-08_THCA	96	62	63	45	69	67	89	85	61	16	53	0	52	70	0	74	106
TCGA-ET-A3BT-10A-01D-A19M-08_THCA	110	5	7	71	113	118	129	110	125	0	0	0	1	0	27	56	124
TCGA-ET-A3BU-10A-01D-A19M-08_THCA	109	71	76	54	95	79	96	87	74	21	42	70	2	91	0	73	142
TCGA-ET-A3BV-10A-01D-A19M-08_THCA	118	1	0	70	116	109	102	114	114	0	0	0	0	0	0	123	126
TCGA-ET-A3BW-10A-01D-A19M-08_THCA	128	1	4	77	145	110	134	93	145	0	0	0	0	0	0	96	183
TCGA-ET-A3BX-10A-01D-A19M-08_THCA	111	3	3	65	109	104	104	85	101	0	0	0	0	0	0	93	137
TCGA-ET-A3DO-10A-01D-A19M-08_THCA	111	71	73	47	67	70	103	118	82	15	39	0	56	72	21	0	131
TCGA-ET-A3DQ-10A-01D-A19M-08_THCA	138	4	1	94	127	105	103	104	127	0	0	0	0	0	0	113	139
TCGA-ET-A3DR-10A-01D-A19M-08_THCA	138	1	0	86	149	117	127	134	154	0	2	0	2	5	0	118	182
TCGA-ET-A3DS-10A-01D-A19M-08_THCA	120	96	111	6	89	80	107	88	121	0	55	74	0	0	40	3	135
TCGA-ET-A3DT-10A-01D-A19M-08_THCA	100	93	103	1	4	3	90	87	86	15	40	0	48	75	24	0	134
TCGA-ET-A3DU-10A-01D-A19M-08_THCA	112	109	117	5	11	7	122	100	125	0	0	0	0	0	54	1	142
TCGA-ET-A40P-10A-01D-A23K-08_THCA	125	1	2	56	104	98	80	88	73	20	55	0	70	76	0	77	108
TCGA-ET-A40Q-10A-01D-A23K-08_THCA	179	0	1	118	181	175	162	160	192	0	0	0	0	1	46	97	216
TCGA-ET-A40R-10A-01D-A23K-08_THCA	137	89	96	66	162	114	127	162	143	0	80	86	4	2	0	174	156
TCGA-ET-A40S-10A-01D-A23K-08_THCA	87	77	73	50	85	68	81	114	115	0	0	0	0	2	31	72	105
TCGA-ET-A40T-10A-01D-A23K-08_THCA	138	7	6	91	107	87	88	151	115	3	4	7	2	11	31	85	103
TCGA-ET-A4KN-10A-01D-A25A-08_THCA	86	1	5	38	70	71	69	64	55	11	35	0	45	60	0	45	73
TCGA-ET-A4KQ-10A-01D-A25A-08_THCA	64	0	1	44	66	66	72	82	64	0	1	0	5	4	0	94	71
TCGA-EU-5904-10A-01D-1669-08_KIRC	106	74	71	46	90	81	97	130	116	0	0	0	0	0	32	67	128
TCGA-EU-5905-10A-01D-1669-08_KIRC	99	1	1	78	106	94	88	96	98	0	0	0	1	1	0	77	128
TCGA-EU-5906-10A-01D-1669-08_KIRC	116	1	0	69	109	96	99	115	123	0	1	0	0	1	34	78	137
TCGA-EU-5907-10A-01D-1669-08_KIRC	108	72	73	50	136	113	103	126	81	23	72	78	66	95	24	3	143
TCGA-EV-5901-10A-01D-1589-08_KIRP	139	2	3	85	105	110	92	128	112	0	0	0	0	0	33	69	104
TCGA-EV-5902-10A-01D-1589-08_KIRP	108	0	3	57	109	106	97	97	110	0	0	2	0	1	0	113	120
TCGA-EV-5903-10A-01D-1589-08_KIRP	111	3	1	84	100	103	96	84	127	0	1	0	0	3	0	92	105
TCGA-EW-A1IW-10A-01D-A13O-09_BRCA	29	0	0	28	73	70	89	59	83	0	0	1	0	0	19	41	67
TCGA-EW-A1IX-10A-01D-A142-09_BRCA	55	0	0	49	110	111	122	100	131	0	0	0	0	0	28	65	86

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EW-A1IY-10A-01D-A13O-09_BRCA	58	0	0	49	103	98	97	93	69	18	53	0	70	69	31	0	72
TCGA-EW-A1IZ-10A-01D-A13O-09_BRCA	39	56	59	29	51	56	98	75	94	0	0	0	0	0	28	40	74
TCGA-EW-A1J1-10A-01D-A13O-09_BRCA	52	67	64	29	119	94	100	92	95	0	48	65	0	0	29	55	82
TCGA-EW-A1J3-10A-01D-A13O-09_BRCA	61	118	112	0	97	82	126	92	129	0	57	87	1	0	37	80	79
TCGA-EW-A1J5-10A-01D-A13O-09_BRCA	54	68	69	30	65	68	108	92	119	0	0	0	0	0	0	72	76
TCGA-EW-A1J6-10A-01D-A13O-09_BRCA	49	1	0	54	111	112	122	124	122	0	0	0	0	0	40	60	83
TCGA-EW-A1OV-10A-01D-A142-09_BRCA	33	46	45	19	70	59	73	74	64	0	31	43	0	0	0	68	58
TCGA-EW-A1OX-10A-01D-A142-09_BRCA	29	0	0	33	70	70	86	57	71	0	0	0	0	0	0	66	55
TCGA-EW-A1OZ-10A-01D-A142-09_BRCA	30	0	45	24	85	62	82	57	72	0	36	0	43	0	24	30	48
TCGA-EW-A1P0-10A-01D-A142-09_BRCA	33	1	0	41	71	66	80	43	82	0	0	0	0	0	18	40	59
TCGA-EW-A1P1-10A-01D-A14G-09_BRCA	33	51	48	25	86	79	99	80	93	0	39	54	0	1	23	31	58
TCGA-EW-A1P3-10A-01D-A142-09_BRCA	32	0	0	50	79	80	83	89	52	14	45	0	40	64	0	35	70
TCGA-EW-A1P4-10A-01D-A142-09_BRCA	38	97	91	0	54	62	94	101	117	0	45	49	0	0	0	99	74
TCGA-EW-A1P5-10A-01D-A142-09_BRCA	39	69	60	31	60	52	87	64	56	13	40	59	0	55	0	51	76
TCGA-EW-A1P6-10A-01D-A142-09_BRCA	28	53	58	25	53	52	89	70	40	16	37	0	51	40	0	40	59
TCGA-EW-A1P7-10A-01D-A142-09_BRCA	19	55	46	20	45	43	85	66	85	0	0	0	0	0	30	0	68
TCGA-EW-A1P8-10A-01D-A142-09_BRCA	62	99	95	43	78	85	123	95	133	0	0	0	0	0	0	100	96
TCGA-EW-A1PA-10A-01D-A142-09_BRCA	34	0	0	37	68	67	78	54	44	15	24	56	1	49	0	36	58
TCGA-EW-A1PB-10A-01D-A142-09_BRCA	44	0	1	47	87	71	73	79	83	1	0	1	0	0	25	36	61
TCGA-EW-A1PC-10A-01D-A21Q-09_BRCA	54	50	2	19	44	53	47	42	64	1	30	2	44	51	0	35	61
TCGA-EW-A1PD-10A-01D-A142-09_BRCA	22	74	69	1	69	70	85	89	79	15	54	64	0	1	0	83	61
TCGA-EW-A1PE-10A-01D-A142-09_BRCA	42	0	0	37	82	76	81	84	76	1	0	0	0	1	21	43	60
TCGA-EW-A1PG-10A-01D-A142-09_BRCA	30	0	0	44	94	80	110	81	57	12	34	0	65	54	0	35	63
TCGA-EW-A1PH-10A-01D-A14K-09_BRCA	46	91	109	49	144	128	133	86	123	1	62	90	0	0	0	106	95
TCGA-EW-A2FR-10A-01D-A21Q-09_BRCA	45	2	2	28	91	104	93	84	119	1	0	0	3	3	53	6	83
TCGA-EW-A2FS-10A-01D-A17D-09_BRCA	29	0	0	33	63	44	44	33	58	0	0	0	0	0	19	0	43
TCGA-EW-A2FV-10A-01D-A17D-09_BRCA	47	1	0	62	35	74	96	123	100	0	0	1	0	0	17	23	87
TCGA-EW-A2FW-10A-01D-A17D-09_BRCA	37	1	1	41	67	67	72	58	46	12	45	0	38	45	17	0	51
TCGA-EW-A3E8-10A-01D-A243-09_BRCA	40	64	47	13	54	46	53	36	9	10	56	2	81	69	0	9	71
TCGA-EW-A3U0-10A-01D-A22A-09_BRCA	40	50	45	15	93	61	70	77	53	9	55	42	42	49	18	1	67
TCGA-EW-A423-10A-01D-A243-09_BRCA	30	0	1	16	67	60	70	64	94	0	1	2	0	0	18	33	53
TCGA-EX-A1H5-10A-01D-A13W-08_CESC	183	1	2	116	168	143	157	130	183	0	1	0	0	0	42	91	216
TCGA-EX-A1H6-10A-01D-A22X-09_CESC	47	66	60	18	56	61	110	99	118	0	1	0	0	0	40	59	79
TCGA-EX-A3L1-10A-01D-A21Q-09_CESC	49	101	94	0	65	63	112	108	83	14	79	103	1	76	39	2	101
TCGA-EX-A449-10A-01D-A243-09_CESC	40	3	1	36	87	75	113	135	126	8	1	0	0	0	37	35	71
TCGA-EY-A1G7-10A-01D-A13O-09_UCEC	47	81	81	1	63	56	91	89	114	0	39	44	0	0	0	81	87
TCGA-EY-A1G8-10A-01D-A13O-09_UCEC	47	52	49	18	101	88	92	71	70	12	60	80	0	57	0	53	74
TCGA-EY-A1GC-10A-01D-A13O-09_UCEC	50	0	2	40	97	87	110	82	138	0	0	2	0	1	0	84	77
TCGA-EY-A1GD-10A-01D-A13O-09_UCEC	42	1	0	32	91	82	106	75	136	0	0	0	0	0	53	0	77
TCGA-EY-A1GE-10A-01D-A13O-09_UCEC	46	53	57	10	53	50	87	70	102	0	0	0	0	1	30	39	72
TCGA-EY-A1GF-10A-01D-A13O-09_UCEC	62	78	73	24	76	73	103	103	130	0	0	0	0	0	40	64	89
TCGA-EY-A1GH-10A-01D-A13O-09_UCEC	45	63	48	16	58	59	91	83	116	0	2	1	0	0	31	48	64
TCGA-EY-A1GI-10A-01D-A13O-09_UCEC	54	3	0	31	85	89	93	82	97	0	0	0	1	0	51	1	77
TCGA-EY-A1GJ-10A-01D-A142-09_UCEC	54	76	69	23	140	101	136	104	126	0	66	70	0	0	59	0	89
TCGA-EY-A1GK-10A-01D-A13O-09_UCEC	43	1	0	43	86	84	93	104	108	0	0	1	0	1	37	49	78
TCGA-EY-A1GL-10A-01D-A13O-09_UCEC	48	58	56	18	54	61	100	94	112	0	0	2	0	0	31	51	75
TCGA-EY-A1GM-10A-01D-A14G-09_UCEC	62	68	58	20	128	90	99	85	110	0	51	65	0	0	49	0	78
TCGA-EY-A1GO-10A-01D-A14G-09_UCEC	42	54	56	11	40	50	57	59	4	9	72	59	50	88	0	1	79
TCGA-EY-A1GP-10A-01D-A13O-09_UCEC	43	65	65	17	97	119	90	96	121	0	47	0	55	0	37	0	52
TCGA-EY-A1GQ-10A-01D-A13O-09_UCEC	44	1	3	27	88	86	90	80	108	0	2	0	2	4	0	83	84
TCGA-EY-A1GR-10A-01D-A13O-09_UCEC	54	67	72	18	107	97	104	114	142	0	54	0	60	1	0	55	51
TCGA-EY-A1GS-10A-01D-A13O-09_UCEC	42	64	64	27	57	67	110	79	97	0	0	0	0	0	52	50	79
TCGA-EY-A1GT-10A-01D-A13O-09_UCEC	45	52	51	15	57	53	86	65	100	0	0	0	0	2	0	76	73
TCGA-EY-A1GU-10A-01D-A13O-09_UCEC	44	0	1	23	92	105	85	78	109	0	0	0	0	0	46	0	74
TCGA-EY-A1GV-10A-01D-A13O-09_UCEC	47	88	95	1	91	81	96	100	115	0	74	89	0	0	29	54	69
TCGA-EY-A1GW-10A-01D-A13O-09_UCEC	47	98	87	0	94	99	92	78	132	0	70	85	0	1	0	116	74
TCGA-EY-A1GX-10A-01D-A13O-09_UCEC	47	1	2	24	85	110	115	113	125	0	0	0	0	3	31	50	85
TCGA-EY-A1H0-10A-01D-A13O-09_UCEC	53	111	97	0	72	75	107	127	135	0	58	68	0	1	52	57	93
TCGA-EY-A210-10A-01D-A159-09_UCEC	44	0	52	15	118	92	82	88	118	0	40	0	52	0	26	37	70
TCGA-EY-A212-10A-01D-A14K-09_UCEC	42	72	59	28	67	75	118	79	101	0	0	0	0	0	0	80	66
TCGA-EY-A214-10A-01D-A159-09_UCEC	50	76	79	1	50	57	81	73	83	0	36	50	0	0	0	61	69
TCGA-EY-A215-10A-01D-A14K-09_UCEC	55	68	68	21	117	97	112	109	112	0	62	67	0	3	44	57	87
TCGA-EY-A2OM-10A-01D-A18P-09_UCEC	49	62	56	20	80	58	53	48	74	0	44	0	65	71	0	49	79
TCGA-EY-A2ON-10A-01D-A18P-09_UCEC	44	0	0	23	72	89	83	79	115	0	0	0	0	1	58	0	81
TCGA-EY-A2OO-10A-01D-A19Y-09_UCEC	46	53	60	18	90	91	86	78	53	10	81	85	0	59	0	53	78
TCGA-EY-A2OP-10A-01D-A19Y-09_UCEC	34	78	79	2	50	45	83	75	102	0	42	44	1	0	32	36	59
TCGA-EY-A2OQ-10A-01D-A19Y-09_UCEC	61	3	4	32	98	101	92	110	148	0	0	0	1	2	0	115	81
TCGA-EY-A3L3-10A-01D-A22A-09_UCEC	50	55	61	14	124	85	111	99	92	13	77	66	58	77	41	1	78
TCGA-EY-A3QX-10A-01D-A22A-09_UCEC	56	59	47	21	115	91	102	89	70	13	56	54	62	50	0	53	84
TCGA-EY-A4KR-10A-01D-A27P-09_UCEC	55	2	0	42	92	78	98	80	93	0	1	0	1	0	51	2	76
TCGA-EY-A547-10A-01D-A27P-09_UCEC	65	1	1	44	135	106	102	119	160	0	0	0	1	2	50	76	94
TCGA-EY-A548-10A-01D-A27P-09_UCEC	60	88	59	0	1	2	4	1	5	0	81	0	88	106	0	1	72
TCGA-EY-A549-10A-01D-A27P-09_UCEC	55	1	0	25	98	85	93	101	101	0	0	0	3	0	0	116	75
TCGA-EY-A54A-10A-01D-A27P-09_UCEC	64	62	2	20	94	99	86	91	86	13	95	53	56	64	49	0	74
TCGA-EY-A5W2-10A-01D-A31U-09_UCEC	36	0	0	16	55	88	83	74	108	0	0	0	0	0	58	0	81
TCGA-EZ-7264-10A-01D-2024-08_LGG	88	65	67	45	114	93	78	80	9	27	75	60	76	88	0	0	108
TCGA-F1-6177-10A-01D-1800-08_STAD	96	71	65	47	127	90	84	109	83	16	88	66	63	71	31	1	108
TCGA-F1-6874-10A-01D-1882-08_STAD	108	72	72	49	78	81	69	64	70	0	62	0	71	80	0	70	115
TCGA-F1-A448-10A-01D-A24F-08_STAD	92	71	69	39	71	61	77	79	80	2	8	0	7	12	35	0	96
TCGA-F1-A72C-10A-01D-A33W-08_STAD	90	0	0	59	91	87	86	80	94	0	0	0	0	0	39	0	104
TCGA-F2-A44G-10A-01D-A26I-08_PAAD	103	1	0	90	117	109	97	89	0	33	83	0	83	106	0	0	145
TCGA-F2-A44H-10A-01D-A26I-08_PAAD	80	1	1	48	75	80	86	71	85	0	0	0	0	0	28	0	91
TCGA-F4-6459-10A-01D-1771-10_COAD	71	0	0	60	55	64	72	58	80	0	0	0	0	0	0	61	67
TCGA-F4-6460-10B-01D-1771-10_COAD	72	0	0	56	77	69	92	60	52	11	19	0	34	43	25	0	84
TCGA-F4-6461-10A-01D-1806-10_COAD	63	0	0	51	82	72	79	102	105	0	0	0	0	0	18	38	79
TCGA-F4-6463-10A-01D-1719-10_COAD	38	35	25	10	34	43	43	37	59	0	9	16	0	0	5	16	52
TCGA-F4-6569-10A-01D-1771-10_COAD	48	0	1	46	45	44	68	51	67	0	0	0	0	0	0	55	73
TCGA-F4-6570-10A-01D-1771-10_COAD	52	23	19	19	22	0	28	14	32	0	0	0	0	24	0	17	30
TCGA-F4-6703-10A-01D-1835-10_COAD	23	0	0	25	23	33	28	26	14	6	7	0	13	15	0	13	49
TCGA-F4-6805-10A-01D-1835-10_COAD	43	60	62	0	42	58	70	50	38	12	39	54	0	34	0	28	75
TCGA-F4-6806-10A-01D-1835-10_COAD	54	15	13	24	24	19	49	33	27	9	14	0	16	21	8	0	46
TCGA-F4-6807-10A-01D-1835-10_COAD	47	0	0	38	52	43	57	37	53	0	0	0	0	1	0	33	63
TCGA-F4-6808-10A-01D-1835-10_COAD	53	0	0	30	42	20	25	13	0	8	16	0	22	37	0	0	38
TCGA-F4-6809-10A-01D-1835-10_COAD	42	0	0	28	35	27	34	22	30	0	0	0	0	23	0	17	36
TCGA-F4-6854-10A-01D-1924-10_COAD	34	0	1	25	34	25	31	36	0	10	24	0	20	29	0	0	52
TCGA-F4-6855-10A-01D-1924-10_COAD	41	29	17	13	34	47	29	33	22	7	31	24	16	21	0	12	59

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-F4-6856-10A-01D-1924-10_COAD	42	9	13	20	14	27	38	47	31	11	13	0	16	23	0	14	49
TCGA-F5-6464-10A-01D-1733-10_READ	77	0	0	40	72	74	82	71	53	12	33	0	36	41	0	26	105
TCGA-F5-6465-10A-01D-1733-10_READ	78	47	46	23	56	32	85	66	66	12	25	0	37	47	22	0	89
TCGA-F5-6571-10A-01D-1826-10_READ	62	0	0	36	45	61	52	49	36	13	14	0	23	37	15	0	58
TCGA-F5-6702-10A-01D-1826-10_READ	46	59	51	0	28	23	57	44	76	0	27	38	0	0	16	21	69
TCGA-F5-6812-10A-01D-1826-10_READ	51	22	22	24	20	20	49	46	44	0	0	0	0	0	0	41	54
TCGA-F5-6813-10A-01D-1826-10_READ	55	34	28	19	19	23	56	44	66	0	0	0	0	0	11	12	68
TCGA-F5-6814-10A-01D-1924-10_READ	35	62	68	0	36	50	58	40	36	11	45	51	26	35	0	24	56
TCGA-F5-6861-10A-01D-1924-10_READ	46	28	28	28	16	29	67	47	54	0	0	0	0	0	25	0	56
TCGA-F5-6863-10A-01D-1924-10_READ	45	18	19	16	38	49	59	35	40	0	11	27	0	0	0	40	51
TCGA-F5-6864-10A-01D-1924-10_READ	51	0	0	44	70	70	81	53	86	0	0	0	0	0	11	27	90
TCGA-F7-7848-10A-01D-2129-08_HNSC	123	64	0	46	123	73	67	66	4	15	49	1	54	89	0	7	77
TCGA-F7-8298-10A-01D-2394-08_HNSC	81	4	3	59	88	82	80	79	68	17	35	0	63	69	0	70	99
TCGA-F7-8489-10A-01D-2394-08_HNSC	87	68	66	45	128	85	82	96	71	13	67	87	0	72	29	3	92
TCGA-F7-A50G-10A-01D-A25Y-08_HNSC	138	84	86	65	161	86	90	71	85	0	50	86	0	96	0	87	121
TCGA-F7-A624-10A-01D-A30H-08_HNSC	150	149	147	0	114	96	158	158	112	26	107	148	0	110	44	0	172
TCGA-F9-A4JJ-10A-01D-A25F-10_KIRP	113	0	2	44	99	108	106	90	120	0	0	0	0	0	37	69	107
TCGA-FA-8693-10A-01D-2397-10_DLBC	90	0	0	65	87	121	102	88	131	0	0	0	0	0	0	54	105
TCGA-FA-A4BB-10A-01D-A31X-10_DLBC	41	0	0	48	41	66	57	54	42	0	0	0	0	0	0	0	45
TCGA-FA-A6HN-10A-01D-A31X-10_DLBC	55	0	0	17	26	54	53	48	30	1	16	0	31	31	0	0	44
TCGA-FA-A6HO-10A-01D-A31X-10_DLBC	48	0	0	32	54	52	63	45	62	0	0	0	1	0	0	0	45
TCGA-FB-A4P5-10A-01D-A26I-08_PAAD	83	43	49	30	61	56	71	87	104	0	1	3	0	1	29	51	95
TCGA-FB-A4P6-10A-01D-A26I-08_PAAD	97	0	0	73	88	92	84	77	78	0	0	0	1	2	0	85	107
TCGA-FB-A545-10A-01D-A26I-08_PAAD	88	0	0	57	82	83	81	77	64	10	41	0	48	70	0	60	103
TCGA-FB-A5VM-10A-01D-A32N-08_PAAD	84	66	54	42	64	55	78	85	109	0	0	0	0	0	24	57	86
TCGA-FB-A78T-10A-01D-A32N-08_PAAD	86	0	0	68	82	83	73	84	95	0	0	0	0	0	30	62	99
TCGA-FB-A7DR-10A-01D-A33W-08_PAAD	97	0	1	59	77	80	66	69	62	11	45	0	47	54	0	53	79
TCGA-FC-7708-10A-01D-2115-08_PRAD	114	68	58	46	129	82	59	56	76	0	44	66	1	91	0	0	95
TCGA-FC-7961-10A-01D-A29Q-08_PRAD	133	0	1	117	121	131	143	136	149	0	0	0	0	0	47	76	145
TCGA-FC-A4JI-10A-01D-A25A-08_PRAD	86	57	66	55	57	70	85	93	99	0	1	2	1	8	33	60	100
TCGA-FC-A5OB-10A-01D-A29Q-08_PRAD	116	83	80	59	82	76	123	100	0	26	81	0	101	119	0	0	132
TCGA-FC-A66V-10A-01D-A30H-08_PRAD	150	0	0	98	155	159	142	154	171	0	0	0	0	0	37	81	184
TCGA-FC-A6HD-10A-01D-A31J-08_PRAD	117	0	0	57	79	85	84	89	72	17	44	62	0	68	0	68	94
TCGA-FD-A3B3-10A-01D-A202-08_BLCA	87	1	1	62	93	83	82	56	50	12	24	0	43	54	0	48	94
TCGA-FD-A3B4-10A-01D-A202-08_BLCA	74	56	0	37	55	51	52	43	4	14	45	0	70	81	0	0	87
TCGA-FD-A3B5-10A-01D-A20D-08_BLCA	89	0	61	45	111	96	83	70	87	0	48	0	51	0	35	2	103
TCGA-FD-A3B6-10A-01D-A20D-08_BLCA	96	63	57	45	83	66	84	95	100	0	0	2	0	2	26	63	107
TCGA-FD-A3B7-10A-01D-A20D-08_BLCA	86	0	0	92	91	88	90	78	108	0	1	0	0	0	26	61	112
TCGA-FD-A3B8-10A-01D-A20D-08_BLCA	89	53	60	43	101	91	79	63	80	0	47	66	0	1	0	79	105
TCGA-FD-A3N5-10A-01D-A21A-08_BLCA	91	0	3	54	88	83	69	87	102	0	0	1	0	2	30	70	108
TCGA-FD-A3N6-10A-01D-A21A-08_BLCA	95	2	0	54	86	77	79	85	87	0	31	45	0	0	25	56	106
TCGA-FD-A3NA-10A-01D-A21A-08_BLCA	137	53	56	47	89	73	90	97	116	0	0	0	0	4	31	69	116
TCGA-FD-A3SJ-10A-01D-A22Z-08_BLCA	145	0	1	112	147	142	138	132	154	0	0	0	0	0	46	75	170
TCGA-FD-A3SL-10A-01D-A22Z-08_BLCA	148	90	89	48	88	108	138	127	148	0	0	0	0	1	35	70	174
TCGA-FD-A3SM-10A-01D-A22Z-08_BLCA	184	102	0	65	183	147	121	130	0	32	99	0	132	154	0	0	167
TCGA-FD-A3SN-10A-01D-A22Z-08_BLCA	153	0	0	111	145	149	123	141	145	0	0	0	0	0	37	77	157
TCGA-FD-A3SO-10A-01D-A22Z-08_BLCA	164	94	92	64	106	105	132	141	113	15	50	0	86	112	52	0	176
TCGA-FD-A3SP-10A-01D-A22Z-08_BLCA	148	102	88	64	97	101	122	164	143	0	0	0	1	0	43	82	176
TCGA-FD-A3SQ-10A-01D-A22Z-08_BLCA	162	0	0	112	219	183	175	179	100	25	116	114	98	110	0	86	186
TCGA-FD-A3SR-10A-01D-A22Z-08_BLCA	137	78	74	49	152	129	118	120	95	16	93	134	0	103	0	74	168
TCGA-FD-A3SS-10A-01D-A22Z-08_BLCA	183	0	1	86	215	172	167	167	0	37	129	94	135	152	0	0	170
TCGA-FD-A43N-10A-01D-A23U-08_BLCA	81	1	4	44	76	70	69	92	82	0	2	1	0	0	23	54	86
TCGA-FD-A43P-10A-01D-A23U-08_BLCA	72	4	63	36	88	84	72	69	86	0	71	71	48	2	37	3	84
TCGA-FD-A43S-10A-01D-A23U-08_BLCA	76	57	58	40	98	73	70	77	94	0	36	59	0	0	0	68	85
TCGA-FD-A43U-10A-01D-A23U-08_BLCA	83	59	63	40	67	67	71	107	110	1	0	0	0	6	0	127	88
TCGA-FD-A43X-10A-01D-A23U-08_BLCA	137	0	0	116	156	140	125	125	124	23	66	0	76	102	0	76	163
TCGA-FD-A43Y-10A-01D-A26K-08_BLCA	103	3	5	64	98	89	63	79	98	0	1	1	0	0	0	94	103
TCGA-FD-A5BR-10A-01D-A26K-08_BLCA	99	0	0	69	75	74	77	67	66	12	31	0	50	59	24	4	96
TCGA-FD-A5BS-10A-01D-A26K-08_BLCA	93	55	64	0	114	92	86	81	59	6	69	65	50	56	0	51	112
TCGA-FD-A5BT-10A-01D-A26K-08_BLCA	86	58	55	38	60	68	85	76	107	0	1	0	4	4	28	50	110
TCGA-FD-A5BU-10A-01D-A26K-08_BLCA	90	80	93	1	68	61	61	55	82	0	58	58	49	63	35	4	100
TCGA-FD-A5BV-10A-01D-A26K-08_BLCA	88	75	82	3	58	65	63	53	9	14	81	76	48	103	0	0	102
TCGA-FD-A5BX-10A-01D-A26K-08_BLCA	98	58	55	41	108	86	84	84	71	18	70	61	55	57	0	65	105
TCGA-FD-A5BY-10A-01D-A289-08_BLCA	105	70	76	49	81	73	99	93	100	0	0	0	0	0	0	121	128
TCGA-FD-A5BZ-10A-01D-A289-08_BLCA	108	71	86	53	128	98	101	101	106	0	50	63	0	0	0	132	137
TCGA-FD-A5C0-10A-01D-A289-08_BLCA	106	0	0	73	118	112	102	107	109	0	0	0	0	0	0	110	127
TCGA-FD-A5C1-10A-01D-A289-08_BLCA	116	63	89	56	138	100	101	123	127	0	57	80	0	0	0	139	150
TCGA-FD-A62N-10A-01D-A30H-08_BLCA	179	105	120	77	213	157	146	146	125	14	112	160	0	113	0	99	199
TCGA-FD-A62O-10A-01D-A30H-08_BLCA	162	93	98	65	167	163	152	136	120	21	108	150	0	110	43	0	191
TCGA-FD-A62P-10A-01D-A30H-08_BLCA	160	147	145	0	1	0	141	137	171	0	0	0	0	0	41	90	180
TCGA-FD-A62S-10A-01D-A30H-08_BLCA	162	83	97	54	151	139	142	117	156	0	55	0	75	1	0	120	181
TCGA-FD-A6TA-10A-21D-A339-08_BLCA	87	0	0	63	86	81	76	64	102	0	0	0	0	0	0	68	101
TCGA-FD-A6TB-10A-21D-A339-08_BLCA	107	0	0	67	87	78	79	88	81	0	0	0	0	1	23	48	90
TCGA-FD-A6TC-10A-21D-A339-08_BLCA	96	75	73	45	77	76	97	130	119	0	0	0	0	0	0	87	106
TCGA-FD-A6TD-10A-21D-A339-08_BLCA	85	0	0	67	92	88	82	75	95	0	0	0	0	0	0	92	89
TCGA-FD-A6TE-10A-21D-A339-08_BLCA	93	56	63	44	107	76	85	85	85	0	37	67	0	0	0	102	95
TCGA-FD-A6TF-10A-21D-A329-08_BLCA	96	67	61	39	111	96	104	80	109	0	34	71	0	2	0	98	107
TCGA-FD-A6TG-10A-01D-A329-08_BLCA	90	62	66	37	129	98	86	84	76	15	60	70	63	71	26	0	112
TCGA-FD-A6TH-10A-01D-A329-08_BLCA	97	52	68	47	121	104	89	103	80	18	68	92	1	64	20	0	117
TCGA-FD-A6TI-10A-01D-A329-08_BLCA	96	59	61	37	98	103	107	85	113	0	30	67	0	0	20	51	113
TCGA-FD-A6TK-10A-21D-A339-08_BLCA	75	81	75	0	0	0	73	81	88	0	0	0	0	0	0	93	100
TCGA-FE-A22Z-10A-01D-A17V-08_THCA	92	81	76	0	68	74	80	116	96	0	43	60	0	1	27	63	107
TCGA-FE-A230-10A-01D-A14W-08_THCA	91	65	61	38	65	66	80	71	120	0	0	0	0	0	0	81	104
TCGA-FE-A231-10A-01D-A14W-08_THCA	86	0	0	80	109	91	90	83	111	0	0	0	1	4	0	76	115
TCGA-FE-A232-10A-01D-A14W-08_THCA	110	63	65	49	121	90	86	94	76	14	67	68	53	64	22	2	109
TCGA-FE-A233-10A-01D-A14W-08_THCA	86	50	68	37	69	64	56	50	84	0	45	0	57	65	0	41	95
TCGA-FE-A234-10A-01D-A14W-08_THCA	94	61	64	46	68	69	82	91	0	26	72	0	77	97	0	2	106
TCGA-FE-A235-10A-01D-A16O-08_THCA	127	0	1	51	82	82	111	108	109	0	0	0	0	0	31	57	136
TCGA-FE-A236-10A-01D-A16O-08_THCA	126	0	1	89	135	120	117	122	104	0	0	0	0	1	0	129	143
TCGA-FE-A237-10A-01D-A16O-08_THCA	119	0	0	77	118	120	107	87	100	0	0	0	0	0	0	96	141
TCGA-FE-A23A-10A-01D-A17V-08_THCA	119	67	68	45	111	86	97	82	90	0	51	68	0	0	39	0	109
TCGA-FE-A3PA-10A-01D-A21Z-08_THCA	97	1	1	69	89	98	75	70	79	0	0	0	0	0	0	70	93
TCGA-FE-A3PB-10A-01D-A21Z-08_THCA	135	72	64	50	129	92	83	95	109	0	46	64	0	1	0	130	105
TCGA-FE-A3PC-10A-01D-A21Z-08_THCA	104	2	0	53	103	103	90	110	85	0	0	0	1	0	26	70	106
TCGA-FE-A3PD-10A-01D-A21Z-08_THCA	122	0	0	54	89	86	87	99	74	18	38	0	60	75	0	71	110
TCGA-FF-8041-10A-01D-2210-10_DLBC	80	0	1	33	88	94	110	62	66	9	30	58	0	50	0	0	90

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-FF-8042-10A-01D-2210-10_DLBC	93	61	54	27	54	54	86	46	66	0	28	60	0	57	0	0	82
TCGA-FF-8043-10A-01D-2210-10_DLBC	97	0	1	38	97	115	117	93	73	11	18	62	0	58	0	0	122
TCGA-FF-8046-10A-01D-2210-10_DLBC	77	113	106	0	53	56	65	46	63	0	69	61	50	73	0	45	127
TCGA-FG-5962-10A-01D-1893-08_LGG	109	2	0	100	125	97	90	121	100	0	0	1	0	0	0	139	123
TCGA-FG-5963-10A-01D-1705-08_LGG	76	1	0	52	93	83	84	70	62	14	33	0	49	71	0	50	102
TCGA-FG-5964-10A-01D-1705-08_LGG	124	1	2	55	112	103	96	86	76	13	35	0	59	74	0	56	117
TCGA-FG-5965-10A-01D-1893-08_LGG	114	69	67	56	140	97	94	93	1	23	93	103	70	103	0	0	117
TCGA-FG-6688-10A-01D-1893-08_LGG	101	0	2	71	106	96	95	95	106	0	1	0	0	0	39	1	125
TCGA-FG-6689-10A-01D-1893-08_LGG	119	80	76	57	94	76	100	86	84	19	52	0	71	89	0	69	120
TCGA-FG-6690-10A-01D-1893-08_LGG	111	82	82	48	149	104	111	144	77	23	83	86	77	87	36	0	127
TCGA-FG-6691-10A-01D-1893-08_LGG	131	1	1	79	114	101	109	93	148	0	0	0	0	1	0	110	155
TCGA-FG-6692-10A-01D-1893-08_LGG	159	0	0	96	110	101	97	107	139	0	0	1	1	4	0	109	146
TCGA-FG-7634-10A-01D-2086-08_LGG	90	56	59	49	70	1	76	83	93	0	0	0	0	0	22	57	101
TCGA-FG-7636-10A-01D-2086-08_LGG	98	61	60	44	60	65	82	79	85	0	0	0	0	1	25	53	95
TCGA-FG-7637-10A-01D-2086-08_LGG	122	0	1	83	90	94	81	77	77	18	56	64	0	75	0	60	97
TCGA-FG-7638-10A-01D-2086-08_LGG	84	0	1	45	80	89	80	80	57	19	40	0	50	67	0	68	102
TCGA-FG-7641-10A-01D-2253-08_LGG	129	0	0	87	94	97	92	90	76	17	53	0	58	72	23	0	106
TCGA-FG-7643-10A-01D-2086-08_LGG	86	1	0	82	83	69	80	64	64	12	40	1	46	62	0	51	94
TCGA-FG-8181-10A-01D-2253-08_LGG	83	52	56	50	66	65	82	84	98	0	0	1	0	0	0	114	96
TCGA-FG-8182-10A-01D-2253-08_LGG	92	0	1	52	87	86	81	106	111	0	0	0	0	0	29	59	95
TCGA-FG-8185-10A-01D-2253-08_LGG	96	0	1	68	99	90	90	81	117	0	1	0	0	1	0	121	101
TCGA-FG-8186-10A-01D-2253-08_LGG	89	64	66	48	72	68	76	90	88	0	0	0	0	0	32	54	104
TCGA-FG-8187-10A-01D-2253-08_LGG	102	69	66	55	76	76	84	91	4	29	67	0	77	102	0	2	123
TCGA-FG-8188-10A-01D-2253-08_LGG	89	53	62	57	71	65	75	76	74	10	44	1	46	63	31	0	106
TCGA-FG-8189-10A-01D-A289-08_LGG	122	0	0	99	97	100	115	102	128	0	0	0	0	0	0	92	129
TCGA-FG-8191-10A-01D-2253-08_LGG	81	2	0	65	101	91	80	67	64	14	41	0	63	73	0	64	121
TCGA-FG-A4MT-10A-01D-A26K-08_LGG	89	1	2	56	78	80	79	90	98	0	0	0	0	0	24	64	95
TCGA-FG-A4MU-10A-01D-A289-08_LGG	105	0	0	84	103	103	107	115	123	0	0	0	0	1	0	130	124
TCGA-FG-A4MW-10A-01D-A26K-08_LGG	95	56	61	41	72	57	86	75	61	11	40	0	46	68	0	54	102
TCGA-FG-A4MX-10A-01D-A26K-08_LGG	93	3	1	68	85	83	79	75	52	13	29	56	3	48	0	53	101
TCGA-FG-A4MY-10A-01D-A26K-08_LGG	94	77	80	2	64	71	78	74	58	15	60	55	50	66	0	60	104
TCGA-FG-A60J-10A-01D-A289-08_LGG	98	0	0	88	91	77	86	77	80	0	0	0	1	0	0	80	99
TCGA-FG-A60K-10A-01D-A29Q-08_LGG	119	77	83	58	91	85	127	110	97	24	46	0	82	93	40	0	157
TCGA-FG-A60L-10A-01D-A31J-08_LGG	84	0	0	45	87	81	78	89	61	20	47	0	57	77	0	52	88
TCGA-FG-A6IZ-10A-01D-A31J-08_LGG	113	2	1	53	86	76	78	90	73	0	0	0	0	0	27	57	81
TCGA-FG-A6J1-10A-01D-A31J-08_LGG	81	0	0	53	81	89	78	76	90	0	0	0	0	0	35	0	94
TCGA-FG-A6J3-10A-01D-A31J-08_LGG	116	1	0	71	80	81	79	82	70	23	56	0	61	76	0	62	92
TCGA-FG-A713-10A-01D-A329-08_LGG	79	0	1	45	78	77	59	68	0	17	56	0	60	82	0	0	92
TCGA-FI-A2CX-10A-01D-A17D-09_UCEC	59	65	65	16	115	91	103	90	135	0	52	62	0	1	45	57	77
TCGA-FI-A2CY-10A-01D-A17D-09_UCEC	51	0	0	39	100	86	92	112	160	0	0	0	0	0	38	45	78
TCGA-FI-A2D0-10A-01D-A17D-09_UCEC	61	0	0	27	103	103	99	123	137	0	0	2	0	0	0	128	77
TCGA-FI-A2D2-10A-01D-A17D-09_UCEC	39	0	0	61	93	98	109	76	90	0	0	0	0	1	0	83	76
TCGA-FI-A2D4-10A-01D-A17D-09_UCEC	41	2	1	22	93	88	84	100	96	0	0	0	0	1	0	99	74
TCGA-FI-A2D5-10A-01D-A17D-09_UCEC	70	1	2	37	98	96	101	96	75	14	49	0	59	69	37	0	73
TCGA-FI-A2D6-10A-01D-A17D-09_UCEC	45	1	0	28	94	82	97	95	140	0	1	1	0	1	39	67	73
TCGA-FI-A2EU-10A-01D-A17D-09_UCEC	57	92	82	42	69	67	116	99	82	19	68	0	67	82	0	65	87
TCGA-FI-A2EW-10A-01D-A17D-09_UCEC	44	74	51	35	113	87	110	70	99	1	37	66	0	0	37	0	81
TCGA-FI-A2EX-10A-01D-A17D-09_UCEC	49	81	67	39	57	61	159	106	62	52	31	0	69	83	23	0	80
TCGA-FI-A2EY-10A-01D-A18P-09_UCEC	70	78	68	24	133	99	102	97	84	16	100	71	78	70	0	75	92
TCGA-FI-A2F4-10B-01D-A17D-09_UCEC	49	0	1	34	108	91	109	108	133	0	0	0	0	0	46	65	92
TCGA-FI-A2F8-10B-01D-A17D-09_UCEC	36	88	83	3	79	80	86	67	48	22	89	71	48	48	0	38	57
TCGA-FI-A2F9-10B-01D-A17D-09_UCEC	48	68	65	13	59	58	99	81	131	0	0	0	0	0	60	3	81
TCGA-FI-A3PV-10A-01D-A22A-09_UCEC	55	0	1	34	101	93	104	93	138	0	0	0	0	0	36	53	81
TCGA-FI-A3PX-10A-01D-A22A-09_UCEC	53	47	10	20	88	94	91	94	62	10	38	2	47	50	0	49	89
TCGA-FJ-A3Z7-10A-01D-A23K-08_BLCA	131	100	4	57	180	143	127	155	161	0	0	0	0	0	0	174	172
TCGA-FJ-A3Z9-10A-01D-A26K-08_BLCA	90	2	1	57	96	91	81	104	79	17	38	2	63	77	0	53	101
TCGA-FJ-A3ZE-10A-01D-A23K-08_BLCA	101	2	3	54	80	79	73	92	77	0	1	1	0	0	0	84	93
TCGA-FJ-A3ZF-10A-01D-A23K-08_BLCA	91	13	9	80	104	85	83	102	69	17	59	13	64	74	0	53	96
TCGA-FK-A3S3-10A-01D-A22D-08_THCA	96	0	1	77	89	92	92	114	106	0	1	0	0	2	33	68	101
TCGA-FK-A3SB-10A-01D-A22D-08_THCA	100	1	3	50	90	139	103	100	78	21	52	0	0	5	0	124	105
TCGA-FK-A3SD-10A-01D-A22D-08_THCA	91	60	59	48	114	75	79	91	65	17	69	59	48	66	29	0	102
TCGA-FK-A3SE-10A-01D-A22D-08_THCA	88	0	1	53	92	92	86	74	68	13	43	1	52	73	0	63	102
TCGA-FK-A3SG-10A-01D-A22D-08_THCA	134	1	4	84	138	117	95	104	76	29	68	70	56	83	0	63	125
TCGA-FK-A3SH-10A-01D-A22D-08_THCA	105	67	68	45	105	84	79	80	94	0	48	70	0	5	37	2	118
TCGA-FK-A4UB-10A-01D-A25A-08_THCA	87	67	81	45	109	81	81	88	68	13	65	73	0	67	0	53	96
TCGA-FN-7833-10A-01D-2086-08_LGG	90	53	57	45	111	79	79	87	101	0	38	61	0	1	31	62	101
TCGA-FP-7735-10A-01D-2053-08_STAD	89	57	61	44	95	84	77	73	78	0	35	57	0	2	24	33	78
TCGA-FP-7829-10A-01D-2053-08_STAD	82	57	55	42	69	70	77	91	100	0	0	0	0	1	0	111	105
TCGA-FP-7916-10A-01D-2201-08_STAD	108	0	0	104	111	104	109	103	83	21	44	2	53	78	24	0	142
TCGA-FP-7998-10A-01D-2201-08_STAD	99	59	68	58	80	73	89	82	70	13	41	0	53	72	23	1	118
TCGA-FP-8099-10A-01D-2341-08_STAD	153	0	3	75	120	112	113	127	122	0	0	0	0	0	35	73	121
TCGA-FP-8211-10A-01D-2341-08_STAD	106	0	0	104	106	112	92	132	111	0	0	0	0	1	0	94	127
TCGA-FP-8631-10A-01D-2394-08_STAD	109	78	79	1	5	6	81	125	102	0	4	0	1	5	32	76	90
TCGA-FP-A4BF-10A-01D-A24F-08_STAD	105	3	8	52	89	77	75	97	104	0	3	2	1	4	0	94	87
TCGA-FR-A2OS-10B-01D-A21A-08_SKCM	99	0	1	77	91	85	81	64	98	0	0	1	0	2	0	82	101
TCGA-FR-A3R1-10B-01D-A23B-08_SKCM	123	83	88	4	69	70	77	114	92	20	38	74	0	0	40	1	92
TCGA-FR-A3YN-10A-01D-A23B-08_SKCM	107	0	0	80	107	101	109	100	102	0	0	0	0	1	28	55	115
TCGA-FR-A3YO-10A-01D-A23B-08_SKCM	114	73	71	44	119	83	76	103	74	19	74	77	61	75	26	0	91
TCGA-FR-A44A-10A-01D-A24R-08_SKCM	86	0	2	70	76	77	80	154	101	19	0	0	0	2	32	66	87
TCGA-FR-A69P-10A-01D-A30X-08_SKCM	88	0	0	62	91	81	76	79	86	0	0	0	0	0	0	73	96
TCGA-FR-A726-10A-01D-A32N-08_SKCM	98	0	0	58	101	89	85	97	118	0	0	0	0	0	29	63	109
TCGA-FR-A728-10A-01D-A32N-08_SKCM	113	0	0	52	111	109	98	103	78	21	53	0	77	84	0	65	132
TCGA-FS-A1YW-10A-01D-A199-08_SKCM	165	1	1	119	127	103	116	126	149	0	0	0	0	2	0	96	141
TCGA-FS-A1YX-10A-01D-A199-08_SKCM	111	0	0	60	106	97	90	89	69	12	53	73	0	72	0	74	113
TCGA-FS-A1YY-10A-01D-A199-08_SKCM	111	0	0	78	66	65	46	77	37	19	37	0	24	40	0	50	118
TCGA-FS-A1Z0-10A-01D-A199-08_SKCM	93	1	1	72	79	92	88	100	55	13	37	0	44	65	0	62	108
TCGA-FS-A1Z3-10A-01D-A199-08_SKCM	97	0	0	72	96	81	86	91	87	0	0	0	0	0	26	54	113
TCGA-FS-A1Z4-10A-01D-A199-08_SKCM	100	0	0	84	86	83	83	111	106	0	0	0	0	0	33	60	100
TCGA-FS-A1Z7-10A-01D-A199-08_SKCM	110	0	0	56	87	90	73	98	100	0	0	0	0	0	16	48	119
TCGA-FS-A1ZA-10A-01D-A199-08_SKCM	125	63	49	52	114	85	93	74	81	0	35	46	0	0	0	102	122
TCGA-FS-A1ZB-10A-01D-A199-08_SKCM	126	0	2	104	112	94	92	116	77	13	36	0	50	80	19	2	146
TCGA-FS-A1ZC-10A-01D-A199-08_SKCM	87	0	0	68	82	40	42	47	46	0	0	0	0	57	0	44	60
TCGA-FS-A1ZD-10A-01D-A199-08_SKCM	114	40	43	45	54	58	66	75	92	0	0	0	0	0	27	0	126
TCGA-FS-A1ZE-10A-01D-A199-08_SKCM	138	0	2	80	108	94	99	90	91	1	0	0	0	1	0	78	137
TCGA-FS-A1ZF-10A-01D-A199-08_SKCM	120	52	48	42	50	56	98	79	94	0	0	0	0	0	29	0	111
TCGA-FS-A1ZG-10A-01D-A199-08_SKCM	121	44	43	41	44	52	86	80	101	0	0	0	0	0	0	74	115

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-FS-A1ZH-10A-01D-A199-08_SKCM	128	0	1	83	120	105	112	89	1	26	64	0	85	122	0	0	144
TCGA-FS-A1ZJ-10A-01D-A199-08_SKCM	101	77	74	56	87	79	99	114	132	0	0	0	0	0	38	59	126
TCGA-FS-A1ZK-10A-01D-A199-08_SKCM	104	59	63	39	65	70	82	110	108	1	0	0	0	0	24	48	101
TCGA-FS-A1ZM-10A-01D-A199-08_SKCM	140	64	67	61	131	103	93	88	77	12	70	81	0	79	0	60	149
TCGA-FS-A1ZN-10A-01D-A199-08_SKCM	104	65	67	53	129	89	92	89	97	0	47	65	0	0	0	96	147
TCGA-FS-A1ZP-10A-01D-A199-08_SKCM	121	53	72	50	109	97	103	107	66	13	65	96	0	80	0	61	129
TCGA-FS-A1ZQ-10A-01D-A199-08_SKCM	127	66	64	47	115	98	86	89	99	0	29	70	0	0	0	106	120
TCGA-FS-A1ZR-10A-01D-A199-08_SKCM	144	78	66	52	131	101	88	87	61	24	93	73	65	87	0	64	129
TCGA-FS-A1ZS-10A-01D-A199-08_SKCM	85	0	0	48	62	58	65	66	74	0	0	0	0	2	10	27	90
TCGA-FS-A1ZT-10A-01D-A199-08_SKCM	127	0	0	82	115	99	100	93	60	19	27	0	31	70	0	57	141
TCGA-FS-A1ZU-10A-01D-A198-08_SKCM	110	0	0	52	93	82	84	69	87	0	0	0	0	0	0	81	101
TCGA-FS-A1ZW-10A-01D-A199-08_SKCM	103	56	48	34	97	91	82	85	56	12	47	82	0	61	0	46	114
TCGA-FS-A1ZY-10A-01D-A199-08_SKCM	113	75	64	45	71	75	103	99	127	0	0	0	0	2	27	72	134
TCGA-FS-A1ZZ-10A-01D-A199-08_SKCM	141	0	1	114	134	61	77	39	53	0	0	0	0	85	0	56	91
TCGA-FS-A4F0-10A-01D-A24R-08_SKCM	83	73	71	46	72	75	77	123	111	1	3	0	2	6	26	61	95
TCGA-FS-A4F2-10A-01D-A24R-08_SKCM	92	7	5	75	91	81	80	105	72	2	11	9	0	7	0	117	93
TCGA-FS-A4F4-10B-01D-A25O-08_SKCM	77	51	52	36	94	78	74	64	52	12	48	72	0	57	0	49	85
TCGA-FS-A4F5-10B-01D-A25O-08_SKCM	70	61	46	0	61	53	68	69	56	14	25	0	47	59	25	1	78
TCGA-FS-A4F8-10B-01D-A25O-08_SKCM	75	55	52	32	52	60	70	76	75	0	0	0	0	0	24	37	85
TCGA-FS-A4F9-10A-01D-A24R-08_SKCM	93	86	78	6	85	72	84	120	103	1	51	70	5	4	30	62	88
TCGA-FS-A4FB-10B-01D-A25O-08_SKCM	67	0	0	41	67	62	61	71	55	13	30	0	40	48	21	0	74
TCGA-FS-A4FC-10A-01D-A24R-08_SKCM	85	0	1	54	78	80	73	89	93	0	0	2	0	3	27	58	91
TCGA-FS-A4FD-10B-01D-A25O-08_SKCM	77	48	52	36	52	53	59	42	55	0	28	0	42	66	0	66	92
TCGA-FT-A3EE-10A-01D-A202-08_BLCA	73	72	75	0	55	60	70	72	58	12	45	56	48	68	0	49	79
TCGA-FT-A61P-10A-01D-A30H-08_BLCA	160	96	104	80	111	101	136	143	170	0	0	0	0	0	0	166	184
TCGA-FU-A23K-10A-01D-A16O-08_CESC	127	0	0	52	111	111	112	135	103	18	54	0	60	1	0	126	118
TCGA-FU-A23L-10A-01D-A16O-08_CESC	126	0	1	93	114	100	102	107	104	0	0	0	0	0	0	128	133
TCGA-FU-A2QG-10A-01D-A18J-09_CESC	54	1	0	33	105	104	110	88	111	0	0	1	0	4	0	121	76
TCGA-FU-A3HY-10A-01D-A21Q-09_CESC	47	98	99	0	73	67	107	103	132	1	42	57	2	2	0	140	92
TCGA-FU-A3HZ-10A-01D-A20U-09_CESC	51	49	50	24	53	61	94	91	129	0	4	1	2	3	32	50	73
TCGA-FU-A3NI-10A-01D-A21Q-09_CESC	47	58	66	13	102	95	106	97	115	0	49	56	0	0	30	65	92
TCGA-FU-A3TQ-10A-01D-A22X-09_CESC	48	1	0	30	93	87	81	102	125	0	3	1	0	1	0	103	81
TCGA-FU-A3TX-10A-01D-A22X-09_CESC	44	59	51	19	62	56	98	90	77	14	42	63	0	66	0	61	85
TCGA-FU-A3WB-10A-01D-A22X-09_CESC	49	72	57	17	122	89	99	92	110	0	38	50	0	0	37	56	78
TCGA-FU-A3YQ-10A-01D-A22X-09_CESC	46	0	0	14	85	89	104	88	71	16	59	0	51	64	0	67	80
TCGA-FU-A40J-10A-01D-A243-09_CESC	52	48	50	16	57	78	105	102	143	0	0	0	0	0	0	107	84
TCGA-FU-A57G-10A-01D-A26G-09_CESC	55	16	9	35	91	83	94	84	114	2	7	6	5	10	0	77	70
TCGA-FU-A5XV-10A-01D-A28E-09_CESC	42	0	2	31	88	89	93	70	131	0	0	0	0	0	0	91	79
TCGA-FV-A2QQ-10B-01D-A22F-10_LIHC	45	30	36	14	21	33	54	53	78	0	0	0	0	0	0	46	58
TCGA-FV-A3I1-10A-01D-A22F-10_LIHC	70	74	61	0	0	0	65	51	86	0	0	0	0	0	0	45	75
TCGA-FV-A3R3-10A-01D-A22F-10_LIHC	70	0	0	42	52	54	67	53	73	0	0	0	0	0	0	48	74
TCGA-FV-A495-10A-01D-A25V-10_LIHC	87	46	43	24	38	44	92	65	92	0	0	0	1	0	19	53	93
TCGA-FV-A496-10A-01D-A25V-10_LIHC	105	0	0	51	105	120	122	91	0	17	67	65	76	97	0	0	93
TCGA-FV-A4ZQ-10A-01D-A25V-10_LIHC	102	61	61	36	97	95	108	68	109	0	40	77	4	0	44	0	101
TCGA-FW-A3I3-10A-01D-A21A-08_SKCM	143	65	73	53	76	68	85	85	106	0	1	0	0	1	40	2	116
TCGA-FW-A3R5-10A-01D-A23B-08_SKCM	104	72	71	46	122	92	83	119	67	26	76	91	2	78	0	79	98
TCGA-FW-A3TU-10A-01D-A23B-08_SKCM	96	0	3	52	87	91	99	118	86	0	0	0	1	0	39	78	93
TCGA-FW-A3TV-10A-01D-A23B-08_SKCM	121	81	80	54	81	75	80	68	75	0	49	0	63	93	0	65	137
TCGA-FW-A5DX-10A-01D-A27N-08_SKCM	115	51	60	35	69	62	73	97	77	0	0	1	0	0	0	74	91
TCGA-FX-A2QS-10A-01D-A21Q-09_SARC	48	1	1	32	73	83	88	79	100	0	1	3	0	1	0	75	65
TCGA-FX-A3NJ-10A-01D-A21Q-09_SARC	56	0	0	38	90	102	112	80	130	0	0	2	0	0	0	95	83
TCGA-FX-A3NK-10A-01D-A21Q-09_SARC	67	2	1	27	81	89	94	103	101	0	0	1	0	2	0	93	78
TCGA-FX-A3RE-10A-01D-A22A-09_SARC	45	47	44	18	102	82	89	80	108	1	40	64	3	2	0	76	76
TCGA-FX-A3TO-10A-01D-A22A-09_SARC	61	0	0	33	75	81	94	78	64	12	29	1	55	44	0	53	78
TCGA-FX-A48G-10A-01D-A24N-09_SARC	41	68	63	21	71	68	106	116	124	0	0	2	3	0	29	54	78
TCGA-FY-A2QD-10A-01D-A19M-08_THCA	114	66	1	44	135	106	101	79	95	0	34	0	70	1	0	105	147
TCGA-FY-A3BL-10A-01D-A19M-08_THCA	111	2	4	92	110	98	94	92	71	17	43	7	62	77	0	61	141
TCGA-FY-A3I4-10A-01D-A21A-08_THCA	85	2	1	73	84	82	77	64	90	0	0	0	0	0	0	104	109
TCGA-FY-A3I5-10A-01D-A21Z-08_THCA	97	71	0	47	133	102	88	88	73	17	47	0	65	81	0	70	125
TCGA-FY-A3NM-10A-01D-A21A-08_THCA	82	0	1	88	81	99	79	107	108	0	1	1	0	3	32	58	86
TCGA-FY-A3NN-10A-01D-A21A-08_THCA	89	0	0	81	94	79	77	81	68	9	38	0	38	74	25	0	103
TCGA-FY-A3NP-10A-01D-A21A-08_THCA	99	90	83	0	81	71	80	97	86	0	46	73	0	2	30	64	99
TCGA-FY-A3ON-10A-01D-A21Z-08_THCA	90	0	0	54	89	88	78	99	90	0	0	0	0	1	30	58	99
TCGA-FY-A3R6-10A-01D-A21Z-08_THCA	103	1	0	63	100	97	86	80	114	0	0	0	0	1	0	79	96
TCGA-FY-A3R7-10A-01D-A21Z-08_THCA	87	1	0	81	92	85	75	80	110	0	0	0	0	0	0	124	118
TCGA-FY-A3R8-10A-01D-A21Z-08_THCA	91	0	0	63	95	86	81	76	120	0	0	0	0	1	0	82	105
TCGA-FY-A3R9-10A-01D-A21Z-08_THCA	94	67	69	42	127	88	84	107	119	0	46	78	0	1	0	126	98
TCGA-FY-A3RA-10A-01D-A21Z-08_THCA	93	70	79	0	81	79	82	85	49	13	75	78	39	67	0	58	96
TCGA-FY-A3TY-10A-01D-A22Z-08_THCA	150	76	79	61	160	132	136	107	98	20	87	142	0	86	0	66	178
TCGA-FY-A3W9-10A-01D-A22D-08_THCA	85	0	1	77	85	90	81	72	96	0	0	0	1	1	0	79	104
TCGA-FY-A3WA-10A-01D-A22D-08_THCA	79	0	2	71	76	76	80	69	97	0	0	0	0	1	0	73	106
TCGA-FY-A3YR-10A-01D-A22Z-08_THCA	197	119	134	96	143	146	194	233	197	0	0	0	0	1	61	118	215
TCGA-FY-A40K-10A-01D-A23K-08_THCA	83	69	71	49	75	64	80	96	109	2	0	1	0	2	0	80	95
TCGA-FY-A40L-10A-01D-A23K-08_THCA	161	81	94	64	91	103	135	123	173	0	0	0	0	0	0	147	196
TCGA-FY-A40M-10A-01D-A23K-08_THCA	87	65	68	41	110	77	84	78	75	18	68	86	4	67	0	52	89
TCGA-FY-A40N-10A-01D-A23K-08_THCA	116	0	0	56	89	83	91	119	71	16	55	0	60	68	28	2	95
TCGA-FY-A4B0-10A-01D-A23U-08_THCA	78	1	5	71	78	65	72	92	97	0	0	0	0	0	0	89	78
TCGA-FY-A4B3-10A-01D-A23U-08_THCA	74	4	0	52	75	71	71	83	86	3	1	3	5	1	26	54	82
TCGA-FY-A4B4-10A-01D-A23U-08_THCA	171	87	91	65	192	145	148	127	172	0	51	97	0	0	0	147	191
TCGA-G2-A2EC-10A-01D-A17V-08_BLCA	123	67	5	55	76	70	74	59	60	0	43	3	59	74	0	71	164
TCGA-G2-A2EF-10A-01D-A18F-08_BLCA	101	60	70	39	102	86	76	97	55	12	70	75	0	71	0	54	97
TCGA-G2-A2EJ-10A-01D-A17V-08_BLCA	146	118	122	1	84	83	164	181	136	19	48	100	1	1	48	0	186
TCGA-G2-A2EK-10A-01D-A18F-08_BLCA	86	74	78	1	85	82	78	95	94	0	68	88	0	0	35	64	93
TCGA-G2-A2EL-10A-01D-A18F-08_BLCA	98	72	73	45	71	65	77	78	88	0	0	1	0	0	33	59	97
TCGA-G2-A3IB-10A-01D-A20D-08_BLCA	73	0	0	51	97	69	68	68	92	0	2	0	0	0	19	54	89
TCGA-G2-A3IE-10A-01D-A20D-08_BLCA	84	0	1	82	95	81	82	86	107	0	0	0	0	0	0	79	90
TCGA-G2-A3VY-10A-01D-A22Z-08_BLCA	174	95	0	131	162	141	132	130	106	37	108	0	122	161	0	105	216
TCGA-G3-A25S-10A-01D-A16V-10_LIHC	41	1	0	46	45	46	57	36	59	0	0	0	0	0	0	43	59
TCGA-G3-A25T-10A-01D-A16V-10_LIHC	38	0	0	28	34	50	51	31	0	6	29	20	12	47	0	0	50
TCGA-G3-A25U-10A-01D-A16V-10_LIHC	44	0	0	29	28	35	54	38	30	12	18	15	0	21	5	0	62
TCGA-G3-A25V-10A-01D-A16V-10_LIHC	37	23	26	19	32	47	54	48	47	0	15	19	0	0	0	29	58
TCGA-G3-A25Y-10A-01D-A16V-10_LIHC	52	0	0	37	45	35	73	34	0	14	30	21	10	49	0	0	67
TCGA-G3-A25Z-10A-01D-A16V-10_LIHC	47	23	28	17	23	19	57	34	31	7	14	0	16	27	0	28	53
TCGA-G3-A3CG-10A-01D-A20W-10_LIHC	75	50	55	20	99	88	105	81	68	7	47	53	46	55	0	29	87
TCGA-G3-A3CI-10A-01D-A20W-10_LIHC	82	75	68	34	62	66	116	97	110	0	0	0	0	0	21	46	90
TCGA-G3-A3CJ-10A-01D-A20W-10_LIHC	103	0	0	56	148	142	126	131	122	0	0	0	0	0	33	62	121

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-G3-A3CK-10A-01D-A20W-10_LIHC	99	1	0	61	81	90	104	95	109	0	0	0	0	0	27	47	93
TCGA-G3-A5SI-10A-01D-A27I-10_LIHC	76	0	1	62	80	98	109	79	1	16	54	0	83	103	0	2	82
TCGA-G3-A5SJ-10A-01D-A27I-10_LIHC	95	0	0	72	94	114	111	107	70	8	35	80	0	95	0	81	108
TCGA-G3-A5SK-10A-01D-A27I-10_LIHC	70	0	0	76	70	107	93	69	95	0	0	0	0	0	0	73	74
TCGA-G3-A5SL-10A-01D-A27I-10_LIHC	73	56	37	36	56	59	90	73	91	0	0	0	0	0	23	58	85
TCGA-G3-A5SM-10A-01D-A28X-10_LIHC	60	55	50	31	83	79	96	64	70	0	24	56	0	0	0	81	68
TCGA-G4-6293-10A-01D-1719-10_COAD	61	0	0	35	60	56	72	49	71	0	0	0	0	0	0	38	62
TCGA-G4-6294-10A-01D-1771-10_COAD	60	0	0	52	53	64	89	45	45	12	25	0	25	34	0	28	83
TCGA-G4-6295-10A-01D-1719-10_COAD	79	52	45	28	103	79	105	58	65	15	47	72	0	63	0	37	102
TCGA-G4-6297-10A-01D-1719-10_COAD	44	0	0	30	66	69	68	47	49	8	18	0	34	36	0	14	65
TCGA-G4-6298-10A-01D-1719-10_COAD	46	20	20	14	23	25	34	20	30	0	16	0	19	30	5	0	73
TCGA-G4-6299-10A-01D-1771-10_COAD	87	0	0	55	61	59	84	78	92	0	0	0	0	0	12	38	88
TCGA-G4-6302-10A-01D-1719-10_COAD	51	45	47	23	43	43	89	49	82	0	0	0	0	0	15	31	76
TCGA-G4-6303-10A-01D-1771-10_COAD	77	2	0	43	63	77	81	56	71	0	0	0	0	0	17	32	88
TCGA-G4-6304-10A-01D-1924-10_COAD	29	0	0	23	21	29	36	31	19	5	11	0	9	18	0	16	39
TCGA-G4-6306-10A-01D-1771-10_COAD	51	31	27	24	42	46	67	45	45	13	31	35	0	40	0	28	62
TCGA-G4-6307-10A-01D-1720-10_COAD	119	69	70	41	136	106	100	95	137	0	42	68	0	0	28	52	113
TCGA-G4-6309-10A-01D-1835-10_COAD	50	0	24	30	30	28	45	34	40	0	18	0	28	27	0	0	38
TCGA-G4-6310-10A-01D-1720-10_COAD	108	71	68	37	63	66	131	100	174	0	0	0	0	2	24	49	139
TCGA-G4-6314-10A-01D-1720-10_COAD	147	92	111	42	190	159	214	135	237	0	50	88	0	0	0	127	208
TCGA-G4-6315-10A-01D-1720-10_COAD	107	66	88	37	99	111	157	116	162	0	34	71	1	0	30	50	140
TCGA-G4-6317-10A-01D-1720-10_COAD	136	1	3	72	140	156	181	128	222	0	0	0	0	1	0	102	179
TCGA-G4-6320-10A-01D-1720-10_COAD	127	0	0	67	144	138	162	109	123	21	48	0	69	79	0	41	162
TCGA-G4-6321-10A-01D-1720-10_COAD	48	0	0	22	57	52	50	52	39	7	23	0	26	28	0	15	62
TCGA-G4-6323-10A-01D-1720-10_COAD	84	0	1	53	108	127	138	96	154	0	0	0	5	3	17	27	155
TCGA-G4-6586-10A-01D-1771-10_COAD	85	0	0	57	69	84	89	72	48	15	20	0	35	54	0	39	84
TCGA-G4-6588-10A-01D-1771-10_COAD	70	38	41	26	32	36	76	51	86	0	0	0	0	0	29	0	75
TCGA-G4-6626-10A-01D-1771-10_COAD	60	32	47	24	60	64	66	41	25	9	34	57	0	40	15	0	77
TCGA-G4-6628-10A-01D-1835-10_COAD	41	27	40	24	44	45	46	27	35	7	26	39	0	28	0	20	57
TCGA-G5-6233-10A-01D-1733-10_READ	102	57	53	22	99	84	105	79	127	0	31	42	0	0	12	29	115
TCGA-G5-6235-10A-01D-1733-10_READ	82	0	0	35	71	74	97	61	50	14	28	0	32	45	10	1	87
TCGA-G5-6572-10A-01D-1826-10_READ	55	19	26	33	28	29	65	51	72	0	0	0	0	0	0	39	68
TCGA-G5-6641-10A-01D-1826-10_READ	57	33	38	26	22	22	65	48	60	0	0	0	0	0	8	30	63
TCGA-G7-6789-10A-01D-1962-08_KIRP	133	1	0	78	116	106	96	146	137	0	0	0	0	3	28	81	137
TCGA-G7-6790-10A-01D-1962-08_KIRP	127	74	86	59	149	107	114	116	82	17	98	127	1	91	0	73	139
TCGA-G7-6792-10A-01D-1962-08_KIRP	129	0	1	115	151	122	115	164	151	0	0	0	1	2	36	88	151
TCGA-G7-6793-10A-01D-1962-08_KIRP	120	0	3	68	115	110	92	102	86	20	59	1	75	83	0	80	125
TCGA-G7-6795-10A-01D-1962-08_KIRP	122	0	1	75	131	104	103	88	69	20	60	1	74	88	0	77	144
TCGA-G7-6796-10A-01D-1962-08_KIRP	169	77	76	58	92	82	92	150	122	0	1	0	1	0	35	82	149
TCGA-G7-6797-10A-01D-1962-08_KIRP	133	0	0	75	163	141	122	151	105	23	91	119	1	85	0	77	139
TCGA-G7-7501-10A-01D-2201-08_KIRP	92	0	0	59	98	90	85	102	106	0	0	1	0	1	0	136	96
TCGA-G7-7502-10A-01D-2201-08_KIRP	99	0	0	58	77	87	87	75	85	0	1	0	0	0	39	0	106
TCGA-G7-A4TM-10B-01D-A31X-10_KIRP	58	0	0	31	58	61	67	47	55	0	0	0	0	0	0	15	54
TCGA-G9-6329-10A-01D-1961-08_PRAD	128	76	77	47	82	78	113	92	89	17	51	1	61	84	0	76	136
TCGA-G9-6332-10A-01D-1786-08_PRAD	114	72	79	64	86	87	94	91	128	0	0	0	0	0	0	99	123
TCGA-G9-6333-10A-01D-1961-08_PRAD	129	0	1	78	120	113	110	127	94	0	0	2	0	1	0	143	151
TCGA-G9-6336-10A-01D-1786-08_PRAD	98	52	66	41	109	82	82	76	2	21	90	61	74	95	0	2	95
TCGA-G9-6338-10A-01D-1961-08_PRAD	182	71	74	53	147	114	113	122	122	0	49	84	0	3	27	76	161
TCGA-G9-6339-10A-01D-A30X-08_PRAD	91	0	1	59	85	76	80	93	101	0	0	0	0	0	30	62	89
TCGA-G9-6342-10A-01D-1961-08_PRAD	138	72	85	54	89	85	106	124	122	0	1	1	0	2	0	95	138
TCGA-G9-6343-10A-01D-1961-08_PRAD	166	0	0	70	110	112	106	124	81	19	55	0	71	87	36	2	145
TCGA-G9-6347-10A-01D-A31J-08_PRAD	73	0	0	48	75	80	71	77	57	16	44	1	54	65	27	0	81
TCGA-G9-6348-10A-01D-1786-08_PRAD	97	1	0	58	94	89	80	91	68	24	48	2	56	65	0	74	101
TCGA-G9-6351-10A-01D-1961-08_PRAD	135	0	0	66	125	116	126	99	67	19	51	0	61	95	0	78	145
TCGA-G9-6353-10A-01D-1961-08_PRAD	127	1	0	75	128	103	97	131	132	0	1	0	0	3	0	100	152
TCGA-G9-6354-10A-01D-A30X-08_PRAD	91	0	0	61	81	82	87	83	62	17	40	69	0	72	28	0	106
TCGA-G9-6356-10A-01D-1786-08_PRAD	97	59	73	48	115	86	94	109	65	11	72	65	50	76	0	63	103
TCGA-G9-6361-10A-01D-1961-08_PRAD	144	0	1	83	109	104	93	114	100	0	0	1	0	0	0	138	140
TCGA-G9-6362-10A-01D-1786-08_PRAD	91	89	81	2	67	64	87	83	99	1	45	62	0	0	0	119	104
TCGA-G9-6363-10A-01D-1786-08_PRAD	103	59	61	49	72	70	85	105	70	15	51	0	57	65	30	1	110
TCGA-G9-6364-10A-01D-1786-08_PRAD	91	0	1	80	87	84	81	103	97	0	0	0	0	1	0	110	99
TCGA-G9-6365-10A-01D-1786-08_PRAD	77	61	73	44	65	61	78	114	103	0	1	0	0	0	0	111	84
TCGA-G9-6366-10A-01D-2115-08_PRAD	70	0	0	69	64	69	69	64	80	0	0	2	0	3	20	49	88
TCGA-G9-6367-10A-01D-1786-08_PRAD	82	2	1	77	91	96	78	120	104	0	0	2	0	1	23	59	92
TCGA-G9-6369-10A-01D-1961-08_PRAD	142	0	1	80	120	110	126	129	133	0	0	0	0	1	33	75	172
TCGA-G9-6370-10A-01D-1786-08_PRAD	97	72	65	45	106	89	83	97	103	0	48	63	0	0	0	124	104
TCGA-G9-6371-10A-01D-1786-08_PRAD	84	64	57	46	100	81	77	100	65	12	56	77	0	76	0	64	97
TCGA-G9-6373-10A-01D-1786-08_PRAD	121	0	1	65	119	100	109	94	88	17	62	0	66	78	0	74	127
TCGA-G9-6377-10A-01D-1961-08_PRAD	121	75	82	54	115	108	103	108	74	10	83	76	71	79	0	75	130
TCGA-G9-6378-10A-01D-1786-08_PRAD	92	62	64	44	101	90	85	83	69	13	62	63	63	62	0	2	88
TCGA-G9-6379-10A-01D-A31J-08_PRAD	88	0	0	55	85	87	75	76	89	0	0	0	0	0	28	66	89
TCGA-G9-6384-10A-01D-1786-08_PRAD	91	1	1	55	94	81	80	108	92	0	0	0	0	0	31	63	108
TCGA-G9-6385-10A-01D-1786-08_PRAD	103	81	84	1	68	64	82	82	2	27	88	85	0	88	0	0	123
TCGA-G9-6494-10A-01D-1786-08_PRAD	99	68	67	47	117	97	83	89	80	20	65	86	1	75	0	63	103
TCGA-G9-6496-10A-01D-1786-08_PRAD	93	1	1	85	80	74	75	109	98	0	1	0	0	1	0	97	99
TCGA-G9-6498-10A-01D-A30X-08_PRAD	82	0	0	48	83	81	79	69	100	0	0	0	0	0	0	77	97
TCGA-G9-6499-10A-01D-1961-08_PRAD	132	69	77	59	80	82	120	106	1	21	79	0	99	129	0	0	138
TCGA-G9-7510-10A-01D-2260-08_PRAD	79	61	55	39	72	64	79	71	83	0	0	0	0	0	28	54	111
TCGA-G9-7519-10A-01D-2260-08_PRAD	82	72	80	2	3	0	86	87	76	12	32	61	0	76	28	0	106
TCGA-G9-7521-10A-01D-2260-08_PRAD	87	70	66	0	89	80	82	63	89	0	58	73	1	3	0	92	97
TCGA-G9-7522-10A-01D-2260-08_PRAD	96	0	0	44	88	82	71	70	68	16	38	0	50	63	22	0	97
TCGA-G9-7523-10A-01D-2260-08_PRAD	84	64	62	39	113	76	80	93	114	0	38	66	0	0	0	122	92
TCGA-G9-7525-10A-01D-2260-08_PRAD	87	0	1	97	92	86	89	99	102	0	0	0	1	1	33	68	102
TCGA-GC-A3BM-10A-01D-A22Z-08_BLCA	149	78	93	63	110	85	144	138	141	0	0	0	0	0	0	164	173
TCGA-GC-A3I6-10A-01D-A20D-08_BLCA	87	1	0	88	97	87	77	67	91	0	0	1	0	1	0	82	105
TCGA-GC-A3OO-10C-01D-A22Z-08_BLCA	138	91	77	54	158	121	129	129	147	0	44	86	0	0	25	66	159
TCGA-GC-A3RB-10A-01D-A21Z-08_BLCA	92	2	0	82	93	88	81	75	106	0	0	0	0	0	0	116	116
TCGA-GC-A3RC-10B-01D-A22Z-08_BLCA	130	0	0	85	137	132	121	115	84	22	53	0	71	98	0	87	161
TCGA-GC-A3RD-10B-01D-A22Z-08_BLCA	161	95	98	58	106	104	127	125	112	17	51	0	88	104	0	76	197
TCGA-GC-A3WC-10A-01D-A22Z-08_BLCA	142	79	75	60	169	141	135	119	144	0	47	77	0	0	0	142	166
TCGA-GC-A3YS-10A-01D-A23K-08_BLCA	176	1	1	88	206	178	152	152	95	29	93	98	87	104	0	78	164
TCGA-GC-A4ZW-10A-01D-A26K-08_BLCA	113	2	5	75	93	83	92	64	82	0	4	5	0	4	0	80	102
TCGA-GC-A6I1-10A-01D-A31J-08_BLCA	99	0	1	65	114	108	106	94	87	18	43	0	61	80	0	59	129
TCGA-GC-A6I3-10A-01D-A31J-08_BLCA	112	100	76	0	0	0	0	1	0	0	73	0	98	104	0	0	107
TCGA-GD-A2C5-10A-01D-A17V-08_BLCA	173	0	2	118	156	127	148	133	80	22	55	0	81	96	0	85	154
TCGA-GD-A3OP-10A-01D-A21Z-08_BLCA	97	62	67	53	76	78	84	108	115	0	3	0	0	1	28	66	104

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-GD-A3OQ-10A-01D-A21Z-08_BLCA	100	1	0	53	92	93	93	81	70	16	48	1	53	89	0	69	113
TCGA-GD-A3OS-10A-01D-A21Z-08_BLCA	93	0	0	81	99	90	90	105	112	0	0	0	0	2	0	147	108
TCGA-GD-A6C6-10A-01D-A31J-08_BLCA	111	74	79	47	87	71	102	105	80	18	44	0	68	79	29	0	103
TCGA-GD-A76B-10A-01D-A329-08_BLCA	97	70	67	40	131	101	89	91	80	10	59	62	42	87	22	0	108
TCGA-GE-A2C6-10A-01D-A16O-08_THCA	102	65	69	44	121	81	89	96	92	0	44	73	0	0	33	68	99
TCGA-GF-A2C7-10A-01D-A199-08_SKCM	128	1	3	94	122	97	106	114	109	1	0	1	0	1	0	134	143
TCGA-GF-A3OT-10A-01D-A23B-08_SKCM	92	61	62	50	75	69	85	115	88	0	0	1	0	1	31	67	99
TCGA-GF-A4EO-10A-01D-A24R-08_SKCM	78	67	66	44	67	66	70	96	95	0	2	3	1	0	31	64	95
TCGA-GF-A6C8-10A-01D-A30X-08_SKCM	82	0	2	77	105	76	73	82	66	11	30	0	56	63	22	0	105
TCGA-GF-A6C9-10A-01D-A30X-08_SKCM	118	83	78	2	0	1	75	87	113	0	0	0	0	0	0	95	98
TCGA-GF-A769-10A-01D-A32N-08_SKCM	87	87	92	0	0	0	92	90	105	0	0	0	0	0	42	0	98
TCGA-GJ-A6C0-10A-01D-A30V-10_LIHC	45	1	1	37	48	49	53	50	64	0	0	0	0	0	10	30	54
TCGA-GL-6846-10A-01D-1962-08_KIRP	128	82	84	50	133	124	112	140	107	0	62	83	0	0	0	140	130
TCGA-GL-7773-10A-01D-2136-08_KIRP	95	75	83	7	75	70	84	86	98	1	52	70	4	2	0	93	107
TCGA-GL-7966-10A-01D-2201-08_KIRP	97	0	2	52	91	89	96	117	112	0	0	0	0	1	0	121	101
TCGA-GL-8500-10A-01D-2396-08_KIRP	83	66	70	49	124	86	82	96	108	1	46	68	3	6	0	127	93
TCGA-GL-A4EM-10A-01D-A25F-10_KIRP	95	0	0	64	93	111	109	103	107	0	0	0	0	1	0	108	117
TCGA-GL-A59R-10A-01D-A26P-10_KIRP	88	0	1	58	77	86	91	105	52	8	33	0	46	68	0	46	93
TCGA-GL-A59T-10A-01D-A28G-10_KIRP	87	52	52	28	47	64	84	99	82	0	0	0	0	0	23	59	71
TCGA-GM-A2DA-10C-01D-A18P-09_BRCA	56	105	108	1	0	1	115	98	128	0	0	0	0	0	58	0	91
TCGA-GM-A2DB-10C-01D-A18P-09_BRCA	43	70	59	30	64	60	103	98	128	0	0	0	0	0	0	108	73
TCGA-GM-A2DC-10C-01D-A18P-09_BRCA	37	0	0	54	75	77	85	80	81	0	0	1	0	0	26	45	63
TCGA-GM-A2DD-10C-01D-A17W-09_BRCA	55	75	72	40	132	111	99	106	108	0	52	84	0	0	38	63	79
TCGA-GM-A2DF-10C-01D-A17W-09_BRCA	63	0	0	79	140	109	129	96	115	0	0	0	0	0	49	69	89
TCGA-GM-A2DH-10C-01D-A17W-09_BRCA	78	2	1	62	121	127	145	110	104	25	71	1	90	98	0	83	95
TCGA-GM-A2DK-10C-01D-A17W-09_BRCA	48	0	0	66	95	95	107	96	107	0	0	0	0	0	0	111	84
TCGA-GM-A2DL-10C-01D-A18P-09_BRCA	45	0	0	67	90	101	119	100	119	0	0	0	0	0	0	97	71
TCGA-GM-A2DM-10C-01D-A17W-09_BRCA	55	80	80	39	132	97	110	102	71	24	103	76	81	72	31	2	72
TCGA-GM-A2DN-10C-01D-A17W-09_BRCA	52	91	79	40	73	75	106	117	108	0	0	0	0	0	33	60	84
TCGA-GM-A2DO-10D-01D-A18P-09_BRCA	45	0	79	42	136	111	130	99	114	3	73	0	76	1	66	0	92
TCGA-GM-A3NW-10A-01D-A22A-09_BRCA	52	66	73	16	64	61	111	82	108	0	2	0	1	0	32	51	83
TCGA-GM-A3NY-10A-01D-A21Q-09_BRCA	69	1	3	22	103	95	111	101	167	0	1	0	4	1	31	51	97
TCGA-GM-A3XG-10A-01D-A243-09_BRCA	52	6	2	24	95	69	93	75	123	0	0	2	2	1	28	40	64
TCGA-GM-A3XL-10A-01D-A22X-09_BRCA	47	48	55	15	52	46	90	64	101	1	0	0	0	3	48	3	67
TCGA-GM-A3XN-10A-01D-A22X-09_BRCA	50	60	63	22	99	86	96	79	113	1	43	64	5	2	0	80	71
TCGA-GM-A4E0-10A-01D-A25Q-09_BRCA	63	112	107	4	11	14	112	133	104	17	55	6	72	79	0	69	106
TCGA-GM-A5PV-10A-01D-A28E-09_BRCA	47	1	2	20	74	77	81	70	93	0	1	0	0	0	0	68	71
TCGA-GM-A5PX-10A-01D-A28E-09_BRCA	56	102	101	0	98	96	106	106	77	15	97	99	0	71	0	51	80
TCGA-GN-A261-10A-01D-A199-08_SKCM	79	64	57	43	101	72	78	92	100	0	41	68	0	1	0	105	86
TCGA-GN-A262-10A-01D-A198-08_SKCM	100	81	92	1	1	1	80	109	74	15	39	0	56	72	28	0	98
TCGA-GN-A263-10A-01D-A198-08_SKCM	98	54	81	44	58	54	79	120	58	26	72	0	64	64	0	54	102
TCGA-GN-A264-10A-01D-A198-08_SKCM	101	0	0	68	91	64	71	47	53	0	0	0	0	68	0	57	76
TCGA-GN-A265-10A-01D-A199-08_SKCM	102	0	0	56	103	102	103	111	93	0	0	1	0	1	0	114	133
TCGA-GN-A266-10A-01D-A199-08_SKCM	120	70	63	44	109	95	80	126	108	0	59	62	0	0	0	143	106
TCGA-GN-A267-10A-01D-A198-08_SKCM	101	1	0	84	92	79	78	93	117	0	0	0	0	0	0	123	112
TCGA-GN-A268-10A-01D-A198-08_SKCM	97	57	44	40	64	64	76	83	51	7	39	0	41	56	29	0	111
TCGA-GN-A269-10A-01D-A19A-08_SKCM	108	0	0	75	108	87	96	93	91	0	0	0	0	0	0	97	121
TCGA-GN-A26A-10A-01D-A19A-08_SKCM	170	66	67	57	72	69	99	117	125	0	0	0	0	0	22	65	132
TCGA-GN-A26C-10A-01D-A19A-08_SKCM	112	42	54	49	55	56	84	69	92	0	2	0	0	0	16	43	113
TCGA-GN-A26D-10A-01D-A19A-08_SKCM	86	0	0	52	83	80	71	84	87	0	0	0	0	2	0	97	89
TCGA-GN-A4U3-10F-01D-A32N-08_SKCM	97	0	0	93	113	84	95	97	125	0	0	0	0	0	0	91	105
TCGA-GN-A4U4-10B-01D-A32N-08_SKCM	113	0	0	47	91	91	98	94	86	18	53	0	67	78	0	75	123
TCGA-GN-A4U5-10B-01D-A32N-08_SKCM	87	0	0	54	101	102	85	77	111	0	0	0	0	0	0	81	116
TCGA-GN-A4U7-10B-01D-A32N-08_SKCM	98	98	88	1	78	71	91	91	96	0	47	74	0	1	35	0	111
TCGA-GN-A4U8-10B-01D-A32N-08_SKCM	92	0	2	60	105	86	89	99	112	0	0	0	0	1	26	63	108
TCGA-GN-A4U9-10B-01D-A32N-08_SKCM	101	70	78	42	117	96	82	84	78	15	87	77	65	81	0	72	113
TCGA-GR-A4D4-10A-01D-A31X-10_DLBC	49	0	0	40	54	58	60	51	56	0	0	0	0	1	0	1	55
TCGA-GR-A4D5-10A-01D-A31X-10_DLBC	40	0	1	31	56	57	60	49	34	4	26	0	36	30	0	33	50
TCGA-GR-A4D6-10A-01D-A31X-10_DLBC	55	1	0	32	34	59	54	49	42	5	19	0	22	36	0	1	57
TCGA-GR-A4D9-10A-01D-A31X-10_DLBC	58	41	28	24	24	34	63	57	67	0	0	0	0	0	0	52	57
TCGA-GU-A42P-10A-01D-A23U-08_BLCA	104	4	2	61	108	73	79	72	64	17	72	63	53	62	0	60	84
TCGA-GU-A42Q-10A-01D-A23U-08_BLCA	70	73	71	4	4	10	65	62	58	17	26	1	48	55	0	35	72
TCGA-GU-A42R-10A-01D-A23K-08_BLCA	126	8	5	76	83	80	82	116	77	20	50	0	70	71	33	5	97
TCGA-GU-A762-10A-01D-A339-08_BLCA	111	0	0	43	96	87	77	79	58	14	32	0	57	65	0	51	102
TCGA-GU-A763-10A-01D-A329-08_BLCA	89	41	47	46	68	61	83	82	92	0	0	0	0	0	23	45	97
TCGA-GU-A766-10A-01D-A329-08_BLCA	119	0	0	82	107	102	102	73	99	0	0	1	1	0	36	0	121
TCGA-GU-A767-10A-01D-A329-08_BLCA	96	67	70	52	71	77	100	75	98	0	0	0	0	0	0	77	123
TCGA-GV-A3JV-10B-01D-A21Z-08_BLCA	93	0	0	66	98	100	100	78	83	0	1	0	0	1	0	87	120
TCGA-GV-A3JW-10A-01D-A20D-08_BLCA	88	76	86	1	72	68	86	102	74	19	65	90	0	83	0	56	100
TCGA-GV-A3JX-10A-01D-A20D-08_BLCA	92	58	61	43	80	68	89	114	112	0	2	0	0	0	33	71	120
TCGA-GV-A3JZ-10A-01D-A21A-08_BLCA	85	0	0	48	91	79	72	69	95	0	0	0	0	1	0	110	88
TCGA-GV-A3QF-10A-01D-A22Z-08_BLCA	136	1	2	104	130	137	132	137	146	0	0	1	0	0	0	121	165
TCGA-GV-A3QG-10A-01D-A21Z-08_BLCA	96	75	71	55	92	78	86	105	98	0	0	0	0	1	0	100	105
TCGA-GV-A3QH-10A-01D-A21Z-08_BLCA	92	0	1	54	84	88	85	88	104	0	0	0	0	0	33	60	120
TCGA-GV-A3QI-10A-01D-A21Z-08_BLCA	99	1	1	61	101	99	85	83	82	20	50	0	63	76	0	68	122
TCGA-GV-A3QK-10A-01D-A23K-08_BLCA	81	66	72	46	67	69	86	107	84	0	1	0	0	1	37	3	91
TCGA-GV-A40E-10A-01D-A23K-08_BLCA	162	97	104	64	108	114	90	82	88	0	67	0	83	110	0	90	189
TCGA-GV-A40G-10A-01D-A23K-08_BLCA	103	2	8	91	90	92	89	112	81	0	2	0	6	4	0	134	108
TCGA-GV-A6ZA-10A-01D-A339-08_BLCA	75	42	48	32	37	43	58	61	50	9	26	0	44	54	13	0	80
TCGA-H2-A26U-10A-01D-A16O-08_THCA	143	75	97	60	93	76	110	126	133	0	0	0	0	3	36	73	151
TCGA-H2-A2K9-10A-01D-A17V-08_THCA	115	82	90	59	89	78	106	121	117	0	0	0	1	2	0	142	131
TCGA-H2-A3RH-10A-01D-A21Z-08_THCA	120	0	0	55	94	102	86	79	103	0	2	3	0	1	0	82	106
TCGA-H2-A3RI-10A-01D-A21Z-08_THCA	87	69	72	52	71	79	64	62	72	0	42	0	55	75	0	61	112
TCGA-H2-A421-10A-01D-A23K-08_THCA	93	2	4	66	100	96	85	100	111	1	1	0	3	13	32	58	95
TCGA-H2-A422-10A-01D-A23K-08_THCA	192	81	89	75	103	111	141	138	163	0	0	0	0	0	38	76	185
TCGA-H4-A2HO-10A-01D-A17V-08_BLCA	111	100	103	3	3	6	95	133	125	1	4	6	3	4	34	85	130
TCGA-H4-A2HQ-10A-01D-A17V-08_BLCA	122	81	82	54	91	90	103	135	143	0	0	1	0	0	0	147	128
TCGA-H5-A2HR-10A-01D-A17W-09_UCEC	46	65	66	13	98	93	101	95	142	0	49	0	69	0	0	48	51
TCGA-H6-8124-10A-01D-2396-08_PAAD	85	66	71	2	1	2	68	82	67	14	53	0	52	63	0	72	76
TCGA-H6-A45N-10A-01D-A26I-08_PAAD	92	0	0	59	95	91	90	68	91	0	0	0	0	0	0	80	113
TCGA-H7-7774-10A-01D-2078-08_HNSC	74	57	55	40	58	57	70	70	85	0	1	6	0	1	31	0	82
TCGA-H7-8501-10A-01D-2394-08_HNSC	85	60	66	43	104	81	80	95	100	0	54	58	0	0	0	115	92
TCGA-H7-8502-10A-01D-2394-08_HNSC	77	52	58	39	90	80	69	99	97	0	49	57	0	0	0	98	86
TCGA-H7-A6C4-10A-01D-A30H-08_HNSC	141	138	133	0	88	95	141	129	182	0	53	94	0	1	0	134	184
TCGA-H7-A6C5-10A-01D-A30H-08_HNSC	165	142	160	0	165	160	156	148	119	20	131	193	0	123	0	75	193
TCGA-H8-A6C1-10A-01D-A32N-08_PAAD	96	64	57	43	68	62	72	82	103	0	0	1	0	0	0	82	98

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-H9-7775-10A-01D-2115-08_PRAD	87	0	1	57	95	90	78	83	85	1	0	0	0	0	0	103	103
TCGA-H9-A6BX-10A-01D-A30X-08_PRAD	85	0	1	59	91	83	87	82	76	0	0	0	0	0	0	96	89
TCGA-H9-A6BY-10A-01D-A30H-08_PRAD	171	110	113	75	123	118	158	151	183	0	0	0	0	0	46	102	184
TCGA-HB-A2OT-10A-01D-A21Q-09_SARC	60	59	56	18	92	98	98	103	130	0	55	50	3	0	36	57	83
TCGA-HB-A3L4-10A-01D-A21Q-09_SARC	48	3	1	32	82	79	82	92	97	1	0	2	0	4	0	82	75
TCGA-HB-A3YV-10A-01D-A24N-09_SARC	40	51	50	10	89	70	86	74	106	0	20	44	0	1	0	71	71
TCGA-HB-A43Z-10A-01D-A24N-09_SARC	67	0	3	35	104	100	101	89	125	0	2	1	0	0	0	90	89
TCGA-HB-A5W3-10A-01D-A29N-09_SARC	42	3	3	28	72	76	80	78	62	9	40	3	47	50	0	49	72
TCGA-HC-7075-10A-01D-1961-08_PRAD	109	1	0	64	113	104	97	112	111	0	0	0	0	1	31	60	121
TCGA-HC-7077-10A-01D-1961-08_PRAD	125	114	125	3	0	1	86	70	98	0	56	0	69	87	25	1	155
TCGA-HC-7078-10A-01D-2115-08_PRAD	111	61	60	43	65	55	83	62	52	15	33	0	42	66	0	54	104
TCGA-HC-7079-10A-01D-1961-08_PRAD	127	0	1	76	128	112	113	104	121	0	0	0	0	1	0	109	153
TCGA-HC-7080-10A-01D-1961-08_PRAD	145	0	2	91	133	131	120	113	117	0	1	0	0	1	0	134	161
TCGA-HC-7081-10A-01D-1962-08_PRAD	126	0	0	101	110	103	93	120	123	0	0	0	0	0	32	71	143
TCGA-HC-7209-10A-01D-2115-08_PRAD	82	0	0	59	87	83	85	93	84	0	0	0	0	1	0	115	102
TCGA-HC-7210-10A-01D-2115-08_PRAD	93	69	70	51	77	70	83	110	96	0	0	1	1	1	37	82	109
TCGA-HC-7212-10A-01D-2115-08_PRAD	92	0	0	71	87	87	77	87	89	0	1	1	0	1	0	82	100
TCGA-HC-7213-10A-01D-2115-08_PRAD	100	62	66	46	75	69	85	119	113	0	0	0	0	1	25	68	107
TCGA-HC-7230-10A-01D-2115-08_PRAD	93	1	1	71	74	80	80	78	88	0	2	0	0	1	18	50	103
TCGA-HC-7231-10A-01D-2115-08_PRAD	102	0	0	67	108	98	85	89	81	16	44	0	49	76	36	1	126
TCGA-HC-7232-10A-01D-2115-08_PRAD	133	68	62	50	69	67	95	104	76	19	49	0	55	70	28	0	102
TCGA-HC-7233-10A-01D-2115-08_PRAD	102	0	0	45	93	94	84	96	76	22	46	61	0	72	0	67	121
TCGA-HC-7736-10A-01D-2115-08_PRAD	100	76	79	49	134	90	101	130	78	32	87	68	70	81	35	3	106
TCGA-HC-7738-10A-01D-2115-08_PRAD	84	48	51	53	74	74	76	80	106	1	1	0	0	0	0	74	98
TCGA-HC-7740-10A-01D-2115-08_PRAD	86	85	94	0	73	66	64	65	3	22	86	63	78	99	0	0	99
TCGA-HC-7742-10A-01D-2115-08_PRAD	93	60	67	43	112	81	74	66	53	13	65	89	0	70	0	50	100
TCGA-HC-7744-10A-01D-2115-08_PRAD	103	1	3	66	98	97	85	78	64	16	52	0	53	73	0	65	116
TCGA-HC-7745-10A-01D-2115-08_PRAD	106	0	0	82	128	102	85	71	123	0	0	0	0	2	24	62	117
TCGA-HC-7747-10A-01D-2115-08_PRAD	160	0	1	70	125	89	98	94	112	0	0	0	0	0	0	99	116
TCGA-HC-7748-10A-01D-2115-08_PRAD	97	4	3	56	92	95	87	121	119	0	0	0	0	0	0	139	117
TCGA-HC-7749-10A-01D-2115-08_PRAD	103	1	0	87	89	86	86	76	70	17	48	0	50	77	29	0	108
TCGA-HC-7750-10A-01D-2115-08_PRAD	91	1	0	61	103	91	72	61	69	18	47	0	50	70	0	54	109
TCGA-HC-7752-10A-01D-2115-08_PRAD	106	0	0	64	101	100	90	105	104	0	0	0	0	1	28	64	106
TCGA-HC-7817-10A-01D-A29Q-08_PRAD	132	90	90	47	156	118	116	131	121	0	57	78	0	0	38	73	157
TCGA-HC-7818-10A-01D-2115-08_PRAD	115	0	0	53	93	90	95	84	78	20	43	0	58	79	0	71	122
TCGA-HC-7819-10A-01D-2115-08_PRAD	87	56	49	44	63	59	72	60	79	0	0	0	0	1	0	74	95
TCGA-HC-7820-10A-01D-2115-08_PRAD	98	0	0	63	102	84	98	88	107	0	0	0	0	0	0	121	109
TCGA-HC-7821-10A-01D-2115-08_PRAD	103	0	0	67	93	90	62	90	74	13	46	0	63	67	0	72	104
TCGA-HC-8213-10A-01D-A29Q-08_PRAD	138	0	1	72	131	134	117	123	125	0	0	0	0	0	0	135	142
TCGA-HC-8216-10A-01D-A29Q-08_PRAD	147	0	0	102	126	111	104	101	99	0	0	0	0	0	0	114	152
TCGA-HC-8256-10A-01D-2260-08_PRAD	90	84	72	0	70	72	77	71	74	16	57	74	49	77	0	68	137
TCGA-HC-8257-10A-01D-2260-08_PRAD	92	74	73	53	126	90	88	106	94	0	50	82	0	1	0	138	103
TCGA-HC-8258-10A-01D-2260-08_PRAD	77	49	60	39	75	70	77	85	104	0	0	0	0	1	31	67	95
TCGA-HC-8259-10A-01D-2260-08_PRAD	89	79	77	0	88	96	87	89	65	15	69	83	42	71	22	0	93
TCGA-HC-8260-10A-01D-2260-08_PRAD	87	0	0	69	88	81	74	98	84	0	0	0	0	0	29	0	74
TCGA-HC-8261-10A-01D-2260-08_PRAD	77	0	1	52	117	88	84	105	95	18	34	60	0	0	0	100	95
TCGA-HC-8262-10A-01D-2260-08_PRAD	85	85	87	0	90	83	91	118	88	17	63	88	0	0	32	3	100
TCGA-HC-8264-10A-01D-2395-08_PRAD	107	74	68	49	75	72	82	90	94	0	0	0	0	0	36	5	107
TCGA-HC-8265-10A-01D-2260-08_PRAD	89	84	87	0	2	3	1	1	0	0	70	0	71	95	0	0	92
TCGA-HC-8266-10A-01D-2260-08_PRAD	111	77	87	1	81	68	81	92	101	0	38	76	0	1	34	66	119
TCGA-HC-A48F-10A-01D-A25A-08_PRAD	94	86	99	2	78	78	81	108	93	0	51	67	1	3	35	74	96
TCGA-HC-A4ZV-10A-01D-A26K-08_PRAD	110	0	0	74	105	103	97	138	130	0	0	0	0	0	30	70	125
TCGA-HC-A631-10A-01D-A29Q-08_PRAD	141	0	1	83	149	119	114	120	146	0	0	0	0	0	0	141	172
TCGA-HC-A632-10A-01D-A29Q-08_PRAD	127	74	95	61	95	85	88	73	95	0	53	0	78	100	0	82	160
TCGA-HC-A6AL-10A-01D-A30H-08_PRAD	161	0	0	143	190	161	141	137	104	14	60	0	112	112	0	98	217
TCGA-HC-A6AN-10A-01D-A30H-08_PRAD	157	0	1	95	181	153	138	127	165	0	0	0	0	0	41	94	181
TCGA-HC-A6AO-10A-01D-A30H-08_PRAD	179	0	0	102	170	167	153	157	156	0	0	0	0	0	0	194	204
TCGA-HC-A6AP-10A-01D-A30H-08_PRAD	167	103	90	71	169	151	140	142	117	17	106	100	84	92	39	0	187
TCGA-HC-A6AQ-10A-01D-A30H-08_PRAD	161	96	0	63	181	152	148	134	119	18	63	0	89	118	0	87	183
TCGA-HC-A6AS-10A-01D-A30H-08_PRAD	159	0	0	120	155	149	139	116	101	10	55	0	98	110	0	75	188
TCGA-HC-A6HX-10A-01D-A31J-08_PRAD	89	0	0	54	79	76	81	78	102	0	0	0	0	0	0	71	93
TCGA-HC-A6HY-10A-01D-A31J-08_PRAD	89	50	66	37	64	65	81	97	74	16	45	0	64	74	27	1	95
TCGA-HC-A76W-10A-01D-A33W-08_PRAD	88	0	1	75	72	79	73	88	83	0	0	0	0	0	0	62	88
TCGA-HC-A76X-10A-01D-A33W-08_PRAD	119	0	0	75	87	76	81	96	75	16	41	0	61	72	24	0	103
TCGA-HD-7229-10A-01D-2013-08_HNSC	131	92	95	62	92	88	115	109	146	0	0	0	0	0	47	0	163
TCGA-HD-7753-10A-01D-2078-08_HNSC	76	1	0	51	79	72	77	85	72	0	0	0	0	0	0	99	89
TCGA-HD-7754-10A-01D-2078-08_HNSC	79	63	60	43	56	64	76	69	72	1	0	0	3	3	0	72	90
TCGA-HD-7831-10A-01D-2129-08_HNSC	87	78	80	1	72	71	73	88	94	0	45	66	4	5	31	69	97
TCGA-HD-7832-10A-01D-2129-08_HNSC	122	73	69	55	125	91	80	87	98	0	51	74	0	6	30	69	106
TCGA-HD-7917-10A-01D-2229-08_HNSC	115	0	0	96	103	115	106	116	90	16	46	0	72	89	31	0	126
TCGA-HD-8224-10A-01D-2394-08_HNSC	80	60	64	45	64	63	74	94	77	1	1	4	0	2	27	60	94
TCGA-HD-8314-10A-01D-2394-08_HNSC	120	68	74	50	74	79	86	109	98	0	0	0	0	0	27	66	105
TCGA-HD-8634-10A-01D-2394-08_HNSC	91	70	64	48	81	70	83	102	73	20	41	64	0	71	33	5	95
TCGA-HD-8635-10A-01D-2394-08_HNSC	96	67	66	41	72	65	85	96	74	20	50	0	63	69	0	56	97
TCGA-HD-A4C1-10A-02D-A24F-08_HNSC	145	0	0	119	144	143	141	126	158	0	0	0	0	0	0	163	173
TCGA-HD-A6HZ-10A-01D-A31J-08_HNSC	83	53	62	40	54	52	79	76	78	0	0	0	0	1	30	43	89
TCGA-HD-A6I0-10A-01D-A31J-08_HNSC	107	0	0	73	83	73	73	88	78	0	0	0	0	0	0	102	90
TCGA-HE-7128-10A-01D-1962-08_KIRP	123	0	1	75	122	155	141	153	138	18	62	1	81	1	0	117	130
TCGA-HE-7129-10A-01D-1962-08_KIRP	159	2	0	107	102	119	124	145	136	0	0	0	0	1	0	144	131
TCGA-HE-7130-10A-01D-1962-08_KIRP	128	91	1	53	154	118	100	108	82	14	67	1	75	87	0	70	163
TCGA-HE-A5NF-10A-01D-A26P-10_KIRP	77	74	44	35	36	65	95	78	87	0	0	0	0	0	22	55	72
TCGA-HE-A5NH-10A-01D-A26P-10_KIRP	63	0	0	51	62	88	90	75	76	0	0	0	0	0	0	76	65
TCGA-HE-A5NI-10A-01D-A26P-10_KIRP	78	66	62	37	78	109	99	74	62	4	59	53	42	69	0	59	85
TCGA-HE-A5NJ-10A-01D-A26P-10_KIRP	76	0	1	76	88	98	91	70	82	1	0	1	0	0	0	89	80
TCGA-HE-A5NK-10A-01D-A26P-10_KIRP	75	49	53	36	105	97	111	83	64	13	65	65	55	64	0	65	88
TCGA-HE-A5NL-10A-01D-A26P-10_KIRP	78	0	1	48	75	91	92	92	107	0	0	0	0	1	0	109	80
TCGA-HF-7131-10A-01D-2053-08_STAD	88	80	68	0	72	66	76	78	58	19	58	65	43	63	34	0	91
TCGA-HF-7132-10A-01D-2053-08_STAD	74	0	55	44	99	85	73	81	76	0	31	0	49	0	25	55	101
TCGA-HF-7133-10A-01D-2053-08_STAD	95	54	64	46	119	90	83	85	96	1	46	64	1	3	24	61	105
TCGA-HF-7134-10A-01D-2053-08_STAD	86	59	61	52	115	85	80	82	110	0	37	61	0	3	31	57	93
TCGA-HF-7136-10A-01D-2053-08_STAD	83	60	54	42	64	60	83	89	100	0	0	2	0	3	29	51	98
TCGA-HF-A5NB-10A-01D-A31J-08_STAD	92	60	67	47	65	1	63	62	76	0	0	0	0	70	30	0	89
TCGA-HG-A2PA-10B-01D-A20U-09_CESC	52	62	61	24	120	83	107	91	154	0	50	49	0	3	31	43	78
TCGA-HI-7168-10A-01D-2115-08_PRAD	86	59	58	41	106	74	75	102	59	15	66	84	0	72	0	62	95
TCGA-HI-7169-10A-01D-2115-08_PRAD	90	58	63	46	74	73	80	109	107	1	0	0	0	4	0	129	120
TCGA-HI-7170-10A-01D-2115-08_PRAD	87	49	42	40	53	53	70	65	56	15	38	0	48	57	0	51	83

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-HI-7171-10A-01D-2115-08_PRAD	86	0	2	63	94	96	72	83	96	0	0	0	0	0	28	67	106
TCGA-HJ-7597-10A-01D-2201-08_STAD	134	0	0	102	111	106	102	82	80	22	28	0	48	76	30	0	128
TCGA-HL-7533-10A-01D-2229-08_HNSC	106	0	1	66	101	110	86	69	83	0	0	0	0	0	0	93	110
TCGA-HM-A3JJ-10A-01D-A21Q-09_CESC	62	2	1	29	110	107	124	99	126	0	0	2	0	0	37	58	97
TCGA-HM-A3JK-10A-01D-A21Q-09_CESC	45	0	0	31	106	95	113	81	111	0	0	0	0	1	0	85	82
TCGA-HM-A4S6-10A-01D-A26G-09_CESC	44	5	8	28	93	77	87	98	72	11	30	6	53	48	0	57	75
TCGA-HN-A2NL-10A-01D-A18P-09_BRCA	48	82	73	46	126	110	113	105	69	23	109	77	70	72	0	56	90
TCGA-HN-A2OB-10B-01D-A27P-09_BRCA	44	2	0	38	86	85	90	80	86	0	2	2	0	0	0	75	80
TCGA-HP-A5MZ-10A-01D-A27I-10_LIHC	73	54	47	32	81	86	85	72	81	0	17	52	1	1	0	56	79
TCGA-HP-A5N0-10A-01D-A28X-10_LIHC	75	59	51	29	53	66	105	96	99	0	0	1	0	0	0	95	63
TCGA-HQ-A2OE-10A-01D-A202-08_BLCA	89	0	0	66	85	86	73	76	98	0	1	0	1	1	23	46	86
TCGA-HQ-A2OF-10B-01D-A26K-08_BLCA	81	1	2	68	80	85	82	66	89	0	3	1	0	1	0	66	99
TCGA-HQ-A5ND-10A-01D-A26K-08_BLCA	163	0	0	117	149	154	144	128	164	0	0	1	0	0	64	6	191
TCGA-HQ-A5NE-10A-01D-A289-08_BLCA	147	0	0	83	116	102	106	138	136	0	0	0	0	1	37	69	125
TCGA-HR-A2OG-10A-01D-A199-08_SKCM	70	37	42	21	41	38	57	67	80	0	0	1	1	0	21	35	93
TCGA-HR-A2OH-10A-01D-A199-08_SKCM	105	50	56	44	50	57	67	50	56	0	35	2	47	64	0	44	108
TCGA-HR-A5NC-10A-01D-A27N-08_SKCM	84	63	66	44	74	70	79	69	83	0	0	0	0	0	37	1	103
TCGA-HS-A5N7-10A-01D-A26G-09_SARC	37	54	45	13	46	47	76	66	90	2	0	0	1	2	30	40	71
TCGA-HS-A5N8-10A-01D-A26G-09_SARC	59	4	6	38	89	93	105	89	124	2	3	0	7	7	0	94	71
TCGA-HS-A5N9-10A-01D-A26G-09_SARC	55	63	62	19	60	58	86	93	126	1	1	0	3	2	35	43	77
TCGA-HT-7467-10A-01D-2024-08_LGG	89	63	67	40	55	60	86	76	89	0	0	0	0	1	40	6	92
TCGA-HT-7468-10A-01D-2024-08_LGG	72	65	64	40	104	73	77	78	82	0	37	60	0	1	0	80	99
TCGA-HT-7469-10B-01D-2253-08_LGG	91	68	52	47	70	66	92	115	109	0	1	1	2	1	30	63	99
TCGA-HT-7470-10A-01D-2086-08_LGG	89	0	1	77	78	76	75	88	101	0	0	0	0	1	0	78	90
TCGA-HT-7471-10B-01D-2253-08_LGG	79	59	55	46	108	92	80	61	83	0	33	61	0	0	0	87	101
TCGA-HT-7472-10A-01D-2024-08_LGG	83	74	81	0	1	1	81	78	95	1	1	5	3	2	0	82	106
TCGA-HT-7473-10A-01D-2024-08_LGG	95	2	0	53	87	85	96	101	75	23	47	1	52	74	21	0	101
TCGA-HT-7474-10A-01D-2024-08_LGG	114	74	79	0	66	68	80	74	87	1	37	61	2	2	0	71	98
TCGA-HT-7475-10A-01D-2024-08_LGG	105	6	3	60	96	79	86	97	110	1	0	1	0	2	27	55	102
TCGA-HT-7476-10A-01D-2024-08_LGG	87	3	2	52	90	77	76	77	100	0	0	0	1	1	0	78	94
TCGA-HT-7477-10A-01D-A289-08_LGG	84	83	79	1	84	79	79	94	97	0	68	86	0	0	0	74	92
TCGA-HT-7478-10A-01D-2024-08_LGG	99	5	2	72	92	90	82	101	110	0	0	1	0	0	31	57	106
TCGA-HT-7479-10A-01D-2024-08_LGG	90	1	7	81	93	95	90	103	79	0	1	4	1	1	0	114	117
TCGA-HT-7480-10A-01D-2086-08_LGG	90	63	49	46	117	79	79	79	97	1	47	59	0	0	23	59	102
TCGA-HT-7481-10A-01D-2024-08_LGG	123	2	0	57	95	91	79	79	64	16	47	0	54	69	0	70	97
TCGA-HT-7482-10A-01D-2024-08_LGG	86	67	63	40	80	69	83	84	91	1	0	4	0	0	30	54	111
TCGA-HT-7483-10A-01D-2024-08_LGG	98	0	3	83	99	90	89	93	105	0	1	2	0	0	0	129	106
TCGA-HT-7485-10A-01D-2024-08_LGG	88	64	69	44	113	80	81	106	104	0	38	67	1	2	0	116	99
TCGA-HT-7601-10A-01D-2086-08_LGG	85	60	63	50	65	59	77	82	92	0	1	0	0	0	28	62	101
TCGA-HT-7602-10A-01D-2086-08_LGG	94	1	0	51	91	87	90	106	106	0	0	0	1	1	27	62	95
TCGA-HT-7603-10A-01D-2086-08_LGG	116	0	0	84	96	92	80	95	120	0	0	0	0	0	0	129	103
TCGA-HT-7604-10A-01D-2086-08_LGG	95	1	67	51	140	90	79	90	75	21	57	0	69	70	28	1	103
TCGA-HT-7605-10A-01D-2086-08_LGG	93	0	0	92	85	84	80	100	96	0	0	0	0	0	0	120	85
TCGA-HT-7606-10A-01D-2086-08_LGG	61	0	0	47	71	74	71	42	77	0	0	1	0	2	0	67	87
TCGA-HT-7607-10A-01D-2086-08_LGG	92	68	61	45	69	84	78	98	111	0	0	0	0	1	32	71	101
TCGA-HT-7608-10A-01D-2086-08_LGG	91	52	61	41	73	66	91	89	91	0	0	0	1	0	0	123	103
TCGA-HT-7609-10A-01D-2086-08_LGG	88	84	79	0	82	83	86	77	65	28	69	79	50	64	0	57	100
TCGA-HT-7610-10A-01D-2086-08_LGG	110	62	59	40	66	62	83	87	90	0	0	0	0	2	27	60	96
TCGA-HT-7611-10B-01D-2396-08_LGG	92	80	95	6	96	95	88	80	69	18	88	81	65	72	0	63	93
TCGA-HT-7616-10A-01D-2253-08_LGG	102	61	57	51	70	70	81	90	104	0	0	0	0	0	30	73	106
TCGA-HT-7620-10A-01D-2253-08_LGG	85	57	50	49	99	64	57	56	80	0	45	50	0	74	26	2	74
TCGA-HT-7676-10B-01D-2396-08_LGG	87	63	65	44	111	90	77	102	75	18	67	83	0	72	29	4	99
TCGA-HT-7677-10A-01D-2253-08_LGG	106	2	1	93	102	87	135	148	116	16	2	2	0	2	34	65	119
TCGA-HT-7680-10A-01D-2253-08_LGG	99	62	58	51	71	75	86	87	69	18	49	0	47	73	0	61	94
TCGA-HT-7681-10C-01D-2396-08_LGG	80	0	3	54	84	73	70	90	104	0	4	1	6	2	0	78	93
TCGA-HT-7684-10A-01D-2253-08_LGG	126	69	58	52	140	113	100	109	62	26	82	96	47	77	0	62	110
TCGA-HT-7686-10A-01D-2253-08_LGG	86	0	0	90	98	98	85	102	123	0	0	0	0	0	35	78	115
TCGA-HT-7687-10A-01D-2253-08_LGG	123	76	80	1	1	2	85	86	91	0	0	0	0	0	38	1	104
TCGA-HT-7688-10A-01D-2253-08_LGG	103	0	0	82	83	78	81	71	107	0	0	0	0	0	0	87	100
TCGA-HT-7689-10A-01D-2253-08_LGG	89	55	0	38	83	89	71	60	79	0	0	0	0	0	0	81	101
TCGA-HT-7690-10A-01D-2253-08_LGG	86	0	0	70	67	58	69	64	37	22	30	41	0	39	0	50	86
TCGA-HT-7691-10A-01D-2253-08_LGG	94	0	0	62	98	105	82	81	82	16	44	0	48	75	0	53	97
TCGA-HT-7692-10A-01D-2253-08_LGG	88	51	59	53	126	92	90	80	75	20	63	84	0	71	36	0	92
TCGA-HT-7693-10A-01D-2253-08_LGG	98	0	72	53	106	101	84	121	114	0	58	0	53	2	35	70	115
TCGA-HT-7694-10A-01D-2253-08_LGG	73	0	0	82	82	86	81	83	77	0	0	0	0	1	0	107	104
TCGA-HT-7695-10A-01D-2253-08_LGG	95	52	61	47	64	63	85	84	108	0	0	0	0	0	0	120	105
TCGA-HT-7854-10A-01D-2253-08_LGG	101	0	0	87	104	102	78	70	86	0	0	0	0	0	0	90	120
TCGA-HT-7855-10A-01D-2396-08_LGG	88	4	4	55	87	84	80	83	64	21	54	2	64	72	0	64	106
TCGA-HT-7856-10A-01D-2396-08_LGG	170	104	100	77	110	110	137	172	169	0	0	0	0	1	47	94	175
TCGA-HT-7857-10A-01D-2396-08_LGG	79	65	58	37	65	72	78	89	80	0	1	4	0	0	0	96	86
TCGA-HT-7858-10A-01D-2396-08_LGG	86	89	70	1	73	70	73	102	72	17	51	0	65	77	32	6	92
TCGA-HT-7860-10A-01D-2396-08_LGG	119	0	3	57	107	82	82	107	119	0	1	0	0	0	29	72	104
TCGA-HT-7873-10A-01D-2396-08_LGG	83	5	4	77	82	82	71	103	100	0	0	0	0	0	0	122	94
TCGA-HT-7874-10A-01D-2396-08_LGG	80	8	4	63	80	73	72	70	80	0	4	5	0	0	0	74	87
TCGA-HT-7875-10A-01D-2396-08_LGG	119	69	70	48	129	90	79	116	66	27	91	80	61	66	0	66	105
TCGA-HT-7877-10A-01D-2396-08_LGG	88	82	81	5	76	74	80	86	85	0	55	63	1	2	0	78	95
TCGA-HT-7879-10A-01D-2396-08_LGG	86	88	77	1	82	72	80	93	106	1	41	74	6	8	0	122	142
TCGA-HT-7880-10A-01D-2396-08_LGG	81	4	3	60	86	85	84	82	85	0	0	0	0	0	0	87	106
TCGA-HT-7881-10A-01D-2396-08_LGG	88	63	66	49	110	83	72	101	97	0	43	6	63	0	0	100	91
TCGA-HT-7882-10A-01D-2396-08_LGG	84	79	69	50	69	72	81	107	72	23	46	6	61	71	35	0	96
TCGA-HT-7884-10A-01D-2396-08_LGG	90	67	66	43	71	72	83	104	82	0	3	4	0	6	0	128	103
TCGA-HT-7902-10A-01D-2396-08_LGG	89	65	74	43	118	90	85	105	92	2	54	68	11	7	33	70	96
TCGA-HT-8010-10A-01D-2396-08_LGG	110	63	61	46	70	58	71	105	97	0	0	4	1	0	24	50	96
TCGA-HT-8011-10A-01D-2396-08_LGG	86	4	3	76	91	80	82	79	100	0	0	0	1	2	0	110	94
TCGA-HT-8012-10A-01D-2396-08_LGG	84	85	86	3	2	3	74	77	71	16	58	61	1	71	0	65	95
TCGA-HT-8013-10A-01D-2396-08_LGG	132	132	132	0	94	88	130	93	128	0	53	93	0	0	0	109	166
TCGA-HT-8015-10A-01D-A289-08_LGG	94	0	0	51	84	82	91	110	79	0	0	1	0	0	0	127	99
TCGA-HT-8018-10A-01D-2396-08_LGG	90	10	8	51	84	84	81	98	108	0	0	0	0	1	0	117	97
TCGA-HT-8019-10A-01D-2396-08_LGG	82	64	61	42	68	68	82	92	85	1	2	3	0	5	28	63	89
TCGA-HT-8104-10A-01D-2396-08_LGG	91	78	73	42	76	73	78	71	88	1	0	0	1	1	0	82	95
TCGA-HT-8105-10A-01D-2396-08_LGG	88	91	90	2	96	88	83	103	78	19	88	83	63	74	28	3	99
TCGA-HT-8106-10A-01D-2396-08_LGG	154	1	1	90	147	137	136	112	153	0	0	0	0	0	0	135	179
TCGA-HT-8107-10A-01D-2396-08_LGG	83	4	6	72	94	81	80	89	83	19	46	66	2	81	0	56	96
TCGA-HT-8108-10A-01D-2396-08_LGG	93	66	69	47	120	84	82	96	89	0	54	63	0	3	0	117	97
TCGA-HT-8109-10A-01D-2396-08_LGG	81	4	5	48	84	79	76	79	93	0	6	5	0	0	35	0	99
TCGA-HT-8110-10A-01D-2396-08_LGG	86	64	67	43	117	79	65	67	5	14	78	67	68	73	0	3	84

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-HT-8111-10A-01D-2396-08_LGG	85	3	1	60	117	85	78	84	64	20	42	2	57	73	0	66	92
TCGA-HT-8113-10A-01D-2396-08_LGG	148	0	0	115	195	190	132	124	151	0	0	1	0	0	0	132	175
TCGA-HT-8114-10A-01D-2396-08_LGG	96	2	8	52	92	79	84	83	113	0	3	0	2	3	0	83	86
TCGA-HT-8558-10A-01D-2396-08_LGG	89	69	66	39	112	89	75	85	88	0	52	74	0	0	39	2	99
TCGA-HT-8563-10A-01D-2396-08_LGG	84	67	66	52	111	87	81	99	95	0	59	67	0	1	31	57	98
TCGA-HT-8564-10A-01D-2396-08_LGG	86	65	75	40	79	74	89	106	85	0	0	0	5	5	34	56	96
TCGA-HT-A4DS-10A-01D-A26K-08_LGG	86	0	0	47	76	76	75	64	79	0	0	0	0	0	0	78	102
TCGA-HT-A4DV-10A-01D-A26K-08_LGG	75	69	74	0	2	6	85	66	64	12	35	3	43	55	24	3	90
TCGA-HT-A5R5-10A-01D-A289-08_LGG	82	0	0	47	90	84	71	97	78	0	0	0	0	0	0	110	92
TCGA-HT-A5R7-10A-01D-A289-08_LGG	113	64	65	45	118	81	87	76	68	21	70	66	60	68	0	60	98
TCGA-HT-A5R9-10A-01D-A289-08_LGG	82	0	0	75	85	90	79	77	59	12	39	0	54	80	0	52	91
TCGA-HT-A5RA-10A-01D-A289-08_LGG	122	58	71	39	118	73	83	121	110	16	42	63	0	0	28	55	98
TCGA-HT-A5RB-10A-01D-A289-08_LGG	84	63	68	40	72	73	85	78	3	22	64	0	81	89	0	0	100
TCGA-HT-A5RC-10A-01D-A289-08_LGG	82	67	62	42	109	68	63	53	74	0	43	60	0	68	0	55	77
TCGA-HT-A614-10A-01D-A29Q-08_LGG	126	0	1	79	130	117	123	111	152	0	0	0	0	0	0	121	146
TCGA-HT-A615-10A-01D-A29Q-08_LGG	128	96	93	61	152	118	107	111	111	0	49	86	0	0	0	104	152
TCGA-HT-A616-10A-01D-A29Q-08_LGG	167	80	93	47	66	80	95	94	97	18	60	0	60	82	30	0	133
TCGA-HT-A617-10A-01D-A29Q-08_LGG	153	0	0	99	126	121	113	105	148	0	0	0	0	0	0	151	154
TCGA-HT-A618-10A-01D-A29Q-08_LGG	116	86	76	52	92	87	109	126	136	0	0	0	0	0	35	75	142
TCGA-HT-A619-10A-01D-A29Q-08_LGG	115	73	75	63	83	85	105	105	121	0	0	0	0	0	47	0	140
TCGA-HT-A61A-10A-01D-A29Q-08_LGG	164	0	0	91	135	122	129	111	151	0	1	0	0	1	38	81	169
TCGA-HT-A61B-10A-01D-A29Q-08_LGG	144	76	85	47	84	85	115	105	90	17	55	0	75	98	0	80	156
TCGA-HT-A61C-10A-01D-A29Q-08_LGG	141	127	130	0	0	0	132	147	140	0	0	0	0	1	43	82	162
TCGA-HT-A74H-10A-01D-A329-08_LGG	114	0	0	90	113	95	110	93	119	0	0	0	0	0	31	51	131
TCGA-HT-A74J-10A-01D-A329-08_LGG	87	62	59	38	93	77	76	76	60	14	58	55	57	67	0	48	89
TCGA-HT-A74K-10A-01D-A329-08_LGG	78	0	0	47	79	78	77	74	63	14	29	57	0	62	17	0	81
TCGA-HT-A74L-10A-01D-A329-08_LGG	80	0	0	66	81	75	77	69	95	0	0	0	0	0	0	80	91
TCGA-HT-A74O-10A-01D-A329-08_LGG	94	1	0	67	81	76	67	65	78	0	0	0	0	0	0	61	89
TCGA-HU-8238-10A-01D-2341-08_STAD	150	0	0	92	95	104	99	121	130	0	0	0	0	0	36	72	127
TCGA-HU-8243-10A-01D-2341-08_STAD	102	0	2	67	115	108	112	121	89	26	57	0	74	74	33	0	122
TCGA-HU-8244-10A-01D-2341-08_STAD	103	1	1	62	116	92	103	109	79	22	43	2	68	86	33	3	111
TCGA-HU-8245-10A-01D-2341-08_STAD	108	84	79	58	84	82	101	116	94	26	62	0	69	75	39	0	135
TCGA-HU-8249-10A-01D-2341-08_STAD	106	0	0	64	103	100	110	88	114	0	0	0	0	0	46	0	130
TCGA-HU-8602-10A-01D-2394-08_STAD	81	2	2	51	88	86	74	85	62	15	44	4	55	74	27	0	98
TCGA-HU-8604-10A-01D-2394-08_STAD	113	6	4	87	82	78	80	91	94	0	1	0	0	1	40	6	99
TCGA-HU-8608-10A-01D-2394-08_STAD	75	65	59	40	65	75	76	96	83	0	0	4	1	0	29	56	95
TCGA-HU-8610-10A-01D-2394-08_STAD	94	0	0	65	90	85	91	81	93	0	0	0	0	0	40	0	94
TCGA-HU-A4G2-10A-01D-A25E-08_STAD	91	0	1	56	88	71	79	76	81	0	0	0	0	1	37	1	95
TCGA-HU-A4G3-10A-01D-A24F-08_STAD	76	5	3	49	77	79	67	100	64	11	44	8	50	60	30	7	82
TCGA-HU-A4G6-10A-01D-A24F-08_STAD	85	0	0	82	88	85	78	108	113	0	0	0	0	0	33	63	88
TCGA-HU-A4G8-10A-01D-A25E-08_STAD	87	0	0	51	83	93	94	94	81	13	47	71	1	0	0	110	89
TCGA-HU-A4G9-10A-01D-A24F-08_STAD	71	3	5	47	73	70	74	75	76	0	0	0	0	0	26	44	85
TCGA-HU-A4GC-10A-01D-A25E-08_STAD	92	0	0	66	97	76	86	94	111	0	0	0	0	1	33	62	91
TCGA-HU-A4GD-10A-01D-A25E-08_STAD	91	1	0	53	96	84	79	100	90	0	1	0	0	0	30	58	93
TCGA-HU-A4GF-10A-01D-A24F-08_STAD	82	1	0	43	79	71	72	79	74	0	0	0	0	0	27	45	95
TCGA-HU-A4GH-10A-01D-A24F-08_STAD	88	0	0	51	87	89	85	87	79	16	58	0	60	80	0	66	90
TCGA-HU-A4GJ-10A-01D-A25E-08_STAD	90	0	0	58	95	89	84	113	117	0	0	0	0	0	35	71	100
TCGA-HU-A4GN-10A-01D-A25E-08_STAD	91	0	1	60	98	73	90	96	78	20	43	67	0	76	0	66	112
TCGA-HU-A4GP-10A-01D-A25E-08_STAD	117	1	2	73	90	82	78	82	79	0	0	0	0	0	0	80	88
TCGA-HU-A4GQ-10A-01D-A25E-08_STAD	87	0	6	61	91	88	83	97	77	19	53	67	0	65	28	1	112
TCGA-HU-A4GT-10A-01D-A25E-08_STAD	127	2	2	85	82	90	88	78	7	25	67	0	79	92	0	0	97
TCGA-HU-A4GU-10A-01D-A25E-08_STAD	101	67	67	42	86	76	92	111	125	1	1	0	0	2	0	101	107
TCGA-HU-A4GX-10A-01D-A25E-08_STAD	101	2	2	56	93	83	80	83	91	0	0	0	0	0	38	3	96
TCGA-HU-A4GY-10A-01D-A24F-08_STAD	75	0	0	49	73	73	71	84	77	0	0	1	0	1	30	54	85
TCGA-HU-A4H2-10A-01D-A25E-08_STAD	93	0	0	47	89	79	84	82	81	0	0	0	0	0	37	1	100
TCGA-HU-A4H3-10A-01D-A25E-08_STAD	94	1	0	57	95	82	79	88	74	1	1	1	0	2	26	4	104
TCGA-HU-A4H6-10A-01D-A25E-08_STAD	90	0	2	56	91	91	86	81	69	0	3	1	0	0	31	3	107
TCGA-HU-A4H8-10A-01D-A25E-08_STAD	93	62	66	50	118	85	92	89	100	0	42	65	0	0	29	76	116
TCGA-HU-A4HB-10A-01D-A25E-08_STAD	97	0	0	66	91	101	94	131	114	0	0	0	0	1	42	75	128
TCGA-HU-A4HD-10A-01D-A25E-08_STAD	88	0	0	53	89	86	69	79	89	0	0	0	0	1	36	0	97
TCGA-HV-A5A3-10A-01D-A26I-08_PAAD	90	1	1	70	95	78	80	65	55	13	34	9	54	59	0	52	97
TCGA-HV-A5A4-10A-01D-A26I-08_PAAD	97	1	4	65	90	93	80	75	66	13	24	4	38	56	22	5	99
TCGA-HV-A5A5-10A-01D-A26I-08_PAAD	87	0	1	52	81	91	78	79	103	0	2	0	2	9	24	49	99
TCGA-HV-A5A6-10A-01D-A26I-08_PAAD	88	0	0	53	88	75	73	63	47	16	32	50	3	56	0	48	92
TCGA-HV-A7OL-10A-01D-A33W-08_PAAD	79	0	1	52	77	79	74	82	84	0	0	0	0	0	26	48	82
TCGA-HV-A7OP-10A-01D-A33W-08_PAAD	71	0	0	46	77	75	65	70	61	9	35	0	46	57	0	38	79
TCGA-HW-7486-10A-01D-2024-08_LGG	95	1	2	60	107	93	100	84	118	0	0	0	0	1	0	84	128
TCGA-HW-7487-10A-01D-2024-08_LGG	88	2	5	52	93	86	83	85	91	0	1	1	0	0	0	78	91
TCGA-HW-7489-10A-01D-2024-08_LGG	88	58	65	43	80	74	77	107	115	0	0	2	2	0	22	58	105
TCGA-HW-7490-10A-01D-2024-08_LGG	97	67	70	39	70	71	74	100	72	14	46	0	59	74	26	1	95
TCGA-HW-7491-10A-01D-2024-08_LGG	115	66	72	40	89	58	94	103	125	0	3	1	0	1	0	102	139
TCGA-HW-7493-10A-01D-2024-08_LGG	92	0	1	58	92	85	92	89	84	0	2	0	4	3	0	89	96
TCGA-HW-7495-10A-01D-2024-08_LGG	92	1	1	49	92	85	79	81	95	0	1	0	1	2	0	76	100
TCGA-HW-8319-10A-01D-2396-08_LGG	84	5	2	56	81	91	72	111	111	2	3	0	4	8	32	63	100
TCGA-HW-8320-10A-01D-2396-08_LGG	86	53	65	39	68	56	74	104	103	0	0	1	0	1	34	68	85
TCGA-HW-8321-10A-01D-2396-08_LGG	77	0	6	55	86	78	81	90	74	19	50	0	57	69	30	0	94
TCGA-HW-8322-10A-01D-2396-08_LGG	95	74	76	46	72	73	91	105	83	0	0	2	0	0	32	74	96
TCGA-HW-A5KJ-10A-01D-A27N-08_LGG	124	0	0	95	111	105	100	98	134	0	0	0	0	0	0	96	113
TCGA-HW-A5KK-10A-01D-A27N-08_LGG	135	79	77	45	129	119	105	124	75	11	80	96	0	83	33	0	127
TCGA-HW-A5KL-10A-01D-A27N-08_LGG	111	0	0	101	116	114	98	114	100	0	0	0	0	0	0	145	134
TCGA-HW-A5KM-10A-01D-A27N-08_LGG	109	72	81	51	82	77	108	94	1	22	69	0	86	107	0	0	129
TCGA-HZ-7920-10B-01D-2201-08_PAAD	98	62	68	48	114	85	85	103	114	0	52	0	54	0	0	128	114
TCGA-HZ-8001-10A-01D-2201-08_PAAD	83	57	54	45	115	81	80	107	103	0	45	57	0	1	0	104	101
TCGA-HZ-8002-10A-01D-2201-08_PAAD	95	66	70	43	70	78	74	63	6	17	75	5	78	90	0	1	103
TCGA-HZ-8003-10A-01D-2201-08_PAAD	86	76	89	3	5	2	78	90	80	1	0	2	1	1	36	58	90
TCGA-HZ-8005-10A-01D-2201-08_PAAD	117	0	2	41	69	69	61	62	76	0	1	0	1	76	0	64	97
TCGA-HZ-8315-10A-01D-2396-08_PAAD	86	56	55	43	58	64	54	56	63	0	41	0	45	62	0	51	91
TCGA-HZ-8317-10A-01D-2396-08_PAAD	76	3	1	70	82	77	73	73	90	0	1	1	0	0	0	68	87
TCGA-HZ-8519-10A-01D-2396-08_PAAD	83	53	71	41	110	77	78	82	62	16	69	70	68	76	0	65	94
TCGA-HZ-8636-10A-01D-2396-08_PAAD	85	50	62	35	62	51	61	63	85	0	0	5	0	0	0	70	81
TCGA-HZ-8637-10A-01D-2396-08_PAAD	113	0	1	71	105	99	91	116	103	0	0	0	0	1	0	134	125
TCGA-HZ-8638-10A-01D-2396-08_PAAD	71	55	60	33	58	57	76	84	81	0	1	0	1	2	20	45	81
TCGA-HZ-A49G-10A-01D-A26I-08_PAAD	103	55	64	38	105	85	89	90	103	2	32	50	0	5	23	57	99
TCGA-HZ-A49H-10A-01D-A26I-08_PAAD	90	0	0	68	101	115	91	85	111	0	2	0	0	2	0	109	100
TCGA-HZ-A49I-10A-01D-A26I-08_PAAD	260	127	143	99	162	153	186	208	267	0	0	0	0	1	73	136	234
TCGA-HZ-A4BH-10A-01D-A26I-08_PAAD	108	0	2	76	89	86	87	81	67	13	37	0	55	72	0	66	99

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-HZ-A4BK-10A-01D-A26I-08_PAAD	86	76	71	0	5	6	77	67	86	1	1	2	0	1	36	5	101
TCGA-HZ-A77O-10A-01D-A33W-08_PAAD	76	0	0	39	75	80	79	80	44	16	32	0	53	65	0	53	86
TCGA-HZ-A77P-10A-01D-A33W-08_PAAD	79	54	61	37	54	64	66	91	91	0	0	0	1	0	30	51	82
TCGA-IA-A40U-10A-01D-A25F-10_KIRP	65	93	98	3	89	99	104	92	65	11	106	86	70	73	0	64	78
TCGA-IA-A40X-10A-01D-A25F-10_KIRP	76	61	46	31	79	90	104	77	99	0	19	40	0	0	21	37	90
TCGA-IA-A40Y-10A-01D-A25F-10_KIRP	75	59	60	33	59	68	93	101	121	0	0	0	0	0	26	56	98
TCGA-IB-7645-10A-01D-2201-08_PAAD	100	61	62	43	72	67	81	85	88	0	1	1	0	1	43	4	102
TCGA-IB-7890-10A-01D-2201-08_PAAD	86	63	67	43	72	66	75	89	117	0	1	1	1	1	33	71	93
TCGA-IB-7891-10A-01D-2201-08_PAAD	91	4	1	87	87	82	80	86	83	0	0	1	0	1	0	94	92
TCGA-IB-7893-10A-01D-2201-08_PAAD	81	61	65	39	67	68	75	81	103	0	2	4	4	3	0	77	99
TCGA-IB-7897-10A-01D-2201-08_PAAD	86	1	2	87	83	82	81	115	105	0	0	0	0	1	0	117	96
TCGA-IB-8126-10A-01D-2396-08_PAAD	74	0	1	49	81	75	68	63	66	12	41	4	54	62	0	49	86
TCGA-IB-8127-10A-01D-2396-08_PAAD	76	59	65	42	69	60	78	92	96	0	0	0	1	0	0	108	87
TCGA-IB-A5SO-10A-01D-A32N-08_PAAD	80	50	57	38	103	78	71	81	53	13	64	74	0	66	0	46	89
TCGA-IB-A5SP-10A-01D-A32N-08_PAAD	114	61	63	34	72	66	58	51	66	0	38	51	0	63	31	0	86
TCGA-IB-A5SQ-10A-01D-A32N-08_PAAD	81	50	60	35	50	57	69	90	93	0	0	0	0	0	29	47	97
TCGA-IB-A5SS-10A-01D-A32N-08_PAAD	84	52	56	44	67	71	71	98	89	0	0	0	0	0	31	59	98
TCGA-IB-A5ST-10A-01D-A32N-08_PAAD	118	0	0	55	88	79	73	101	59	17	48	0	53	63	0	64	93
TCGA-IB-A6UF-10A-01D-A33W-08_PAAD	84	78	77	0	80	83	73	86	78	0	51	73	0	0	0	110	89
TCGA-IB-A6UG-10A-01D-A33W-08_PAAD	104	0	0	50	73	74	74	87	89	0	1	0	0	0	28	51	82
TCGA-IE-A4EH-10A-01D-A24N-09_SARC	42	2	1	30	82	91	93	96	88	16	37	2	55	57	0	44	83
TCGA-IE-A4EI-10A-01D-A24N-09_SARC	51	3	0	29	98	93	93	91	136	0	1	1	3	1	42	51	79
TCGA-IE-A4EJ-10A-01D-A24N-09_SARC	67	80	84	14	116	104	124	117	131	0	78	80	0	0	35	54	72
TCGA-IE-A4EK-10A-01D-A24N-09_SARC	56	2	4	36	99	92	104	127	127	0	0	3	1	3	0	105	74
TCGA-IE-A6BZ-10A-01D-A307-09_SARC	67	1	0	58	141	129	157	117	181	0	0	0	0	0	74	0	110
TCGA-IH-A3EA-10A-01D-A20D-08_SKCM	102	72	61	50	65	64	95	74	60	14	50	0	55	72	0	64	101
TCGA-IK-7675-10A-01D-2086-08_LGG	88	53	58	48	103	81	83	80	84	0	45	65	0	0	0	107	99
TCGA-IK-8125-10A-01D-2253-08_LGG	118	70	56	0	92	82	63	72	71	15	75	64	43	62	22	0	99
TCGA-IM-A3EB-10A-01D-A202-08_THCA	100	57	67	44	114	83	87	93	113	0	39	60	0	2	0	122	101
TCGA-IM-A3ED-10A-01D-A202-08_THCA	106	0	0	72	108	83	98	112	106	0	0	0	0	0	35	74	95
TCGA-IM-A3U2-10A-01D-A22D-08_THCA	99	0	0	59	90	91	85	79	111	0	0	1	0	3	0	86	101
TCGA-IM-A3U3-10A-01D-A22D-08_THCA	81	58	49	39	106	77	82	81	106	0	35	64	0	0	29	56	95
TCGA-IM-A41Y-10A-01D-A23U-08_THCA	71	3	1	65	94	66	73	65	92	0	0	0	0	0	0	69	75
TCGA-IM-A41Z-10A-01D-A23K-08_THCA	102	69	75	51	119	88	79	90	72	17	74	92	6	83	0	66	117
TCGA-IM-A420-10A-01D-A23K-08_THCA	89	77	78	52	92	76	89	132	119	1	1	2	0	1	0	145	110
TCGA-IM-A4EB-10A-01D-A25A-08_THCA	71	2	3	34	65	60	61	76	70	0	0	0	0	0	26	49	69
TCGA-IN-7806-10A-01D-2053-08_STAD	89	0	0	83	87	87	79	78	88	0	1	0	0	1	0	82	107
TCGA-IN-7808-10A-01D-2201-08_STAD	154	0	0	84	150	124	105	115	75	24	70	62	46	82	0	60	124
TCGA-IN-8462-10A-01D-2341-08_STAD	113	73	75	48	83	79	92	98	113	0	0	0	0	0	33	86	114
TCGA-IN-8663-10A-01D-2394-08_STAD	76	89	80	5	2	2	82	78	94	1	3	0	2	4	0	79	99
TCGA-IN-A6RI-10A-01D-A32N-08_STAD	101	0	0	99	99	91	95	89	107	0	0	0	0	1	0	112	119
TCGA-IN-A6RJ-10A-21D-A33W-08_STAD	92	0	1	60	95	88	89	85	89	0	0	0	0	1	33	54	96
TCGA-IN-A6RL-10A-01D-A32N-08_STAD	105	88	90	2	127	104	103	91	0	22	92	83	90	91	0	0	109
TCGA-IN-A6RN-10A-01D-A33W-08_STAD	98	0	0	60	94	84	89	106	108	0	0	0	0	0	27	64	114
TCGA-IN-A6RO-10A-01D-A33W-08_STAD	121	0	1	56	97	95	102	104	100	15	0	0	0	0	0	93	118
TCGA-IN-A6RP-10A-01D-A33W-08_STAD	121	0	0	71	106	97	103	117	93	18	52	67	0	81	30	0	110
TCGA-IN-A6RR-10A-01D-A32N-08_STAD	113	63	74	44	125	96	85	89	85	16	88	78	64	85	0	76	111
TCGA-IP-7968-10A-01D-2201-08_STAD	93	0	0	52	103	99	88	97	121	0	0	0	0	0	26	55	118
TCGA-IQ-7630-10A-01D-2078-08_HNSC	86	55	64	41	97	76	71	81	61	13	62	62	51	63	0	54	91
TCGA-IQ-7631-10A-01D-2078-08_HNSC	80	5	1	59	99	86	80	66	70	12	31	3	49	63	0	45	94
TCGA-IQ-7632-10A-01D-2078-08_HNSC	78	2	58	46	112	86	79	70	96	0	37	0	52	6	34	0	105
TCGA-IQ-A61E-10A-01D-A30H-08_HNSC	168	0	1	96	173	158	144	164	173	0	0	0	0	0	45	82	185
TCGA-IQ-A61G-10A-01D-A30H-08_HNSC	183	84	0	57	179	156	152	151	107	24	59	0	72	109	42	0	198
TCGA-IQ-A61H-10A-01D-A30H-08_HNSC	216	0	0	111	186	175	164	202	217	0	0	0	1	1	55	110	203
TCGA-IQ-A61I-10A-01D-A30H-08_HNSC	175	0	0	118	148	141	153	164	157	0	0	0	0	0	0	158	179
TCGA-IQ-A61J-10A-01D-A30H-08_HNSC	174	0	1	64	162	152	146	145	104	21	54	0	108	99	0	70	189
TCGA-IQ-A61K-10A-01D-A30H-08_HNSC	160	101	97	77	190	150	152	135	133	0	60	113	0	0	0	158	192
TCGA-IQ-A61L-10A-01D-A30H-08_HNSC	152	148	102	0	109	108	103	88	2	19	135	108	136	171	0	0	175
TCGA-IQ-A61O-10A-01D-A30H-08_HNSC	161	0	1	149	172	164	164	165	184	0	0	0	0	0	48	92	192
TCGA-IR-A3L7-10A-01D-A20U-09_CESC	50	59	44	11	50	55	107	104	123	11	1	1	1	2	0	93	69
TCGA-IR-A3LA-10A-01D-A22X-09_CESC	59	0	0	28	100	93	96	98	69	12	45	0	61	64	37	4	75
TCGA-IR-A3LB-10A-01D-A243-09_CESC	43	0	1	31	96	111	102	84	79	12	62	0	63	70	0	63	78
TCGA-IR-A3LC-10A-01D-A20U-09_CESC	45	61	46	10	52	46	90	90	98	0	3	1	1	2	0	87	71
TCGA-IR-A3LF-10A-01D-A22X-09_CESC	68	0	1	34	99	107	115	114	152	0	1	1	0	0	0	136	94
TCGA-IR-A3LH-10A-01D-A20U-09_CESC	42	49	49	11	80	83	80	58	64	8	64	42	49	47	28	1	69
TCGA-IR-A3LI-10A-01D-A20U-09_CESC	49	1	2	27	81	81	87	93	103	1	2	1	0	1	0	91	73
TCGA-IR-A3LK-10A-01D-A20U-09_CESC	63	91	85	1	3	3	99	106	82	13	49	0	64	67	41	3	74
TCGA-IR-A3LL-10A-01D-A20U-09_CESC	51	3	3	31	111	98	111	98	62	12	68	1	61	56	0	59	79
TCGA-IS-A3K6-10A-01D-A21Q-09_SARC	47	57	50	12	55	52	103	67	101	0	0	0	1	2	0	70	65
TCGA-IS-A3K7-10A-01D-A21Q-09_SARC	42	59	58	18	54	60	92	88	103	0	0	0	1	0	0	86	86
TCGA-IS-A3K8-10A-01D-A21Q-09_SARC	34	0	1	26	86	88	90	77	101	0	1	0	0	0	34	47	77
TCGA-IS-A3KA-10A-01D-A21Q-09_SARC	49	57	44	18	106	94	89	102	78	12	75	87	2	66	30	1	65
TCGA-IW-A3M4-10B-01D-A21Q-09_SARC	52	71	59	18	106	99	93	82	68	14	91	69	68	70	0	60	80
TCGA-IW-A3M5-10A-01D-A21Q-09_SARC	52	2	1	23	87	85	100	82	117	0	0	0	0	0	27	47	73
TCGA-IW-A3M6-10A-01D-A21Q-09_SARC	60	1	0	23	91	102	86	94	77	13	52	0	57	74	0	56	75
TCGA-IZ-8195-10A-01D-2396-08_KIRP	95	1	1	87	89	82	85	114	112	0	2	2	0	0	0	121	98
TCGA-IZ-8196-10A-01D-2396-08_KIRP	88	1	0	53	84	84	70	90	75	0	1	0	1	0	0	134	92
TCGA-IZ-A6M8-10A-01D-A31X-10_KIRP	57	39	26	32	28	35	65	46	66	0	0	0	0	0	28	0	57
TCGA-IZ-A6M9-10A-01D-A31X-10_KIRP	56	0	0	39	54	64	62	60	40	5	23	0	31	31	12	2	53
TCGA-J1-A4AH-10A-01D-A24F-08_LUSC	80	0	2	47	82	82	78	71	64	17	42	0	57	59	0	54	87
TCGA-J2-8192-10A-01D-2238-08_LUAD	130	70	69	52	85	72	93	103	76	14	42	1	55	76	33	0	107
TCGA-J2-8194-10A-01D-2238-08_LUAD	111	1	1	54	87	100	84	77	92	0	0	0	1	0	27	69	106
TCGA-J2-A4AD-10A-01D-A24F-08_LUAD	78	68	62	44	68	62	74	76	86	0	0	0	0	1	37	1	87
TCGA-J2-A4AE-10A-01D-A24F-08_LUAD	78	0	0	50	77	74	69	72	82	0	0	0	0	0	0	69	80
TCGA-J2-A4AG-10A-01D-A24F-08_LUAD	87	67	61	43	105	80	73	105	56	17	79	72	1	66	0	66	80
TCGA-J4-8198-10A-01D-2260-08_PRAD	91	59	62	48	113	105	90	82	74	17	76	64	59	82	0	68	98
TCGA-J4-8200-10A-01D-A29Q-08_PRAD	128	149	82	53	145	121	113	119	94	26	81	77	85	106	0	65	141
TCGA-J4-A67K-10A-01D-A30H-08_PRAD	164	1	0	92	157	144	143	127	173	0	0	0	0	0	42	88	193
TCGA-J4-A67L-10A-01D-A30H-08_PRAD	167	85	104	69	105	105	145	137	169	0	0	0	0	0	0	168	187
TCGA-J4-A67M-10A-01D-A30H-08_PRAD	147	89	103	69	114	93	131	139	169	0	0	0	0	1	0	172	166
TCGA-J4-A67N-10A-01D-A30H-08_PRAD	164	0	1	100	151	141	117	126	101	16	52	0	84	102	0	65	152
TCGA-J4-A67O-10A-01D-A30H-08_PRAD	139	0	1	110	142	135	130	132	148	0	0	0	0	0	0	127	159
TCGA-J4-A67Q-10A-01D-A30H-08_PRAD	130	83	90	0	156	126	148	124	70	16	76	136	0	99	0	74	179
TCGA-J4-A67R-10A-01D-A30H-08_PRAD	138	0	0	88	148	136	125	115	127	0	0	0	0	0	0	124	163
TCGA-J4-A67S-10A-01D-A30H-08_PRAD	166	93	97	59	103	105	140	132	140	0	0	0	0	0	0	131	177
TCGA-J4-A67T-10A-01D-A30X-08_PRAD	88	67	63	40	69	64	82	92	71	10	42	0	58	72	28	0	100

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-J4-A6G1-10A-01D-A30X-08_PRAD	89	0	1	50	93	85	71	78	64	14	33	0	48	68	21	0	92
TCGA-J4-A6G3-10A-01D-A30X-08_PRAD	118	0	0	71	96	85	73	82	110	0	0	0	2	0	0	92	98
TCGA-J4-A6M7-10A-01D-A31J-08_PRAD	84	1	0	57	83	77	65	68	86	0	0	0	0	0	0	80	96
TCGA-J7-6720-10A-01D-2136-08_KIRP	88	63	67	45	63	77	95	100	73	17	40	0	56	71	36	4	105
TCGA-J7-8537-10A-01D-2396-08_KIRP	81	74	80	4	10	6	73	88	68	20	43	73	0	75	0	65	87
TCGA-J8-A3NZ-10A-01D-A21A-08_THCA	97	52	54	51	59	70	75	76	89	0	0	0	0	1	28	67	101
TCGA-J8-A3O0-10A-01D-A21A-08_THCA	89	0	0	77	91	89	81	68	62	14	43	0	43	63	0	65	133
TCGA-J8-A3O1-10A-01D-A21A-08_THCA	79	59	45	53	68	66	82	76	102	0	0	0	0	1	44	0	116
TCGA-J8-A3O2-10A-01D-A23K-08_THCA	127	0	0	115	135	124	155	131	0	43	75	0	110	132	0	0	174
TCGA-J8-A3YD-10A-01D-A22Z-08_THCA	76	1	1	61	73	73	77	66	73	0	0	0	0	0	0	65	72
TCGA-J8-A3YE-10A-01D-A23K-08_THCA	88	2	7	53	94	74	92	133	107	1	0	0	0	0	32	69	91
TCGA-J8-A3YF-10A-01D-A23K-08_THCA	167	101	0	64	194	155	148	126	92	26	60	0	86	112	0	85	204
TCGA-J8-A3YG-10A-01D-A22Z-08_THCA	65	0	0	54	67	66	63	84	80	0	0	0	0	0	0	80	82
TCGA-J8-A3YH-10A-01D-A22Z-08_THCA	101	0	0	44	70	72	67	64	70	0	0	0	0	1	35	0	88
TCGA-J8-A42S-10A-01D-A23K-08_THCA	97	76	74	51	75	74	89	88	71	23	57	7	66	81	0	71	95
TCGA-J8-A4HW-10A-01D-A25A-08_THCA	81	69	74	1	73	72	73	77	3	22	77	80	2	69	0	0	79
TCGA-J8-A4HY-10A-01D-A25A-08_THCA	181	0	1	120	199	172	164	137	99	32	95	90	82	107	0	66	178
TCGA-J9-A52B-10A-01D-A26K-08_PRAD	110	0	0	48	94	73	74	64	77	2	0	0	1	6	0	73	95
TCGA-J9-A52C-10A-01D-A26K-08_PRAD	82	0	1	37	97	86	73	68	60	13	27	1	46	65	0	56	98
TCGA-J9-A52D-10A-01D-A29Q-08_PRAD	138	0	0	52	125	132	120	114	86	20	51	0	75	94	0	75	143
TCGA-J9-A52E-10A-01D-A26K-08_PRAD	80	51	63	34	107	88	79	82	91	0	26	59	2	0	0	86	102
TCGA-JL-A3YW-10B-01D-A23C-09_BRCA	52	103	109	2	96	102	112	96	107	0	72	104	2	4	34	50	88
TCGA-JL-A3YX-10A-01D-A22X-09_BRCA	52	69	54	15	87	94	95	110	89	14	74	65	57	60	26	3	75
TCGA-JV-A5VE-10A-01D-A29N-09_SARC	42	54	58	19	49	64	107	83	102	0	1	1	1	1	0	74	69
TCGA-JV-A5VF-10A-01D-A29N-09_SARC	55	68	60	21	102	97	99	85	108	1	42	70	0	0	0	112	83
TCGA-JW-A5VG-10A-01D-A28E-09_CESC	52	74	54	14	107	116	114	87	111	0	42	73	0	0	60	1	91
TCGA-JW-A5VH-10A-01D-A28E-09_CESC	68	76	67	12	77	70	148	97	143	0	2	0	1	0	0	95	89
TCGA-JW-A5VI-10A-01D-A28E-09_CESC	67	1	0	34	114	129	135	111	159	0	0	0	0	0	82	0	106
TCGA-JW-A5VJ-10A-01D-A28E-09_CESC	54	1	0	28	121	106	132	101	85	10	57	2	69	73	0	60	103
TCGA-JW-A5VK-10A-01D-A28E-09_CESC	59	87	71	20	75	74	127	117	156	0	1	1	0	0	0	124	97
TCGA-JW-A5VL-10A-01D-A28E-09_CESC	61	2	1	27	83	94	101	83	115	0	0	0	0	1	55	1	91
TCGA-JX-A3PZ-10A-01D-A21Q-09_CESC	50	0	0	34	97	107	108	99	152	0	0	0	0	0	42	59	97
TCGA-JX-A3Q0-10A-01D-A21Q-09_CESC	61	1	3	31	103	103	113	107	146	0	3	1	0	1	32	72	96
TCGA-JX-A3Q8-10A-01D-A21Q-09_CESC	53	1	1	37	111	104	124	99	127	0	2	3	0	0	52	0	100
TCGA-JX-A5QV-10A-01D-A28E-09_CESC	49	58	50	13	110	97	115	92	79	11	81	53	52	61	0	59	82
TCGA-K1-A3PN-10A-01D-A22A-09_SARC	33	0	1	29	75	74	90	67	91	0	1	0	0	0	0	64	61
TCGA-K1-A3PO-10A-01D-A21Q-09_SARC	40	3	1	19	65	90	88	93	62	7	38	53	0	52	0	52	77
TCGA-K1-A42W-10A-01D-A24N-09_SARC	46	2	0	22	109	103	99	92	4	20	74	41	73	85	0	0	68
TCGA-K4-A3WS-10A-01D-A22Z-08_BLCA	163	152	154	1	0	1	147	168	122	19	61	0	91	109	0	88	174
TCGA-K4-A3WU-10A-01D-A23K-08_BLCA	85	54	57	48	70	61	69	80	86	0	0	1	0	0	29	62	95
TCGA-K4-A3WV-10A-01D-A22Z-08_BLCA	150	147	141	0	0	0	133	122	149	0	0	0	0	0	0	123	176
TCGA-K4-A4AB-10A-01D-A289-08_BLCA	116	0	0	97	118	124	115	103	104	0	0	0	0	0	0	105	136
TCGA-K4-A4AC-10A-01D-A26K-08_BLCA	100	84	88	37	102	83	92	114	123	0	28	56	0	0	0	94	106
TCGA-K4-A54R-10A-01D-A26K-08_BLCA	90	62	60	39	67	66	80	79	90	0	1	0	0	0	32	61	105
TCGA-K4-A5RH-10A-01D-A30H-08_BLCA	169	0	1	150	174	163	193	227	197	25	0	0	1	0	47	81	197
TCGA-K4-A5RI-10A-01D-A289-08_BLCA	124	97	103	0	84	75	94	123	136	0	56	74	0	1	35	75	156
TCGA-K4-A5RJ-10A-01D-A289-08_BLCA	113	92	111	0	108	105	101	122	82	15	91	115	57	81	0	70	139
TCGA-K4-A6FZ-10A-01D-A31J-08_BLCA	106	0	3	65	110	101	105	123	124	0	0	0	0	1	34	64	119
TCGA-K4-A6MB-10A-01D-A31J-08_BLCA	96	0	0	60	82	80	86	100	97	0	0	0	0	0	0	100	105
TCGA-K6-A3WQ-10A-01D-A22A-09_UCEC	30	30	36	8	51	33	72	52	63	0	2	1	2	3	0	59	50
TCGA-K7-A5RF-10B-01D-A28X-10_LIHC	56	52	40	24	66	84	111	90	63	5	19	53	0	0	26	56	59
TCGA-K7-A5RG-10A-01D-A28X-10_LIHC	72	64	51	27	87	95	93	81	92	0	45	56	0	0	30	57	58
TCGA-K7-A6G5-10A-01D-A30V-10_LIHC	47	25	22	15	26	25	54	39	28	5	17	0	15	24	12	0	34
TCGA-KB-A6F5-10A-01D-A33W-08_STAD	103	75	74	58	122	93	98	86	74	20	80	88	0	69	0	68	119
TCGA-KB-A6F7-10A-01D-A32N-08_STAD	108	0	0	53	96	90	91	89	82	19	59	0	65	69	0	64	109
TCGA-KC-A4BL-10A-01D-A25A-08_PRAD	105	0	79	55	75	87	84	67	93	0	69	0	66	96	0	66	116
TCGA-KC-A4BN-10A-01D-A25A-08_PRAD	96	77	79	43	119	81	82	97	96	0	47	73	0	1	42	1	95
TCGA-KC-A4BO-10A-01D-A25A-08_PRAD	87	0	1	75	105	84	80	97	95	1	0	1	0	2	28	49	102
TCGA-KC-A4BR-10A-01D-A25A-08_PRAD	122	80	74	54	135	112	122	101	123	0	71	80	1	0	0	153	140
TCGA-KC-A4BV-10A-01D-A26K-08_PRAD	96	53	63	32	65	59	61	48	74	0	37	0	44	61	0	50	95
TCGA-KC-A7F3-10A-01D-A33W-08_PRAD	85	0	0	49	93	89	71	94	104	0	0	0	0	0	0	105	86
TCGA-KC-A7F5-10A-01D-A33W-08_PRAD	89	2	1	88	96	88	78	116	103	0	0	4	1	2	27	58	113
TCGA-KC-A7F6-10A-01D-A33W-08_PRAD	83	75	79	18	75	65	79	94	65	16	55	73	10	64	0	57	85
TCGA-KC-A7FA-10A-01D-A33W-08_PRAD	68	0	0	40	66	69	67	73	90	0	0	0	0	0	0	75	79
TCGA-KC-A7FD-10A-01D-A33W-08_PRAD	79	59	68	43	108	84	80	67	82	0	35	60	0	0	0	74	94
TCGA-KC-A7FE-10A-01D-A33W-08_PRAD	90	0	0	53	87	89	74	66	69	14	42	0	52	67	0	58	102
TCGA-KD-A5QS-10A-01D-A27P-09_SARC	43	1	3	29	77	52	48	45	70	0	1	2	1	46	0	47	36
TCGA-KD-A5QT-10A-01D-A27P-09_SARC	59	0	0	30	99	96	101	89	73	13	48	1	60	56	38	1	90
TCGA-KD-A5QU-10A-01D-A27P-09_SARC	51	1	0	36	91	92	95	93	130	0	0	0	0	1	0	99	84
TCGA-KF-A41W-10A-01D-A24N-09_SARC	56	50	59	17	48	65	100	90	102	0	1	0	0	1	0	108	72
TCGA-KJ-A3U4-10A-01D-A22A-09_UCEC	51	73	67	17	66	74	103	102	141	0	2	2	3	2	38	58	82
TCGA-KM-8438-10A-01D-2311-10_KICH	54	31	34	14	27	28	33	23	47	0	18	0	18	43	0	28	74
TCGA-KM-8439-10A-01D-2311-10_KICH	75	68	40	1	37	32	73	61	0	17	56	0	55	74	0	0	77
TCGA-KM-8440-10A-01D-2311-10_KICH	71	1	0	49	62	116	70	66	89	0	0	0	0	0	0	0	80
TCGA-KM-8441-10A-01D-2311-10_KICH	60	0	0	36	78	38	54	46	69	0	0	0	0	44	0	1	50
TCGA-KM-8442-10A-01D-2311-10_KICH	59	0	0	39	56	68	75	58	90	0	0	0	0	0	0	52	77
TCGA-KM-8443-10A-01D-2311-10_KICH	60	0	0	41	48	64	71	56	80	0	0	0	0	0	0	48	65
TCGA-KM-8476-10A-01D-2311-10_KICH	67	0	0	32	50	50	72	53	86	0	0	0	0	0	0	42	72
TCGA-KM-8477-10A-01D-2311-10_KICH	59	54	62	1	0	0	69	50	52	8	14	0	28	34	0	26	72
TCGA-KM-8639-10A-01D-2397-10_KICH	114	0	0	44	106	116	110	94	120	0	0	0	0	0	0	129	98
TCGA-KP-A3VZ-10A-01D-A22A-09_UCEC	55	87	85	0	1	2	81	82	82	20	58	1	65	57	0	65	80
TCGA-KP-A3W0-10A-01D-A22A-09_UCEC	44	1	1	27	90	68	59	63	71	0	0	1	0	63	41	0	50
TCGA-KP-A3W1-10A-01D-A22A-09_UCEC	71	73	65	30	74	63	124	134	128	0	1	0	0	1	37	68	110
TCGA-KP-A3W3-10A-01D-A22A-09_UCEC	42	1	1	23	74	64	80	67	42	16	28	0	47	41	20	0	59
TCGA-KP-A3W4-10A-01D-A22A-09_UCEC	55	71	60	26	87	108	108	91	122	0	1	0	2	4	34	65	81
TCGA-KQ-A41N-10D-01D-A339-08_BLCA	70	0	54	33	102	71	73	65	78	0	30	0	50	0	32	0	89
TCGA-KQ-A41P-10F-01D-A339-08_BLCA	79	0	0	41	90	89	79	78	79	0	0	1	0	0	0	104	96
TCGA-KQ-A41Q-10D-01D-A339-08_BLCA	76	80	80	0	62	58	75	66	93	0	31	54	0	0	0	63	90
TCGA-KQ-A41S-10C-01D-A339-08_BLCA	84	79	84	0	0	0	85	88	65	14	47	68	0	68	35	0	93
TCGA-KT-A74X-10A-01D-A329-08_LGG	112	60	59	43	62	67	74	65	106	0	0	0	0	0	0	71	90
TCGA-KU-A66S-10A-01D-A30H-08_HNSC	145	1	0	108	157	114	111	96	117	0	1	0	0	127	0	102	147
TCGA-KU-A66T-10A-01D-A30H-08_HNSC	151	86	102	62	172	149	146	151	109	16	100	103	104	110	0	74	188
TCGA-KU-A6H7-10A-01D-A31J-08_HNSC	83	0	0	74	94	72	75	72	94	0	0	0	0	1	24	62	94
TCGA-KV-A6GD-10A-01D-A31X-10_KIRP	45	0	0	48	49	68	69	57	71	0	0	0	0	0	12	34	49
TCGA-KV-A6GE-10A-01D-A31X-10_KIRP	59	35	37	14	16	30	69	49	68	1	0	0	0	2	0	52	50
TCGA-L3-A4E7-10A-01D-A25A-08_LUSC	80	83	89	3	61	59	74	82	6	21	83	93	65	84	0	4	94

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-L3-A524-10A-01D-A25L-08_LUSC	90	7	6	89	91	90	82	103	123	0	0	0	6	5	0	87	106
TCGA-L4-A4E5-10A-01D-A24P-08_LUAD	80	55	61	42	68	63	75	95	60	16	46	0	59	55	0	48	83
TCGA-L4-A4E6-10A-01D-A24F-08_LUAD	111	95	107	0	113	97	114	95	127	17	60	100	1	1	0	102	133
TCGA-L6-A4EP-10A-01D-A25A-08_THCA	54	0	0	34	49	53	53	49	54	0	1	0	0	0	0	48	62
TCGA-L6-A4EQ-10A-01D-A25A-08_THCA	167	0	0	112	146	142	133	107	110	18	47	0	73	111	0	59	175
TCGA-L6-A4ET-10A-01D-A25A-08_THCA	70	55	49	33	84	68	63	79	91	0	40	44	4	4	18	55	77
TCGA-L6-A4EU-10A-01D-A25A-08_THCA	69	51	56	33	95	65	63	87	84	0	35	49	0	0	21	41	71
TCGA-L9-A443-10A-01D-A24F-08_LUAD	118	0	1	53	86	83	82	120	103	0	0	0	1	1	27	64	93
TCGA-L9-A444-10A-01D-A24F-08_LUAD	84	70	68	47	111	79	76	102	70	11	72	63	60	69	0	58	88
TCGA-LA-A446-10A-01D-A25A-08_LUSC	80	3	3	57	87	86	81	87	67	13	47	2	58	69	0	56	103
TCGA-LB-A7SX-10A-01D-A33W-08_PAAD	76	0	0	65	71	73	77	68	74	0	0	0	0	0	0	91	84
TCGA-LC-A66R-10A-01D-A30H-08_BLCA	184	159	172	1	123	122	97	85	110	0	121	121	95	123	0	110	196
TCGA-LD-A66U-10A-01D-A31U-09_BRCA	35	53	53	6	103	93	89	82	72	9	71	51	61	58	0	41	76
TCGA-LG-A6GG-10A-01D-A30V-10_LIHC	58	44	32	19	34	43	65	56	66	0	0	0	0	0	19	37	52
TCGA-LI-A67I-10A-01D-A307-09_SARC	75	107	95	28	102	100	135	164	191	0	0	1	0	0	58	82	103
TCGA-LL-A440-10A-01D-A243-09_BRCA	47	1	1	18	67	59	77	59	73	0	4	3	0	0	0	47	57
TCGA-LL-A441-10A-01D-A243-09_BRCA	35	49	44	9	75	70	74	81	94	0	25	32	1	2	25	0	41
TCGA-LL-A50Y-10A-01D-A25Q-09_BRCA	56	1	5	29	98	92	92	81	109	1	1	3	0	3	33	51	81
TCGA-LL-A5YL-10A-01D-A29N-09_BRCA	40	55	60	13	59	64	102	94	75	8	42	0	53	58	42	3	72
TCGA-LL-A5YM-10A-01D-A28E-09_BRCA	45	68	66	23	62	52	106	103	117	0	0	0	0	0	33	47	75
TCGA-LL-A5YN-10A-01D-A28E-09_BRCA	53	2	3	31	98	91	94	96	133	0	1	0	0	0	40	61	82
TCGA-LL-A5YO-10A-01D-A28E-09_BRCA	49	64	60	16	56	62	68	50	83	0	42	0	60	67	0	56	75
TCGA-LL-A5YP-10A-01D-A28E-09_BRCA	50	1	1	21	79	89	91	76	90	0	0	0	0	0	55	0	77
TCGA-LL-A6FP-10A-01D-A31U-09_BRCA	41	0	1	37	87	95	112	93	126	1	0	0	2	4	0	114	71
TCGA-LL-A6FQ-10A-01D-A31U-09_BRCA	27	0	0	29	84	91	83	73	86	8	40	0	47	48	0	51	68
TCGA-LL-A6FR-10B-01D-A31U-09_BRCA	27	0	1	23	89	95	99	77	77	10	35	64	0	53	0	48	84
TCGA-LP-A4AU-10A-01D-A243-09_CESC	37	0	0	29	84	85	87	77	127	0	1	0	2	1	0	82	85
TCGA-LP-A4AV-10A-01D-A243-09_CESC	45	1	1	23	82	98	88	68	111	0	1	0	1	0	35	60	77
TCGA-LP-A4AW-10A-01D-A243-09_CESC	57	2	1	22	93	100	102	99	137	0	0	0	1	1	37	60	79
TCGA-LP-A4AX-10A-01D-A243-09_CESC	52	60	51	22	120	95	129	136	106	14	49	72	2	0	41	46	88
TCGA-LP-A5U2-10A-01D-A28E-09_CESC	57	52	47	8	86	80	95	71	104	0	41	51	0	0	46	0	63
TCGA-LP-A5U3-10A-01D-A28E-09_CESC	58	0	1	28	98	117	119	109	127	0	0	0	2	0	0	83	109
TCGA-LQ-A4E4-10A-01D-A25Q-09_BRCA	53	97	81	3	61	61	95	88	103	2	38	50	3	7	0	67	85
TCGA-LT-A5Z6-10A-01D-A289-08_BLCA	93	69	67	40	74	78	102	96	66	14	44	0	51	93	0	70	127
TCGA-M7-A71Y-10A-01D-A329-08_PRAD	97	0	1	59	107	89	93	73	105	0	0	0	0	1	0	74	94
TCGA-M7-A71Z-10A-01D-A329-08_PRAD	99	0	2	65	108	99	94	83	73	15	44	0	70	81	0	49	114
TCGA-M7-A720-10A-01D-A329-08_PRAD	99	1	0	85	108	89	80	94	66	15	33	0	52	72	0	48	113
TCGA-M7-A721-10A-01D-A329-08_PRAD	107	77	83	56	84	77	79	75	75	0	58	0	64	81	0	71	119
TCGA-M7-A723-10A-01D-A329-08_PRAD	115	83	87	56	137	99	103	126	79	21	93	90	79	77	0	82	152
TCGA-M7-A724-10A-01D-A329-08_PRAD	103	0	0	53	91	88	92	63	61	12	29	0	59	70	0	48	115
TCGA-M7-A725-10A-01D-A329-08_PRAD	113	79	84	50	141	98	84	122	133	0	60	80	0	1	36	74	116
TCGA-M8-A5N4-10A-01D-A26I-08_PAAD	86	50	57	34	102	81	84	65	85	0	32	46	0	1	32	4	85
TCGA-MB-A5Y8-10A-01D-A29N-09_SARC	33	2	1	19	71	73	86	63	92	0	0	0	1	0	0	74	62
TCGA-MB-A5Y9-10A-01D-A29N-09_SARC	41	50	66	15	39	59	100	81	64	16	60	0	81	53	0	33	75
TCGA-MB-A5YA-10A-01D-A29N-09_SARC	40	57	43	11	54	45	71	76	62	9	33	2	50	49	0	38	58
TCGA-MF-A522-10A-01D-A25L-08_LUSC	83	74	74	42	111	81	90	82	114	0	53	58	1	1	0	87	96
TCGA-MH-A55W-10A-01D-A26P-10_KIRP	89	0	0	60	77	125	102	80	91	0	0	0	0	0	40	0	96
TCGA-MH-A55Z-10A-01D-A26P-10_KIRP	71	0	59	0	53	106	102	95	89	0	31	0	49	1	31	69	81
TCGA-MH-A560-10A-01D-A26P-10_KIRP	85	0	1	48	99	106	99	94	123	0	2	0	0	2	0	95	76
TCGA-MH-A561-10A-01D-A26P-10_KIRP	73	0	0	70	73	111	107	82	55	6	32	0	43	71	32	0	87
TCGA-MH-A562-10A-01D-A26P-10_KIRP	76	58	52	38	84	102	96	80	83	0	40	60	1	1	50	3	73
TCGA-MJ-A68H-10A-01D-A307-09_SARC	65	95	89	33	166	143	138	161	184	0	66	84	0	0	0	175	109
TCGA-MJ-A68J-10A-01D-A307-09_SARC	72	101	128	0	181	132	143	197	184	0	112	1	152	0	66	95	106
TCGA-MK-A4N6-10A-01D-A25A-08_THCA	77	0	0	41	53	66	53	89	49	14	37	0	38	52	26	0	72
TCGA-MK-A4N7-10A-01D-A25A-08_THCA	77	0	3	53	70	77	61	91	69	16	42	1	52	59	29	0	77
TCGA-MK-A4N9-10A-01D-A25A-08_THCA	74	58	57	33	50	53	65	79	52	12	39	0	48	53	31	4	77
TCGA-MM-A563-10A-01D-A25V-10_KIRC	97	0	1	52	99	110	113	86	123	0	0	0	1	0	23	64	112
TCGA-MM-A564-10A-01D-A25V-10_KIRC	86	84	100	0	3	4	93	58	65	10	31	0	56	61	0	62	95
TCGA-MN-A4N1-10A-01D-A24P-08_LUAD	81	3	6	52	81	86	78	82	86	1	1	1	1	2	0	82	98
TCGA-MN-A4N4-10A-01D-A24P-08_LUAD	81	2	5	56	93	77	79	76	99	0	0	0	1	1	0	79	93
TCGA-MN-A4N5-10A-01D-A24P-08_LUAD	123	3	5	42	76	76	72	130	101	0	2	0	5	3	31	69	86
TCGA-MO-A47P-10A-01D-A24N-09_SARC	49	69	61	16	62	65	107	87	84	10	45	2	49	68	36	4	88
TCGA-MO-A47R-10A-01D-A24N-09_SARC	44	3	3	33	83	86	82	83	96	0	0	2	0	0	29	45	67
TCGA-MP-A4SV-10A-01D-A24P-08_LUAD	75	82	80	10	8	6	79	71	74	20	48	1	65	63	0	63	92
TCGA-MP-A4SW-10A-01D-A24P-08_LUAD	76	3	4	73	81	79	77	68	66	15	46	2	60	64	0	58	80
TCGA-MP-A4SY-10A-01D-A24P-08_LUAD	80	64	58	44	109	81	77	127	105	0	48	64	3	2	29	54	93
TCGA-MP-A4T2-10A-01D-A24P-08_LUAD	127	0	0	57	146	108	105	98	65	21	41	1	75	87	0	66	144
TCGA-MP-A4T4-10A-01D-A25L-08_LUAD	93	1	3	63	94	97	89	86	95	0	3	0	2	11	0	91	107
TCGA-MP-A4T6-10A-01D-A25L-08_LUAD	110	89	96	4	10	1	88	95	76	12	51	0	60	73	28	9	98
TCGA-MP-A4T7-10A-01D-A24P-08_LUAD	112	1	1	51	80	82	82	75	82	0	0	5	0	0	26	64	89
TCGA-MP-A4T8-10A-01D-A24P-08_LUAD	86	77	78	4	74	62	85	85	71	15	68	68	54	65	29	8	85
TCGA-MP-A4T9-10A-01D-A24P-08_LUAD	93	73	72	42	64	71	85	93	93	0	0	0	2	0	33	60	99
TCGA-MP-A4TA-10A-01D-A24P-08_LUAD	85	0	1	61	85	79	91	75	81	14	39	0	62	74	0	57	98
TCGA-MP-A4TC-10A-01D-A24P-08_LUAD	118	68	74	46	117	83	78	100	67	16	76	68	64	69	0	55	101
TCGA-MP-A4TD-10A-01D-A25L-08_LUAD	98	0	1	84	111	107	104	96	74	19	50	0	69	79	0	60	132
TCGA-MP-A4TE-10A-01D-A25L-08_LUAD	94	66	77	43	75	69	83	110	76	12	41	0	69	69	0	63	101
TCGA-MP-A4TF-10A-01D-A25L-08_LUAD	90	93	97	3	72	76	87	102	77	25	82	68	56	65	0	67	106
TCGA-MP-A4TH-10A-01D-A25L-08_LUAD	98	70	72	47	79	70	96	104	117	0	0	0	6	5	29	71	108
TCGA-MP-A4TI-10A-01D-A24P-08_LUAD	102	7	12	94	99	90	103	89	78	22	50	0	62	79	0	74	101
TCGA-MP-A4TJ-10A-01D-A25L-08_LUAD	104	93	102	3	77	72	87	104	73	16	77	79	1	70	30	6	108
TCGA-MP-A4TK-10A-01D-A24P-08_LUAD	91	75	69	52	77	67	79	102	115	1	0	0	0	0	23	63	98
TCGA-MP-A5C7-10A-01D-A25L-08_LUAD	91	93	88	1	3	4	88	101	70	19	50	1	65	75	31	5	107
TCGA-MR-A520-10A-01D-A25V-10_LIHC	99	1	4	47	90	97	125	74	64	8	35	0	52	63	27	0	99
TCGA-MS-A51U-10A-01D-A25Q-09_BRCA	48	6	5	31	105	104	106	107	152	0	0	2	2	3	32	59	98
TCGA-MT-A51W-10A-01D-A25Y-08_HNSC	116	0	0	72	100	83	84	105	101	0	1	0	1	1	33	59	94
TCGA-MT-A51X-10A-01D-A25Y-08_HNSC	89	72	64	43	71	55	65	60	71	0	46	60	0	78	0	61	111
TCGA-MT-A67A-10A-01D-A30H-08_HNSC	193	100	105	70	113	98	140	146	164	0	0	0	0	0	43	93	202
TCGA-MT-A67D-10A-01D-A30H-08_HNSC	168	94	97	0	110	101	100	84	1	20	104	1	127	152	0	1	190
TCGA-MT-A67F-10A-01D-A30H-08_HNSC	172	0	0	109	163	151	166	123	185	0	0	0	0	1	0	162	204
TCGA-MT-A67G-10A-01D-A30H-08_HNSC	165	0	105	0	201	155	155	157	113	17	91	0	135	115	41	0	181
TCGA-MU-A51Y-10A-01D-A26G-09_CESC	50	2	6	27	71	66	81	78	110	1	1	1	0	3	22	54	79
TCGA-MV-A51V-10A-01D-A26K-08_BLCA	82	46	55	39	96	84	70	78	50	13	52	73	0	56	0	59	86
TCGA-MW-A4EC-10A-01D-A25V-10_KIRC	88	54	63	30	106	103	105	91	115	0	34	61	0	0	0	117	105
TCGA-MX-A5UG-10A-01D-A31J-08_STAD	78	0	0	57	84	72	81	86	71	15	46	0	57	70	30	0	85
TCGA-MX-A5UJ-10A-01D-A31J-08_STAD	77	55	60	33	96	83	70	86	97	0	39	60	0	0	0	100	81
TCGA-MX-A663-10A-01D-A31J-08_STAD	77	0	1	46	88	82	74	85	106	0	0	0	1	1	0	111	85

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-MX-A666-10A-01D-A31J-08_STAD	79	56	55	42	71	62	79	93	70	17	36	0	52	72	29	0	89
TCGA-MY-A5BD-10A-01D-A26G-09_CESC	46	51	42	20	57	61	76	60	94	1	2	1	2	2	45	5	67
TCGA-MY-A5BE-10A-01D-A26G-09_CESC	49	5	6	25	88	76	109	109	95	1	6	0	1	6	0	49	52
TCGA-MY-A5BF-10A-01D-A26G-09_CESC	56	97	91	4	65	73	88	77	12	19	118	96	59	94	0	5	79
TCGA-MZ-A6I9-10A-01D-A31J-08_HNSC	89	54	60	39	108	84	87	123	91	15	32	58	0	0	24	48	95
TCGA-NC-A5HD-10A-01D-A26K-08_LUSC	85	0	3	51	84	77	82	86	78	0	0	0	0	1	0	117	102
TCGA-NC-A5HE-10A-01D-A26K-08_LUSC	92	0	0	56	92	86	92	89	63	9	40	0	53	64	0	70	107
TCGA-NC-A5HF-10A-01D-A26K-08_LUSC	82	0	0	76	86	79	79	96	98	0	0	0	0	0	0	102	86
TCGA-NC-A5HG-10A-01D-A26K-08_LUSC	97	0	0	56	93	89	80	91	93	0	0	1	0	1	28	72	91
TCGA-NC-A5HH-10A-01D-A26K-08_LUSC	104	0	2	81	93	93	92	110	104	0	1	2	0	1	0	125	108
TCGA-NC-A5HI-10A-01D-A26K-08_LUSC	95	58	56	40	60	64	85	101	90	1	3	0	1	0	0	92	110
TCGA-NC-A5HJ-10A-01D-A26K-08_LUSC	88	0	1	75	98	81	78	74	87	0	1	0	1	3	47	0	99
TCGA-NC-A5HK-10A-01D-A26K-08_LUSC	85	0	2	75	99	86	110	111	110	15	0	0	0	1	0	80	120
TCGA-NC-A5HL-10A-01D-A26K-08_LUSC	103	64	59	42	67	76	78	80	93	0	1	0	0	0	42	2	104
TCGA-NC-A5HM-10A-01D-A26K-08_LUSC	98	2	2	60	93	97	93	96	99	2	1	1	2	2	32	55	104
TCGA-NC-A5HN-10A-01D-A26K-08_LUSC	84	51	59	34	99	76	81	86	91	0	35	61	1	0	31	60	97
TCGA-NC-A5HO-10A-01D-A26K-08_LUSC	109	0	0	70	90	84	75	90	110	0	0	0	0	2	32	52	100
TCGA-NC-A5HP-10A-01D-A26K-08_LUSC	88	1	1	60	80	80	80	76	72	0	1	0	2	2	0	89	98
TCGA-NC-A5HQ-10A-01D-A26K-08_LUSC	94	53	53	37	93	72	74	84	61	11	48	46	52	60	0	50	88
TCGA-NC-A5HR-10A-01D-A26K-08_LUSC	100	70	61	38	72	64	56	51	5	20	66	5	79	101	0	5	109
TCGA-NC-A5HT-10A-01D-A26K-08_LUSC	99	76	60	46	69	61	85	113	110	0	0	0	2	0	30	57	96
TCGA-NH-A50T-10A-01D-A28G-10_COAD	77	1	2	62	93	96	107	86	86	0	2	0	0	1	30	57	81
TCGA-NH-A50V-10A-01D-A28G-10_COAD	61	63	39	27	48	57	97	73	40	6	41	0	48	57	28	1	62
TCGA-NI-A4U2-10A-01D-A28X-10_LIHC	81	2	3	22	70	97	99	93	93	0	1	4	0	0	0	113	72
TCGA-NJ-A4YF-10A-01D-A25L-08_LUAD	94	0	4	81	101	95	96	101	79	0	2	0	2	9	0	69	104
TCGA-NJ-A4YG-10A-01D-A25L-08_LUAD	136	0	1	73	109	116	100	116	85	18	49	0	56	85	0	76	124
TCGA-NJ-A4YI-10A-01D-A25L-08_LUAD	100	2	11	80	93	94	83	90	76	12	48	1	71	82	0	73	109
TCGA-NJ-A4YP-10A-01D-A25L-08_LUAD	91	89	96	5	8	6	87	83	69	13	47	0	63	75	0	62	97
TCGA-NJ-A4YQ-10A-01D-A25L-08_LUAD	136	2	3	64	152	106	108	125	125	26	83	70	61	70	0	64	102
TCGA-NJ-A55A-10A-01D-A25L-08_LUAD	117	0	0	67	94	93	82	110	119	0	1	1	1	0	25	65	105
TCGA-NJ-A55O-10A-01D-A25L-08_LUAD	80	0	0	62	90	92	81	88	82	0	2	1	1	5	0	78	91
TCGA-NJ-A55R-10A-01D-A25L-08_LUAD	256	199	215	125	341	243	246	298	205	50	224	198	179	207	0	174	295
TCGA-NK-A5CR-10A-01D-A26K-08_LUSC	100	68	66	49	78	76	87	97	72	10	44	70	0	76	0	59	105
TCGA-NK-A5CT-10A-01D-A26K-08_LUSC	97	71	75	45	78	77	96	99	72	17	51	0	70	70	32	3	111
TCGA-NK-A5CX-10A-01D-A26K-08_LUSC	94	66	70	42	68	73	88	97	72	16	48	0	58	65	31	5	91
TCGA-NK-A5D1-10A-01D-A26K-08_LUSC	86	1	0	57	92	84	86	81	64	12	45	0	47	71	0	60	105
TCGA-O1-A52J-10A-01D-A25L-08_LUAD	91	2	7	51	87	80	77	111	102	0	1	3	0	1	26	60	94
TCGA-O2-A52N-10A-01D-A26K-08_LUSC	112	67	74	44	85	72	102	95	79	16	46	0	70	80	0	55	118
TCGA-O2-A52Q-10A-01D-A26K-08_LUSC	82	69	62	43	108	84	77	101	107	0	36	54	0	0	30	62	89
TCGA-O2-A52S-10A-01D-A25L-08_LUSC	96	62	65	40	78	65	94	99	77	15	43	3	63	80	37	2	97
TCGA-O2-A52V-10A-01D-A25L-08_LUSC	85	2	3	56	96	88	89	96	90	0	0	1	0	0	39	1	108
TCGA-O2-A52W-10A-01D-A26K-08_LUSC	90	51	61	27	61	65	83	71	76	0	2	3	1	8	37	0	86
TCGA-O2-A5IB-10A-01D-A27N-08_LUSC	117	0	0	51	91	78	78	93	99	0	0	0	0	0	28	57	92
TCGA-OD-A75X-10A-01D-A32N-08_SKCM	100	68	77	45	79	68	90	94	83	15	62	1	77	76	0	76	120
TCGA-OE-A75W-10A-01D-A32N-08_PAAD	81	0	0	51	83	84	68	91	82	0	0	0	1	0	25	57	89
TCGA-OK-A5Q2-10A-01D-A27P-09_BRCA	35	1	0	23	93	75	88	86	98	0	0	0	0	2	55	2	68
TCGA-OL-A5D6-10A-01D-A27P-09_BRCA	34	0	1	28	83	84	99	81	91	0	0	0	0	0	0	74	76
TCGA-OL-A5D7-10A-01D-A27P-09_BRCA	33	59	33	12	84	67	75	69	89	0	34	43	0	0	39	0	62
TCGA-OL-A5D8-10A-01D-A27P-09_BRCA	48	4	2	32	84	78	94	97	111	1	3	1	1	0	33	43	64
TCGA-OL-A5DA-10A-01D-A27P-09_BRCA	44	89	75	0	76	87	82	75	67	11	82	95	0	57	0	42	63
TCGA-OL-A5RU-10A-01D-A28E-09_BRCA	58	0	60	18	110	91	89	108	121	0	45	0	57	0	44	48	78
TCGA-OL-A5RV-10A-01D-A28E-09_BRCA	53	0	94	0	67	67	90	86	93	0	39	1	58	0	55	3	72
TCGA-OL-A5RW-10A-01D-A28E-09_BRCA	39	0	1	35	93	75	84	82	89	0	1	0	0	0	24	0	41
TCGA-OL-A5RX-10A-01D-A28E-09_BRCA	52	91	75	1	86	86	79	77	98	0	64	53	52	1	26	42	74
TCGA-OL-A5RY-10A-01D-A28E-09_BRCA	49	58	52	19	56	53	59	48	70	0	36	0	54	59	0	46	71
TCGA-OL-A5RZ-10A-01D-A28E-09_BRCA	40	3	1	30	100	77	98	77	109	0	0	0	0	0	54	0	76
TCGA-OL-A5S0-10A-01D-A28E-09_BRCA	56	101	85	0	0	0	95	73	124	0	0	0	0	0	58	0	72
TCGA-OL-A66H-10A-01D-A29N-09_BRCA	34	61	51	15	101	85	82	80	104	0	40	0	50	0	0	71	67
TCGA-OL-A66I-10A-01D-A29N-09_BRCA	47	56	58	14	101	87	98	71	102	0	38	61	1	0	0	97	67
TCGA-OL-A66J-10A-01D-A29N-09_BRCA	71	80	61	23	82	77	111	127	110	0	1	0	0	0	0	88	81
TCGA-OL-A66K-10A-01D-A29N-09_BRCA	52	62	1	15	113	99	92	91	2	22	71	0	87	91	0	0	103
TCGA-OL-A66L-10A-01D-A31U-09_BRCA	32	0	1	30	79	105	93	75	127	0	0	0	0	0	0	71	76
TCGA-OL-A66N-10A-01D-A31U-09_BRCA	36	73	55	16	57	60	97	82	68	13	54	61	0	64	0	55	81
TCGA-OL-A66O-10A-01D-A31U-09_BRCA	37	60	46	13	58	126	102	89	138	0	1	0	1	0	26	53	90
TCGA-OL-A66P-10A-01D-A31U-09_BRCA	29	56	0	23	84	87	100	94	130	12	61	78	0	0	40	47	69
TCGA-OR-A5J1-10A-01D-A29L-10_ACC	81	0	0	59	92	116	111	89	49	10	33	0	59	68	35	0	81
TCGA-OR-A5J2-10A-01D-A29L-10_ACC	71	0	1	53	94	98	95	85	70	0	0	0	3	0	32	65	80
TCGA-OR-A5J3-10A-01D-A29L-10_ACC	95	53	58	26	91	92	98	75	91	0	35	71	0	0	0	93	79
TCGA-OR-A5J4-10A-01D-A29L-10_ACC	71	1	1	61	74	93	90	84	81	0	1	2	0	0	0	88	61
TCGA-OR-A5J7-10A-01D-A29L-10_ACC	77	65	53	31	107	90	98	80	53	8	68	59	63	64	26	0	80
TCGA-OR-A5J8-10A-01D-A29L-10_ACC	76	62	53	20	84	96	91	68	42	2	47	78	0	61	0	32	65
TCGA-OR-A5J9-10A-01D-A29L-10_ACC	79	0	0	53	130	118	125	113	110	4	36	59	0	0	31	77	76
TCGA-OR-A5JA-10A-01D-A29L-10_ACC	70	0	3	53	65	93	92	77	85	0	1	4	1	3	0	78	69
TCGA-OR-A5JB-10A-01D-A29L-10_ACC	56	54	58	24	94	81	81	56	1	8	80	46	67	87	0	0	59
TCGA-OR-A5JD-10B-01D-A29L-10_ACC	72	62	53	21	62	67	91	97	94	0	0	0	0	0	0	100	69
TCGA-OR-A5JE-10A-01D-A29L-10_ACC	60	53	58	24	83	94	80	87	83	0	33	56	0	0	28	45	77
TCGA-OR-A5JF-10A-01D-A29L-10_ACC	75	2	0	49	91	94	89	69	44	5	30	0	51	54	21	0	77
TCGA-OR-A5JG-10A-01D-A29L-10_ACC	84	56	53	34	62	75	91	77	85	0	2	0	6	0	0	47	76
TCGA-OR-A5JH-10A-01D-A30A-10_ACC	64	53	42	23	43	55	54	47	0	7	50	0	67	86	0	0	65
TCGA-OR-A5JI-10A-01D-A29L-10_ACC	65	60	48	34	87	97	103	103	54	4	66	89	0	70	0	42	76
TCGA-OR-A5JJ-10A-01D-A29L-10_ACC	73	0	1	61	76	87	91	87	59	6	33	1	44	74	0	46	68
TCGA-OR-A5JK-10A-01D-A29L-10_ACC	78	3	2	55	75	84	101	77	93	0	0	0	1	0	27	64	79
TCGA-OR-A5JL-10A-01D-A29L-10_ACC	73	56	55	27	46	59	95	69	47	4	28	0	58	58	0	55	75
TCGA-OR-A5JM-10B-01D-A29L-10_ACC	95	57	51	31	51	69	88	76	55	6	43	0	47	67	0	62	67
TCGA-OR-A5JO-10A-01D-A29L-10_ACC	74	1	0	44	80	86	93	72	76	0	0	0	0	1	0	86	65
TCGA-OR-A5JP-10A-01D-A29L-10_ACC	68	0	1	39	76	97	92	66	66	2	1	1	3	1	29	61	67
TCGA-OR-A5JQ-10A-01D-A29L-10_ACC	78	60	50	26	104	88	74	63	38	4	61	53	59	67	0	39	65
TCGA-OR-A5JR-10A-01D-A29L-10_ACC	68	53	0	23	74	89	77	80	56	7	25	0	40	51	19	1	51
TCGA-OR-A5JS-10A-01D-A29L-10_ACC	64	67	45	22	48	65	96	74	84	0	0	0	1	3	0	90	62
TCGA-OR-A5JT-10A-01D-A29L-10_ACC	75	41	49	25	31	56	76	76	40	0	25	1	40	53	0	47	68
TCGA-OR-A5JU-10A-01D-A30A-10_ACC	90	42	40	30	42	65	82	83	83	0	0	0	3	1	25	48	70
TCGA-OR-A5JV-10A-01D-A29L-10_ACC	59	35	44	27	60	77	86	80	36	7	34	55	1	51	0	34	59
TCGA-OR-A5JW-10A-01D-A29L-10_ACC	71	51	50	30	87	91	95	94	85	0	25	38	0	1	0	100	75
TCGA-OR-A5JX-10B-01D-A29L-10_ACC	87	57	62	31	89	114	107	87	60	10	62	56	64	70	27	1	81
TCGA-OR-A5JY-10A-01D-A29L-10_ACC	100	66	57	35	64	75	73	46	63	0	36	1	59	69	0	72	77
TCGA-OR-A5JZ-10A-01D-A29L-10_ACC	63	83	87	1	46	48	89	69	69	0	28	37	0	2	41	2	55

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-OR-A5K0-10B-01D-A29L-10_ACC	88	0	2	38	77	108	89	73	85	0	0	0	0	0	27	59	85
TCGA-OR-A5K1-10A-01D-A29L-10_ACC	77	57	55	24	39	65	84	67	53	9	35	0	44	55	0	54	63
TCGA-OR-A5K2-10B-01D-A29L-10_ACC	69	0	0	42	77	92	95	68	87	1	2	0	2	1	0	92	67
TCGA-OR-A5K3-10A-01D-A29L-10_ACC	72	0	1	40	96	92	92	64	1	6	61	0	83	88	0	4	71
TCGA-OR-A5K4-10A-01D-A29L-10_ACC	93	1	1	45	83	118	103	112	95	0	0	0	0	0	0	112	79
TCGA-OR-A5K5-10A-01D-A29L-10_ACC	76	65	54	30	34	62	98	93	96	0	0	0	0	0	0	112	65
TCGA-OR-A5K6-10A-01D-A29L-10_ACC	89	62	58	27	51	70	116	85	92	0	0	0	0	4	45	0	87
TCGA-OR-A5K8-10A-01D-A29L-10_ACC	68	1	0	41	76	98	97	77	47	5	30	0	47	63	21	0	67
TCGA-OR-A5KP-10A-01D-A30A-10_ACC	59	40	45	26	29	53	74	65	76	0	1	0	0	0	24	47	62
TCGA-OR-A5KQ-10A-01D-A30A-10_ACC	68	2	0	38	72	74	81	63	70	0	0	0	3	1	0	80	62
TCGA-OR-A5KS-10A-01D-A30A-10_ACC	71	48	46	39	39	61	82	85	47	7	37	0	46	57	0	54	68
TCGA-OR-A5KT-10A-01D-A29L-10_ACC	80	93	85	1	0	2	91	92	93	0	0	0	0	0	0	95	76
TCGA-OR-A5KU-10A-01D-A29L-10_ACC	67	0	1	43	73	94	84	81	88	0	0	0	0	0	0	93	68
TCGA-OR-A5KV-10A-01D-A29L-10_ACC	84	65	4	29	106	100	105	88	54	9	33	0	58	64	0	58	78
TCGA-OR-A5KW-10A-01D-A29L-10_ACC	77	61	38	30	47	51	91	77	82	0	0	0	1	1	19	42	63
TCGA-OR-A5KX-10A-01D-A29L-10_ACC	79	0	0	44	87	95	108	74	86	1	0	0	1	3	0	92	72
TCGA-OR-A5KY-10A-01D-A29L-10_ACC	88	0	0	39	89	87	106	80	44	6	34	0	51	65	0	48	69
TCGA-OR-A5KZ-10A-01D-A29L-10_ACC	84	0	0	64	69	87	98	82	91	0	0	0	0	0	24	41	60
TCGA-OR-A5L1-10A-01D-A30A-10_ACC	68	0	1	41	71	84	70	79	78	0	0	0	0	0	0	98	69
TCGA-OR-A5L2-10A-01D-A30A-10_ACC	71	0	0	45	68	99	90	73	56	5	24	0	38	56	20	1	62
TCGA-OR-A5L3-10A-01D-A29L-10_ACC	55	0	1	42	69	72	66	56	68	0	0	0	0	0	0	54	56
TCGA-OR-A5L4-10A-01D-A29L-10_ACC	73	68	47	35	39	73	106	68	81	0	1	0	0	3	23	61	70
TCGA-OR-A5L6-10C-01D-A29L-10_ACC	89	57	57	29	41	69	97	81	88	0	0	0	1	2	21	39	72
TCGA-OR-A5L8-10A-01D-A29L-10_ACC	82	59	60	25	49	70	109	71	58	3	30	0	54	59	0	42	76
TCGA-OR-A5L9-10B-01D-A29L-10_ACC	84	0	0	61	73	99	91	84	80	0	0	0	0	0	0	101	80
TCGA-OR-A5LA-10A-01D-A29L-10_ACC	79	0	0	45	76	73	79	74	72	0	0	0	0	0	20	42	60
TCGA-OR-A5LB-10A-01D-A29L-10_ACC	71	52	58	26	52	67	101	79	67	0	0	0	0	0	0	88	63
TCGA-OR-A5LC-10A-01D-A29L-10_ACC	71	60	41	27	44	59	93	68	86	0	0	0	0	0	24	58	60
TCGA-OR-A5LD-10A-01D-A29L-10_ACC	77	64	49	33	88	97	89	85	44	11	52	92	0	65	25	1	80
TCGA-OR-A5LE-10A-01D-A29L-10_ACC	78	56	52	24	100	102	90	70	50	7	56	83	0	61	0	51	74
TCGA-OR-A5LF-10A-01D-A30A-10_ACC	71	71	70	1	71	90	91	85	80	0	58	86	0	1	0	99	67
TCGA-OR-A5LG-10A-01D-A29L-10_ACC	75	1	2	45	82	94	78	61	69	0	2	0	0	1	0	83	70
TCGA-OR-A5LH-10A-01D-A29L-10_ACC	75	47	46	23	51	58	83	92	50	7	40	0	44	66	0	55	74
TCGA-OR-A5LI-10A-01D-A30A-10_ACC	62	45	37	33	69	85	86	80	40	6	54	75	2	50	20	2	60
TCGA-OR-A5LJ-10A-01D-A29L-10_ACC	78	83	75	2	44	79	90	86	62	2	80	63	51	54	31	1	75
TCGA-OR-A5LK-10A-01D-A29L-10_ACC	71	1	0	44	75	89	89	81	75	0	1	0	0	2	0	105	73
TCGA-OR-A5LL-10A-01D-A29L-10_ACC	75	38	44	27	72	77	64	75	77	0	23	37	0	0	0	83	64
TCGA-OR-A5LN-10A-01D-A29L-10_ACC	84	62	53	26	77	87	82	83	92	0	29	66	1	0	32	44	76
TCGA-OR-A5LO-10A-01D-A29L-10_ACC	65	65	44	30	75	90	73	67	40	9	44	44	32	52	0	40	61
TCGA-OR-A5LP-10A-01D-A29L-10_ACC	79	90	87	0	44	56	84	87	108	0	35	58	0	0	30	61	66
TCGA-OR-A5LR-10A-01D-A29L-10_ACC	74	86	83	0	37	77	93	73	98	0	42	57	0	0	30	47	73
TCGA-OR-A5LS-10A-01D-A29L-10_ACC	83	0	1	48	74	103	87	70	51	9	29	0	57	62	25	2	65
TCGA-OR-A5LT-10A-01D-A29L-10_ACC	80	0	2	46	88	109	116	114	92	0	0	0	2	3	0	126	83
TCGA-OU-A5PI-10A-01D-A29L-10_ACC	84	54	52	25	88	110	121	124	69	7	26	60	0	2	25	40	72
TCGA-OX-A56R-10A-01D-A33W-08_GBM	83	0	0	50	77	83	69	83	51	12	40	0	49	61	0	59	86
TCGA-P5-A5ET-10A-01D-A27N-08_LGG	92	78	109	59	76	75	119	131	84	26	80	0	105	83	0	71	121
TCGA-P5-A5EU-10A-01D-A27N-08_LGG	117	93	114	0	1	0	102	122	74	19	51	0	69	82	0	63	110
TCGA-P5-A5EV-10A-01D-A27N-08_LGG	112	75	75	47	152	106	92	107	79	13	80	70	62	92	0	67	119
TCGA-P5-A5EW-10A-01D-A27N-08_LGG	137	76	82	52	146	106	115	123	120	0	49	76	0	0	36	63	129
TCGA-P5-A5EX-10A-01D-A289-08_LGG	80	0	0	78	89	72	75	69	74	0	0	0	0	0	0	75	87
TCGA-P5-A5EY-10A-01D-A27N-08_LGG	126	76	69	48	87	88	106	111	119	0	0	0	0	1	39	76	142
TCGA-P5-A5EZ-10A-01D-A27N-08_LGG	138	67	77	95	120	76	116	115	130	0	0	0	0	0	0	104	131
TCGA-P5-A5F0-10A-01D-A289-08_LGG	84	59	67	44	106	84	86	109	96	14	37	63	0	0	30	55	88
TCGA-P5-A5F1-10A-01D-A289-08_LGG	89	63	67	48	113	88	86	122	67	23	66	86	0	77	26	0	101
TCGA-P5-A5F2-10A-01D-A289-08_LGG	84	0	1	85	90	91	80	98	69	18	42	62	0	75	0	65	98
TCGA-P5-A5F4-10A-01D-A289-08_LGG	78	79	85	0	0	0	76	78	64	18	47	0	62	65	0	58	92
TCGA-P5-A5F6-10A-01D-A289-08_LGG	85	0	1	81	95	79	74	68	81	0	0	0	0	0	0	72	97
TCGA-P5-A72U-10A-01D-A329-08_LGG	84	50	51	33	52	55	71	71	56	12	24	1	51	62	0	46	85
TCGA-P5-A72W-10A-01D-A329-08_LGG	105	0	1	59	117	98	93	93	120	0	0	0	0	4	0	76	128
TCGA-P5-A72X-10A-01D-A329-08_LGG	86	53	58	39	109	74	78	97	76	0	28	58	0	1	0	69	87
TCGA-P5-A72Z-10A-01D-A329-08_LGG	83	0	2	73	81	81	70	68	0	20	55	59	58	78	0	0	86
TCGA-P5-A730-10A-01D-A329-08_LGG	77	1	0	66	79	77	75	85	81	0	0	0	0	0	0	100	94
TCGA-P5-A731-10A-01D-A329-08_LGG	85	50	51	35	65	71	76	91	67	18	33	57	0	62	20	0	85
TCGA-P5-A733-10A-01D-A329-08_LGG	82	49	56	65	69	61	85	78	85	0	0	0	0	0	0	59	87
TCGA-P5-A735-10A-01D-A329-08_LGG	88	0	1	51	81	76	65	65	0	21	60	0	73	91	0	0	99
TCGA-P5-A736-10A-01D-A329-08_LGG	87	75	76	0	82	76	74	84	65	13	76	78	54	65	0	0	92
TCGA-P5-A737-10A-01D-A329-08_LGG	78	0	0	47	83	77	76	70	72	0	0	0	0	1	0	69	89
TCGA-P5-A77W-10A-01D-A329-08_LGG	89	0	1	85	92	92	88	90	112	0	0	0	0	0	0	79	92
TCGA-P5-A77X-10A-01D-A329-08_LGG	79	0	0	61	78	70	71	64	63	11	27	62	0	61	0	54	85
TCGA-P5-A780-10A-01D-A329-08_LGG	82	54	56	37	104	81	76	61	66	13	61	68	51	71	0	50	84
TCGA-P5-A781-10A-01D-A329-08_LGG	81	52	51	31	55	56	77	68	81	0	0	0	0	0	0	73	90
TCGA-P6-A5OF-10A-01D-A29L-10_ACC	88	1	1	49	80	117	130	96	55	3	32	2	55	67	25	1	74
TCGA-P6-A5OG-10A-01D-A29L-10_ACC	66	49	52	27	83	98	100	65	52	3	56	67	49	58	0	61	75
TCGA-PA-A5YG-10A-01D-A29L-10_ACC	72	52	41	24	47	53	90	78	41	10	35	0	53	62	0	55	77
TCGA-PC-A5DK-10A-01D-A27P-09_SARC	65	82	70	19	119	114	105	125	79	12	90	110	1	72	49	3	89
TCGA-PC-A5DL-10A-01D-A26G-09_SARC	35	4	2	25	74	71	76	84	88	0	2	0	1	3	25	37	68
TCGA-PC-A5DM-10A-01D-A27P-09_SARC	60	0	1	35	94	107	112	122	136	0	1	0	2	0	38	65	79
TCGA-PC-A5DN-10A-01D-A27P-09_SARC	82	0	1	41	115	116	115	119	140	0	0	0	3	2	0	128	96
TCGA-PC-A5DO-10A-01D-A26G-09_SARC	37	5	6	29	70	68	79	74	91	0	0	0	3	2	27	33	64
TCGA-PC-A5DP-10A-01D-A26G-09_SARC	36	5	2	29	80	85	81	73	94	0	2	0	4	1	0	83	71
TCGA-PD-A5DF-10A-01D-A27I-10_LIHC	74	0	3	44	63	77	77	60	43	6	25	0	44	52	19	3	66
TCGA-PE-A5DC-10A-01D-A27P-09_BRCA	40	0	2	31	86	83	82	88	89	0	1	0	0	0	0	81	60
TCGA-PE-A5DD-10A-01D-A27P-09_BRCA	49	67	64	21	120	89	97	100	100	0	42	57	0	0	0	112	66
TCGA-PE-A5DE-10A-01D-A27P-09_BRCA	55	85	80	1	59	64	91	86	61	10	78	51	62	54	29	0	77
TCGA-PG-A5BC-10A-01D-A27P-09_UCEC	62	0	1	22	86	126	84	118	75	13	69	0	66	66	34	2	74
TCGA-PG-A6IB-10A-01D-A31U-09_UCEC	28	51	49	13	53	41	80	76	112	0	0	0	0	1	30	42	84
TCGA-PJ-A5Z8-10A-01D-A28G-10_KIRP	86	52	57	27	50	62	125	119	61	8	45	0	45	65	0	68	81
TCGA-PJ-A5Z9-10A-01D-A28G-10_KIRP	83	1	0	47	87	105	107	82	116	0	2	0	2	1	0	94	69
TCGA-PK-A5H8-10A-01D-A29L-10_ACC	89	78	53	36	49	68	105	79	100	0	0	0	1	1	42	0	75
TCGA-PK-A5H9-10A-01D-A29L-10_ACC	76	0	2	54	65	89	101	83	53	4	29	1	46	60	0	36	61
TCGA-PK-A5HA-10A-01D-A29L-10_ACC	79	0	0	46	101	104	97	86	54	3	38	0	40	57	0	53	76
TCGA-PQ-A6FI-10A-01D-A31J-08_BLCA	98	0	0	93	106	90	95	113	108	0	0	0	0	0	0	115	115
TCGA-PQ-A6FN-10A-01D-A31J-08_BLCA	130	72	66	48	84	70	95	91	74	19	36	79	0	81	30	0	116
TCGA-PZ-A5RE-10B-01D-A32N-08_PAAD	74	0	0	50	74	69	69	75	63	0	0	0	0	0	0	88	79
TCGA-Q1-A5R1-10A-01D-A28E-09_CESC	40	0	0	31	82	89	96	79	58	10	35	56	0	50	0	45	68
TCGA-Q1-A5R2-10A-01D-A28E-09_CESC	56	80	68	16	68	62	123	102	93	18	57	0	60	70	43	0	110

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-Q1-A5R3-10B-01D-A28E-09_CESC	39	0	0	19	88	87	104	71	109	0	0	0	0	0	0	79	79
TCGA-Q2-A5QZ-10A-01D-A28G-10_KIRP	39	23	31	14	53	51	45	38	50	0	9	24	0	0	9	18	30
TCGA-Q3-A5QY-10A-01D-A32N-08_PAAD	88	0	0	69	83	78	70	90	54	19	38	0	54	68	29	0	84
TCGA-QB-A6FS-10A-01D-A30X-08_SKCM	79	0	1	56	85	84	80	83	76	0	0	0	0	0	0	87	87
TCGA-QF-A5YS-10A-01D-A31U-09_UCEC	41	0	0	27	116	94	120	112	130	0	0	0	0	0	35	51	89
TCGA-QF-A5YT-10A-01D-A31U-09_UCEC	35	0	0	23	80	79	86	67	90	0	0	0	0	0	47	0	76
TCGA-QG-A5YV-10A-01D-A28G-10_COAD	78	59	52	21	91	87	79	51	84	0	39	64	0	1	37	0	40
TCGA-QG-A5YW-10A-01D-A28G-10_COAD	58	0	0	31	77	84	97	71	68	0	0	0	0	0	35	0	66
TCGA-QG-A5YX-10A-01D-A28G-10_COAD	78	1	1	52	107	123	93	81	89	0	38	56	2	2	35	0	77
TCGA-QG-A5Z1-10A-01D-A28G-10_COAD	70	63	83	0	72	79	75	64	33	2	84	46	83	52	12	0	67
TCGA-QG-A5Z2-10A-01D-A28G-10_COAD	63	2	0	51	86	91	85	57	78	0	0	0	0	0	36	0	76
TCGA-QH-A65R-10A-01D-A31J-08_LGG	90	61	64	39	68	71	84	92	93	0	0	0	0	0	0	121	92
TCGA-QH-A65S-10A-01D-A29Q-08_LGG	139	121	118	0	121	120	121	109	150	0	88	133	0	0	0	141	148
TCGA-QH-A65V-10A-01D-A29Q-08_LGG	129	0	0	67	117	104	103	99	72	15	37	66	0	77	0	60	133
TCGA-QH-A65X-10D-01D-A329-08_LGG	80	1	0	52	87	92	91	65	90	0	0	0	0	0	0	69	110
TCGA-QH-A65Z-10A-01D-A29Q-08_LGG	143	0	0	49	128	131	113	122	82	15	54	0	76	97	0	63	161
TCGA-QH-A6CS-10A-01D-A31J-08_LGG	84	0	1	73	94	79	79	77	101	0	0	0	0	0	0	78	84
TCGA-QH-A6CU-10A-01D-A31J-08_LGG	86	72	68	43	107	77	83	109	99	0	39	72	0	2	0	122	79
TCGA-QH-A6CV-10A-01D-A31J-08_LGG	86	1	1	48	86	118	77	97	64	15	40	65	0	65	31	0	90
TCGA-QH-A6CW-10B-01D-A329-08_LGG	109	64	74	47	84	76	105	82	110	0	0	1	0	1	0	76	124
TCGA-QH-A6CX-10A-01D-A329-08_LGG	88	60	61	35	129	105	88	76	75	20	58	74	54	74	0	41	125
TCGA-QH-A6CY-10A-01D-A329-08_LGG	103	1	0	74	91	99	94	80	77	16	43	0	57	76	0	50	118
TCGA-QH-A6CZ-10B-01D-A329-08_LGG	91	61	68	46	124	91	85	77	0	18	75	91	48	96	0	0	98
TCGA-QH-A6X3-10B-01D-A329-08_LGG	76	76	67	36	114	78	85	68	70	18	62	76	0	64	0	63	89
TCGA-QH-A6X4-10B-01D-A329-08_LGG	92	48	50	34	102	82	75	71	98	0	26	58	0	1	0	71	103
TCGA-QH-A6X5-10B-01D-A329-08_LGG	70	0	1	69	75	71	79	85	95	0	1	0	0	0	0	63	94
TCGA-QH-A6X8-10B-01D-A329-08_LGG	80	53	54	40	59	52	79	67	70	0	0	0	0	0	0	71	99
TCGA-QH-A6X9-10B-01D-A329-08_LGG	108	56	63	40	60	63	86	77	100	0	0	0	0	1	12	44	103
TCGA-QH-A6XA-10B-01D-A329-08_LGG	107	49	53	33	104	83	70	74	88	0	23	63	0	0	16	38	105
TCGA-QH-A6XC-10B-01D-A329-08_LGG	106	1	2	62	105	98	83	103	104	0	0	0	0	0	0	82	136
TCGA-QK-A64Z-10A-01D-A30H-08_HNSC	175	159	151	0	106	107	148	135	134	22	96	112	90	118	0	93	198
TCGA-QK-A652-10A-01D-A30H-08_HNSC	143	90	87	67	183	144	154	129	81	24	111	151	0	107	0	91	176
TCGA-QK-A6IF-10A-01D-A31J-08_HNSC	134	73	65	40	68	69	78	131	101	0	0	0	0	0	25	58	97
TCGA-QK-A6IG-10A-01D-A31J-08_HNSC	78	61	63	41	102	110	77	92	82	0	47	65	0	0	0	109	96
TCGA-QK-A6IH-10A-01D-A31J-08_HNSC	81	59	58	34	60	59	73	99	104	0	0	0	0	0	0	107	95
TCGA-QK-A6II-10A-01D-A31J-08_HNSC	87	61	57	42	67	66	86	97	67	13	37	1	56	67	25	0	94
TCGA-QK-A6IJ-10A-01D-A31J-08_HNSC	107	61	55	42	111	70	59	59	0	17	69	74	64	91	0	2	89
TCGA-QS-A5YQ-10A-01D-A31U-09_UCEC	34	0	41	12	105	78	81	64	103	0	34	0	43	0	47	0	89
TCGA-QS-A5YR-10A-01D-A31U-09_UCEC	40	0	0	28	98	82	97	80	128	0	0	0	0	1	33	0	52
TCGA-QU-A6IL-10A-01D-A31J-08_PRAD	85	61	62	45	67	61	57	57	65	0	36	59	0	66	28	0	83
TCGA-QU-A6IM-10A-01D-A31J-08_PRAD	77	0	0	77	87	82	53	89	80	0	0	0	0	0	22	47	92
TCGA-QU-A6IN-10A-01D-A31J-08_PRAD	86	0	1	57	79	83	81	78	0	20	69	0	77	93	0	0	96
TCGA-QU-A6IO-10A-01D-A31J-08_PRAD	81	0	0	50	111	78	73	111	93	0	0	0	0	0	24	59	88
TCGA-QU-A6IP-10A-01D-A31J-08_PRAD	79	0	1	52	91	85	85	96	75	0	0	0	0	0	0	121	106
TCGA-R3-A69X-10A-01D-A30H-08_BLCA	151	1	0	96	155	151	145	143	94	16	77	0	78	102	0	87	176
TCGA-R5-A7O7-10A-01D-A33W-08_STAD	95	0	0	53	83	86	74	78	59	19	50	0	57	75	0	64	106
TCGA-R8-A6MK-10A-01D-A329-08_LGG	98	50	65	42	80	73	100	86	126	0	0	1	0	2	0	104	124
TCGA-R8-A6ML-10A-01D-A329-08_LGG	80	0	1	51	83	71	79	76	76	0	0	0	0	0	18	47	82
TCGA-R8-A6YH-10B-01D-A329-08_LGG	76	0	0	70	102	78	67	76	60	10	32	0	52	59	24	0	95
TCGA-R8-A73M-10C-01D-A329-08_LGG	101	72	73	0	0	0	74	79	53	10	38	0	49	55	0	42	92
TCGA-RB-A7B8-10A-01D-A33W-08_PAAD	71	75	71	0	59	49	68	79	52	11	61	69	0	52	0	46	81
TCGA-RD-A7BS-10A-01D-A32N-08_STAD	105	2	0	66	101	97	100	108	117	0	0	0	0	0	37	77	112
TCGA-RD-A7BT-10A-01D-A33W-08_STAD	87	57	60	36	51	58	77	78	69	12	39	0	55	54	0	47	94
TCGA-RD-A7BW-10A-01D-A32N-08_STAD	104	0	1	92	94	110	87	122	102	0	0	0	0	0	31	74	119
TCGA-RD-A7C1-10A-01D-A32N-08_STAD	97	89	99	1	127	121	112	102	0	29	121	119	85	109	0	0	136
TCGA-RN-A68Q-10A-01D-A307-09_SARC	59	73	71	20	81	64	109	74	119	0	0	0	0	0	55	0	92
TCGA-RP-A690-10A-01D-A30X-08_SKCM	81	0	0	79	77	82	80	78	101	0	0	0	0	0	0	75	92
TCGA-RP-A693-10A-01D-A30X-08_SKCM	86	0	1	81	92	88	82	76	104	0	0	0	0	0	0	82	94
TCGA-RP-A694-10A-01D-A30X-08_SKCM	90	0	1	78	98	98	90	86	110	0	0	0	0	1	32	60	100
TCGA-RP-A695-10A-01D-A30X-08_SKCM	77	77	94	0	65	62	73	84	102	0	28	49	0	0	0	78	82
TCGA-RQ-A68N-10A-01D-A31X-10_DLBC	49	0	0	33	52	52	60	47	58	0	0	0	0	0	0	32	46
TCGA-RQ-A6JB-10A-01D-A31X-10_DLBC	45	32	34	20	33	19	62	42	46	0	0	0	0	0	0	35	48
TCGA-RR-A6KA-10A-01D-A33W-08_GBM	78	52	52	35	79	66	72	78	92	0	35	51	0	0	25	53	85
TCGA-RR-A6KB-10A-01D-A33W-08_GBM	75	70	68	0	60	55	58	53	65	0	67	57	52	65	24	0	80
TCGA-RR-A6KC-10A-01D-A33W-08_GBM	98	0	0	53	111	77	77	98	71	18	65	52	47	59	24	0	84
TCGA-S5-A6DX-10A-01D-A31J-08_BLCA	137	68	65	51	85	72	92	127	125	0	0	0	0	0	33	62	120
TCGA-S9-A6TU-10A-01D-A329-08_LGG	79	51	56	46	70	65	77	89	86	0	0	0	0	0	19	49	89
TCGA-S9-A6TW-10A-01D-A329-08_LGG	83	0	0	71	79	73	77	63	0	27	47	0	65	75	0	0	86
TCGA-S9-A6TX-10A-01D-A329-08_LGG	78	48	51	32	87	69	70	73	95	0	31	52	0	0	19	43	77
TCGA-S9-A6TY-10A-01D-A329-08_LGG	81	0	0	61	77	87	78	68	64	18	32	0	50	60	0	53	93
TCGA-S9-A6TZ-10A-01D-A329-08_LGG	73	1	1	69	83	71	72	63	56	14	25	0	47	58	17	0	83
TCGA-S9-A6U0-10A-01D-A329-08_LGG	82	0	1	52	77	83	79	101	103	0	0	0	0	0	25	55	87
TCGA-S9-A6U9-10A-01D-A329-08_LGG	79	0	1	69	91	80	80	92	84	0	0	1	0	0	28	62	96
TCGA-SL-A6J9-10A-01D-A31U-09_UCEC	35	0	0	19	85	81	96	93	127	0	0	0	0	0	38	46	74
TCGA-SL-A6JA-10A-01D-A31U-09_UCEC	36	0	0	33	100	99	101	99	113	0	0	0	0	0	39	48	81
TCGA-SU-A7E7-10A-01D-A33W-08_PRAD	93	0	0	52	83	79	84	70	83	0	0	0	0	0	36	0	101
TCGA-TM-A7C3-10A-01D-A329-08_LGG	89	0	0	67	90	80	85	89	82	0	0	0	0	2	0	105	97
TCGA-TM-A7C4-10A-01D-A329-08_LGG	84	45	55	31	59	57	72	64	83	0	0	0	0	0	23	42	84
TCGA-TM-A7C5-10A-01D-A329-08_LGG	102	0	0	76	117	105	80	106	99	0	0	0	0	1	22	39	131
TCGA-TM-A7CF-10A-01D-A329-08_LGG	79	0	0	47	81	72	75	76	80	0	0	0	0	0	27	46	81
TCGA-UY-A78K-10A-01D-A339-08_BLCA	85	0	0	68	90	81	88	90	107	0	0	0	0	0	0	117	98
TCGA-UY-A78L-10A-01D-A339-08_BLCA	89	0	2	61	93	91	85	75	74	0	0	0	0	0	0	73	111
TCGA-UY-A78N-10A-01D-A339-08_BLCA	78	0	0	52	84	70	71	65	57	8	33	0	36	60	0	29	125
TCGA-UY-A78O-10A-01D-A339-08_BLCA	76	77	80	0	82	83	86	105	92	15	63	76	0	1	23	58	82

Table A2 Normalized counts of reads containing high frequency KIR-specific motifs for 2535 OKG and 5512 TCGA samples

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG00096.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.53	-2.47	-2.48	0.00	0.00	0.00	-2.48	-2.44	-2.38	0.00	0.00	0.00	0.00	0.00	-2.87	-2.68	-2.61
HG00097.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.23	0.00	-4.04	-2.62	-2.47	-2.37	-2.30	-2.42	-2.38	0.00	0.00	0.00	0.00	0.00	-2.64	0.00	-2.23
HG00099.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.34	0.00	-3.92	-2.64	-2.46	-2.39	-2.39	-2.54	-2.69	-3.18	-3.22	0.00	-2.66	-2.55	0.00	-2.78	-2.33
HG00100.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.54	0.00	0.00	-2.86	-2.58	-2.56	-2.65	-2.77	-2.82	-3.45	-2.99	0.00	-2.93	-2.77	0.00	-3.01	-2.60
HG00101.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.60	0.00	0.00	-2.67	-2.51	-2.49	-2.48	-2.37	-2.37	0.00	0.00	0.00	0.00	0.00	-2.88	-2.65	-2.60
HG00102.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.68	0.00	0.00	-2.64	-2.52	-2.55	-2.50	-2.51	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.66
HG00103.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.58	0.00	0.00	-2.67	-2.52	-2.57	-2.51	-2.61	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.64
HG00105.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.31	-2.72	0.00	-2.88	-2.45	-2.36	-2.29	-2.61	-2.62	-3.18	-3.31	0.00	-2.67	-2.69	0.00	-2.58	-2.35
HG00106.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.25	0.00	0.00	-2.62	-2.56	-2.35	-2.36	-2.55	-2.23	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.27
HG00107.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.70	-2.70	-2.66	-3.06	-2.66	-2.69	-2.54	-2.48	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.44	-2.69
HG00108.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.96	-2.90	-2.94	-3.15	-2.71	-2.86	-2.83	-2.92	-3.10	-3.36	-2.87	-2.99	-3.03	-2.98	0.00	-3.01	-2.86
HG00109.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.79	-2.80	-2.85	-2.99	-2.80	-2.88	-2.67	-2.84	-2.71	0.00	0.00	0.00	0.00	0.00	-3.12	-2.87	-2.75
HG00110.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.95	-2.88	-2.89	-3.22	-2.66	-2.80	-2.82	-2.87	-3.04	-3.28	-2.92	-2.98	-2.98	-2.92	0.00	-3.02	-2.88
HG00111.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.73	-2.73	-2.72	-3.05	-2.75	-2.86	-2.67	-2.69	-2.71	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.68
HG00112.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.35	0.00	0.00	-2.66	-2.59	-2.47	-2.29	-2.46	0.00	-2.98	-2.79	0.00	-2.49	-2.41	0.00	0.00	-2.26
HG00113.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.82	0.00	-4.68	-2.80	-2.72	-2.65	-2.69	-2.80	-2.71	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.74
HG00114.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.60	0.00	0.00	-2.81	-2.43	-2.49	-2.44	-2.47	-2.42	0.00	0.00	0.00	0.00	0.00	-2.89	-2.71	-2.53
HG00115.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.29	0.00	0.00	-2.58	-2.47	-2.39	-2.27	-2.60	-2.67	-3.24	-3.09	0.00	-2.75	-2.56	0.00	-2.77	-2.29
HG00116.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.69	-2.91	-2.86	-3.14	-2.64	-2.73	-2.75	-2.77	-2.88	-3.66	-2.84	-2.90	-2.93	-2.90	0.00	-2.91	-2.60
HG00117.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.49	-2.78	-2.76	-3.04	-2.73	-2.74	-2.64	-2.65	-2.58	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.51
HG00118.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.33	0.00	0.00	-2.50	-2.61	-2.31	-2.26	-2.54	-2.27	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.19
HG00119.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.61	0.00	0.00	-2.84	-2.64	-2.60	-2.63	-2.66	-2.55	0.00	0.00	0.00	0.00	0.00	-3.29	-2.92	-2.57
HG00120.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.60	-2.85	-2.81	-3.06	-2.52	-2.63	-2.67	-2.72	-2.65	0.00	-3.10	-2.80	0.00	0.00	0.00	-2.67	-2.59
HG00121.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.92	-2.89	-2.88	-3.12	-2.71	-2.74	-2.80	-2.80	-2.83	0.00	-3.13	-2.98	0.00	0.00	-3.11	-3.00	-2.84
HG00122.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.34	-2.71	-2.68	-2.96	-2.70	-2.43	-2.34	-2.39	-2.67	-3.05	-2.76	-2.63	-2.93	-2.78	0.00	-2.86	-2.43
HG00123.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.56	0.00	0.00	-2.80	-2.55	-2.68	-2.67	-2.66	-2.77	-3.54	-2.96	0.00	-2.86	-2.73	0.00	-2.97	-2.63
HG00124.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.63	0.00	-4.71	-2.74	-2.59	-2.56	-2.68	-2.67	-2.68	0.00	0.00	0.00	0.00	-4.71	0.00	-2.63	-2.57
HG00125.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.83	-2.76	-2.57	-3.05	-2.80	-2.81	-2.66	-2.66	-2.67	-4.66	0.00	0.00	-4.66	0.00	0.00	-2.57	-2.71
HG00126.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.31	-2.63	-2.58	-2.70	-2.60	-2.53	-2.27	-2.50	-2.32	0.00	0.00	0.00	0.00	0.00	-3.01	-2.46	-2.23
HG00127.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.54	0.00	0.00	-2.63	-2.43	-2.46	-2.41	-2.42	-2.39	0.00	-4.38	0.00	0.00	0.00	-2.86	-2.72	-2.46
HG00128.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.47	0.00	-4.37	-2.80	-2.40	-2.45	-2.32	-2.39	-2.43	-3.16	-3.04	-2.75	-4.37	-4.37	-3.11	-2.82	-2.40
HG00129.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.39	-2.76	-2.65	-2.97	-2.45	-2.39	-2.42	-2.73	-2.37	0.00	-3.13	-2.65	-4.17	0.00	-3.22	-2.92	-2.29
HG00130.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.28	0.00	0.00	-2.78	-2.49	-2.35	-2.35	-2.52	-2.27	0.00	0.00	0.00	0.00	0.00	0.00	-2.38	-2.28
HG00131.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.52	0.00	-4.77	-2.83	-2.53	-2.60	-2.64	-2.70	-2.53	0.00	0.00	0.00	0.00	-4.47	-2.99	0.00	-2.52
HG00132.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.29	0.00	0.00	-2.64	-2.48	-2.25	-2.20	-2.36	-2.27	0.00	0.00	0.00	0.00	0.00	0.00	-2.23	-2.21
HG00133.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.61	-2.91	-2.93	-3.15	-2.58	-2.68	-2.79	-2.74	-2.89	-3.54	-2.86	-2.89	-2.90	-2.88	0.00	-2.95	-2.66
HG00136.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.85	-2.85	-2.92	-3.07	-2.64	-2.77	-2.76	-2.85	-2.83	0.00	-2.97	-2.92	0.00	-4.84	-3.18	-2.89	-2.81
HG00137.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.76	-2.79	-2.87	-3.12	-2.80	-2.91	-2.68	-2.76	-2.69	0.00	0.00	0.00	0.00	0.00	-3.19	-2.90	-2.66
HG00138.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.78	-2.57	-2.59	0.00	-4.62	0.00	-2.69	-2.62	-2.65	0.00	0.00	0.00	0.00	0.00	-2.90	-2.82	-2.65
HG00139.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.76	0.00	-4.14	-2.76	-2.66	-2.75	-2.72	-2.70	-2.79	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.75
HG00140.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.92	-2.91	-2.93	-3.24	-2.69	-2.79	-2.85	-2.92	-3.18	-3.29	-2.90	-2.96	-3.00	-2.99	0.00	-3.01	-2.89
HG00141.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.27	-2.53	-2.58	-2.82	-2.69	-2.50	-2.23	-2.36	-2.34	0.00	0.00	0.00	0.00	-3.52	-2.97	-2.51	-2.23
HG00142.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.20	0.00	0.00	-2.50	-2.30	-2.36	-2.44	-2.63	-2.52	0.00	0.00	0.00	0.00	-2.53	-2.79	-4.07	-2.29
HG00143.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.32	-2.55	-2.64	-2.82	-2.63	-2.44	-2.33	-2.49	-2.28	0.00	0.00	0.00	0.00	0.00	-3.06	-2.68	-2.31
HG00145.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.57	-2.83	-2.79	-3.03	-2.76	-2.82	-2.69	-2.63	-2.63	0.00	0.00	0.00	0.00	0.00	-3.16	-2.84	-2.54
HG00146.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.48	-4.14	-4.31	-2.72	-2.53	-2.60	-2.64	-2.56	-2.79	-3.33	-2.91	0.00	-2.80	-2.69	0.00	-2.76	-2.55
HG00148.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.24	-2.62	-2.59	-2.82	-2.70	-2.49	-2.30	-2.52	-2.31	0.00	0.00	0.00	-4.10	0.00	0.00	-2.24	-2.17
HG00149.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.24	-3.80	0.00	-2.65	-2.50	-2.43	-2.39	-2.61	-2.19	0.00	0.00	0.00	0.00	0.00	-3.25	-2.53	-2.11
HG00150.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.33	-2.65	-2.63	-2.78	-2.57	-2.34	-2.35	-2.35	-2.66	-3.21	-2.57	-2.38	0.00	-2.60	0.00	-2.70	-2.25
HG00151.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.36	0.00	0.00	-2.67	-2.55	-2.37	-2.28	-2.65	-2.27	0.00	0.00	-4.03	0.00	0.00	0.00	-2.42	-2.25
HG00154.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.80	0.00	0.00	-2.91	-2.65	-2.53	-2.68	-2.75	-2.75	0.00	0.00	0.00	0.00	0.00	-2.99	-2.86	-2.68
HG00155.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.47	-4.59	-4.59	-2.82	-2.56	-2.60	-2.58	-2.44	-2.50	0.00	0.00	-4.59	0.00	-4.11	-3.13	-2.69	-2.45
HG00157.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.52	-2.75	-2.77	-2.94	-2.77	-2.81	-2.61	-2.67	-2.53	0.00	0.00	0.00	0.00	0.00	-3.19	-2.83	-2.53
HG00158.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.59	0.00	0.00	-2.92	-2.67	-2.68	-2.75	-2.84	-2.80	-3.47	-3.20	0.00	-2.94	-2.84	-3.44	0.00	-2.63
HG00159.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.68	0.00	0.00	-2.98	-2.53	-2.62	-2.75	-2.70	-2.89	-3.46	-2.94	-2.97	-2.97	-2.91	0.00	-2.94	-2.66
HG00160.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.47	-2.74	-2.68	-2.90	-2.59	-2.64	-2.61	-2.52	-2.52	0.00	-4.48	0.00	0.00	0.00	-3.30	-2.81	-2.40
HG00171.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.86	0.00	-4.72	-2.86	-2.66	-2.68	-2.70	-2.82	-2.74	0.00	0.00	0.00	0.00	0.00	-3.14	-2.83	-2.76
HG00173.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.38	0.00	0.00	-2.54	-2.37	-2.30	-2.23	-2.50	-2.57	-3.22	-2.64	0.00	-2.61	-2.50	-3.13	-4.17	-2.37
HG00174.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.80	0.00	0.00	-2.80	-2.64	-2.65	-2.73	-2.85	-2.71	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.78
HG00176.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.49	-4.55	-4.25	-2.64	-2.50	-2.56	-2.54	-2.56	-2.60	0.00	0.00	0.00	0.00	-4.55	0.00	-2.52	-2.47
HG00177.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.20	0.00	-3.83	-2.67	-2.45	-2.34	-2.29	-2.42	-2.30	0.00	0.00	0.00	0.00	-3.83	-2.93	-2.74	-2.27
HG00178.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.63	0.00	0.00	-2.73	-2.49	-2.54	-2.50	-2.55	-2.69	-3.84	-2.84	-4.75	-2.77	-2.70	-3.12	0.00	-2.62
HG00179.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.18	0.00	0.00	-2.50	-2.30	-2.35	-2.33	-2.55	-2.45	0.00	0.00	0.00	0.00	-2.40	0.00	-2.37	-2.31
HG00180.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.26	0.00	0.00	-2.51	-2.60	-2.30	-2.23	-2.61	-2.35	0.00	0.00	0.00	0.00	0.00	-3.23	-2.75	-2.21
HG00181.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.68	0.00	0.00	-2.79	-2.52	-2.54	-2.41	-2.39	-2.51	-3.82	0.00	0.00	0.00	-4.77	-2.91	-2.74	-2.61
HG00182.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.69	0.00	0.00	-2.86	-2.56	-2.53	-2.58	-2.54	-2.65	-3.51	-2.75	-4.68	-2.73	-2.65	0.00	-2.73	-2.62
HG00183.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.75	-2.68	-2.68	-3.07	-2.47	-2.57	-2.57	-2.56	-2.69	-3.71	-2.60	-2.80	-2.76	-2.69	-3.08	0.00	-2.66
HG00185.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.72	-2.77	-2.75	-3.14	-2.47	-2.62	-2.55	-2.41	-2.54	-3.78	-2.87	-2.76	0.00	0.00	-3.03	-2.83	-2.73
HG00186.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.73	0.00	-4.70	-2.83	-2.60	-2.62	-2.56	-2.48	-2.73	-3.70	-2.79	0.00	-2.76	-2.71	0.00	-2.78	-2.66
HG00187.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.62	0.00	0.00	-2.86	-2.48	-2.47	-2.48	-2.46	-2.42	0.00	0.00	0.00	0.00	0.00	-2.86	-2.63	-2.54
HG00188.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.55	0.00	0.00	-2.60	-2.48	-2.49	-2.40	-2.51	-2.44	0.00	0.00	0.00	0.00	0.00	-2.71	-4.58	-2.59
HG00189.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.54	0.00	0.00	-2.81	-2.47	-2.62	-2.59	-2.67	0.00	-3.69	-2.68	0.00	-2.69	-2.46	0.00	0.00	-2.62
HG00190.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.51	-2.61	-2.60	-2.90	-2.61	-2.64	-2.48	-2.53	-2.38	0.00	0.00	0.00	0.00	0.00	-2.71	0.00	-2.62
HG00231.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.24	0.00	-4.11	-2.60	-2.34	-2.31	-2.24	-2.50	-2.34	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.20
HG00232.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.78	-2.71	-2.80	-3.11	-2.77	-2.83	-2.68	-2.72	-2.70	0.00	0.00	0.00	-4.69	0.00	-2.99	-2.81	-2.71
HG00233.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.72	-2.57	-2.56	0.00	-2.67	-2.67	-2.53	-2.49	-2.67	-3.70	-2.67	-2.56	0.00	-2.65	0.00	-2.75	-2.64
HG00234.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.32	0.00	-3.72	-2.77	-2.36	-2.31	-2.21	-2.36	-2.31	0.00	0.00	0.00	0.00	-4.02	0.00	-2.21	-2.21
HG00235.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.33	0.00	0.00	-2.50	-2.46	-2.35	-2.23	-2.45	-2.30	0.00	0.00	0.00	0.00	0.00	0.00	-2.31	-2.20
HG00236.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.85	-2.73	-2.78	-4.81	-2.88	-2.97	-2.80	-2.82	-3.03	-3.37	-2.87	-2.99	-2.94	-2.95	-3.23	0.00	-2.83
HG00237.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.83	0.00	-4.38	-2.89	-2.64	-2.68	-2.68	-2.84	-2.69	0.00	0.00	0.00	0.00	0.00	-3.13	-2.86	-2.71
HG00238.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.65	0.00	0.00	-2.82	-2.46	-2.54	-2.49	-2.49	-2.37	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.56
HG00239.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.59	-2.85	-2.82	-3.03	-2.76	-2.79	-2.69	-2.74	-2.75	-3.54	-3.02	0.00	-2.90	-2.75	0.00	-2.88	-2.54
HG00240.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.58	-4.70	-4.70	-2.69	-2.43	-2.53	-2.46	-2.50	-2.40	0.00	-4.70	0.00	0.00	0.00	0.00	-2.46	-2.58
HG00242.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.58	0.00	-4.80	-2.82	-2.63	-2.59	-2.73	-2.62	-2.66	0.00	0.00	0.00	0.00	0.00	-3.29	-2.84	-2.64
HG00243.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.52	-2.61	-2.60	0.00	0.00	0.00	-2.63	-2.54	-2.52	0.00	0.00	0.00	0.00	0.00	-3.14	-2.75	-2.55
HG00244.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.55	0.00	-4.71	-2.83	-2.57	-2.60	-2.67	-2.68	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.68	-2.60
HG00245.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.58	-2.72	-2.68	-2.95	-2.69	-2.71	-2.68	-2.62	-2.70	-3.33	-2.90	0.00	-2.80	-2.73	0.00	-2.81	-2.56
HG00246.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.78	-2.76	-2.76	-3.09	-2.76	-2.79	-2.70	-2.74	-2.67	0.00	0.00	0.00	0.00	0.00	-3.03	-2.94	-2.75
HG00250.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.79	0.00	0.00	-2.74	-2.61	-2.72	-2.67	-2.65	-2.69	0.00	0.00	0.00	0.00	0.00	-3.06	-2.83	-2.67
HG00251.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.89	-2.83	-2.94	-3.11	-2.66	-2.77	-2.81	-2.75	-3.00	-3.38	-2.82	-3.05	-2.97	-2.94	0.00	-3.08	-2.84
HG00252.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.84	-4.78	0.00	-2.93	-2.68	-2.69	-2.68	-2.75	-2.70	0.00	0.00	0.00	0.00	0.00	0.00	-2.64	-2.72
HG00253.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.94	-2.96	-2.95	-3.10	-2.70	-2.79	-2.77	-2.85	-2.99	-3.23	-2.82	-3.00	-2.99	-2.99	0.00	-2.94	-2.81
HG00254.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.87	-2.87	-2.92	-3.16	-2.87	-3.03	-2.78	-2.86	-3.01	-3.29	-3.04	0.00	-2.89	-2.95	0.00	-2.99	-2.84
HG00255.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.58	-2.81	-2.77	-3.08	-2.76	-2.88	-2.66	-2.66	-2.85	-3.42	-3.06	0.00	-2.86	-2.74	0.00	-2.90	-2.59

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG00256.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.83	0.00	0.00	-2.93	-2.67	-2.73	-2.91	-3.15	0.00	-3.19	-3.00	-2.97	-4.68	-2.85	-3.29	0.00	-2.87
HG00257.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.76	0.00	-4.76	-2.94	-2.61	-2.70	-2.75	-2.76	-2.73	0.00	0.00	-4.76	0.00	-4.76	-3.08	-2.80	-2.78
HG00258.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.73	-2.87	-2.86	-3.03	-2.59	-2.68	-2.76	-2.68	-2.63	0.00	-2.92	-2.82	0.00	-4.74	0.00	-2.68	-2.67
HG00259.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.84	0.00	0.00	-2.99	-2.71	-2.78	-2.77	-2.74	-2.69	0.00	0.00	-4.83	0.00	-4.83	-3.03	-2.83	-2.79
HG00260.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.76	-2.75	-2.76	-2.97	-2.76	-2.87	-2.67	-2.75	-2.69	0.00	0.00	-4.64	0.00	0.00	-3.05	-2.77	-2.69
HG00261.mapped.ILLUMINA.bwa.GBR.exome.20121211	-2.69	-2.57	-2.59	-4.56	-4.56	-4.56	-2.59	-2.63	-2.61	0.00	0.00	0.00	0.00	-4.56	-2.89	-2.78	-2.61
HG00262.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.67	-2.93	-2.90	-3.07	-2.58	-2.69	-2.74	-2.72	-4.85	-3.38	-2.82	-2.72	-2.91	-2.71	0.00	0.00	-2.67
HG00263.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.76	0.00	0.00	-2.82	-2.66	-2.67	-2.72	-2.73	-2.71	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.77
HG00264.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.65	-2.93	-2.85	-3.10	-2.62	-2.69	-2.77	-2.74	-2.90	-3.64	-2.90	-2.67	0.00	-2.87	0.00	-3.00	-2.62
HG00265.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.52	-2.71	-2.65	0.00	-2.76	-2.84	-2.68	-2.72	-2.58	0.00	-2.92	-2.84	0.00	0.00	-3.39	-2.91	-2.58
HG00266.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.31	0.00	0.00	-2.59	-2.49	-2.33	-2.33	-2.43	0.00	-3.13	-2.53	0.00	-2.56	-2.34	0.00	0.00	-2.29
HG00267.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.29	-2.53	-2.59	-2.86	-2.63	-2.48	-2.31	-2.35	-2.30	0.00	0.00	0.00	0.00	-4.16	0.00	-2.26	-2.28
HG00268.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.75	0.00	0.00	-2.94	-2.71	-2.69	-2.72	-2.77	-2.70	-4.75	0.00	0.00	0.00	0.00	-3.14	-2.87	-2.82
HG00269.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.37	0.00	0.00	-2.65	-2.47	-2.40	-2.20	-2.28	-2.40	-3.41	0.00	0.00	0.00	0.00	-2.97	-2.63	-2.31
HG00271.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.78	0.00	0.00	-2.98	-2.67	-2.69	-2.79	-2.82	-2.76	-4.77	0.00	0.00	0.00	0.00	-2.93	0.00	-2.79
HG00272.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.41	-2.60	-2.62	-2.82	-2.60	-2.56	-2.47	-2.57	-2.49	0.00	0.00	0.00	0.00	0.00	-2.86	0.00	-2.37
HG00273.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.74	-2.79	-2.97	-2.99	-2.73	-2.98	-2.70	-2.70	-2.65	0.00	0.00	0.00	0.00	0.00	0.00	-2.64	-2.78
HG00274.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.93	-2.84	-2.93	-3.15	-2.71	-2.79	-2.69	-2.69	-2.80	-3.32	-3.11	-2.98	0.00	0.00	-3.19	-2.96	-2.79
HG00275.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.85	0.00	0.00	-2.85	-2.70	-2.74	-2.74	-2.96	-3.14	-3.28	-3.07	0.00	-2.96	-2.91	0.00	-2.99	-2.83
HG00276.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.83	-2.87	-2.87	-3.11	-2.60	-2.69	-2.76	-2.87	-2.80	0.00	-3.22	-2.97	0.00	0.00	-2.95	0.00	-2.82
HG00277.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.84	0.00	0.00	-2.87	-2.63	-2.58	-2.68	-2.81	-2.74	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.71
HG00278.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.72	-2.75	-2.79	-2.96	-2.81	-2.83	-2.67	-2.79	-2.68	0.00	0.00	0.00	0.00	0.00	-2.86	0.00	-2.66
HG00280.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.88	0.00	0.00	-2.99	-2.74	-2.93	-2.77	-2.89	-3.08	-3.27	-3.25	0.00	-2.94	-2.96	0.00	-2.99	-2.83
HG00281.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.81	-2.75	-2.80	-2.95	-2.84	-2.84	-2.68	-2.67	-2.67	0.00	0.00	0.00	0.00	0.00	-3.04	-2.85	-2.65
HG00282.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.77	-2.83	-2.80	-3.07	-2.86	-2.88	-2.70	-2.79	-2.72	0.00	0.00	0.00	0.00	0.00	-3.07	-2.93	-2.74
HG00284.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.87	0.00	0.00	-2.79	-2.72	-2.69	-2.76	-2.85	-2.83	0.00	0.00	0.00	0.00	0.00	-3.43	-2.98	-2.72
HG00285.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.93	-2.91	-2.94	-3.28	-2.70	-2.82	-2.89	-2.98	-3.02	-3.41	-2.99	-3.07	-2.99	-2.96	-3.42	0.00	-2.86
HG00288.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.83	-4.79	-4.79	-2.71	-2.59	-2.54	-2.51	-2.59	-2.59	0.00	0.00	0.00	-4.79	0.00	-2.93	0.00	-2.74
HG00290.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.89	-4.85	-4.85	-2.96	-2.64	-2.67	-2.50	-2.49	-2.58	-3.51	0.00	0.00	0.00	-4.85	-3.10	-2.83	-2.78
HG00304.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.72	-4.02	0.00	-3.00	-2.44	-2.49	-2.42	-2.52	-2.29	0.00	0.00	-4.32	0.00	0.00	0.00	-2.52	-2.49
HG00306.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.40	0.00	0.00	-2.74	-2.50	-2.51	-2.59	-2.52	-2.55	-3.44	-3.14	0.00	-2.80	-2.54	0.00	-2.74	-2.39
HG00308.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.55	-2.74	-2.73	-2.91	-2.68	-2.73	-2.61	-2.54	-2.51	-4.61	0.00	0.00	-4.61	-4.61	-3.06	-2.69	-2.50
HG00309.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.85	-2.86	-2.92	-3.22	-2.71	-2.81	-2.75	-2.82	-2.81	0.00	-3.17	-2.94	0.00	0.00	-3.14	-3.00	-2.82
HG00310.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.75	0.00	0.00	-2.80	-2.68	-2.66	-2.68	-2.80	-2.68	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.79
HG00311.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.51	0.00	-4.45	-2.70	-2.44	-2.51	-2.49	-2.55	-2.73	-3.45	-3.03	0.00	-2.89	-2.70	0.00	-2.74	-2.44
HG00313.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.93	-2.93	-2.99	-3.27	-2.73	-2.81	-2.78	-2.88	-3.07	-3.39	-2.86	-3.01	-3.01	-2.98	0.00	-2.99	-2.84
HG00315.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.81	0.00	0.00	-2.97	-2.66	-2.73	-2.75	-2.80	-3.03	-3.31	-3.01	0.00	-2.88	-2.83	0.00	-2.90	-2.79
HG00318.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.73	0.00	0.00	-2.69	-2.63	-2.66	-2.68	-2.69	-2.75	0.00	0.00	0.00	-4.67	0.00	0.00	-2.52	-2.69
HG00319.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.90	-2.69	-2.78	0.00	-2.89	-3.02	-2.77	-2.91	-3.02	-3.31	-2.81	-3.07	-3.01	-2.94	-3.23	-4.83	-2.78
HG00320.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.84	0.00	0.00	-2.84	-2.65	-2.63	-2.72	-2.79	-2.80	0.00	-4.77	0.00	0.00	-4.77	0.00	-2.66	-2.68
HG00321.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.92	-2.83	-3.00	-3.32	-2.68	-2.82	-2.82	-2.85	-3.16	-3.40	-2.85	-2.84	0.00	-2.98	0.00	-2.96	-2.87
HG00323.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.86	-2.87	-2.90	-3.10	-2.59	-2.76	-2.71	-2.87	-2.79	0.00	-3.03	-3.02	0.00	-4.76	0.00	-2.60	-2.86
HG00324.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.81	-2.85	-2.86	-3.16	-2.65	-2.71	-2.82	-2.97	-2.83	0.00	-3.12	-3.07	0.00	0.00	0.00	-2.79	-2.74
HG00325.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.87	-2.89	-2.89	-3.17	-2.68	-2.78	-2.67	-2.76	-2.84	-3.31	-3.20	-2.92	0.00	0.00	-3.09	-2.99	-2.83
HG00326.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.89	-2.89	-2.91	-3.15	-2.63	-2.72	-2.83	-2.95	-2.84	0.00	-3.11	-2.97	0.00	-4.83	0.00	-2.72	-2.79
HG00327.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.82	-2.75	-2.93	-3.10	-2.89	-2.83	-2.74	-2.80	-3.01	-3.21	-3.10	0.00	-2.86	-2.82	0.00	-2.82	-2.76
HG00328.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.86	-2.86	-2.93	-3.20	-2.71	-2.75	-2.82	-2.94	-3.10	-3.29	-2.89	-2.83	0.00	-2.94	0.00	-2.92	-2.80
HG00329.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.69	0.00	0.00	-2.98	-2.61	-2.83	-2.93	-3.05	0.00	-3.19	-2.92	0.00	-2.86	-2.59	0.00	-4.64	-2.87
HG00330.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.76	0.00	0.00	-2.74	-2.60	-2.63	-2.67	-2.75	-2.72	0.00	-4.69	0.00	0.00	0.00	-3.00	-2.81	-2.70
HG00331.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.82	-4.75	-4.45	-2.86	-2.72	-2.72	-2.76	-2.82	-2.76	0.00	0.00	0.00	0.00	0.00	-3.21	-2.90	-2.76
HG00332.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.74	0.00	-4.72	-2.78	-2.69	-2.70	-2.74	-2.76	-2.76	0.00	0.00	0.00	0.00	0.00	-3.11	-2.89	-2.73
HG00334.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.73	-2.80	-2.86	-3.06	-2.53	-2.81	-2.93	-3.12	-3.12	0.00	-3.07	-2.86	0.00	-2.88	0.00	-2.92	-2.88
HG00335.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.81	-2.72	-2.86	-3.05	-2.86	-2.89	-2.68	-2.75	-2.68	0.00	0.00	-4.69	0.00	0.00	-3.03	-2.78	-2.67
HG00336.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.84	-4.75	0.00	-2.99	-2.70	-2.74	-2.73	-2.88	-2.97	-3.25	-3.08	-2.95	0.00	-2.85	-3.25	0.00	-2.79
HG00337.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.79	0.00	0.00	-2.98	-2.77	-2.73	-2.63	-2.77	-3.06	-3.10	-3.08	0.00	-2.83	-2.94	-3.17	0.00	-2.79
HG00338.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.77	0.00	0.00	-2.81	-2.67	-2.81	-2.72	-2.74	-3.03	-3.22	-3.13	0.00	-2.94	-2.89	0.00	-2.94	-2.76
HG00339.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.88	0.00	0.00	-2.79	-2.70	-2.68	-2.76	-2.82	-3.06	-3.19	-3.07	0.00	-2.95	-2.84	0.00	-2.92	-2.76
HG00341.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.70	-2.68	-2.73	-2.95	-2.77	0.00	-2.78	-2.81	-2.88	0.00	0.00	0.00	0.00	-2.68	0.00	-2.70	-2.72
HG00342.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.82	-2.94	-2.78	-3.14	-2.92	-2.95	-2.75	-2.67	-3.06	-3.23	-2.85	0.00	-2.79	-2.88	0.00	-3.00	-2.81
HG00343.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.78	-4.64	0.00	-2.73	-2.63	-2.67	-2.64	-2.83	-2.76	0.00	0.00	0.00	0.00	-4.64	0.00	-2.61	-2.72
HG00344.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.80	0.00	0.00	-2.88	-2.63	-2.68	-2.79	-2.85	-2.98	-3.25	-3.01	0.00	-2.87	-2.81	0.00	-2.85	-2.78
HG00345.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.74	0.00	0.00	-2.76	-2.69	-2.68	-2.74	-2.81	-2.79	-4.70	0.00	0.00	0.00	0.00	0.00	-2.64	-2.76
HG00346.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.72	0.00	0.00	-3.00	-2.68	-2.68	-2.72	-2.81	-3.04	-3.21	-3.06	0.00	-2.84	-2.86	0.00	-2.80	-2.75
HG00349.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.30	0.00	0.00	-2.58	-2.40	-2.32	-2.24	-2.40	-2.27	0.00	0.00	0.00	0.00	0.00	-2.89	-2.74	-2.32
HG00350.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.36	0.00	0.00	-2.68	-2.44	-2.31	-2.31	-2.45	-2.62	-3.19	-2.99	-2.56	0.00	-2.58	0.00	-2.74	-2.28
HG00351.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.25	-2.45	-2.76	-2.87	-2.64	-2.57	-2.33	-2.50	-2.24	0.00	0.00	0.00	0.00	0.00	-2.90	-2.58	-2.20
HG00353.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.82	-2.81	-2.87	-3.21	-2.93	-2.94	-2.70	-2.84	-2.93	-3.22	-3.07	0.00	-2.87	-2.87	-3.07	0.00	-2.72
HG00355.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.25	-2.49	-2.71	-2.76	-2.64	-2.50	-2.22	-2.50	-2.38	0.00	0.00	0.00	0.00	0.00	-2.85	0.00	-2.21
HG00356.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.30	-2.56	-2.70	-2.94	-2.68	-2.70	-2.26	-2.39	-2.30	0.00	0.00	0.00	0.00	0.00	0.00	-2.30	-2.23
HG00357.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.54	-2.77	-2.74	-2.99	-2.50	-2.57	-2.65	-2.68	-2.57	0.00	-3.00	-2.70	0.00	0.00	0.00	-2.61	-2.54
HG00358.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.26	-3.98	-3.98	-2.46	-2.48	-2.24	-2.22	-2.48	-2.25	0.00	0.00	0.00	0.00	0.00	-3.02	-2.47	-2.25
HG00360.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.36	0.00	0.00	-2.51	-2.61	-2.32	-2.39	-2.55	-2.65	-3.17	-2.99	0.00	-2.87	-2.71	-2.99	0.00	-2.31
HG00361.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.52	-3.52	-3.72	-2.72	-2.56	-2.53	-2.53	-2.47	-2.49	0.00	-4.56	-4.56	-4.26	-4.08	0.00	-2.48	-2.46
HG00362.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.34	-2.48	-2.45	-4.10	-2.87	-2.72	-2.28	-2.48	-2.37	0.00	-3.15	-2.64	0.00	0.00	-2.69	-4.10	-2.26
HG00364.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.34	-2.55	-2.49	-2.79	-2.51	-2.34	-2.21	-2.30	-2.32	0.00	0.00	0.00	0.00	0.00	0.00	-2.27	-2.20
HG00365.mapped.ILLUMINA.bwa.FIN.exome.20130415	-2.31	0.00	0.00	-2.62	-2.58	-2.32	-2.40	-2.34	-2.54	-3.25	-2.93	0.00	-2.63	-2.69	-2.88	0.00	-2.23
HG00366.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.55	-2.60	-2.56	-4.22	-2.53	-2.56	-2.61	-2.63	-2.65	0.00	-2.84	-2.56	0.00	-4.22	0.00	-2.75	-2.48
HG00367.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.52	-4.51	0.00	-2.78	-2.48	-2.50	-2.58	-2.68	-2.72	-3.47	-2.92	0.00	-2.78	-2.62	0.00	-2.79	-2.43
HG00368.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.45	-4.10	-4.40	-2.63	-2.47	-2.42	-2.51	-2.56	-2.39	0.00	-4.40	0.00	0.00	0.00	0.00	-2.53	-2.40
HG00369.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.51	-2.77	-2.69	-2.95	-2.43	-2.55	-2.57	-2.69	-2.61	0.00	-3.11	-2.69	0.00	-4.55	0.00	-2.65	-2.48
HG00371.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.52	-2.74	-4.53	-2.95	-2.45	-2.57	-2.64	-2.61	-2.47	0.00	-3.13	-2.70	0.00	-4.53	0.00	-2.68	-2.48
HG00372.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.49	0.00	-4.17	-2.57	-2.40	-2.47	-2.53	-2.63	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.43
HG00373.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.56	-2.81	-2.82	-2.98	-2.50	-2.55	-2.65	-2.70	-2.71	-3.30	-2.81	-2.61	0.00	-2.66	0.00	-2.85	-2.51
HG00375.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.76	0.00	0.00	-2.79	-2.65	-2.66	-2.70	-2.76	-2.80	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.70
HG00376.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.81	-2.71	-2.76	-3.00	-2.88	-2.88	-2.70	-2.71	-2.66	0.00	0.00	0.00	0.00	0.00	-2.98	-2.82	-2.70
HG00378.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.77	0.00	0.00	-2.82	-2.70	-2.78	-2.75	-2.82	-2.87	-3.30	-3.21	0.00	-2.93	-2.92	0.00	-2.95	-2.83
HG00379.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.51	-2.76	-2.76	-2.93	-2.41	-2.53	-2.54	-2.69	-2.76	-3.32	-2.85	-2.80	-2.83	-2.75	0.00	-2.87	-2.44
HG00380.mapped.ILLUMINA.bwa.FIN.exome.20120522	-2.49	-2.80	-2.74	-2.90	-2.51	-2.53	-2.62	-2.59	-2.43	0.00	-2.97	-2.69	0.00	0.00	-3.54	-2.93	-2.45
HG00381.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.75	0.00	0.00	-2.72	-2.64	-2.69	-2.74	-2.79	-2.68	0.00	0.00	0.00	0.00	0.00	0.00	-2.69	-2.75
HG00382.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.81	0.00	0.00	-2.85	-2.70	-2.73	-2.75	-2.77	-3.03	-3.30	-3.24	0.00	-2.88	-2.91	0.00	-3.03	-2.80
HG00383.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.80	-4.65	-4.65	-2.75	-2.63	-2.68	-2.68	-2.74	-2.75	0.00	0.00	0.00	-4.65	0.00	-3.03	-2.92	-2.73
HG00384.mapped.ILLUMINA.bwa.FIN.exome.20121211	-2.47	-2.66	-2.66	-2.86	-2.59	-2.59	-2.50	-2.53	-2.48	0.00	0.00	0.00	0.00	0.00	-3.13	-2.74	-2.45
HG00403.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.52	0.00	-4.47	-2.70	-2.52	-2.48	-2.53	-2.52	-2.41	0.00	0.00	0.00	-4.47	-4.47	-3.26	-2.81	-2.47
HG00404.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.49	0.00	-4.24	-2.73	-2.52	-2.63	-2.54	-2.57	-2.52	0.00	0.00	0.00	0.00	-4.55	-3.17	-2.86	-2.48
HG00406.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.80	0.00	0.00	-2.87	-2.69	-2.77	-2.74	-2.80	-2.96	-3.30	-3.11	-2.87	0.00	-2.88	-3.15	0.00	-2.81
HG00407.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.76	0.00	0.00	-2.72	-2.66	-2.68	-2.69	-2.79	-2.75	0.00	0.00	0.00	0.00	0.00	-2.86	0.00	-2.75

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG00409.mapped.ILLUMINA.bwa.CHS.exome.20130415	-2.57	0.00	0.00	-2.74	-2.56	-2.51	-2.65	-2.64	-2.70	-3.35	-2.89	-3.92	-2.86	-2.69	0.00	-2.75	-2.42
HG00410.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.50	0.00	-4.14	-2.74	-2.50	-2.50	-2.48	-2.61	-2.43	0.00	0.00	0.00	0.00	0.00	-2.87	0.00	-2.39
HG00419.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.81	0.00	0.00	-2.98	-2.79	-2.70	-2.79	-2.83	-3.06	-3.30	-3.18	-3.04	0.00	-2.92	-3.17	0.00	-2.79
HG00421.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.80	0.00	0.00	-2.86	-2.67	-2.67	-2.67	-2.73	-2.71	0.00	0.00	0.00	0.00	0.00	-3.06	-2.96	-2.70
HG00422.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.76	0.00	0.00	-2.79	-2.69	-2.72	-2.67	-2.92	-2.83	0.00	0.00	0.00	0.00	0.00	-2.99	-2.87	-2.78
HG00428.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.81	0.00	0.00	-2.84	-2.56	-2.70	-2.77	-2.81	-2.72	0.00	0.00	0.00	0.00	0.00	0.00	-2.63	-2.74
HG00436.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.84	-4.80	0.00	-2.86	-2.70	-2.70	-2.74	-2.78	-2.70	0.00	0.00	0.00	0.00	-4.80	-3.20	-2.89	-2.78
HG00437.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.85	0.00	0.00	-2.89	-2.65	-2.70	-2.66	-2.82	-2.67	0.00	0.00	0.00	0.00	0.00	-2.97	0.00	-2.74
HG00442.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.85	0.00	0.00	-2.97	-2.67	-2.73	-2.69	-2.83	-2.78	0.00	0.00	0.00	0.00	-4.69	-2.87	0.00	-2.74
HG00443.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.71	0.00	0.00	-2.83	-2.70	-2.69	-2.78	-2.90	-2.97	-3.24	-3.05	0.00	-3.01	-2.91	0.00	-2.98	-2.80
HG00445.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.80	0.00	-4.70	-2.99	-2.71	-2.71	-2.78	-2.85	-3.06	-3.22	-3.11	-2.94	0.00	-2.93	-3.07	0.00	-2.77
HG00446.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.85	0.00	0.00	-2.93	-2.74	-2.70	-2.77	-2.77	-2.78	0.00	0.00	0.00	0.00	0.00	-3.12	-2.92	-2.81
HG00448.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.84	0.00	-4.70	-2.97	-2.72	-2.73	-2.75	-2.86	-2.77	-4.70	0.00	0.00	0.00	0.00	-2.94	0.00	-2.83
HG00449.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.80	0.00	0.00	-2.95	-2.67	-2.72	-2.63	-2.78	-2.73	0.00	0.00	0.00	0.00	0.00	-2.95	-4.75	-2.76
HG00451.mapped.ILLUMINA.bwa.CHS.exome.20121211	-3.00	-2.94	-3.10	-3.29	-2.74	-2.89	-2.83	-2.83	-3.13	-3.30	-2.96	-3.16	-3.06	-2.96	-3.36	0.00	-2.93
HG00452.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.86	0.00	0.00	-3.02	-2.77	-2.82	-2.84	-2.90	-3.02	-3.34	-2.99	0.00	-2.87	-2.86	0.00	-2.87	-2.72
HG00457.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.70	0.00	-4.74	-2.94	-2.86	-2.80	-2.76	-2.76	-2.82	0.00	0.00	0.00	0.00	0.00	-2.89	-4.74	-2.82
HG00458.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.78	0.00	0.00	-2.89	-2.62	-2.68	-2.66	-2.84	-2.74	0.00	0.00	0.00	0.00	0.00	-2.79	-4.63	-2.69
HG00463.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.88	0.00	0.00	-2.90	-2.73	-2.69	-2.72	-2.86	-2.77	0.00	0.00	0.00	-4.71	0.00	-2.91	0.00	-2.69
HG00464.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.88	-2.88	-2.93	-3.18	-2.96	-2.94	-2.81	-2.98	-4.50	-3.18	-2.86	0.00	-2.81	-2.74	0.00	0.00	-2.85
HG00472.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.73	0.00	0.00	-2.82	-2.69	-2.73	-2.71	-2.77	-2.74	0.00	0.00	0.00	0.00	0.00	-3.07	-2.87	-2.74
HG00473.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.79	0.00	-4.83	-3.09	-2.76	-2.78	-2.76	-2.81	-2.94	-3.33	-3.02	-2.92	0.00	-2.88	-3.17	0.00	-2.84
HG00475.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.71	0.00	0.00	-3.04	-2.83	-2.81	-2.80	-2.72	-2.87	0.00	-4.70	0.00	0.00	0.00	-2.85	0.00	-2.87
HG00476.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.83	0.00	-4.76	-2.95	-2.73	-2.75	-2.78	-2.76	-2.97	-3.20	-3.03	0.00	-2.87	-2.88	-3.11	-4.76	-2.79
HG00478.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.82	-2.78	-2.86	-3.07	-2.83	-2.91	-2.72	-2.85	-3.01	-3.25	-3.06	-2.90	0.00	-2.83	0.00	-2.87	-2.78
HG00479.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.68	0.00	0.00	-2.91	-2.60	-2.63	-2.67	-2.78	-2.66	0.00	0.00	0.00	0.00	0.00	-2.88	0.00	-2.83
HG00500.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.90	-4.71	-4.23	-2.84	-2.68	-2.70	-2.71	-2.85	-2.74	0.00	0.00	0.00	0.00	0.00	0.00	-2.75	-2.75
HG00501.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.74	0.00	0.00	-2.78	-2.65	-2.71	-2.68	-2.88	-2.83	0.00	0.00	0.00	0.00	0.00	0.00	-2.72	-2.73
HG00513.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.78	0.00	0.00	-2.93	-2.68	-2.69	-2.57	-2.73	-2.75	0.00	0.00	0.00	0.00	0.00	-3.09	-2.86	-2.74
HG00524.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.74	-4.75	-4.75	-2.72	-2.62	-2.72	-2.72	-2.77	-2.72	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.70
HG00525.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.81	0.00	-4.71	-2.94	-2.68	-2.67	-2.73	-2.71	-2.64	0.00	0.00	0.00	0.00	-4.41	-3.04	-2.79	-2.71
HG00530.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.80	0.00	0.00	-2.91	-2.64	-2.67	-2.67	-2.75	-2.79	0.00	0.00	0.00	0.00	0.00	-3.05	-2.96	-2.70
HG00531.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.89	0.00	0.00	-2.93	-2.73	-2.76	-2.73	-2.80	-2.96	-3.30	-3.11	-2.94	0.00	-2.87	0.00	-2.93	-2.80
HG00533.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.82	-2.83	-2.84	-3.09	-2.89	-2.92	-2.74	-2.87	-3.10	-3.19	-3.18	0.00	-2.91	-2.92	0.00	-2.95	-2.67
HG00534.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.78	-2.78	-2.86	-3.14	-2.85	-2.88	-2.73	-2.82	-2.79	0.00	0.00	0.00	0.00	0.00	-3.17	-2.93	-2.74
HG00536.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.77	0.00	0.00	-2.99	-2.74	-2.75	-2.76	-2.80	-3.00	-3.25	-3.15	0.00	-2.90	-2.90	-3.08	0.00	-2.75
HG00537.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.87	0.00	0.00	-2.77	-2.69	-2.74	-2.72	-2.73	-2.99	-3.22	-2.97	0.00	-2.87	-2.90	-3.09	-4.46	-2.83
HG00542.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.83	0.00	0.00	-2.81	-2.70	-2.74	-2.75	-2.90	-3.08	-3.21	-3.15	0.00	-2.98	-2.86	0.00	-2.90	-2.69
HG00543.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.88	0.00	0.00	-2.85	-2.74	-2.82	-2.82	-2.89	-3.00	-3.39	-3.01	0.00	-2.98	-2.93	0.00	-2.89	-2.81
HG00551.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.47	-2.78	-2.68	-2.99	-2.70	-2.75	-2.64	-2.49	-2.54	0.00	0.00	0.00	0.00	-4.64	-3.06	-2.77	-2.55
HG00553.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.60	0.00	-4.77	-2.72	-2.42	-2.47	-2.44	-2.50	-2.52	0.00	0.00	0.00	0.00	0.00	-2.93	-2.72	-2.58
HG00554.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.66	0.00	0.00	-2.88	-2.43	-2.49	-2.47	-2.57	-2.43	0.00	0.00	0.00	0.00	-4.74	-2.96	-2.70	-2.57
HG00556.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.75	0.00	0.00	-3.03	-2.72	-2.70	-2.71	-2.72	-2.76	0.00	0.00	0.00	-4.83	0.00	-2.89	0.00	-2.78
HG00557.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.52	0.00	0.00	-2.86	-2.64	-2.62	-2.91	-2.74	0.00	0.00	0.00	0.00	-4.59	0.00	-2.97	0.00	-2.95
HG00559.mapped.ILLUMINA.bwa.CHS.exome.20130415	-2.37	0.00	0.00	-2.61	-2.41	-2.30	-2.32	-2.39	-2.32	0.00	0.00	0.00	0.00	-3.88	-2.98	-2.56	-2.27
HG00560.mapped.ILLUMINA.bwa.CHS.exome.20130415	-2.28	-2.66	-2.68	-2.96	-2.41	-2.39	-2.36	-2.46	-2.36	0.00	-2.82	-2.58	-4.22	0.00	-3.44	-2.64	-2.32
HG00565.mapped.ILLUMINA.bwa.CHS.exome.20130415	-2.30	-2.59	-2.71	-2.85	-2.69	-2.59	-2.26	-2.48	-2.39	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.31
HG00566.mapped.ILLUMINA.bwa.CHS.exome.20130415	-2.26	0.00	-3.97	-2.67	-2.48	-2.24	-2.24	-2.69	-2.55	0.00	0.00	0.00	0.00	0.00	-2.74	0.00	-2.29
HG00580.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.77	-2.74	-2.81	-3.08	-2.84	-2.99	-2.93	-3.20	-2.85	0.00	-2.91	-2.95	0.00	-2.82	-3.06	0.00	-2.66
HG00581.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.91	-2.89	-2.95	-3.17	-2.65	-2.75	-2.73	-2.78	-2.86	-3.23	-3.19	-2.98	0.00	0.00	-3.15	-3.00	-2.82
HG00583.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.82	0.00	-4.66	-2.81	-2.71	-2.72	-2.75	-2.89	-2.97	-3.26	-3.20	0.00	-2.90	-2.80	-3.17	0.00	-2.76
HG00584.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.83	-2.82	-2.91	-3.12	-2.91	-2.90	-2.69	-2.91	-2.75	-4.78	0.00	0.00	0.00	0.00	-3.22	-2.97	-2.70
HG00589.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.92	-2.86	-3.00	-3.16	-2.67	-2.76	-2.84	-2.98	-3.18	-3.32	-2.89	-2.80	0.00	-2.96	0.00	-2.94	-2.87
HG00590.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.84	0.00	0.00	-2.92	-2.68	-2.67	-2.71	-2.80	-2.73	0.00	0.00	0.00	0.00	0.00	-3.09	-2.96	-2.73
HG00592.mapped.ILLUMINA.bwa.CHS.exome.20130415	-2.32	0.00	0.00	-2.62	-2.40	-2.25	-2.35	-2.50	-2.40	0.00	0.00	0.00	0.00	0.00	-2.71	-4.05	-2.23
HG00593.mapped.ILLUMINA.bwa.CHS.exome.20130415	-2.36	0.00	0.00	-2.65	-2.52	-2.32	-2.25	-2.36	-2.32	0.00	0.00	0.00	0.00	-4.08	-2.97	-2.80	-2.25
HG00595.mapped.ILLUMINA.bwa.CHS.exome.20130415	-2.27	-4.06	0.00	-2.61	-2.61	-2.25	-2.22	-2.45	-2.66	-3.36	-3.16	0.00	-2.83	-2.51	0.00	-2.78	-2.25
HG00596.mapped.ILLUMINA.bwa.CHS.exome.20130415	-2.26	-2.68	-2.56	-2.81	-2.70	-2.39	-2.26	-2.45	-2.41	0.00	0.00	0.00	-3.76	-4.06	-2.83	-2.54	-2.23
HG00598.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.60	-2.81	-2.82	-2.89	-2.54	-2.63	-2.64	-2.53	-2.76	-3.25	-2.74	-2.82	-2.85	-2.73	-3.10	-4.63	-2.58
HG00599.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.44	0.00	0.00	-2.65	-2.59	-2.59	-2.63	-2.59	-2.70	-3.41	-2.97	0.00	-2.76	-2.65	-3.04	0.00	-2.50
HG00607.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.91	0.00	0.00	-2.93	-2.71	-2.77	-2.77	-2.81	-3.02	-3.25	-3.13	-2.87	-4.74	-2.91	-3.15	0.00	-2.79
HG00608.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.84	0.00	0.00	-2.95	-2.71	-2.75	-2.81	-2.87	-3.08	-3.28	-3.09	0.00	-2.95	-2.90	-3.24	0.00	-2.80
HG00610.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.51	-2.61	-2.59	0.00	-2.70	-2.70	-2.53	-2.59	-2.65	-3.35	-2.81	-2.65	-2.84	-2.65	-3.42	-4.53	-2.47
HG00611.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.49	-2.79	-2.70	-2.91	-2.48	-2.59	-2.60	-2.66	-2.69	-3.29	-2.90	-2.61	0.00	-2.68	-3.34	0.00	-2.50
HG00613.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.92	0.00	0.00	-2.99	-2.69	-2.79	-2.85	-2.89	-3.08	-3.28	-3.19	-2.98	0.00	-2.93	-3.15	0.00	-2.79
HG00614.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.81	0.00	-4.72	-2.95	-2.75	-2.70	-2.79	-2.90	-3.03	-3.20	-3.10	-4.72	-2.89	-2.85	-3.26	0.00	-2.77
HG00619.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.86	0.00	0.00	-2.94	-2.70	-2.76	-2.76	-2.84	-3.09	-3.32	-3.14	-2.98	0.00	-2.85	-3.10	0.00	-2.82
HG00620.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.88	0.00	0.00	-2.93	-2.66	-2.73	-2.76	-2.82	-2.93	-3.25	-3.09	0.00	-2.93	-2.87	-3.06	0.00	-2.74
HG00622.mapped.ILLUMINA.bwa.CHS.exome.20130415	-2.53	0.00	0.00	-2.51	-2.51	-2.46	-2.53	-2.59	-2.51	0.00	-4.48	0.00	0.00	-4.48	-2.85	-4.48	-2.46
HG00623.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.49	-2.67	-2.74	-2.78	-2.69	-2.70	-2.53	-2.58	-2.61	-3.24	-2.90	0.00	-2.82	-2.66	0.00	-2.74	-2.42
HG00625.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.41	0.00	-4.38	-2.67	-2.46	-2.39	-2.51	-2.52	-2.47	0.00	0.00	0.00	0.00	-4.08	-2.90	0.00	-2.40
HG00626.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.45	-4.52	-4.52	-2.65	-2.50	-2.57	-2.59	-2.60	-2.62	-3.29	-3.04	0.00	-2.86	-2.66	-3.19	0.00	-2.53
HG00628.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.31	0.00	-4.38	-2.67	-2.41	-2.44	-2.51	-2.51	-2.39	0.00	0.00	0.00	0.00	-4.38	-2.91	0.00	-2.41
HG00629.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.47	0.00	0.00	-2.73	-2.44	-2.50	-2.52	-2.64	-2.48	0.00	0.00	0.00	0.00	0.00	-2.93	0.00	-2.37
HG00631.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.56	-2.80	-2.78	-2.93	-2.51	-2.63	-2.58	-2.55	-2.56	-3.40	-2.97	-2.79	-4.28	0.00	-2.99	0.00	-2.50
HG00632.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.52	0.00	0.00	-2.75	-2.51	-2.54	-2.56	-2.47	-2.47	0.00	0.00	-4.00	-4.48	0.00	-3.01	-2.61	-2.50
HG00634.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.48	0.00	0.00	-2.61	-2.47	-2.50	-2.56	-2.61	-2.75	-3.25	-3.03	0.00	-2.80	-2.65	0.00	-2.79	-2.46
HG00635.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.52	-2.84	-2.73	-2.90	-2.44	-2.57	-2.54	-2.51	-2.60	-3.34	-3.01	-2.76	0.00	0.00	-3.06	0.00	-2.52
HG00637.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.61	0.00	-4.71	-2.75	-2.51	-2.47	-2.45	-2.43	-2.42	0.00	0.00	0.00	-4.71	0.00	0.00	-2.40	-2.52
HG00638.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.52	0.00	0.00	-2.86	-2.45	-2.48	-2.47	-2.51	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.47
HG00640.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.64	-2.73	-2.73	-3.00	-2.68	-2.75	-2.59	-2.56	-2.69	-3.80	-2.82	0.00	-2.76	-2.65	-2.88	-4.15	-2.62
HG00641.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.55	-2.88	-2.85	-3.03	-2.69	-2.75	-2.68	-2.58	-2.62	0.00	-4.83	-4.83	0.00	-4.53	-3.28	-2.84	-2.52
HG00650.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.83	0.00	0.00	-2.96	-2.62	-2.73	-2.73	-2.82	-2.72	0.00	0.00	0.00	0.00	0.00	-3.06	-2.87	-2.71
HG00651.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.87	0.00	-4.76	-2.86	-2.61	-2.65	-2.72	-2.92	-2.72	0.00	0.00	0.00	0.00	0.00	-3.13	-2.87	-2.67
HG00653.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.70	-2.52	-2.56	0.00	0.00	-4.68	-2.63	-2.77	-2.68	0.00	0.00	0.00	0.00	0.00	-2.83	-4.68	-2.60
HG00654.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.78	-4.73	0.00	-2.84	-2.59	-2.82	-2.66	-2.88	-2.75	0.00	0.00	0.00	0.00	-4.73	-2.82	0.00	-2.67
HG00656.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.75	0.00	0.00	-2.87	-2.57	-2.70	-2.73	-2.80	-2.74	0.00	0.00	0.00	0.00	0.00	-3.11	-2.96	-2.73
HG00657.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.58	-2.53	-2.60	-2.85	-2.61	-2.64	-2.67	-2.80	-4.49	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-2.74
HG00662.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.80	0.00	-4.75	-2.95	-2.62	-2.70	-2.68	-2.92	-2.74	0.00	0.00	0.00	0.00	0.00	-3.20	-2.87	-2.70
HG00663.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.90	0.00	0.00	-3.01	-2.68	-2.75	-2.74	-2.95	-3.00	-3.22	-3.12	-2.98	0.00	-2.92	-3.17	0.00	-2.78
HG00671.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.87	-2.82	-2.81	-3.11	-2.90	-3.06	-2.79	-2.84	-4.69	-3.15	-2.81	0.00	-2.68	-2.78	0.00	0.00	-2.70
HG00672.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.74	0.00	0.00	-2.75	-2.64	-2.65	-2.73	-2.76	-2.74	0.00	0.00	0.00	0.00	0.00	0.00	-2.63	-2.71
HG00674.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.57	-2.64	-2.76	-2.86	-2.70	-2.65	-2.59	-2.51	-2.62	-3.32	-2.86	0.00	-2.80	-2.63	-3.00	0.00	-2.47
HG00675.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.48	-4.16	0.00	-2.69	-2.47	-2.50	-2.55	-2.58	-2.48	0.00	-4.46	-4.46	0.00	0.00	-2.81	0.00	-2.44
HG00683.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.84	0.00	0.00	-3.06	-2.75	-2.75	-2.76	-2.84	-2.97	-3.30	-3.09	-2.95	0.00	-2.95	0.00	-2.97	-2.83
HG00684.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.86	0.00	0.00	-2.98	-2.70	-2.74	-2.78	-2.80	-3.01	-3.35	-3.09	0.00	-2.96	-2.93	-3.15	-4.78	-2.84

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG00689.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.82	0.00	-4.41	-2.83	-2.66	-2.71	-2.75	-2.82	-2.79	0.00	0.00	0.00	0.00	0.00	-3.18	-2.99	-2.75
HG00690.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.82	0.00	-4.72	-3.01	-2.77	-2.82	-2.78	-2.82	-2.93	-3.31	-3.02	-2.90	0.00	-2.90	-3.15	-4.72	-2.78
HG00692.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.80	0.00	0.00	-2.81	-2.70	-2.71	-2.74	-2.85	-2.74	0.00	0.00	0.00	0.00	0.00	-2.91	0.00	-2.75
HG00693.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.86	-2.80	-2.82	-3.03	-2.80	-2.89	-2.91	-3.12	-2.96	0.00	-3.25	-2.91	0.00	-2.89	-3.21	0.00	-2.72
HG00698.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.80	0.00	0.00	-2.88	-2.66	-2.61	-2.70	-2.86	-2.71	0.00	0.00	0.00	0.00	0.00	-3.17	-2.81	-2.69
HG00699.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.73	0.00	0.00	-2.88	-2.61	-2.68	-2.67	-2.85	-2.73	0.00	0.00	0.00	0.00	0.00	-2.92	0.00	-2.72
HG00701.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.82	-4.75	0.00	-2.89	-2.69	-2.67	-2.83	-2.91	-2.74	0.00	0.00	0.00	0.00	0.00	-2.97	0.00	-2.69
HG00702.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.77	-2.77	-2.91	-3.08	-2.90	-2.89	-2.73	-2.87	-2.68	0.00	0.00	0.00	0.00	-4.76	0.00	-2.67	-2.71
HG00704.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.81	0.00	-4.86	-3.01	-2.68	-2.71	-2.81	-2.93	-3.09	-3.26	-3.25	-3.02	0.00	-2.95	-3.36	0.00	-2.81
HG00705.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.82	0.00	0.00	-2.90	-2.62	-2.70	-2.70	-2.94	-2.69	0.00	0.00	-4.79	0.00	0.00	-2.94	0.00	-2.77
HG00707.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.79	-2.73	-2.83	-3.11	-2.75	-2.79	-2.70	-2.81	-2.73	0.00	0.00	0.00	0.00	0.00	-3.33	-2.84	-2.67
HG00708.mapped.ILLUMINA.bwa.CHS.exome.20120522	-2.81	0.00	0.00	-2.76	-2.69	-2.75	-2.72	-2.85	-3.02	-3.26	-3.26	-4.85	-2.92	-2.94	-3.32	0.00	-2.76
HG00717.mapped.ILLUMINA.bwa.CHS.exome.20130415	-2.73	-3.84	-3.94	-2.93	-2.49	-2.48	-2.43	-2.56	-2.45	0.00	0.00	0.00	-4.54	0.00	0.00	-2.52	-2.56
HG00728.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.47	0.00	-4.46	-2.69	-2.51	-2.49	-2.52	-2.52	-2.39	0.00	-3.86	0.00	0.00	-3.99	-2.97	-2.67	-2.40
HG00729.mapped.ILLUMINA.bwa.CHS.exome.20121211	-2.43	-4.23	0.00	-2.75	-2.53	-2.59	-2.60	-2.55	-2.63	-3.26	-2.86	-4.53	-2.83	-2.64	-3.04	0.00	-2.45
HG00731.mapped.ILLUMINA.bwa.PUR.exome.20130422	-2.62	-2.85	-2.81	-5.05	-2.85	-2.88	-2.66	-2.58	-2.72	-3.56	-3.06	-2.83	-4.45	-4.15	-3.29	-2.89	-2.64
HG00732.mapped.ILLUMINA.bwa.PUR.exome.20130422	-2.37	-4.20	-4.20	-4.10	-4.80	-3.76	-2.63	-2.67	-3.85	-3.30	-2.72	0.00	-2.70	-2.56	0.00	-4.32	-2.54
HG00733.mapped.ILLUMINA.bwa.PUR.exome.20130422	-2.69	-2.78	-2.86	-2.93	-2.60	-2.71	-2.69	-2.59	-2.69	-3.40	-2.93	-2.84	-4.14	-4.04	-3.22	-2.86	-2.57
HG00734.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.17	0.00	-4.45	-4.15	-4.45	-3.97	-2.44	-2.37	-3.85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-2.35
HG00736.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.50	-2.79	-2.80	-3.02	-2.69	-2.71	-2.68	-2.66	-2.76	-3.46	-2.96	0.00	-2.85	-2.74	0.00	-2.69	-2.54
HG00737.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.47	-2.79	-2.76	-2.95	-2.71	-2.71	-2.76	-2.69	-4.26	-3.48	-2.81	0.00	-2.75	-2.71	-3.15	0.00	-2.65
HG00739.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.37	-2.70	-2.68	-2.86	-2.60	-4.59	-2.63	-2.64	-2.56	0.00	0.00	0.00	0.00	-2.60	-3.07	0.00	-2.51
HG00740.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.67	-2.87	-2.84	-3.12	-2.59	-2.69	-2.73	-2.80	-2.57	0.00	-3.13	-2.79	0.00	0.00	0.00	-2.71	-2.63
HG00742.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.86	-2.56	-2.61	-3.81	-2.70	-2.77	-2.52	-2.51	-2.67	-3.47	-2.79	-2.59	0.00	-2.79	-2.90	-4.03	-2.65
HG00743.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.87	-2.70	-2.78	-3.37	-2.67	-2.70	-2.43	-2.48	-2.60	-3.46	-2.86	-3.71	-2.78	-2.65	0.00	-2.75	-2.61
HG00759.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.78	-2.67	-2.79	-3.08	-2.81	-2.77	-2.64	-2.66	-2.83	-3.26	-2.86	0.00	-2.75	-2.76	-3.17	-4.23	-2.82
HG00766.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.88	0.00	0.00	-2.80	-2.66	-2.68	-2.61	-2.67	-2.80	-3.41	-2.83	0.00	-2.78	-2.79	0.00	-2.79	-2.82
HG00844.mapped.ILLUMINA.bwa.CDX.exome.20121211	-2.74	0.00	0.00	-2.88	-2.61	-2.57	-2.66	-2.72	-2.62	0.00	0.00	0.00	0.00	0.00	-2.81	-4.58	-2.59
HG00851.mapped.ILLUMINA.bwa.CDX.exome.20121211	-2.88	-2.85	-2.92	-3.10	-2.65	-2.81	-2.77	-2.82	-2.95	-3.25	-2.83	-2.97	-2.93	-3.04	-3.22	0.00	-2.79
HG00864.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.74	0.00	0.00	-2.82	-2.61	-2.66	-2.71	-2.81	-2.71	0.00	0.00	0.00	0.00	0.00	0.00	-2.65	-2.72
HG00867.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.95	-4.90	-4.42	-3.06	-2.64	-2.68	-2.63	-2.56	-2.73	-3.48	-2.81	0.00	-2.77	-2.81	-3.15	-4.42	-2.80
HG00879.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.73	0.00	0.00	-2.83	-2.61	-2.68	-2.58	-2.75	-2.71	0.00	0.00	0.00	0.00	0.00	-2.88	0.00	-2.70
HG00881.mapped.ILLUMINA.bwa.CDX.exome.20121211	-2.73	0.00	0.00	-2.90	-2.66	-2.67	-2.72	-2.86	-2.93	-3.15	-3.05	-2.87	0.00	-2.80	-3.01	0.00	-2.71
HG00956.mapped.ILLUMINA.bwa.CDX.exome.20121211	-2.85	-2.88	-2.92	-3.10	-2.69	-2.75	-2.77	-2.91	-3.05	-3.29	-2.80	-2.98	-3.01	-2.94	0.00	-2.90	-2.84
HG00978.mapped.ILLUMINA.bwa.CDX.exome.20121211	-2.67	-2.70	-2.78	-3.03	-2.81	-2.82	-2.67	-2.77	-2.71	0.00	0.00	0.00	0.00	0.00	-2.86	0.00	-2.71
HG00982.mapped.ILLUMINA.bwa.CDX.exome.20121211	-2.78	-4.67	0.00	-2.76	-2.64	-2.69	-2.71	-2.74	-2.89	-3.24	-2.97	0.00	-2.86	-2.89	-3.19	0.00	-2.76
HG01028.mapped.ILLUMINA.bwa.CDX.exome.20121211	-2.77	0.00	0.00	-2.79	-2.68	-2.70	-2.73	-2.82	-2.95	-3.22	-3.00	0.00	-2.84	-2.89	0.00	-2.84	-2.79
HG01029.mapped.ILLUMINA.bwa.CDX.exome.20121211	-2.79	0.00	0.00	-2.89	-2.74	-2.74	-2.80	-2.83	-2.92	-3.27	-3.00	-2.94	0.00	-2.92	0.00	-2.81	-2.81
HG01031.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.80	-4.65	0.00	-2.79	-2.66	-2.73	-2.71	-2.82	-3.04	-3.27	-2.95	0.00	-2.98	-2.82	0.00	-2.83	-2.78
HG01046.mapped.ILLUMINA.bwa.CDX.exome.20121211	-2.70	0.00	0.00	-2.89	-2.65	-2.66	-2.71	-2.76	-2.93	-3.18	-2.95	0.00	-2.77	-2.83	-3.08	0.00	-2.89
HG01047.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.53	-2.63	-2.63	0.00	0.00	0.00	-2.65	-2.55	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.48
HG01048.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.55	0.00	0.00	-2.80	-2.56	-2.64	-2.66	-2.61	-2.58	0.00	0.00	0.00	0.00	-4.88	-3.27	-2.86	-2.51
HG01049.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.69	-3.01	-2.97	-3.12	-2.66	-2.71	-2.81	-2.64	-2.96	-3.69	-2.95	-2.70	-4.95	-2.87	0.00	-2.92	-2.66
HG01051.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.73	0.00	0.00	-2.89	-2.62	-2.68	-2.72	-2.74	-2.63	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.70
HG01052.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.81	0.00	-2.93	-3.12	-2.63	-2.75	-2.79	-2.78	-2.74	0.00	-2.98	0.00	-2.99	0.00	-3.22	-2.92	-2.78
HG01054.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.52	0.00	-4.91	-2.77	-2.57	-2.57	-2.64	-2.67	-2.56	0.00	0.00	0.00	0.00	-4.91	0.00	-2.65	-2.53
HG01055.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.56	0.00	0.00	-2.71	-2.57	-2.55	-2.66	-2.60	-2.55	0.00	0.00	0.00	0.00	-4.83	-3.04	0.00	-2.54
HG01058.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.92	-4.11	-3.51	-2.89	-2.45	-2.50	-2.47	-2.55	-2.34	-4.41	-4.41	0.00	0.00	-4.41	0.00	-2.56	-2.51
HG01060.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.76	-2.62	-2.65	0.00	0.00	0.00	-2.73	-2.94	-2.70	0.00	0.00	0.00	0.00	0.00	-3.01	0.00	-2.71
HG01061.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.90	-2.92	-2.94	-3.24	-2.65	-2.72	-2.79	-3.06	-2.86	0.00	-3.21	-3.03	0.00	0.00	0.00	-2.88	-2.78
HG01063.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.66	-2.72	-2.77	-3.13	-2.69	-2.67	-2.47	-2.46	-2.44	0.00	-4.09	-4.09	0.00	-4.09	-3.07	-2.79	-2.55
HG01064.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.71	-4.40	0.00	-3.03	-2.48	-2.50	-2.42	-2.50	-2.40	0.00	-4.09	0.00	0.00	0.00	-2.89	-2.66	-2.60
HG01066.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.51	0.00	-4.86	-2.86	-2.57	-2.56	-2.63	-2.62	-2.59	0.00	0.00	-4.86	0.00	0.00	0.00	-2.63	-2.53
HG01067.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.65	-2.91	-2.91	-3.09	-2.59	-2.71	-2.79	-2.76	-2.71	0.00	-3.18	-2.94	0.00	-4.87	0.00	-2.74	-2.58
HG01069.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.78	0.00	0.00	-2.91	-2.70	-2.68	-2.68	-2.72	-2.75	-4.70	0.00	0.00	0.00	0.00	0.00	-2.56	-2.72
HG01070.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.72	0.00	0.00	-2.76	-2.66	-2.67	-2.68	-2.77	-2.69	0.00	0.00	0.00	0.00	0.00	-3.01	-2.84	-2.73
HG01072.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.75	0.00	0.00	-2.93	-2.64	-2.66	-2.74	-2.64	-2.65	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.73
HG01073.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.76	-2.61	-2.62	-4.59	0.00	0.00	-2.91	-2.96	-4.59	-3.18	-2.70	-2.86	-2.85	-2.63	0.00	0.00	-2.65
HG01075.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.55	-2.73	-2.71	-3.00	-2.66	-2.73	-2.61	-2.63	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.55
HG01077.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.81	-3.70	-3.70	-2.92	-2.47	-2.45	-2.45	-2.62	-2.43	-4.39	0.00	-4.09	-4.09	0.00	-2.73	-4.39	-2.55
HG01079.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.59	0.00	-4.70	-2.75	-2.60	-2.59	-2.66	-2.63	-2.57	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.59
HG01080.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.50	0.00	0.00	-2.94	-2.53	-2.61	-2.65	-2.54	-2.78	-3.57	-2.94	0.00	-2.85	-2.71	0.00	-2.88	-2.60
HG01082.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.75	-2.77	-2.81	-3.08	-2.84	-2.86	-2.72	-2.72	-2.65	0.00	0.00	0.00	0.00	0.00	0.00	-2.68	-2.78
HG01083.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.88	-2.87	-2.91	-3.17	-2.70	-2.79	-2.80	-2.88	-3.12	-3.32	-2.92	-3.02	-2.97	-2.99	0.00	-2.99	-2.80
HG01085.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.80	-2.79	-2.83	-3.03	-2.78	-2.80	-2.68	-2.78	-2.75	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.71
HG01086.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.79	0.00	0.00	-2.73	-2.64	-2.69	-2.70	-2.83	-2.74	0.00	0.00	0.00	0.00	-4.67	0.00	-2.61	-2.66
HG01088.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.82	-4.12	-3.94	-3.14	-2.54	-2.56	-2.47	-2.52	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.59
HG01089.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.83	-2.61	-2.59	-4.50	-2.80	-2.76	-2.49	-2.46	-2.47	-3.59	-2.93	-2.85	-4.50	-4.50	-3.02	-2.90	-2.68
HG01092.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.80	-2.68	-2.54	-4.39	-2.93	-2.71	-2.50	-2.58	-2.48	0.00	-2.74	0.00	-2.76	0.00	-2.70	-4.39	-2.53
HG01094.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.51	-2.77	-2.77	-2.92	-2.71	-2.70	-2.61	-2.58	-2.53	0.00	0.00	0.00	0.00	0.00	-2.89	0.00	-2.54
HG01095.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.61	0.00	-4.68	-2.86	-2.53	-2.64	-2.64	-2.71	-2.59	0.00	-2.92	-2.83	0.00	-4.68	0.00	-2.86	-2.78
HG01097.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.60	0.00	0.00	-2.83	-2.46	-2.55	-2.49	-2.50	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.57
HG01098.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.68	-2.79	-2.68	-3.09	-2.45	-2.56	-2.51	-2.58	-2.49	0.00	-2.86	-2.69	0.00	0.00	-3.09	-2.87	-2.62
HG01101.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.56	0.00	-4.61	-2.67	-2.56	-2.60	-2.67	-2.52	-2.65	-4.61	-4.61	-4.61	0.00	-4.61	0.00	-2.48	-2.53
HG01102.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.58	-2.71	-2.66	0.00	0.00	-4.72	-2.69	-2.67	-2.95	-3.46	-2.88	0.00	-2.86	-2.78	0.00	-2.85	-2.57
HG01104.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.91	-4.74	0.00	-2.98	-2.73	-2.78	-2.67	-2.84	-2.98	-3.27	-2.92	0.00	-2.86	-2.87	-3.12	0.00	-2.79
HG01105.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.85	-2.79	-2.82	-3.02	-2.86	-2.92	-2.69	-2.92	-3.10	-3.21	-3.11	-2.97	0.00	-2.82	-3.22	0.00	-2.78
HG01107.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.90	-2.85	-2.90	-3.09	-2.64	-2.76	-2.78	-2.86	-2.85	-4.82	-3.15	-3.02	0.00	0.00	-3.30	-3.02	-2.79
HG01108.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.68	-4.25	-4.12	-2.77	-2.55	-2.69	-2.72	-2.79	-2.65	0.00	-4.42	-4.42	-4.72	-4.42	0.00	-2.66	-2.78
HG01110.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.62	-2.92	-2.86	-3.09	-2.55	-2.67	-2.68	-2.65	-2.65	0.00	-2.97	-2.84	0.00	-4.82	-3.35	-2.95	-2.60
HG01111.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.55	-2.89	-2.77	-3.01	-2.76	-2.76	-2.70	-2.57	-2.65	0.00	0.00	0.00	0.00	0.00	-3.21	-2.83	-2.54
HG01112.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.59	0.00	0.00	-2.78	-2.40	-2.41	-2.44	-2.51	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.52
HG01113.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.62	0.00	0.00	-2.68	-2.51	-2.54	-2.49	-2.60	-2.66	-3.54	-2.80	0.00	-2.71	-2.63	0.00	-2.84	-2.62
HG01119.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.92	0.00	-4.55	-2.78	-2.61	-2.62	-2.52	-2.49	-2.57	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.77
HG01121.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.96	-3.66	-2.80	-3.16	-2.72	-2.68	-2.56	-2.63	-2.81	-3.32	-2.69	-4.07	-2.72	-2.84	0.00	-4.13	-2.95
HG01122.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.93	-2.65	-2.66	-4.54	-2.75	-2.81	-2.56	-2.51	-2.56	-4.24	-2.82	-2.79	-3.61	-3.80	-3.11	-2.82	-2.81
HG01124.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.16	0.00	0.00	-2.72	-2.27	-2.51	-2.42	-2.53	0.00	-3.17	-2.56	0.00	-2.59	-2.19	0.00	0.00	-2.08
HG01125.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.37	0.00	0.00	-2.67	-2.44	-2.45	-2.37	-2.38	-2.28	0.00	0.00	0.00	0.00	-4.08	-3.13	-2.56	-2.29
HG01130.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.89	-2.67	-2.68	-3.00	-2.69	-2.72	-2.55	-2.41	-2.45	0.00	0.00	0.00	0.00	0.00	-3.07	-2.74	-2.70
HG01131.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.83	0.00	-4.48	-2.99	-2.54	-2.62	-2.58	-2.47	-2.56	-4.78	-4.78	0.00	-4.78	-4.48	-3.02	-2.73	-2.72
HG01133.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.26	0.00	-4.11	-2.63	-2.57	-2.40	-2.34	-2.51	-2.35	0.00	-4.11	0.00	0.00	-4.11	0.00	-2.39	-2.25
HG01134.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.31	0.00	0.00	-2.66	-2.44	-2.28	-2.32	-2.49	-2.63	-3.39	-2.89	0.00	-2.65	-2.50	-2.98	-4.09	-2.35
HG01136.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.31	-4.04	0.00	-2.55	-2.39	-2.29	-2.22	-2.43	-2.27	0.00	0.00	0.00	0.00	0.00	-2.69	0.00	-2.22
HG01137.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.30	-3.66	-4.14	-2.72	-2.41	-2.33	-2.29	-2.50	-2.57	-3.54	-2.61	0.00	-2.65	-2.66	-3.18	-4.14	-2.26
HG01139.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.23	0.00	0.00	-2.63	-2.56	-2.28	-2.18	-2.47	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.26	-2.23
HG01140.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.26	0.00	0.00	-2.67	-2.62	-2.28	-2.23	-2.34	-2.46	-3.61	-3.18	-2.72	-4.08	0.00	0.00	-2.38	-2.35

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG01142.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.90	0.00	-4.57	-2.97	-2.67	-2.68	-2.58	-2.55	-2.75	-3.49	-2.78	0.00	-2.76	-2.82	-3.10	-4.57	-2.83
HG01148.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.26	0.00	0.00	-2.65	-2.37	-2.25	-2.33	-2.34	-2.29	0.00	0.00	0.00	0.00	0.00	-2.82	0.00	-2.22
HG01149.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.32	-2.67	-2.64	-3.00	-2.82	-2.64	-2.23	-2.25	-2.66	-3.00	-2.90	0.00	-2.61	-2.59	0.00	-2.71	-2.34
HG01161.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.78	0.00	-4.33	-3.03	-2.51	-2.54	-2.46	-2.53	-2.64	-3.21	-2.95	0.00	-2.76	-2.65	0.00	-2.74	-2.60
HG01162.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.90	-4.03	-4.33	-2.98	-2.53	-2.56	-2.53	-2.55	-2.60	-3.25	-2.86	0.00	-2.74	-2.67	0.00	-2.75	-2.52
HG01164.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.87	-2.60	-2.58	0.00	-2.57	-2.63	-2.54	-2.67	-2.55	0.00	-2.68	-2.58	-4.55	0.00	0.00	-2.67	-2.63
HG01167.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.50	-2.64	-2.62	-4.60	-4.12	-4.30	-2.63	-2.51	-2.64	-3.30	-2.86	0.00	-2.75	-2.63	-3.11	-4.30	-2.52
HG01168.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.53	-2.88	-2.86	-3.03	-2.79	-2.82	-2.71	-2.58	-2.81	-3.47	-2.99	-2.77	0.00	-2.77	-3.30	0.00	-2.50
HG01170.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.75	-4.11	-4.71	-2.79	-2.66	-2.72	-2.75	-2.70	-2.71	0.00	-4.71	-4.24	0.00	0.00	-3.12	-2.86	-2.78
HG01171.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.75	0.00	0.00	-2.95	-2.69	-2.71	-2.72	-2.99	-2.73	0.00	0.00	0.00	0.00	0.00	-3.17	-2.92	-2.74
HG01173.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.72	-2.57	-2.64	0.00	0.00	0.00	-2.64	-2.85	-2.92	-3.19	-3.00	-2.94	0.00	-2.82	-3.02	0.00	-2.66
HG01174.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.78	0.00	0.00	-2.92	-2.64	-2.68	-2.72	-2.75	-2.75	0.00	0.00	0.00	0.00	0.00	0.00	-2.70	-2.69
HG01176.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.67	-2.86	-2.91	-3.11	-2.61	-2.71	-2.77	-2.72	-2.94	-3.54	-2.80	-2.73	0.00	-2.84	0.00	-2.95	-2.71
HG01177.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.54	0.00	0.00	-2.84	-2.58	-2.62	-2.69	-2.60	-2.56	0.00	0.00	0.00	0.00	-4.63	-2.97	0.00	-2.52
HG01182.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.64	-2.80	-2.77	-3.00	-2.51	-2.63	-2.57	-2.63	-2.62	0.00	-2.99	-2.75	0.00	0.00	-3.15	-2.95	-2.62
HG01183.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.63	-2.78	-2.78	-2.89	-2.67	-2.77	-2.65	-2.55	-2.70	-3.35	-3.02	-4.65	-2.71	-2.71	-3.10	-4.65	-2.53
HG01187.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.63	0.00	0.00	-2.90	-2.55	-2.68	-2.72	-2.75	-2.83	-3.55	-3.05	0.00	-2.93	-2.83	-3.29	0.00	-2.58
HG01188.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.51	0.00	0.00	-2.85	-2.57	-2.55	-2.64	-2.64	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.54
HG01190.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.65	0.00	0.00	-2.72	-2.64	-2.64	-2.70	-2.70	-2.62	0.00	0.00	0.00	0.00	0.00	0.00	-2.64	-2.55
HG01191.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.63	-2.74	-2.71	-4.69	-2.74	-2.81	-2.60	-2.48	-2.57	-3.39	-3.05	-2.78	-4.69	-4.21	-3.21	-2.90	-2.65
HG01197.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.59	-2.78	-2.77	-2.98	-2.52	-2.69	-2.69	-2.70	-2.65	0.00	-2.97	-2.82	0.00	-4.36	0.00	-2.65	-2.57
HG01198.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.58	-2.66	-2.70	-2.86	-2.61	-2.66	-2.61	-2.59	-2.59	-4.55	0.00	0.00	-4.55	-4.25	0.00	-2.60	-2.48
HG01200.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.74	-4.11	-4.41	-3.02	-2.54	-2.56	-2.51	-2.53	-2.67	-3.30	-2.80	-4.41	-2.76	-2.77	0.00	-2.91	-2.61
HG01204.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.57	-2.74	-2.82	-2.95	-2.49	-2.64	-2.72	-2.58	-2.60	0.00	-2.94	-2.76	-4.18	0.00	-3.21	-2.76	-2.51
HG01205.mapped.ILLUMINA.bwa.PUR.exome.20121211	-2.57	-2.72	-2.64	-4.70	-2.81	-2.73	-2.85	-2.90	-2.70	0.00	-2.74	-2.65	0.00	-2.79	0.00	-2.82	-2.61
HG01241.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.49	-2.57	-2.65	0.00	0.00	-4.56	-4.56	0.00	0.00	0.00	-2.61	-4.56	-2.58	-2.42	0.00	0.00	-2.44
HG01242.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.62	-2.81	-2.62	0.00	0.00	-2.82	-2.81	-3.02	-2.74	0.00	-3.04	0.00	-2.92	-2.77	-3.27	0.00	-2.53
HG01247.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.61	0.00	-4.69	-2.77	-2.58	-2.55	-2.65	-2.71	-2.63	0.00	0.00	0.00	0.00	0.00	0.00	-2.72	-2.54
HG01248.mapped.ILLUMINA.bwa.PUR.exome.20120522	-2.58	-4.69	-4.69	-2.71	-2.59	-2.54	-2.66	-2.62	-2.61	0.00	0.00	0.00	0.00	-4.69	0.00	-2.64	-2.53
HG01250.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.57	0.00	0.00	-2.57	-2.40	-2.48	-2.48	-2.52	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.54
HG01251.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.55	-2.59	-2.56	-2.84	-2.62	-2.57	-2.40	-2.38	-2.37	0.00	0.00	0.00	0.00	0.00	-3.02	-2.71	-2.38
HG01253.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.59	-2.69	-2.63	-2.94	-2.65	-2.64	-2.46	-2.49	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.77	-2.54
HG01254.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.57	0.00	0.00	-2.75	-2.40	-2.43	-2.39	-2.54	-2.37	0.00	0.00	-4.77	0.00	-4.77	-2.70	0.00	-2.48
HG01256.mapped.ILLUMINA.bwa.CLM.exome.20121211	-2.51	-2.73	-2.70	-2.93	-2.61	-2.60	-2.61	-2.54	-2.70	-3.24	-3.00	0.00	-2.76	-2.62	0.00	-2.96	-2.40
HG01257.mapped.ILLUMINA.bwa.CLM.exome.20121211	-2.44	-2.73	-2.70	-2.88	-2.67	-2.68	-2.56	-2.66	-4.19	-3.11	-2.86	0.00	-2.70	-2.46	0.00	0.00	-2.45
HG01259.mapped.ILLUMINA.bwa.CLM.exome.20121211	-2.48	-2.61	-2.62	-4.13	-2.59	-2.60	-2.66	-2.81	-2.58	0.00	-2.93	0.00	-2.76	-2.53	0.00	-2.80	-2.41
HG01260.mapped.ILLUMINA.bwa.CLM.exome.20121211	-2.52	-2.77	-2.70	-2.90	-2.69	-2.72	-2.59	-2.65	-2.69	-3.41	-3.08	0.00	-2.79	-2.69	0.00	-2.76	-2.46
HG01269.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.85	-4.12	-4.05	-2.93	-2.54	-2.60	-2.56	-2.63	-2.54	-4.90	0.00	0.00	0.00	0.00	-2.98	0.00	-2.74
HG01271.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.35	-2.85	-2.77	-2.81	-2.57	-2.37	-2.38	-2.42	-2.37	0.00	-2.94	-2.57	0.00	0.00	-3.25	-2.73	-2.33
HG01272.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.28	0.00	0.00	-2.81	-2.59	-2.30	-2.28	-2.50	-2.70	-3.24	-2.94	0.00	-2.88	-2.72	-2.91	0.00	-2.22
HG01275.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.37	0.00	-3.88	-2.69	-2.47	-2.28	-2.34	-2.41	-2.53	-3.18	-2.61	0.00	-2.86	-2.58	0.00	-2.66	-2.32
HG01277.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.27	0.00	0.00	-2.60	-2.57	-2.34	-2.27	-2.40	-2.50	-3.09	-3.02	0.00	-2.62	-2.57	0.00	-2.51	-2.34
HG01280.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.83	-2.53	-2.54	-4.73	-4.13	-4.25	-2.48	-2.44	-2.55	0.00	0.00	0.00	0.00	0.00	-2.94	-2.73	-2.64
HG01281.mapped.ILLUMINA.bwa.CLM.exome.20130415	-3.00	-2.85	-2.85	-3.27	-2.63	-2.75	-2.63	-2.56	-2.65	-3.47	-2.92	-2.84	-4.99	-4.39	0.00	-2.60	-2.85
HG01284.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.94	-2.72	-2.74	-3.11	-2.77	-2.83	-2.61	-2.57	-2.79	-3.44	-2.86	0.00	-2.82	-2.82	0.00	-2.84	-2.77
HG01286.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.82	-2.48	-2.48	-3.98	-3.81	-3.38	-2.39	-2.54	-2.59	-3.28	-2.85	-2.78	0.00	-2.60	0.00	-2.70	-2.55
HG01302.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.87	-2.59	-2.75	-3.27	-2.60	-2.64	-2.60	-2.71	-2.67	-4.32	-2.77	0.00	-2.63	-2.59	0.00	-2.71	-2.57
HG01303.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.73	-2.61	-2.72	-3.14	-2.70	-2.66	-2.66	-2.64	-2.57	0.00	-2.84	-4.07	-2.78	-2.64	0.00	-2.71	-2.56
HG01305.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.83	-2.83	-2.76	-3.27	-2.71	-2.69	-2.56	-2.58	-3.75	-3.30	-2.65	-4.15	-2.53	-2.57	0.00	0.00	-2.63
HG01308.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.73	-3.88	-3.76	-2.90	-2.60	-2.51	-2.37	-2.55	-2.42	0.00	0.00	-4.36	-4.36	-4.06	-2.66	-4.06	-2.56
HG01311.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.70	-2.74	-2.74	-3.26	-2.71	-2.64	-2.50	-2.50	-2.39	0.00	0.00	-4.47	-4.17	-4.47	0.00	-2.44	-2.61
HG01312.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.88	-2.66	-2.74	-3.25	-2.74	-2.75	-2.55	-2.56	-2.66	-3.65	-2.86	-2.74	0.00	-2.72	-2.87	0.00	-2.63
HG01323.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.78	-4.05	-3.75	-2.89	-2.53	-2.48	-2.49	-2.45	-2.32	0.00	0.00	-4.35	0.00	0.00	-2.85	-2.73	-2.59
HG01325.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.89	-4.42	-3.82	-3.21	-2.60	-2.50	-2.51	-2.53	-2.69	-3.52	-2.87	-4.12	-2.72	-2.64	0.00	-2.82	-2.57
HG01326.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.80	-2.74	-2.72	-3.21	-2.79	-2.72	-2.56	-2.59	-2.67	-3.39	-2.80	-3.86	-2.73	-2.77	0.00	-2.78	-2.65
HG01334.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.74	0.00	0.00	-2.93	-2.64	-2.62	-2.63	-2.69	-2.63	0.00	0.00	0.00	0.00	0.00	-3.03	-2.82	-2.69
HG01341.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.59	-4.58	-4.28	-2.73	-2.58	-2.57	-2.61	-2.67	-2.58	0.00	0.00	0.00	0.00	-4.58	0.00	-2.60	-2.49
HG01342.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.72	-2.70	-2.70	0.00	-2.61	-2.70	-2.69	-2.85	-2.86	-3.43	-2.73	-2.71	-2.96	-2.89	0.00	-2.98	-2.58
HG01344.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.31	0.00	-4.10	-2.76	-2.51	-2.34	-2.33	-2.52	-2.29	0.00	0.00	0.00	-4.10	0.00	0.00	-2.40	-2.27
HG01345.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.30	-2.62	-2.66	-2.89	-2.57	-2.45	-2.41	-2.51	0.00	-2.96	-2.52	-2.58	-2.98	-2.41	0.00	0.00	-2.35
HG01348.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.36	-2.69	-2.78	-2.80	-2.60	-2.41	-2.46	-2.45	-2.66	-3.52	-2.70	-2.84	-2.94	-2.78	0.00	-2.80	-2.29
HG01350.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.89	-2.89	-2.91	-3.13	-2.66	-2.74	-2.77	-2.90	-2.84	0.00	-3.02	-2.96	0.00	0.00	-3.17	-2.98	-2.85
HG01351.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.83	0.00	0.00	-2.69	-2.65	-2.69	-2.71	-2.76	-2.68	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.69
HG01353.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.86	-2.58	-2.69	0.00	-2.87	-2.82	-2.79	-2.91	-2.75	0.00	-3.15	-3.02	0.00	0.00	-3.18	-2.82	-2.79
HG01354.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.55	0.00	-4.57	-2.60	-2.44	-2.64	-4.57	0.00	-4.57	0.00	0.00	0.00	0.00	-2.69	0.00	0.00	-2.66
HG01356.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.27	0.00	0.00	-2.67	-2.58	-2.26	-2.30	-2.39	-2.36	0.00	0.00	-3.52	0.00	0.00	-2.99	-2.55	-2.29
HG01357.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.22	-2.49	-2.50	-2.92	-2.64	-2.49	-2.59	-2.62	-4.04	-3.26	-2.46	0.00	-2.39	-2.23	0.00	0.00	-2.06
HG01359.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.60	0.00	-4.49	-2.75	-2.58	-2.56	-2.69	-2.72	-2.58	0.00	0.00	0.00	-4.49	0.00	0.00	-2.66	-2.50
HG01360.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.70	-2.57	-2.59	0.00	-2.70	-2.73	-2.60	-2.60	0.00	-3.78	-2.44	-2.72	-2.63	-2.56	0.00	0.00	-2.64
HG01362.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.77	-2.55	-2.52	0.00	-4.77	0.00	-2.52	-2.45	-2.38	0.00	-4.77	-4.17	0.00	0.00	-2.94	-2.73	-2.66
HG01363.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.95	-2.63	-2.64	0.00	-2.82	-2.79	-2.59	-2.54	-2.58	0.00	-2.88	-2.78	-4.99	0.00	0.00	-2.55	-2.77
HG01365.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.82	-2.77	-2.81	-3.07	-2.81	-2.85	-2.68	-2.83	-2.94	-3.20	-2.98	0.00	-2.85	-2.86	0.00	-2.78	-2.78
HG01366.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.81	-2.74	-2.74	-3.06	-2.79	-2.85	-2.69	-2.78	-2.67	0.00	0.00	0.00	0.00	0.00	-3.04	-2.81	-2.72
HG01369.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.94	-2.78	-2.76	-3.12	-2.54	-2.66	-2.62	-2.53	-2.55	0.00	-2.87	-2.79	0.00	0.00	-3.15	-2.79	-2.78
HG01372.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.85	-2.75	-2.70	-3.08	-2.76	-2.75	-2.61	-2.67	-2.76	-3.48	-2.83	0.00	-2.72	-2.79	0.00	-2.81	-2.73
HG01374.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.82	0.00	0.00	-2.92	-2.67	-2.71	-2.71	-2.82	-2.76	0.00	0.00	0.00	0.00	0.00	-2.87	0.00	-2.81
HG01375.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.89	0.00	0.00	-2.96	-2.69	-2.76	-2.74	-2.73	-2.96	-3.26	-3.03	0.00	-2.87	-2.85	-3.06	0.00	-2.78
HG01377.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.43	-4.55	0.00	-2.74	-2.45	-2.50	-2.57	-2.58	-2.51	0.00	0.00	0.00	0.00	-4.07	-2.94	-4.25	-2.46
HG01378.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.50	-4.14	-4.44	-2.75	-2.43	-2.46	-2.54	-2.59	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.37
HG01383.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.40	-2.72	-2.69	-2.96	-2.58	-2.68	-2.49	-2.50	-2.59	-3.46	-2.83	0.00	-2.71	-2.63	-3.26	-4.41	-2.46
HG01384.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.53	-2.79	-2.79	-2.94	-2.50	-2.54	-2.59	-2.63	-2.75	-3.65	-2.78	-2.72	-2.79	-2.68	0.00	-2.93	-2.49
HG01389.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.79	-2.81	-4.79	-3.12	-2.64	-2.71	-2.78	-2.87	-2.94	-3.25	-2.99	0.00	-2.86	-2.88	0.00	-2.91	-2.86
HG01390.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.74	-2.81	-2.83	-3.08	-2.80	-2.87	-2.89	-2.99	-2.93	0.00	-2.90	-2.90	0.00	-2.83	0.00	-2.93	-2.71
HG01392.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.92	-2.81	-2.78	-3.13	-2.56	-2.69	-2.67	-2.71	-2.65	0.00	-2.81	-2.84	0.00	0.00	-3.00	0.00	-2.81
HG01393.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.89	-2.75	-2.78	-3.11	-2.52	-2.69	-2.65	-2.59	-2.60	0.00	-2.86	-2.82	0.00	0.00	-3.15	-2.88	-2.81
HG01395.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.87	-4.82	-4.82	-2.77	-2.63	-2.60	-2.54	-2.49	-2.52	0.00	0.00	0.00	0.00	-4.21	0.00	-2.49	-2.75
HG01396.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.87	-2.69	-2.75	-3.00	-2.74	-2.70	-2.74	-2.74	-2.69	-4.81	-2.77	0.00	-2.75	-2.72	-3.05	-4.81	-2.76
HG01398.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.74	-2.65	-2.69	-3.10	-2.70	-2.68	-2.49	-2.52	-2.48	0.00	0.00	0.00	-4.40	-4.10	-2.93	-2.78	-2.58
HG01402.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.86	0.00	-4.57	-2.80	-2.61	-2.66	-2.60	-2.65	-4.09	-3.26	-2.64	0.00	-2.63	-2.63	0.00	0.00	-2.78
HG01403.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.84	0.00	0.00	-2.76	-2.44	-2.60	-2.54	-2.50	-2.58	0.00	0.00	0.00	-4.77	-4.77	-3.00	-2.76	-2.70
HG01405.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.88	-2.63	-2.69	-4.90	-2.80	-2.82	-2.63	-2.56	-2.57	0.00	-2.84	-2.74	0.00	0.00	0.00	-2.52	-2.78
HG01412.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.80	-4.51	-4.51	-2.76	-2.57	-2.59	-2.52	-2.61	-2.57	0.00	-4.11	-4.81	0.00	0.00	0.00	-2.56	-2.66
HG01413.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.95	-2.76	-2.76	-3.07	-2.82	-2.80	-2.60	-2.54	-2.74	-3.39	-2.80	-2.78	-4.56	-2.78	0.00	-2.84	-2.72
HG01414.mapped.ILLUMINA.bwa.PUR.exome.20130415	-2.85	-2.73	-2.77	-3.02	-2.82	-2.79	-2.64	-2.54	-2.76	-3.44	-2.82	0.00	-2.76	-2.77	0.00	-2.82	-2.83
HG01431.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.94	-2.75	-2.81	-3.13	-2.78	-2.79	-2.62	-2.70	-2.81	-3.56	-2.79	0.00	-2.77	-2.81	0.00	-2.81	-2.79
HG01432.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.89	-2.71	-2.71	-3.07	-2.75	-2.75	-2.61	-2.62	-2.65	0.00	-4.53	0.00	0.00	-4.53	0.00	-2.66	-2.74

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG01435.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.90	0.00	-4.75	-2.75	-2.59	-2.61	-2.55	-2.50	-2.50	0.00	0.00	-4.75	0.00	0.00	0.00	-2.44	-2.71
HG01437.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.57	-2.65	-2.65	-4.62	-2.73	-2.81	-2.62	-2.63	-2.62	0.00	-3.05	-2.91	-4.62	0.00	-3.28	-2.90	-2.57
HG01438.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.53	-2.78	-2.74	-2.90	-2.72	-2.75	-2.59	-2.70	-2.54	0.00	-4.51	0.00	0.00	0.00	0.00	-2.47	-2.45
HG01440.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.61	-2.82	-2.77	-2.87	-2.74	-2.81	-2.62	-2.77	0.00	-3.30	-2.75	0.00	-2.71	-2.56	0.00	0.00	-2.52
HG01441.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.54	-2.85	-2.78	-2.92	-2.78	-2.79	-2.54	-2.54	-2.61	0.00	0.00	0.00	0.00	0.00	-3.19	-2.82	-2.48
HG01443.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.90	-2.81	-2.78	-3.16	-2.80	-2.83	-2.62	-2.56	-2.79	-3.44	-2.82	0.00	-2.80	-2.76	-3.12	-4.88	-2.84
HG01444.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.81	-2.74	-2.74	-3.04	-2.76	-2.73	-2.60	-2.44	-2.55	0.00	0.00	-4.83	0.00	0.00	-3.13	-2.83	-2.80
HG01447.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.80	-4.51	-4.51	-3.00	-2.57	-2.58	-2.58	-2.45	-2.43	0.00	0.00	-4.81	0.00	0.00	-2.99	-2.76	-2.71
HG01455.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.53	0.00	0.00	-2.75	-2.41	-2.46	-2.45	-2.41	-2.32	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.52
HG01456.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.66	-2.44	-4.66	0.00	-2.51	-2.45	-2.45	-2.52	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.57
HG01459.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.84	-4.68	0.00	-2.91	-2.55	-2.58	-2.55	-2.50	-2.46	0.00	0.00	0.00	0.00	0.00	-3.01	-2.77	-2.70
HG01461.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.61	-2.84	-2.66	0.00	-2.63	-2.66	-2.72	-2.70	-2.62	0.00	-2.82	-2.86	-2.90	0.00	-3.44	-2.89	-2.57
HG01462.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.58	-2.77	-2.78	-2.84	-2.71	-2.76	-2.59	-2.64	-2.61	0.00	0.00	-4.54	0.00	0.00	0.00	-2.54	-2.44
HG01464.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.66	-2.82	-2.70	-4.66	-2.57	-2.65	-2.73	-2.71	-2.57	0.00	-2.80	-2.88	-2.96	-4.36	-3.16	-2.91	-2.58
HG01465.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.50	-2.79	0.00	-2.88	-2.49	-2.54	-2.56	-2.71	-2.63	0.00	0.00	-4.55	0.00	0.00	-3.27	-2.83	-2.52
HG01468.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.83	-2.66	-2.63	-4.59	-2.80	-2.77	-2.59	-2.61	-2.74	-3.44	-2.71	-2.83	-2.83	-2.76	-2.94	-4.59	-2.71
HG01474.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.92	-2.72	-2.76	-3.26	-2.53	-2.59	-2.54	-2.60	-2.66	-3.50	-2.70	-2.76	-2.76	-2.69	0.00	-2.88	-2.67
HG01479.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.81	-2.69	-2.80	-3.29	-2.71	-2.70	-2.53	-2.54	-2.66	-3.45	-2.87	-4.49	-2.82	-2.75	-3.02	-4.19	-2.68
HG01485.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.83	0.00	-4.80	-2.89	-2.58	-2.61	-2.53	-2.61	-2.50	0.00	0.00	0.00	0.00	0.00	-2.89	0.00	-2.75
HG01486.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.82	0.00	-4.85	-2.93	-2.58	-2.59	-2.46	-2.64	-2.49	0.00	0.00	-4.85	0.00	-4.85	-2.96	0.00	-2.77
HG01488.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.59	-4.57	0.00	-2.73	-2.57	-2.60	-2.62	-2.68	-2.82	-3.46	-3.00	0.00	-2.87	-2.77	0.00	-2.94	-2.54
HG01489.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.50	0.00	0.00	-2.62	-2.45	-2.50	-2.57	-2.58	-2.49	0.00	0.00	0.00	0.00	0.00	-3.24	0.00	-2.66
HG01491.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.60	0.00	-4.57	-2.66	-2.52	-2.57	-2.62	-2.68	-2.50	0.00	0.00	0.00	0.00	-4.57	0.00	-2.60	-2.48
HG01492.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.61	-2.77	-2.78	-2.97	-2.75	-2.82	-2.68	-2.69	-2.80	-3.48	-2.89	0.00	-2.82	-2.80	-3.31	0.00	-2.53
HG01494.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.65	-2.59	-2.57	0.00	-2.70	-2.65	-2.58	-2.53	-2.69	-3.81	-2.66	-2.56	0.00	-2.66	0.00	-2.74	-2.62
HG01495.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.61	-2.66	-2.67	-2.95	-2.42	-2.58	-2.59	-2.59	-2.50	0.00	-2.76	-2.70	0.00	0.00	-2.78	0.00	-2.64
HG01497.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.72	-2.70	-2.71	-3.04	-2.44	-2.57	-2.54	-2.50	-2.45	0.00	-2.80	-2.71	0.00	-4.67	0.00	-2.47	-2.68
HG01498.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.67	0.00	-4.63	-2.88	-2.55	-2.53	-2.50	-2.52	-2.61	-3.51	-2.66	0.00	-2.69	-2.64	0.00	-2.74	-2.65
HG01500.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.51	-2.67	-2.71	-2.86	-2.51	-2.44	-2.43	-2.42	-2.65	-3.24	-2.96	-2.47	0.00	-2.64	0.00	-3.33	-2.35
HG01501.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.35	-2.61	-2.91	-2.94	-2.94	-2.79	-2.38	-2.44	0.00	-3.07	-2.52	0.00	-2.49	-2.41	0.00	-4.12	-2.35
HG01503.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.41	-2.78	-3.00	-3.13	-2.45	-2.56	-2.39	-2.44	-2.44	0.00	-3.18	-2.80	0.00	-3.78	0.00	-2.78	-2.31
HG01504.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.39	0.00	0.00	-2.57	-2.47	-2.46	-2.38	-2.44	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.23
HG01506.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.80	0.00	0.00	-2.75	-2.64	-2.65	-2.68	-2.68	-2.71	0.00	0.00	0.00	0.00	0.00	0.00	-2.62	-2.69
HG01507.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.71	0.00	-4.64	-2.75	-2.61	-2.64	-2.66	-2.69	-2.71	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.69
HG01509.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.76	0.00	0.00	-2.86	-2.61	-2.66	-2.73	-2.64	-2.69	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.72
HG01510.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.78	-2.76	-2.88	-3.12	-2.82	-2.99	-2.75	-2.87	0.00	-3.12	-2.74	0.00	-2.71	-2.70	0.00	0.00	-2.80
HG01512.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.87	0.00	0.00	-3.02	-2.58	-2.75	-2.75	-2.81	-3.14	-3.19	-3.17	0.00	-3.01	-3.01	0.00	-2.85	-2.76
HG01513.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.74	0.00	0.00	-2.85	-2.64	-2.70	-2.67	-2.71	-2.69	-4.70	-4.70	0.00	0.00	0.00	0.00	-2.56	-2.68
HG01515.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.72	-2.73	-2.67	0.00	-2.78	-2.78	-2.66	-2.61	-2.87	-4.02	-2.65	-2.83	-2.79	-2.87	0.00	-2.83	-2.77
HG01516.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.65	-2.55	-2.55	0.00	0.00	0.00	-2.57	-2.54	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.64
HG01518.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.59	-2.75	-2.75	-3.05	-2.73	-2.69	-2.53	-2.51	-2.53	0.00	0.00	0.00	0.00	-4.45	0.00	-2.54	-2.63
HG01519.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.65	0.00	0.00	-2.79	-2.53	-2.58	-2.57	-2.56	-2.61	0.00	0.00	0.00	0.00	0.00	-3.01	-2.72	-2.69
HG01521.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.80	-2.86	-2.80	0.00	-2.74	-2.75	-2.79	-2.66	-2.90	-3.88	-2.55	-2.74	-2.92	-2.90	-3.02	0.00	-2.87
HG01522.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.74	0.00	0.00	-3.02	-2.65	-2.56	-2.65	-2.53	-2.61	-3.90	-2.93	0.00	-2.85	0.00	0.00	-2.65	-2.79
HG01524.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.86	-2.87	-2.91	-3.20	-2.65	-2.73	-2.77	-2.78	-2.74	0.00	-3.01	-2.95	0.00	-4.83	0.00	-2.59	-2.82
HG01525.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.76	-2.72	-2.75	-3.06	-2.79	-2.90	-2.86	-3.02	-2.93	0.00	-2.97	-2.86	0.00	-2.89	0.00	-2.79	-2.73
HG01527.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.71	-4.64	0.00	-2.84	-2.63	-2.66	-2.67	-2.71	-2.73	0.00	0.00	-4.64	0.00	0.00	-3.01	-2.79	-2.72
HG01528.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.78	0.00	0.00	-2.72	-2.62	-2.70	-2.70	-2.67	-2.75	0.00	0.00	0.00	0.00	0.00	0.00	-2.48	-2.73
HG01530.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.84	-4.42	-4.72	-2.85	-2.67	-2.68	-2.68	-2.78	-2.70	0.00	0.00	0.00	0.00	0.00	-3.09	-2.80	-2.71
HG01531.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.88	-2.90	-2.88	-3.17	-2.64	-2.78	-2.79	-2.85	-2.83	0.00	-3.11	-2.96	0.00	0.00	-3.23	-2.89	-2.85
HG01536.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.79	-2.86	-2.87	-3.12	-2.88	-2.86	-2.81	-2.75	-2.98	-3.25	-3.01	0.00	-2.81	-2.89	0.00	-2.82	-2.76
HG01537.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.78	-2.73	-2.84	-3.03	-2.80	-2.85	-2.70	-2.68	-2.64	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.70
HG01550.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.69	-2.49	-2.50	0.00	-2.73	-2.68	-2.54	-2.52	-2.69	-3.60	-2.59	-2.56	0.00	-2.66	-2.96	0.00	-2.63
HG01551.mapped.ILLUMINA.bwa.CLM.exome.20120522	-2.62	0.00	0.00	-2.68	-2.41	-2.36	-2.35	-2.44	-2.34	0.00	0.00	0.00	0.00	-4.72	0.00	-2.47	-2.40
HG01556.mapped.ILLUMINA.bwa.CLM.exome.20130415	-2.85	-2.71	-2.72	-3.15	-2.72	-2.78	-2.59	-2.49	-2.47	0.00	0.00	0.00	0.00	0.00	-3.05	-2.78	-2.75
HG01565.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.40	-2.78	-2.71	-2.96	-2.48	-2.43	-2.46	-2.62	-2.44	0.00	-2.83	0.00	-2.71	-4.00	-2.89	-4.30	-2.39
HG01566.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.39	-2.54	-2.61	-2.87	-2.64	-2.73	-2.35	-2.54	-2.27	0.00	0.00	-3.85	0.00	0.00	-2.83	0.00	-2.24
HG01571.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.31	0.00	0.00	-2.67	-2.55	-2.32	-2.37	-2.44	-2.36	0.00	0.00	0.00	0.00	0.00	-2.81	0.00	-2.19
HG01572.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.29	0.00	0.00	-2.58	-2.40	-2.40	-2.29	-2.42	-2.24	0.00	-4.06	0.00	0.00	0.00	-2.76	-4.06	-2.21
HG01577.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.78	0.00	0.00	-2.85	-2.62	-2.64	-2.67	-2.75	-2.67	0.00	0.00	0.00	0.00	-4.71	-2.90	0.00	-2.73
HG01578.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.82	-2.79	-2.86	-3.15	-2.86	-2.91	-2.77	-2.82	-2.92	-3.20	-2.81	-2.91	-2.92	-2.92	-3.14	0.00	-2.78
HG01583.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.81	-2.51	-2.57	0.00	-2.74	-2.76	-2.50	-2.59	-2.47	0.00	-2.87	-2.76	-4.42	-4.42	0.00	-2.53	-2.62
HG01586.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.77	-4.37	-4.37	-3.04	-2.45	-2.63	-2.49	-2.62	-2.63	-3.41	-2.90	-4.06	-2.81	-2.79	-2.85	-4.06	-2.60
HG01589.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.79	-2.74	-2.96	-3.37	-2.52	-2.62	-2.54	-2.62	-2.69	-3.49	-2.80	-2.65	-4.15	-2.88	0.00	-2.96	-2.66
HG01593.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.77	-2.62	-2.66	-3.14	-2.68	-2.70	-2.42	-2.47	-2.36	0.00	0.00	-4.35	-4.05	0.00	0.00	-2.48	-2.58
HG01595.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.67	0.00	-4.73	-2.87	-2.62	-2.68	-2.70	-2.70	-2.76	0.00	0.00	0.00	0.00	0.00	-2.97	-2.87	-2.74
HG01596.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.73	0.00	0.00	-2.85	-2.60	-2.69	-2.67	-2.80	-2.71	0.00	0.00	0.00	0.00	0.00	-2.89	0.00	-2.72
HG01597.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.80	0.00	0.00	-2.75	-2.63	-2.71	-2.72	-2.68	-2.76	0.00	0.00	0.00	0.00	0.00	-3.09	-2.78	-2.68
HG01598.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.79	-4.60	0.00	-2.71	-2.62	-2.62	-2.67	-2.72	-2.64	0.00	0.00	0.00	-4.60	0.00	-2.83	-4.60	-2.70
HG01599.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.70	0.00	0.00	-2.89	-2.58	-2.62	-2.63	-2.74	-2.64	0.00	0.00	0.00	0.00	-4.60	-2.89	0.00	-2.67
HG01600.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.75	0.00	0.00	-2.87	-2.60	-2.64	-2.65	-2.78	-2.69	0.00	0.00	0.00	0.00	0.00	-2.89	0.00	-2.71
HG01602.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.47	-2.49	-2.57	0.00	-2.62	-2.52	-2.39	-2.56	-2.43	-3.48	-2.81	-2.46	0.00	-4.26	-3.18	-2.91	-2.48
HG01603.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.43	-4.13	0.00	-2.70	-2.58	-2.36	-2.31	-2.41	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.28
HG01605.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.35	0.00	0.00	-2.67	-2.54	-2.50	-2.35	-2.73	-2.67	-3.31	-3.04	0.00	-2.82	-2.70	0.00	-2.82	-2.25
HG01606.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.37	0.00	0.00	-2.73	-2.57	-2.40	-2.36	-2.57	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.36	-2.31
HG01607.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.39	-4.07	0.00	-2.62	-2.41	-2.32	-2.39	-2.46	-2.54	-3.77	-3.22	0.00	-2.84	-2.61	0.00	-2.99	-2.24
HG01608.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.24	-2.71	-2.60	-2.91	-2.71	-2.60	-2.36	-2.56	-2.33	0.00	0.00	0.00	0.00	0.00	-2.82	0.00	-2.21
HG01610.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.35	-4.18	0.00	-2.70	-2.58	-2.49	-2.35	-2.72	-2.63	-3.33	-3.03	0.00	-2.76	-2.76	0.00	-2.76	-2.38
HG01612.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.37	-2.80	-2.63	-2.98	-2.50	-2.54	-2.35	-2.58	0.00	-3.06	-2.59	-2.44	-3.06	-2.41	0.00	0.00	-2.36
HG01613.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.34	-4.25	-4.25	-2.58	-2.53	-2.47	-2.36	-2.47	-2.58	-3.30	-2.85	0.00	-2.73	-2.75	0.00	-2.69	-2.31
HG01615.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.30	0.00	-4.05	-2.67	-2.60	-2.45	-2.35	-2.63	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.29
HG01617.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.24	0.00	0.00	-2.50	-2.48	-2.38	-2.32	-2.40	-2.35	0.00	0.00	0.00	0.00	-4.03	0.00	-2.35	-2.24
HG01618.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.37	-2.55	-2.64	-3.02	-2.55	-2.39	-2.36	-2.47	-2.39	0.00	-3.02	-2.59	0.00	0.00	0.00	-2.38	-2.28
HG01619.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.27	-2.65	-2.61	-2.98	-2.76	-2.51	-2.38	-2.32	-2.60	-3.16	-2.95	0.00	-2.80	-2.61	0.00	-2.59	-2.23
HG01620.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.33	-3.82	-4.12	-2.51	-2.48	-2.39	-2.30	-2.57	-2.63	-3.16	-3.08	0.00	-2.80	-2.56	0.00	-2.61	-2.28
HG01623.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.22	0.00	0.00	-2.51	-2.38	-2.29	-2.27	-2.53	-2.40	-3.81	0.00	0.00	0.00	-4.11	-3.03	-2.51	-2.21
HG01624.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.28	-2.64	-2.60	-3.18	-2.82	-2.49	-2.29	-2.59	-2.62	-3.33	-2.98	-4.18	-2.73	-2.56	0.00	-2.82	-2.32
HG01625.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.20	-2.87	-2.64	-2.83	-2.83	-2.48	-2.22	-2.35	-2.35	0.00	-3.98	0.00	0.00	0.00	0.00	-2.22	-2.18
HG01626.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.20	0.00	0.00	-2.63	-2.72	-2.18	-2.16	-2.37	-2.29	0.00	0.00	0.00	0.00	0.00	-3.26	-2.36	-2.17
HG01628.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.14	-2.50	-2.73	-2.91	-2.83	-2.50	-2.29	-2.49	-2.32	0.00	0.00	0.00	0.00	0.00	-2.86	-2.67	-2.19
HG01630.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.21	-2.26	-2.31	0.00	0.00	-4.07	-2.27	-2.33	-2.33	0.00	0.00	0.00	-3.76	-3.76	0.00	-2.23	-2.24
HG01631.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.71	0.00	0.00	-2.81	-2.66	-2.70	-2.73	-2.71	-2.86	-3.28	-3.07	0.00	-2.91	-2.86	0.00	-2.86	-2.76
HG01632.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.90	-2.85	-2.92	-3.16	-2.71	-2.79	-2.81	-2.86	0.00	-3.27	-2.72	-3.00	-2.77	-2.75	0.00	0.00	-2.83
HG01668.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.41	-4.18	0.00	-2.70	-2.52	-2.28	-2.41	-2.50	-2.35	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.25
HG01669.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.41	0.00	0.00	-2.73	-2.66	-2.42	-2.28	-2.62	-2.56	-3.31	-3.05	0.00	-2.74	-2.86	0.00	-2.76	-2.25
HG01670.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.34	0.00	0.00	-2.66	-2.61	-2.40	-2.32	-2.57	-2.31	0.00	0.00	0.00	0.00	0.00	-2.86	0.00	-2.33

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG01672.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.32	-3.90	-4.20	-2.63	-2.56	-2.42	-2.31	-2.77	-2.61	-3.42	-3.25	-4.20	-2.84	-2.80	0.00	-2.88	-2.29
HG01673.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.75	0.00	0.00	-2.68	-2.63	-2.70	-2.72	-2.66	-2.64	0.00	0.00	0.00	0.00	0.00	-3.03	-2.83	-2.76
HG01675.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.81	0.00	0.00	-2.72	-2.61	-2.68	-2.66	-2.72	-2.67	0.00	0.00	0.00	0.00	0.00	-3.07	-2.81	-2.72
HG01676.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.69	0.00	-4.65	-2.70	-2.65	-2.69	-2.66	-2.73	-2.67	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.72
HG01678.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.74	-2.75	-2.81	-3.08	-2.82	-2.81	-2.85	-2.97	-2.90	0.00	-2.97	0.00	-2.80	-2.77	0.00	-2.79	-2.73
HG01679.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.70	0.00	-4.72	-2.93	-2.69	-2.73	-2.77	-2.74	-2.89	-3.20	-3.00	0.00	-2.86	-2.82	0.00	-2.90	-2.69
HG01680.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.74	0.00	0.00	-2.70	-2.70	-2.67	-2.70	-2.68	-2.65	-4.72	0.00	0.00	0.00	0.00	0.00	-2.54	-2.75
HG01682.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.81	0.00	0.00	-2.74	-2.58	-2.62	-2.71	-2.64	-2.69	0.00	0.00	0.00	0.00	0.00	-3.08	-2.80	-2.71
HG01684.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.81	0.00	0.00	-2.91	-2.66	-2.67	-2.69	-2.72	-2.68	0.00	0.00	0.00	-4.68	0.00	0.00	-2.54	-2.67
HG01685.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.80	0.00	0.00	-2.70	-2.58	-2.64	-2.65	-2.82	-2.67	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.70
HG01686.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.72	-2.75	-2.81	-3.06	-2.79	-2.83	-2.88	-2.94	-2.85	0.00	-3.03	-2.82	0.00	-2.76	0.00	-2.80	-2.71
HG01694.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.93	-2.86	-2.95	-3.14	-2.65	-2.73	-2.76	-2.88	-2.97	-3.37	-2.82	-2.80	-4.79	-2.95	0.00	-2.93	-2.89
HG01695.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.74	-2.74	-2.80	-3.06	-2.82	-2.78	-2.65	-2.69	-2.68	0.00	0.00	-4.71	0.00	0.00	-3.03	-2.87	-2.72
HG01697.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.63	-3.09	-3.01	-3.12	-3.01	-3.04	-2.70	-2.63	-2.81	0.00	-5.14	-4.66	-4.66	-4.19	0.00	-2.78	-2.55
HG01699.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.54	-2.72	-2.70	-2.92	-2.68	-2.72	-2.66	-2.64	-2.73	-3.43	-2.92	-4.64	-2.83	-2.66	0.00	-2.77	-2.51
HG01700.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.72	0.00	0.00	-2.72	-2.68	-2.62	-2.67	-2.60	-2.63	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.74
HG01702.mapped.ILLUMINA.bwa.IBS.exome.20121211	-2.70	-2.70	-2.81	-2.96	-2.78	-2.86	-2.61	-2.67	-2.70	0.00	0.00	0.00	0.00	0.00	-3.06	-2.80	-2.66
HG01704.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.62	0.00	-4.46	-2.83	-2.61	-2.65	-2.67	-2.60	-2.80	-3.53	-2.96	0.00	-2.83	-2.78	0.00	-2.82	-2.54
HG01705.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.61	-2.79	-2.83	-2.99	-2.56	-2.67	-2.67	-2.61	-2.56	0.00	-2.98	-2.87	0.00	-4.77	0.00	-2.74	-2.55
HG01707.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.48	-4.69	-4.39	-2.62	-2.60	-2.58	-2.63	-2.56	-2.55	0.00	0.00	0.00	0.00	-4.69	-3.10	-2.76	-2.45
HG01708.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.49	-4.70	-4.70	-2.83	-2.39	-2.55	-2.64	-2.55	-2.54	0.00	-4.70	-4.70	0.00	-4.09	-3.07	-2.77	-2.51
HG01709.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.65	-2.73	-2.80	0.00	-2.74	-2.73	-2.65	-2.57	-2.69	-3.60	-2.85	-2.77	0.00	-4.86	-3.16	-4.86	-2.63
HG01710.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.52	-2.78	-2.76	-2.91	-2.65	-2.74	-2.61	-2.49	-2.55	0.00	-4.69	0.00	-4.69	0.00	0.00	-2.46	-2.50
HG01746.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.65	-2.90	-2.90	-3.04	-2.60	-2.69	-2.73	-2.68	-2.84	-3.49	-2.84	-2.83	-2.92	-2.78	0.00	-2.90	-2.59
HG01747.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.55	-4.71	-4.71	-2.76	-2.60	-2.62	-2.61	-2.54	-2.48	0.00	0.00	0.00	0.00	-4.41	0.00	-2.48	-2.46
HG01756.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.79	-2.66	-2.61	0.00	-2.79	-2.78	-2.57	-2.52	-2.76	-3.65	-2.65	-2.84	-2.79	-2.81	-3.06	-4.72	-2.72
HG01757.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.74	0.00	-4.80	-2.82	-2.66	-2.67	-2.61	-2.66	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.78
HG01761.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.79	0.00	-4.38	-3.02	-2.64	-2.68	-2.68	-2.64	0.00	-3.60	-2.74	0.00	-2.69	-2.65	0.00	0.00	-2.72
HG01762.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.90	-2.85	-2.87	-3.16	-2.61	-2.79	-2.71	-2.63	-2.80	-3.70	-2.74	-2.76	0.00	-2.84	0.00	-2.86	-2.82
HG01765.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.85	-3.61	-3.85	-2.83	-2.57	-2.57	-2.55	-2.45	-2.42	0.00	0.00	-4.69	0.00	0.00	0.00	-2.41	-2.69
HG01766.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.89	-2.67	-2.75	-3.11	-2.47	-2.62	-2.58	-2.66	-2.62	0.00	-2.79	-2.72	0.00	-4.73	-2.94	0.00	-2.77
HG01767.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.78	0.00	-4.75	-2.78	-2.53	-2.60	-2.54	-2.60	-2.55	0.00	-4.27	0.00	0.00	-4.45	0.00	-2.61	-2.75
HG01768.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.92	0.00	0.00	-2.98	-2.59	-2.66	-2.62	-2.52	-2.70	-3.37	-2.78	0.00	-2.76	-2.72	0.00	-2.75	-2.77
HG01770.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.31	-2.60	-2.58	-2.70	-2.75	-2.54	-2.28	-2.54	-2.29	-4.13	0.00	0.00	0.00	-4.13	0.00	-2.37	-2.30
HG01771.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.40	-2.69	-2.73	-2.98	-2.57	-2.45	-2.36	-2.63	-4.12	-3.17	-2.57	-2.60	-2.98	-2.47	0.00	0.00	-2.38
HG01773.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.41	-2.65	-2.69	-2.96	-2.54	-2.42	-2.39	-2.51	-2.71	-3.30	-2.67	-2.70	-2.87	-2.65	0.00	-2.92	-2.43
HG01775.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.37	-4.08	0.00	-2.54	-2.62	-2.47	-2.36	-2.38	0.00	-3.08	-2.85	0.00	-2.49	-2.33	0.00	0.00	-2.33
HG01776.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.24	-2.72	-2.76	-2.70	-2.66	-2.62	-2.33	-2.49	-2.22	0.00	0.00	0.00	0.00	-4.02	-3.12	-2.82	-2.32
HG01777.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.33	-2.56	-2.63	-2.76	-2.80	-2.52	-2.37	-2.51	-2.32	0.00	0.00	0.00	0.00	0.00	-3.30	-2.59	-2.27
HG01779.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.43	-2.70	-2.73	-2.84	-2.59	-2.50	-2.45	-2.50	-2.65	-3.39	-2.73	-2.73	-2.69	-2.84	0.00	-2.77	-2.37
HG01781.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.34	-2.58	-2.69	-2.84	-2.80	-2.69	-2.33	-2.58	-2.38	0.00	0.00	0.00	-4.14	0.00	-3.10	-2.68	-2.28
HG01783.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.36	-2.60	-2.66	-3.18	-2.85	-2.68	-2.35	-2.52	-2.32	0.00	0.00	0.00	0.00	0.00	-3.00	-2.78	-2.32
HG01784.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.38	-2.75	-2.76	-3.00	-2.59	-2.41	-2.42	-2.57	-2.33	0.00	-3.19	-2.68	0.00	0.00	-3.00	-2.84	-2.35
HG01785.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.87	-2.75	-2.77	-3.47	-2.50	-2.62	-2.55	-2.63	-2.47	0.00	-2.93	-2.73	0.00	0.00	-3.02	-2.79	-2.67
HG01786.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.75	-3.94	-4.12	-2.91	-2.49	-2.55	-2.42	-2.53	-2.39	0.00	0.00	0.00	0.00	-4.12	0.00	-2.59	-2.49
HG01789.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.44	-2.75	-2.73	-3.15	-2.47	-2.41	-2.41	-2.58	-2.57	-3.66	-2.77	-2.67	-2.71	-2.73	0.00	-2.72	-2.43
HG01790.mapped.ILLUMINA.bwa.GBR.exome.20130415	-2.44	-2.66	-2.82	-2.82	-2.82	-2.62	-2.29	-2.68	-2.60	-3.38	-3.23	0.00	-2.76	-2.74	0.00	-2.85	-2.32
HG01791.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.73	-2.73	-2.79	-2.96	-2.77	-2.79	-2.72	-2.64	-2.67	0.00	0.00	0.00	0.00	0.00	-3.05	-2.75	-2.70
HG01794.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.90	-2.73	-2.75	0.00	-2.89	-2.92	-2.75	-2.84	0.00	-3.18	-2.77	-2.94	-2.76	-2.76	0.00	0.00	-2.79
HG01795.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.98	-2.86	-2.88	-3.12	-2.68	-2.80	-2.76	-2.78	-2.81	-3.30	-3.10	-2.98	-4.82	0.00	-3.05	0.00	-2.90
HG01796.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.73	0.00	-4.70	-2.86	-2.62	-2.67	-2.68	-2.76	-2.68	0.00	0.00	0.00	0.00	0.00	-2.92	0.00	-2.73
HG01797.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.77	0.00	0.00	-2.89	-2.69	-2.74	-2.75	-2.74	-2.93	-3.20	-2.96	0.00	-2.83	-2.89	-3.06	0.00	-2.76
HG01798.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.78	0.00	-4.69	-2.76	-2.65	-2.68	-2.73	-2.77	-2.65	0.00	0.00	0.00	0.00	0.00	-3.04	-2.83	-2.73
HG01799.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.79	-2.78	-2.80	-3.04	-2.80	-2.78	-2.73	-2.77	-2.65	0.00	0.00	0.00	0.00	0.00	0.00	-2.67	-2.71
HG01800.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.80	0.00	0.00	-2.95	-2.71	-2.74	-2.71	-2.85	-2.95	-3.25	-3.02	-2.89	0.00	-2.79	0.00	-2.83	-2.80
HG01801.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.82	0.00	0.00	-2.98	-2.71	-2.73	-2.74	-2.83	-2.93	-3.26	-3.03	0.00	-2.92	-2.89	0.00	-2.85	-2.78
HG01802.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.80	0.00	-4.67	-2.84	-2.63	-2.65	-2.63	-2.79	-2.71	0.00	0.00	0.00	0.00	0.00	-2.89	0.00	-2.76
HG01804.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.80	0.00	-4.73	-2.73	-2.70	-2.67	-2.70	-2.69	-2.70	0.00	0.00	0.00	0.00	0.00	-3.08	-2.79	-2.70
HG01805.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.91	-4.78	0.00	-2.85	-2.75	-2.78	-2.81	-2.81	-4.48	-3.21	-2.87	0.00	-2.79	-2.77	0.00	0.00	-2.83
HG01806.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.85	-2.89	-2.90	-3.08	-2.90	-2.93	-2.79	-2.81	-2.91	-3.25	-3.01	0.00	-2.90	-2.89	-3.18	0.00	-2.80
HG01807.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.78	0.00	0.00	-2.73	-2.74	-2.76	-2.76	-2.83	-2.87	-3.24	-3.00	0.00	-2.89	-2.87	0.00	-2.90	-2.82
HG01808.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.75	0.00	0.00	-2.88	-2.61	-2.68	-2.70	-2.80	-2.68	0.00	0.00	0.00	0.00	0.00	-2.90	-4.67	-2.69
HG01809.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.86	-2.82	-2.86	-3.04	-2.85	-2.89	-2.76	-2.84	-4.77	-3.17	-2.72	-2.91	-2.98	-2.73	0.00	0.00	-2.84
HG01810.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.88	-2.92	-2.95	-3.15	-2.69	-2.82	-2.86	-2.86	-3.05	-3.26	-2.79	-2.97	-2.92	-2.92	0.00	-2.92	-2.81
HG01811.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.74	-2.75	-2.80	-2.98	-2.81	-2.86	-2.88	-2.99	-2.90	0.00	-2.93	0.00	-2.76	-2.79	-3.05	0.00	-2.77
HG01812.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.77	0.00	0.00	-2.86	-2.64	-2.67	-2.65	-2.63	-2.61	0.00	0.00	0.00	0.00	0.00	-3.05	-2.79	-2.68
HG01813.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.85	-2.83	-2.91	-3.10	-2.65	-2.78	-2.80	-2.86	-2.97	-3.26	-2.87	-2.97	-2.94	-2.93	-3.20	0.00	-2.86
HG01815.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.71	-2.79	-2.84	-3.05	-2.88	-2.85	-2.76	-2.75	-2.91	-3.26	-3.05	0.00	-2.82	-2.81	-3.08	0.00	-2.78
HG01816.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.83	-2.66	-2.70	0.00	-2.85	-2.90	-2.74	-2.73	-2.67	0.00	-3.01	-2.82	0.00	0.00	-3.10	-2.86	-2.81
HG01817.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.68	-4.70	-4.70	-2.75	-2.63	-2.69	-2.68	-2.83	-2.76	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.74
HG01840.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.89	-2.88	-2.93	-3.15	-2.66	-2.79	-2.71	-2.76	-2.85	-3.27	-3.01	-2.98	0.00	0.00	-3.01	0.00	-2.84
HG01841.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.84	-4.74	-4.44	-2.95	-2.73	-2.74	-2.81	-2.86	-3.05	-3.24	-3.05	-2.94	0.00	-2.91	0.00	-2.90	-2.82
HG01842.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.78	-2.80	-2.86	-3.10	-2.81	-2.87	-2.69	-2.75	-2.97	-3.21	-3.01	0.00	-2.89	-2.80	-3.04	0.00	-2.80
HG01843.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.82	-4.70	-4.70	-2.84	-2.64	-2.64	-2.73	-2.77	-2.70	-4.70	0.00	0.00	0.00	0.00	-3.08	-2.75	-2.70
HG01844.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.84	0.00	0.00	-2.97	-2.68	-2.71	-2.70	-2.72	-2.86	-3.15	-3.00	-2.91	0.00	-2.85	-3.04	0.00	-2.79
HG01845.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.73	0.00	0.00	-2.85	-2.64	-2.62	-2.71	-2.59	-2.56	0.00	-4.66	0.00	0.00	0.00	-3.00	-2.75	-2.69
HG01846.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.68	-2.73	-2.80	-2.96	-2.76	-2.77	-2.80	-2.92	-2.87	0.00	-2.93	-2.84	0.00	-2.74	0.00	-2.79	-2.72
HG01847.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.70	-4.62	0.00	-2.70	-2.63	-2.67	-2.61	-2.75	-2.63	0.00	0.00	0.00	0.00	0.00	-3.08	-2.75	-2.67
HG01848.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.71	0.00	-4.68	-2.83	-2.64	-2.65	-2.67	-2.70	-2.72	0.00	0.00	0.00	-4.68	0.00	0.00	-2.66	-2.70
HG01849.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.79	0.00	0.00	-2.91	-2.62	-2.69	-2.69	-2.72	-2.71	0.00	0.00	0.00	0.00	0.00	-3.01	-2.86	-2.75
HG01850.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.74	0.00	-4.36	-2.85	-2.68	-2.65	-2.68	-2.71	-2.64	0.00	0.00	0.00	0.00	0.00	-2.87	0.00	-2.69
HG01851.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.74	0.00	0.00	-2.71	-2.63	-2.61	-2.65	-2.75	-2.71	0.00	0.00	0.00	0.00	0.00	-3.06	-2.78	-2.69
HG01852.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.78	-2.76	-2.80	-3.02	-2.80	-2.91	-2.69	-2.77	-4.43	-3.17	-2.92	0.00	-2.87	-2.84	0.00	-2.87	-2.74
HG01853.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.80	-4.68	0.00	-2.87	-2.70	-2.65	-2.68	-2.71	-2.60	0.00	0.00	0.00	0.00	0.00	-2.99	-2.83	-2.65
HG01855.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.82	0.00	0.00	-2.93	-2.71	-2.69	-2.75	-2.75	-2.97	-3.24	-2.93	-2.89	0.00	-2.86	0.00	-2.89	-2.79
HG01857.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.77	0.00	0.00	-2.90	-2.63	-2.57	-2.66	-2.72	-2.71	-4.70	0.00	0.00	0.00	0.00	0.00	-2.54	-2.71
HG01858.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.76	0.00	0.00	-2.72	-2.68	-2.62	-2.75	-2.82	-2.87	-3.20	-3.01	-2.85	0.00	0.00	0.00	-2.81	-2.78
HG01859.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.69	0.00	-4.37	-2.91	-2.60	-2.62	-2.69	-2.77	-2.66	0.00	0.00	0.00	0.00	0.00	-2.87	-4.67	-2.75
HG01860.mapped.ILLUMINA.bwa.KHV.exome.20121211	-2.74	-4.58	-4.58	-2.87	-2.63	-2.65	-2.63	-2.73	-2.67	0.00	0.00	0.00	0.00	0.00	-2.83	0.00	-2.67
HG01861.mapped.ILLUMINA.bwa.KHV.exome.20121211	-2.65	0.00	0.00	-2.72	-2.66	-2.64	-2.69	-2.79	-2.72	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.67
HG01862.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.52	-2.71	-2.72	-2.84	-2.71	-2.67	-2.77	-2.72	-2.74	0.00	-2.83	0.00	-2.77	-2.69	0.00	-2.80	-2.44
HG01863.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.41	-2.78	-2.67	-2.88	-2.71	-2.69	-2.60	-2.49	-2.51	0.00	0.00	0.00	0.00	-4.68	-3.12	-2.75	-2.48
HG01864.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.51	-4.70	0.00	-2.75	-2.60	-2.61	-2.61	-2.56	-2.56	0.00	-4.70	-4.70	-4.40	0.00	-3.16	-2.82	-2.51
HG01865.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.54	-4.71	-4.41	-2.62	-2.53	-2.57	-2.63	-2.63	-2.50	0.00	-4.71	-4.71	-4.71	-4.71	0.00	-2.66	-2.44
HG01866.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.57	-4.67	-4.19	-2.74	-2.55	-2.64	-2.65	-2.61	-2.56	0.00	0.00	-4.37	0.00	-4.67	0.00	-2.51	-2.46
HG01867.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.52	0.00	-4.36	-2.69	-2.58	-2.57	-2.63	-2.60	-2.53	0.00	0.00	0.00	0.00	0.00	-3.01	-4.66	-2.51

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG01868.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.55	-4.71	-4.41	-2.83	-2.60	-2.67	-2.64	-2.60	-2.76	-3.60	-2.93	-4.41	-2.84	-2.77	-3.19	-4.71	-2.44
HG01869.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.44	-2.74	-2.74	-2.88	-2.67	-2.74	-2.60	-2.57	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.48	-2.48
HG01870.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.64	0.00	0.00	-3.06	-2.66	-2.70	-2.70	-2.55	-2.71	-3.61	-2.84	-2.75	0.00	-2.77	-2.98	0.00	-2.79
HG01871.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.68	0.00	-4.79	-2.85	-2.52	-2.55	-2.56	-2.49	-2.54	0.00	0.00	0.00	-4.79	0.00	-2.89	-2.77	-2.59
HG01872.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.79	0.00	0.00	-2.76	-2.66	-2.63	-2.59	-2.63	0.00	-3.54	-2.68	0.00	-2.68	-2.57	0.00	0.00	-2.77
HG01873.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.70	0.00	0.00	-2.98	-2.63	-2.66	-2.64	-2.53	-2.53	0.00	0.00	0.00	0.00	-4.30	-2.98	-2.74	-2.67
HG01874.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.67	0.00	0.00	-2.78	-2.58	-2.63	-2.54	-2.52	-2.46	0.00	0.00	0.00	0.00	-4.84	-3.00	-2.73	-2.63
HG01878.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.62	-2.74	-2.76	-3.08	-2.74	-2.72	-2.71	-2.73	-2.71	0.00	-2.77	-2.74	0.00	-2.73	-3.01	0.00	-2.67
HG01879.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.86	-2.80	-2.88	-3.06	-2.75	-2.90	-2.86	-3.04	-4.71	-3.23	-2.71	0.00	-2.70	-2.71	0.00	-4.71	-2.76
HG01880.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.73	-2.77	-2.80	-3.04	-2.76	-2.83	-2.95	-2.98	-2.88	0.00	-2.92	0.00	-2.79	-2.79	0.00	-2.80	-2.72
HG01882.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.85	-2.80	-2.90	-3.07	-2.62	-2.70	-2.75	-2.88	-2.71	0.00	-2.98	-2.87	0.00	-4.43	-2.94	0.00	-2.75
HG01883.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.71	0.00	0.00	-2.73	-2.59	-2.61	-2.63	-2.65	-2.86	-3.08	-2.95	-2.81	0.00	-2.71	0.00	0.00	-2.78
HG01885.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.54	-4.38	0.00	-2.71	-2.56	-2.53	-2.57	-2.56	-2.56	0.00	0.00	-4.68	-4.68	-4.68	-2.98	0.00	-2.48
HG01886.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.70	0.00	0.00	-2.92	-2.60	-2.59	-2.60	-2.51	-2.52	0.00	0.00	0.00	0.00	-4.82	0.00	-2.45	-2.63
HG01889.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.35	-2.77	-2.74	-2.82	-2.58	-2.42	-2.44	-2.65	-2.41	0.00	-3.24	0.00	-2.77	0.00	-2.99	-2.88	-2.31
HG01890.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.35	0.00	0.00	-2.69	-2.37	-2.39	-2.27	-2.62	-2.36	0.00	0.00	0.00	0.00	0.00	-3.09	0.00	-2.54
HG01892.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.81	0.00	0.00	-2.87	-2.62	-2.66	-2.64	-2.72	-2.69	0.00	0.00	0.00	0.00	-4.65	0.00	-2.62	-2.67
HG01893.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.66	0.00	0.00	-2.82	-2.60	-2.61	-2.70	-2.70	-2.63	0.00	0.00	0.00	0.00	0.00	-2.80	0.00	-2.73
HG01894.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.43	0.00	0.00	-2.73	-2.55	-2.45	-2.33	-2.53	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.30
HG01896.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.78	0.00	0.00	-2.71	-2.57	-2.67	-2.68	-2.69	-2.63	0.00	0.00	0.00	0.00	0.00	-3.02	-2.83	-2.71
HG01912.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.43	-2.53	-2.56	-2.95	-2.45	-2.43	-2.31	-2.61	-2.33	-4.18	-2.86	-2.69	0.00	-4.18	0.00	-2.84	-2.43
HG01914.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.77	0.00	-4.67	-2.70	-2.62	-2.66	-2.65	-2.69	-2.68	0.00	0.00	0.00	0.00	0.00	-3.03	-2.72	-2.74
HG01915.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.72	-2.65	-2.74	-2.97	-2.74	-2.81	-2.63	-2.63	-2.63	0.00	0.00	0.00	0.00	0.00	-2.98	0.00	-2.77
HG01917.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.79	0.00	-4.73	-2.86	-2.64	-2.70	-2.69	-2.72	-2.93	-3.18	-2.88	0.00	-2.91	-2.82	0.00	-4.26	-2.74
HG01918.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.74	0.00	0.00	-2.88	-2.61	-2.66	-2.66	-2.78	-2.72	-4.67	0.00	0.00	-4.67	-4.37	-3.03	-2.79	-2.66
HG01920.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.84	-2.74	-2.84	-3.05	-2.80	-2.79	-2.73	-2.72	-2.89	-3.22	-2.96	0.00	-2.85	-2.82	-3.04	-4.75	-2.75
HG01921.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.83	0.00	0.00	-2.77	-2.68	-2.69	-2.74	-2.72	-2.94	-3.23	-2.94	0.00	-2.91	-2.88	0.00	-2.85	-2.79
HG01923.mapped.ILLUMINA.bwa.PEL.exome.20121211	-2.76	-4.72	0.00	-2.92	-2.67	-2.68	-2.77	-2.68	-2.90	-3.24	-2.98	0.00	-2.82	-2.82	-3.01	0.00	-2.70
HG01924.mapped.ILLUMINA.bwa.PEL.exome.20121211	-2.69	0.00	0.00	-2.80	-2.58	-2.56	-2.62	-2.73	-2.60	0.00	0.00	0.00	0.00	0.00	-2.98	-2.71	-2.61
HG01926.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.52	0.00	-4.70	-2.71	-2.57	-2.62	-2.59	-2.59	-2.53	0.00	-4.70	0.00	-4.70	-4.70	-3.01	0.00	-2.47
HG01927.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.51	-4.66	-4.36	-2.74	-2.51	-2.55	-2.59	-2.61	-2.47	0.00	0.00	0.00	-4.66	0.00	-2.98	-4.66	-2.44
HG01932.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.63	-2.82	-2.75	-2.94	-2.57	-2.63	-2.68	-2.61	-2.56	0.00	-2.96	-2.76	-4.75	0.00	-3.17	-2.84	-2.54
HG01933.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.42	-2.62	-2.69	-2.83	-2.64	-4.59	-2.67	-2.67	-2.65	0.00	0.00	0.00	0.00	-2.63	-3.02	-4.59	-2.39
HG01935.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.52	0.00	0.00	-2.76	-2.51	-2.60	-2.56	-2.63	-2.50	0.00	0.00	-4.69	0.00	0.00	-3.02	-4.69	-2.49
HG01936.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.53	-4.66	0.00	-2.59	-2.59	-2.59	-2.60	-2.59	-2.49	0.00	0.00	-4.36	0.00	-4.36	-3.15	-2.79	-2.49
HG01938.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.50	-2.73	-2.70	-2.83	-2.68	-2.68	-2.59	-2.58	-2.56	0.00	0.00	0.00	-4.66	-4.66	-2.97	-4.66	-2.45
HG01939.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.62	-2.78	-2.76	-2.92	-2.73	-2.75	-2.67	-2.57	-2.81	-3.54	-2.92	0.00	-2.82	-2.71	0.00	-2.80	-2.54
HG01941.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.58	0.00	-4.22	-2.66	-2.55	-2.57	-2.56	-2.50	-2.53	0.00	0.00	0.00	0.00	0.00	-3.09	-2.82	-2.48
HG01942.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.49	-4.63	-4.63	-2.75	-2.54	-2.57	-2.56	-2.57	-2.52	0.00	0.00	-4.63	-4.63	-4.63	-2.97	0.00	-2.47
HG01944.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.54	0.00	-3.87	-2.72	-2.57	-2.56	-2.66	-2.60	-2.54	0.00	-4.65	0.00	0.00	0.00	-3.00	0.00	-2.48
HG01945.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.50	0.00	-4.37	-2.75	-2.52	-2.56	-2.54	-2.59	-2.62	0.00	0.00	-4.68	0.00	-4.37	-2.99	-4.37	-2.44
HG01947.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.60	-2.65	-2.67	0.00	-2.81	-2.80	-2.67	-2.66	-2.75	-3.42	-2.77	-2.88	-2.89	-2.75	-3.20	0.00	-2.53
HG01948.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.48	0.00	0.00	-2.73	-2.51	-2.60	-2.59	-2.51	-2.49	0.00	-4.65	-4.65	-4.65	0.00	-3.09	-2.74	-2.43
HG01950.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.60	-2.82	-2.77	-2.93	-2.50	-2.69	-2.71	-2.50	-2.58	0.00	-2.92	-2.83	-4.75	-4.45	-3.10	-2.84	-2.54
HG01951.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.51	-4.65	-4.35	-2.71	-2.54	-2.60	-2.61	-2.64	-2.51	0.00	-4.65	-4.65	-4.65	-4.65	-3.06	0.00	-2.45
HG01953.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.76	-2.72	-2.73	-3.11	-2.75	-2.80	-2.59	-2.57	-2.73	-3.77	-2.84	0.00	-2.78	-2.74	-3.03	0.00	-2.68
HG01954.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.65	-4.49	0.00	-2.94	-2.62	-2.58	-2.59	-2.50	-2.49	0.00	-4.49	0.00	0.00	-4.79	-2.95	-2.75	-2.68
HG01956.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.57	-2.69	-2.74	-2.90	-2.70	-2.73	-2.64	-2.44	-2.52	0.00	0.00	0.00	-4.67	-4.37	-3.18	-2.77	-2.52
HG01958.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.86	-2.84	-2.89	-3.04	-2.59	-2.74	-2.70	-2.80	-2.80	0.00	-2.98	-2.93	0.00	-4.78	-2.94	0.00	-2.79
HG01961.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.72	-2.67	-2.63	-3.26	-2.61	-2.65	-2.54	-2.78	-2.54	0.00	-2.84	-4.41	-2.64	-2.66	-2.99	-4.11	-2.51
HG01965.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.91	-4.51	-4.51	-2.91	-2.52	-2.51	-2.51	-2.56	-2.48	-4.20	-4.20	0.00	-4.03	-3.66	-2.91	-2.74	-2.60
HG01967.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.72	-4.77	0.00	-3.01	-2.61	-2.61	-2.56	-2.51	-2.57	0.00	0.00	0.00	0.00	-4.77	-2.91	-2.71	-2.63
HG01968.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.70	0.00	-4.73	-2.86	-2.55	-2.58	-2.60	-2.55	-2.55	0.00	0.00	0.00	0.00	0.00	-2.80	0.00	-2.57
HG01970.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.73	0.00	-4.49	-2.93	-2.60	-2.62	-2.60	-2.50	-2.54	0.00	0.00	0.00	0.00	0.00	-2.96	-2.72	-2.72
HG01971.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.68	0.00	-4.77	-2.95	-2.58	-2.58	-2.58	-2.59	-2.53	0.00	0.00	-4.77	0.00	0.00	-2.85	0.00	-2.65
HG01973.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.70	0.00	-4.77	-2.72	-2.62	-2.58	-2.57	-2.65	-2.60	0.00	0.00	0.00	0.00	-4.77	-2.86	0.00	-2.65
HG01974.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.62	0.00	-4.48	-2.95	-2.54	-2.57	-2.58	-2.60	-2.53	-4.78	0.00	0.00	-4.78	0.00	-2.84	0.00	-2.66
HG01976.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.70	0.00	-4.75	-2.91	-2.54	-2.61	-2.60	-2.43	-2.43	-4.75	0.00	0.00	0.00	-4.75	-2.91	-2.73	-2.60
HG01977.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.59	0.00	0.00	-2.92	-2.54	-2.56	-2.58	-2.58	-2.51	0.00	0.00	0.00	0.00	-4.75	-2.81	-4.75	-2.65
HG01979.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.24	0.00	0.00	-2.74	-2.43	-2.33	-2.27	-2.39	-2.31	0.00	0.00	0.00	0.00	0.00	0.00	-2.32	-2.31
HG01980.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.25	-2.56	-2.69	-2.94	-2.48	-2.38	-2.33	-2.44	-2.63	-3.54	-2.65	-2.46	0.00	-2.56	0.00	-2.65	-2.36
HG01982.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.75	0.00	0.00	-2.90	-2.62	-2.61	-2.68	-2.72	-2.71	0.00	0.00	0.00	0.00	0.00	-2.92	-4.69	-2.69
HG01983.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.79	-2.74	-2.83	-3.01	-2.83	-2.67	-2.72	-2.79	-2.75	-4.69	-3.08	0.00	-2.95	0.00	-3.12	-2.85	-2.77
HG01985.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.89	-2.82	-2.92	-3.08	-2.74	-2.71	-2.73	-2.85	-2.75	0.00	-2.97	0.00	-2.88	-4.76	-3.02	0.00	-2.78
HG01986.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.77	0.00	-4.64	-2.86	-2.63	-2.63	-2.69	-2.62	-2.74	0.00	0.00	0.00	0.00	0.00	-3.01	-2.74	-2.68
HG01988.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.54	0.00	-4.62	-2.59	-2.54	-2.59	-2.61	-2.60	-2.53	0.00	0.00	0.00	0.00	-4.32	-3.02	-4.62	-2.44
HG01989.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.53	-2.84	-2.78	-2.97	-2.53	-2.64	-2.69	-2.68	-2.87	-3.48	-2.81	-2.81	-2.87	-2.75	0.00	-2.79	-2.55
HG01990.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.80	0.00	0.00	-2.69	-2.55	-2.71	-2.69	-2.78	-2.66	-4.72	-4.72	0.00	-4.72	-4.42	-2.90	-4.42	-2.72
HG01991.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.29	0.00	0.00	-2.69	-2.60	-2.40	-2.34	-2.55	-2.41	0.00	-4.03	0.00	0.00	0.00	-2.88	-2.77	-2.25
HG01992.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.31	-2.66	-2.62	-2.81	-2.62	-2.51	-2.31	-2.62	-2.30	0.00	0.00	0.00	0.00	0.00	-2.78	0.00	-2.30
HG01997.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.51	0.00	-3.99	-2.81	-2.55	-2.37	-2.36	-2.55	-2.31	0.00	0.00	0.00	0.00	0.00	-2.78	0.00	-2.21
HG02002.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.37	-2.78	-2.60	-2.87	-2.73	-2.55	-2.36	-2.49	-2.35	0.00	-4.01	0.00	0.00	0.00	-2.87	-4.01	-2.21
HG02003.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.44	-2.66	-2.63	-3.10	-2.57	-2.41	-2.48	-2.65	-2.41	0.00	-2.95	-2.71	0.00	0.00	-3.34	-2.90	-2.32
HG02006.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.81	0.00	-4.78	-2.83	-2.54	-2.57	-2.53	-2.57	-2.54	-4.17	-4.08	0.00	-3.93	-4.00	0.00	-2.59	-2.67
HG02008.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.39	-2.68	-2.87	-3.22	-2.60	-2.59	-2.42	-2.62	-2.74	-3.70	-2.77	-2.63	0.00	-2.81	0.00	-2.79	-2.32
HG02009.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.37	-2.63	-3.00	-2.89	-2.37	-2.40	-2.39	-2.64	-2.55	-4.04	-2.72	-2.70	-2.86	-2.64	0.00	0.00	-2.54
HG02010.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.37	0.00	0.00	-2.55	-2.60	-2.43	-2.32	-2.47	-2.32	0.00	0.00	0.00	0.00	-4.09	0.00	-2.58	-2.37
HG02012.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.90	-2.86	-2.91	-3.16	-2.66	-2.78	-2.80	-2.86	-3.07	-3.36	-2.84	-2.95	-2.95	-2.95	-3.15	0.00	-2.81
HG02013.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.81	0.00	0.00	-2.78	-2.56	-2.67	-2.64	-2.83	-2.68	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.71
HG02014.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.81	0.00	-4.87	-2.84	-2.51	-2.73	-2.67	-2.55	-2.81	-3.83	-2.88	0.00	-2.77	-2.77	-3.06	0.00	-2.78
HG02016.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.39	-2.88	-2.63	-2.90	-2.76	-2.68	-2.41	-2.43	-2.64	-3.38	-2.93	0.00	-2.61	-2.52	-3.04	-3.86	-2.26
HG02017.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.37	0.00	0.00	-2.67	-2.44	-2.44	-2.31	-2.42	-2.34	0.00	0.00	0.00	-3.73	0.00	0.00	-2.46	-2.37
HG02019.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.30	-2.57	-2.70	-3.07	-2.69	-2.50	-2.29	-2.42	-2.28	0.00	0.00	0.00	0.00	-4.15	0.00	-2.41	-2.32
HG02020.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.29	0.00	0.00	-2.74	-2.45	-2.33	-2.40	-2.47	-2.29	0.00	-4.14	0.00	0.00	0.00	-3.29	-2.76	-2.32
HG02023.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.61	-2.81	-2.82	-2.91	-2.55	-2.67	-2.66	-2.65	-2.75	0.00	-2.92	-2.81	0.00	-4.73	-3.20	-2.83	-2.54
HG02024.mapped.ILLUMINA.bwa.KHV.exome.20130422	-2.67	-2.74	-2.66	-3.94	-2.74	-2.77	-2.70	-2.75	-3.68	-3.29	-2.70	-2.81	-2.74	-2.70	0.00	-4.42	-2.60
HG02025.mapped.ILLUMINA.bwa.KHV.exome.20130422	-2.69	-2.95	-2.93	-3.02	-2.66	-2.70	-2.72	-2.85	-2.91	-3.50	-2.88	-2.92	-2.96	-2.88	0.00	-2.90	-2.61
HG02026.mapped.ILLUMINA.bwa.KHV.exome.20130422	-2.67	-2.88	-2.80	-2.96	-2.79	-2.82	-2.76	-2.67	-2.81	-3.33	-2.90	-4.01	-2.89	-2.78	0.00	-2.90	-2.55
HG02028.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.59	0.00	-4.40	-2.75	-2.57	-2.63	-2.69	-2.58	-2.72	-3.50	-2.97	0.00	-2.88	-2.72	-3.08	0.00	-2.55
HG02029.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.48	0.00	-4.06	-2.76	-2.54	-2.55	-2.55	-2.62	-2.57	0.00	-4.66	-4.66	0.00	-3.96	-2.95	-4.66	-2.46
HG02031.mapped.ILLUMINA.bwa.KHV.exome.20121211	-2.66	0.00	0.00	-2.89	-2.63	-2.66	-2.63	-2.63	-2.70	0.00	0.00	0.00	0.00	0.00	-3.06	-2.91	-2.69
HG02032.mapped.ILLUMINA.bwa.KHV.exome.20121211	-2.78	0.00	0.00	-2.75	-2.64	-2.62	-2.68	-2.76	-2.68	0.00	0.00	0.00	-4.63	-4.63	-3.07	-2.70	-2.73
HG02035.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.46	0.00	0.00	-2.78	-2.44	-2.45	-2.37	-2.58	-2.54	-3.22	-3.08	0.00	-2.95	-2.82	-2.98	-3.65	-2.43
HG02040.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.49	0.00	0.00	-2.71	-2.53	-2.54	-2.53	-2.54	-2.48	0.00	0.00	0.00	-4.60	-4.60	-3.12	-2.70	-2.42
HG02046.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.51	-2.89	-2.83	-3.00	-2.61	-2.69	-2.62	-2.56	-2.54	-3.50	-3.03	-2.81	0.00	0.00	-3.21	-2.88	-2.55
HG02047.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.59	0.00	-4.64	-2.80	-2.62	-2.66	-2.57	-2.67	-2.70	-3.53	-2.90	-2.74	0.00	-2.73	0.00	-2.81	-2.51

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02048.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.71	0.00	-4.79	-2.94	-2.60	-2.58	-2.57	-2.49	-2.43	0.00	0.00	0.00	-4.79	0.00	-2.92	-2.76	-2.67
HG02049.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.70	0.00	0.00	-2.94	-2.56	-2.64	-2.60	-2.59	-2.53	0.00	0.00	0.00	0.00	-4.79	-2.81	0.00	-2.65
HG02050.mapped.ILLUMINA.bwa.KHV.exome.20121211	-2.69	0.00	-4.66	-2.70	-2.57	-2.65	-2.71	-2.71	-2.64	0.00	0.00	0.00	0.00	0.00	-3.01	-2.78	-2.69
HG02051.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.83	0.00	-2.87	-3.06	-2.60	-2.75	-2.74	-2.69	-2.75	0.00	-3.03	0.00	-2.91	0.00	-3.10	-2.89	-2.74
HG02052.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.48	0.00	-4.59	-2.74	-2.58	-2.57	-2.58	-2.56	-2.50	0.00	-4.59	-4.59	0.00	-4.59	-3.05	-2.80	-2.49
HG02053.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.95	-2.84	-2.98	-3.20	-2.78	-2.76	-2.81	-2.76	-2.98	-3.31	-2.80	-2.95	-2.98	-2.90	0.00	-3.00	-2.84
HG02054.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.33	0.00	-3.86	-2.70	-2.50	-2.41	-2.30	-2.54	-2.36	0.00	0.00	0.00	0.00	-4.16	-2.93	0.00	-2.34
HG02057.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.67	0.00	-4.26	-2.86	-2.55	-2.60	-2.60	-2.47	-2.56	0.00	0.00	-4.86	0.00	-4.86	-2.97	-2.76	-2.68
HG02058.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.77	-2.85	-2.90	-3.18	-2.60	-2.73	-2.74	-2.62	-2.79	-3.92	-2.68	-2.90	-2.87	-2.84	-3.08	-4.62	-2.77
HG02060.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.75	-2.76	-2.78	-3.02	-2.78	-2.83	-2.68	-2.69	-2.64	0.00	0.00	0.00	-4.69	0.00	-3.03	-2.81	-2.70
HG02061.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.86	-2.81	-2.87	-2.86	-2.74	-2.72	-2.71	-2.83	-3.01	-3.23	-2.97	0.00	-2.98	-2.88	0.00	-2.90	-2.77
HG02064.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.91	-2.87	-2.91	-3.21	-2.68	-2.78	-2.82	-2.89	-4.50	-3.22	-2.69	-3.08	-2.75	-2.75	0.00	0.00	-2.79
HG02067.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.89	-2.88	-2.89	-3.13	-2.66	-2.77	-2.69	-2.72	-2.80	-3.25	-3.10	-2.96	0.00	-4.80	-3.02	0.00	-2.80
HG02069.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.70	-2.78	-2.76	-3.16	-2.76	-2.78	-2.61	-2.54	-2.73	-3.89	-2.81	0.00	-2.76	-2.75	-3.05	-4.93	-2.66
HG02070.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.61	-2.80	-2.76	-3.17	-2.78	-2.74	-2.63	-2.58	0.00	-3.61	-2.62	-4.61	-2.69	-2.64	0.00	-4.91	-2.69
HG02072.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.71	-2.73	-2.76	-3.12	-2.74	-2.79	-2.59	-2.57	-2.46	0.00	0.00	-4.79	0.00	0.00	0.00	-2.44	-2.65
HG02073.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.65	0.00	-4.54	-2.91	-2.52	-2.56	-2.54	-2.51	-2.50	0.00	-4.54	-4.54	-4.54	0.00	-2.93	-2.75	-2.60
HG02075.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.33	-2.67	-2.72	-2.89	-2.64	-2.60	-2.35	-2.47	-2.38	0.00	0.00	0.00	0.00	0.00	-2.94	-2.85	-2.33
HG02076.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.37	0.00	-4.13	-2.57	-2.54	-2.45	-2.37	-2.56	-2.32	0.00	-4.13	-4.13	0.00	-3.83	-2.98	-2.95	-2.31
HG02078.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.40	-2.65	-2.68	-3.04	-2.78	-2.60	-2.35	-2.59	-2.59	-3.20	-3.25	0.00	-2.68	-2.57	0.00	-2.79	-2.37
HG02079.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.30	0.00	0.00	-2.77	-2.46	-2.30	-2.33	-2.50	-2.39	0.00	0.00	0.00	0.00	0.00	-2.69	0.00	-2.34
HG02081.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.40	0.00	-3.80	-2.58	-2.45	-2.41	-2.40	-2.65	-2.37	0.00	-3.80	0.00	0.00	0.00	-2.95	-4.10	-2.32
HG02082.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.41	-2.65	-2.60	-3.06	-2.75	-2.70	-2.44	-2.55	-2.32	0.00	0.00	0.00	-3.84	0.00	-3.10	-2.65	-2.32
HG02084.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.37	0.00	0.00	-2.59	-2.53	-2.38	-2.34	-2.60	-4.13	-3.44	-2.64	0.00	-2.69	-2.41	0.00	0.00	-2.34
HG02085.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.40	0.00	0.00	-2.70	-2.50	-2.38	-2.37	-2.63	-2.34	0.00	0.00	0.00	0.00	0.00	-2.77	0.00	-2.30
HG02086.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.45	0.00	0.00	-2.70	-2.68	-2.45	-2.39	-2.41	-2.72	-3.26	-2.96	0.00	-2.75	-2.58	0.00	-3.00	-2.28
HG02087.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.34	0.00	-4.21	-2.63	-2.58	-2.45	-2.50	-2.54	-2.59	-3.43	-3.09	0.00	-2.78	-2.83	0.00	-2.95	-2.35
HG02088.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.36	0.00	0.00	-2.78	-2.49	-2.41	-2.41	-2.48	-2.34	0.00	-4.11	0.00	0.00	0.00	-2.60	0.00	-2.32
HG02089.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.26	-2.62	-2.57	-2.82	-2.70	-2.67	-2.35	-2.49	-2.61	-3.21	-2.97	0.00	-2.65	-2.62	-3.04	0.00	-2.27
HG02090.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.33	0.00	0.00	-2.56	-2.53	-2.30	-2.37	-2.41	-2.35	0.00	0.00	0.00	0.00	0.00	0.00	-2.33	-2.26
HG02095.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.51	0.00	0.00	-2.69	-2.53	-2.54	-2.72	-2.74	-2.66	0.00	-2.84	0.00	-2.78	-2.63	-3.09	-4.58	-2.46
HG02102.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.91	-2.71	-2.75	-3.10	-2.75	-2.73	-2.60	-2.54	-2.75	-3.44	-2.77	0.00	-2.75	-2.75	-3.09	-4.00	-2.75
HG02104.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.33	-2.67	-2.68	-2.87	-2.70	-2.57	-2.38	-2.46	-2.57	-3.32	-2.74	0.00	-2.62	-2.50	0.00	-2.52	-2.25
HG02105.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.29	-3.95	0.00	-2.70	-2.65	-2.43	-2.34	-2.54	-2.16	0.00	0.00	0.00	0.00	0.00	-3.35	-2.54	-2.24
HG02107.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.45	-4.63	0.00	-2.68	-2.61	-2.66	-2.67	-2.66	-2.69	-3.55	-2.93	0.00	-2.83	-2.72	0.00	-2.78	-2.50
HG02108.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.57	-2.72	-4.29	-2.86	-2.69	-2.68	-2.76	-2.74	-2.65	0.00	-2.83	0.00	-2.74	-2.71	-3.07	-4.59	-2.49
HG02111.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.48	-2.76	-2.70	-2.84	-2.61	-2.71	-2.61	-2.54	-2.52	-4.58	0.00	0.00	0.00	-4.58	-3.09	-2.76	-2.46
HG02113.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.33	-4.25	0.00	-2.81	-2.55	-2.50	-2.41	-2.51	-2.67	-3.35	-3.02	-2.62	0.00	-2.54	0.00	-2.73	-2.37
HG02116.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.48	0.00	-4.59	-2.71	-2.53	-2.53	-2.55	-2.48	-2.54	0.00	0.00	0.00	0.00	-4.11	-3.07	-2.81	-2.44
HG02121.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.29	0.00	0.00	-2.58	-2.43	-2.37	-2.38	-2.32	-2.37	0.00	0.00	0.00	0.00	0.00	-2.97	-2.63	-2.35
HG02122.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.29	-2.65	-2.58	-2.85	-2.76	-2.67	-2.29	-2.60	-2.32	0.00	0.00	0.00	0.00	0.00	-2.74	0.00	-2.27
HG02127.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.44	-2.66	-2.75	-2.91	-2.55	-2.47	-2.42	-2.58	-2.69	-3.33	-2.75	-2.79	-2.79	-2.61	-3.20	0.00	-2.37
HG02128.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.37	0.00	0.00	-2.74	-2.47	-2.39	-2.37	-2.44	-2.63	-3.12	-2.88	-3.90	-2.69	-2.65	-3.08	0.00	-2.37
HG02130.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.74	-2.77	-2.82	-3.00	-2.76	-2.85	-2.66	-2.68	-2.70	0.00	0.00	0.00	0.00	-4.65	-3.10	-2.90	-2.68
HG02131.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.84	-2.78	-2.89	-3.12	-2.83	-2.96	-2.74	-2.77	-2.99	-3.22	-2.97	-2.91	0.00	-2.91	0.00	-2.87	-2.70
HG02133.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.76	0.00	0.00	-2.71	-2.63	-2.65	-2.67	-2.65	-2.71	0.00	0.00	0.00	0.00	0.00	-3.05	-2.80	-2.71
HG02134.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.79	0.00	0.00	-2.89	-2.67	-2.65	-2.74	-2.79	-2.90	-3.21	-3.03	0.00	-2.81	-2.83	-3.08	-4.77	-2.75
HG02136.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.75	0.00	-4.65	-2.73	-2.65	-2.66	-2.64	-2.74	-2.69	0.00	0.00	0.00	0.00	0.00	-3.05	-2.78	-2.69
HG02137.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.71	0.00	0.00	-2.90	-2.62	-2.65	-2.68	-2.73	-2.70	0.00	0.00	0.00	0.00	0.00	-2.82	0.00	-2.67
HG02138.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.48	0.00	0.00	-2.85	-2.42	-2.45	-2.32	-2.50	-2.58	-3.42	-3.35	-2.81	0.00	-2.65	0.00	-2.75	-2.35
HG02139.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.34	0.00	0.00	-2.71	-2.49	-2.36	-2.33	-2.45	-2.32	0.00	0.00	0.00	0.00	0.00	-3.24	-2.78	-2.31
HG02140.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.36	-2.78	-2.64	-2.83	-2.64	-2.55	-2.34	-2.57	-2.24	0.00	-4.11	0.00	0.00	0.00	-2.90	-2.60	-2.27
HG02141.mapped.ILLUMINA.bwa.KHV.exome.20130415	-2.41	0.00	0.00	-2.83	-2.43	-2.40	-2.33	-2.48	-2.33	0.00	0.00	0.00	0.00	0.00	-2.98	-2.66	-2.29
HG02142.mapped.ILLUMINA.bwa.KHV.exome.20121211	-2.66	-4.40	-4.71	-2.70	-2.63	-2.65	-2.66	-2.72	-2.66	0.00	0.00	0.00	0.00	-4.40	0.00	-2.58	-2.71
HG02143.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.57	0.00	-4.33	-2.82	-2.51	-2.63	-2.62	-2.55	-2.67	-3.43	-2.87	0.00	-2.73	-2.70	-3.22	0.00	-2.49
HG02144.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.62	-2.81	-2.79	-2.97	-2.54	-2.63	-2.68	-2.69	-2.62	0.00	-2.72	-2.80	-2.86	-4.69	-3.12	-4.69	-2.55
HG02146.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.74	0.00	0.00	-2.72	-2.62	-2.69	-2.67	-2.70	-2.69	0.00	0.00	0.00	0.00	0.00	-3.10	-2.77	-2.72
HG02147.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.78	0.00	0.00	-2.62	-2.55	-2.60	-2.68	-2.76	-2.74	0.00	0.00	0.00	0.00	0.00	-2.87	0.00	-2.67
HG02150.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.94	-4.37	-4.85	-2.99	-2.67	-2.66	-2.54	-2.59	-4.15	-3.23	-2.65	0.00	-2.64	-2.63	0.00	-4.55	-2.78
HG02151.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.79	-4.47	0.00	-2.95	-2.68	-2.71	-2.75	-2.74	-2.92	-3.24	-2.94	0.00	-2.85	-2.89	-3.06	0.00	-2.75
HG02152.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.40	-4.23	0.00	-2.78	-2.58	-2.39	-2.30	-2.36	-2.43	-3.39	0.00	0.00	0.00	0.00	-2.80	0.00	-2.39
HG02153.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.23	0.00	0.00	-2.58	-2.58	-2.30	-2.35	-2.58	-2.33	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.20
HG02154.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.34	0.00	0.00	-2.72	-2.51	-2.36	-2.37	-2.53	-2.62	-3.71	-2.86	-2.56	0.00	-2.49	0.00	-2.72	-2.31
HG02155.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.36	-2.49	-2.38	-4.13	-2.81	-2.57	-2.42	-2.44	-2.70	-3.43	-2.67	-2.54	0.00	-2.54	0.00	-2.83	-2.33
HG02156.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.33	0.00	0.00	-2.71	-2.49	-2.45	-2.43	-2.43	-2.27	0.00	0.00	0.00	0.00	0.00	-3.28	-2.94	-2.32
HG02164.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.29	0.00	0.00	-2.82	-2.55	-2.33	-2.24	-2.57	-2.42	0.00	0.00	0.00	0.00	0.00	-3.08	-2.67	-2.23
HG02165.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.35	0.00	0.00	-2.61	-2.50	-2.34	-2.36	-2.59	-2.33	0.00	0.00	0.00	-3.93	0.00	-3.03	-2.93	-2.21
HG02166.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.31	-4.17	0.00	-2.68	-2.43	-2.36	-2.36	-2.59	-2.34	0.00	0.00	-3.87	0.00	0.00	-2.77	0.00	-2.30
HG02178.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.34	0.00	0.00	-2.73	-2.41	-2.42	-2.35	-2.58	-2.30	0.00	0.00	0.00	0.00	0.00	-2.62	0.00	-2.26
HG02179.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.40	-2.50	-2.57	-4.05	-2.76	-2.67	-2.38	-2.44	-2.43	-3.35	-2.95	-2.76	0.00	0.00	-2.87	0.00	-2.39
HG02180.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.35	0.00	-4.05	-2.59	-2.42	-2.49	-2.41	-2.51	-2.53	-3.45	-2.94	0.00	-2.67	-2.67	-3.10	0.00	-2.31
HG02181.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.30	0.00	0.00	-2.58	-2.42	-2.40	-2.28	-2.60	-2.34	0.00	0.00	0.00	0.00	0.00	-2.80	-4.03	-2.30
HG02182.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.31	0.00	0.00	-2.62	-2.40	-2.27	-2.26	-2.51	-2.34	0.00	0.00	0.00	0.00	0.00	-2.86	0.00	-2.27
HG02184.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.43	0.00	0.00	-2.59	-2.37	-2.47	-2.35	-2.49	-2.62	-3.34	-3.43	0.00	-2.92	-2.61	-3.08	-4.04	-2.29
HG02185.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.32	0.00	0.00	-2.56	-2.49	-2.29	-2.34	-2.36	-2.35	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.17
HG02186.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.35	0.00	0.00	-2.64	-2.64	-2.28	-2.27	-2.52	-2.58	-3.26	-2.93	0.00	-2.55	-2.66	0.00	-2.51	-2.20
HG02187.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.35	-2.70	-2.62	-2.82	-2.50	-2.67	-2.23	-2.46	-2.35	0.00	0.00	0.00	0.00	0.00	-3.30	-2.60	-2.30
HG02188.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.41	0.00	0.00	-2.59	-2.39	-2.36	-2.35	-2.69	-2.59	-3.42	-2.86	0.00	-2.61	-2.54	0.00	-2.89	-2.35
HG02190.mapped.ILLUMINA.bwa.CDX.exome.20130415	-2.27	-2.65	-2.54	-2.87	-2.82	-2.72	-2.27	-2.55	0.00	-2.87	-2.68	0.00	-2.43	-2.32	0.00	0.00	-2.28
HG02215.mapped.ILLUMINA.bwa.GBR.exome.20120522	-2.79	-2.71	-2.73	-3.03	-2.79	-2.81	-2.66	-2.65	-2.59	-4.69	0.00	0.00	0.00	-4.69	0.00	-2.51	-2.79
HG02219.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.76	-4.46	-4.46	-2.98	-2.53	-2.52	-2.43	-2.59	-2.46	0.00	0.00	-4.46	0.00	0.00	0.00	-2.64	-2.58
HG02220.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.19	-2.67	-2.58	-2.90	-2.81	-2.62	-2.19	-2.58	-2.31	0.00	0.00	0.00	0.00	0.00	-3.06	-2.63	-2.23
HG02221.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.33	-2.51	-2.55	-2.98	-2.71	-2.54	-2.32	-2.55	-2.31	0.00	0.00	0.00	0.00	0.00	-2.83	-2.45	-2.26
HG02223.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.54	-2.74	-2.70	-2.91	-2.69	-2.67	-2.58	-2.65	-2.64	-3.43	-2.98	0.00	-2.73	-2.66	0.00	-2.75	-2.56
HG02224.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.55	-2.79	-2.74	-2.90	-2.71	-2.76	-2.62	-2.65	-4.36	-3.28	-2.72	-2.79	-2.80	-2.62	0.00	0.00	-2.46
HG02230.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.50	0.00	0.00	-2.74	-2.53	-2.62	-2.63	-2.63	-2.48	0.00	0.00	0.00	0.00	-4.12	0.00	-2.66	-2.49
HG02231.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.46	-2.69	-2.59	-2.83	-2.61	-2.66	-2.60	-2.57	-2.48	0.00	0.00	0.00	0.00	-4.59	-3.08	-2.74	-2.44
HG02232.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.86	-2.82	-2.97	-3.13	-2.72	-2.79	-2.78	-2.88	-2.97	-3.28	-2.84	-2.94	-2.91	-2.92	0.00	-2.96	-2.84
HG02233.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.75	0.00	0.00	-2.82	-2.65	-2.63	-2.66	-2.70	-2.67	-4.68	0.00	0.00	0.00	0.00	-3.07	-2.82	-2.72
HG02235.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.28	0.00	-3.77	-2.54	-2.42	-2.37	-2.33	-2.58	-2.44	-3.11	-2.81	0.00	-2.65	-2.60	0.00	-2.77	-2.26
HG02236.mapped.ILLUMINA.bwa.IBS.exome.20130415	-2.27	0.00	0.00	-2.64	-2.56	-2.25	-2.25	-2.31	-2.29	0.00	0.00	0.00	0.00	0.00	-3.15	-2.67	-2.22
HG02238.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.85	0.00	0.00	-2.93	-2.74	-2.74	-2.69	-2.75	-2.92	-3.29	-2.96	0.00	-2.82	-2.85	0.00	-2.79	-2.75
HG02239.mapped.ILLUMINA.bwa.IBS.exome.20120522	-2.78	0.00	0.00	-2.80	-2.66	-2.66	-2.71	-2.75	-2.70	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.73
HG02250.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.84	-2.81	-2.84	-3.06	-2.86	-2.96	-2.78	-2.88	0.00	-3.14	-2.84	-2.90	-2.92	-2.72	0.00	0.00	-2.73
HG02252.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.84	0.00	-4.57	-2.75	-2.62	-2.58	-2.57	-2.49	-2.45	-4.87	0.00	0.00	-4.87	0.00	-3.02	-2.79	-2.74
HG02253.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.88	0.00	0.00	-3.01	-2.62	-2.66	-2.60	-2.62	-2.67	-3.46	-2.79	0.00	-2.78	-2.72	0.00	-2.81	-2.74

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02255.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.39	0.00	-2.72	-3.10	-2.49	-2.41	-2.33	-2.41	-2.44	0.00	-3.06	-2.68	-4.10	0.00	0.00	-2.44	-2.22
HG02256.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.38	-2.75	-2.73	-2.89	-2.40	-2.26	-2.24	-2.62	-2.24	0.00	-3.03	-2.67	0.00	0.00	-2.96	-2.62	-2.24
HG02259.mapped.ILLUMINA.bwa.PEL.exome.20121211	-2.78	-2.80	-2.86	-3.07	-2.85	-2.86	-2.73	-2.78	-2.93	-3.19	-3.00	-4.74	-2.90	-2.84	-3.13	-4.74	-2.72
HG02260.mapped.ILLUMINA.bwa.PEL.exome.20121211	-2.75	0.00	0.00	-2.86	-2.61	-2.66	-2.69	-2.75	-2.62	-4.66	0.00	-4.66	0.00	0.00	-3.07	-2.77	-2.65
HG02262.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.76	-2.65	-2.62	-2.99	-2.71	-2.67	-2.57	-2.56	-2.54	-4.24	0.00	0.00	0.00	-4.72	-2.84	-4.72	-2.74
HG02265.mapped.ILLUMINA.bwa.PEL.exome.20130422	-2.47	-2.78	-2.74	-2.81	-2.42	-2.47	-2.54	-2.52	-2.44	-4.59	-2.99	-2.74	0.00	-4.11	-3.03	-2.71	-2.39
HG02266.mapped.ILLUMINA.bwa.PEL.exome.20130422	-2.36	-4.23	-4.54	-2.47	-2.45	-2.47	-2.47	-2.48	-2.38	0.00	-4.06	0.00	-4.06	-4.23	-3.03	-2.68	-2.33
HG02271.mapped.ILLUMINA.bwa.PEL.exome.20121211	-2.82	0.00	-4.74	-2.95	-2.62	-2.65	-2.69	-2.69	-2.64	0.00	-4.44	0.00	-4.44	-4.74	-3.00	-2.85	-2.71
HG02272.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.32	0.00	0.00	-2.84	-2.59	-2.32	-2.20	-2.45	-2.24	0.00	0.00	0.00	0.00	0.00	-2.79	-4.04	-2.23
HG02274.mapped.ILLUMINA.bwa.PEL.exome.20130422	-2.37	0.00	0.00	-2.62	-2.38	-2.37	-2.43	-2.53	-2.40	0.00	0.00	0.00	0.00	-4.53	-2.88	-4.05	-2.33
HG02275.mapped.ILLUMINA.bwa.PEL.exome.20130422	-2.37	-2.82	-3.73	-2.89	-2.46	-2.48	-2.53	-2.50	-2.62	-3.27	-2.92	-4.10	-2.89	-2.57	-3.10	-4.10	-2.39
HG02277.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.36	-3.87	0.00	-2.71	-2.52	-2.44	-2.30	-2.34	-2.68	-3.33	-2.94	0.00	-2.92	-2.60	-2.99	0.00	-2.31
HG02278.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.27	0.00	0.00	-2.64	-2.44	-2.32	-2.33	-2.43	-2.35	0.00	0.00	-4.02	0.00	0.00	-2.98	0.00	-2.30
HG02281.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.23	-2.47	-2.85	-2.91	-2.64	-2.56	-2.31	-2.36	-2.24	0.00	-4.05	0.00	-3.75	0.00	-3.05	-2.67	-2.14
HG02282.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.30	0.00	0.00	-2.71	-2.47	-2.20	-2.36	-2.47	-2.35	0.00	-3.94	0.00	0.00	0.00	-3.04	-2.71	-2.22
HG02283.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.48	-2.74	-4.57	-2.89	-2.65	-2.72	-2.72	-2.74	-2.68	0.00	-2.84	0.00	-2.72	-2.68	-3.04	-4.27	-2.43
HG02284.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.57	-2.85	-2.74	-2.88	-2.58	-2.62	-2.65	-2.65	-2.58	0.00	-2.85	0.00	-2.79	-4.37	0.00	-2.66	-2.56
HG02285.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.28	-2.55	-2.48	-2.86	-2.89	-2.52	-2.25	-2.44	-2.27	0.00	0.00	0.00	0.00	0.00	-3.11	-2.55	-2.19
HG02286.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.28	0.00	0.00	-2.66	-2.45	-2.29	-2.30	-2.45	-2.28	0.00	0.00	0.00	-4.11	0.00	-2.69	0.00	-2.24
HG02291.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.57	0.00	0.00	-2.80	-2.42	-2.44	-2.46	-2.53	-2.34	0.00	0.00	-4.67	0.00	-4.67	-3.01	-2.70	-2.49
HG02292.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.63	0.00	-4.83	-2.82	-2.43	-2.45	-2.43	-2.65	-2.65	-3.88	-2.91	-2.71	0.00	-2.62	-3.11	0.00	-2.52
HG02298.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.54	0.00	0.00	-2.81	-2.41	-2.43	-2.44	-2.49	-2.41	0.00	0.00	0.00	0.00	0.00	-2.68	-4.32	-2.48
HG02299.mapped.ILLUMINA.bwa.PEL.exome.20120522	-2.58	-2.69	-2.64	-3.03	-2.62	-2.68	-2.44	-2.55	-2.59	-3.74	-2.88	0.00	-2.73	-2.62	-3.17	0.00	-2.52
HG02301.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.35	0.00	-4.03	-2.58	-2.30	-2.30	-2.35	-2.54	-2.35	0.00	-4.03	0.00	0.00	0.00	-2.85	0.00	-2.27
HG02304.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.86	-2.79	-2.79	-3.09	-2.78	-2.78	-2.61	-2.56	-2.81	-3.34	-2.80	0.00	-2.75	-2.79	0.00	-2.86	-2.80
HG02307.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.57	-4.34	-2.70	-2.92	-2.59	-2.57	-2.63	-2.54	-2.57	0.00	-2.93	-4.64	-2.78	0.00	-3.12	-2.72	-2.50
HG02308.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.54	-4.31	-4.31	-2.62	-2.53	-2.58	-2.59	-2.45	-2.51	0.00	0.00	0.00	0.00	0.00	-3.03	-2.77	-2.44
HG02309.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.49	-2.72	-4.55	-2.86	-2.60	-2.67	-2.72	-2.70	-2.62	0.00	-2.86	0.00	-2.76	-2.66	0.00	-2.67	-2.43
HG02312.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.84	0.00	0.00	-2.86	-2.44	-2.60	-2.58	-2.51	-2.67	-3.33	-2.73	0.00	-2.73	-2.66	-3.09	0.00	-2.78
HG02314.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.53	-2.78	-2.69	-2.83	-2.66	-2.70	-2.60	-2.44	-2.47	0.00	0.00	-4.61	0.00	0.00	-3.06	-2.70	-2.51
HG02315.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.50	0.00	0.00	-2.64	-2.55	-2.59	-2.59	-2.53	-2.55	0.00	0.00	-4.59	-4.29	-4.29	-3.10	-2.79	-2.50
HG02317.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.29	-2.67	-2.56	-2.97	-2.77	-2.58	-2.39	-2.66	-2.37	0.00	0.00	0.00	0.00	0.00	-2.97	-2.67	-2.27
HG02318.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.28	-2.32	-2.47	0.00	0.00	-3.58	-2.45	-2.63	-2.45	0.00	-2.74	0.00	-2.65	-2.56	0.00	-2.81	-2.18
HG02322.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.50	0.00	-4.10	-2.69	-2.53	-2.57	-2.57	-2.57	-2.53	0.00	0.00	0.00	0.00	-4.27	-2.95	0.00	-2.46
HG02323.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.47	-4.26	-4.56	-2.59	-2.45	-2.50	-2.55	-2.39	-2.48	0.00	-4.56	-4.56	0.00	0.00	-3.08	-4.56	-2.54
HG02325.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.43	-2.75	-2.73	-2.97	-2.69	-2.57	-2.61	-2.47	-2.50	0.00	-4.64	0.00	0.00	-3.94	-3.17	-2.78	-2.46
HG02330.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.57	0.00	-4.60	-2.61	-2.61	-2.58	-2.56	-2.51	-2.47	0.00	-4.60	0.00	0.00	-4.60	0.00	-2.47	-2.48
HG02332.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.55	-4.66	-4.36	-2.66	-2.55	-2.59	-2.53	-2.60	-2.54	-3.36	0.00	0.00	0.00	0.00	0.00	-2.59	-2.55
HG02334.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.54	-2.65	-2.66	-2.87	-2.70	-2.71	-2.55	-2.46	-2.50	0.00	0.00	-4.59	0.00	-4.12	0.00	-2.42	-2.45
HG02337.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.50	-4.58	-4.28	-2.74	-2.53	-2.53	-2.58	-2.46	-2.59	0.00	-4.28	0.00	0.00	0.00	0.00	-2.74	-2.45
HG02339.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.51	0.00	-4.61	-2.69	-2.47	-2.55	-2.61	-2.50	-2.55	0.00	-4.61	-4.61	-4.61	-4.61	-3.14	-2.67	-2.50
HG02343.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.60	-2.72	-2.78	-2.94	-2.58	-2.60	-2.66	-2.71	-2.56	-4.66	-2.93	-2.76	0.00	-4.66	-3.03	-4.66	-2.51
HG02345.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.74	0.00	-4.40	-3.04	-2.44	-2.45	-2.49	-2.61	-2.39	-4.40	-4.40	0.00	0.00	0.00	-2.77	-4.10	-2.52
HG02348.mapped.ILLUMINA.bwa.PEL.exome.20130415	-2.86	-2.72	-2.73	-3.04	-2.76	-2.75	-2.55	-2.58	-2.69	-3.41	-2.77	0.00	-2.75	-2.78	-3.07	0.00	-2.70
HG02351.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.85	0.00	0.00	-2.76	-2.65	-2.70	-2.75	-2.77	-2.95	-3.30	-3.24	-2.97	0.00	-2.85	0.00	-2.91	-2.84
HG02353.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.80	0.00	-4.72	-2.84	-2.61	-2.66	-2.68	-2.72	-2.70	0.00	0.00	0.00	0.00	0.00	-2.86	0.00	-2.70
HG02355.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.81	-2.76	-2.79	-2.98	-2.77	-2.86	-2.67	-2.66	-2.71	0.00	0.00	0.00	0.00	0.00	-3.07	-2.78	-2.71
HG02356.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.70	0.00	0.00	-2.89	-2.60	-2.60	-2.61	-2.81	-2.66	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.68
HG02360.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.85	0.00	0.00	-2.93	-2.67	-2.68	-2.75	-2.78	-2.98	-3.24	-3.01	0.00	-2.91	-2.85	-3.14	0.00	-2.77
HG02363.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.86	-2.77	-2.86	-3.07	-2.85	-2.84	-2.70	-2.83	0.00	-3.12	-2.77	0.00	-2.70	-2.71	0.00	0.00	-2.76
HG02364.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.75	-4.71	0.00	-2.84	-2.68	-2.68	-2.71	-2.77	-2.67	-4.41	0.00	0.00	-4.71	-4.23	-2.87	0.00	-2.72
HG02367.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.77	-2.73	-2.75	-2.96	-2.77	-2.81	-2.66	-2.74	-2.65	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.70
HG02371.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.78	-2.65	-2.66	-4.77	-4.77	-4.77	-2.72	-2.80	0.00	-3.12	-2.73	-2.81	-2.84	-2.73	0.00	0.00	-2.80
HG02372.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.81	-2.56	-2.64	-4.69	0.00	0.00	-2.69	-2.74	-2.93	-3.17	-2.95	-2.85	0.00	-2.83	0.00	-2.74	-2.73
HG02373.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.72	-4.45	-4.15	-2.91	-2.62	-2.68	-2.68	-2.81	-2.68	0.00	-4.75	0.00	0.00	-4.15	-2.88	-4.45	-2.76
HG02374.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.85	-4.79	-4.79	-2.93	-2.75	-2.79	-2.63	-2.66	-2.97	-3.13	-2.95	-4.79	-2.85	-2.85	-3.07	0.00	-2.81
HG02375.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.82	-2.78	-2.83	-3.03	-2.86	-2.89	-2.66	-2.71	-2.90	-3.25	-2.95	0.00	-2.86	-2.84	-3.15	0.00	-2.78
HG02377.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.78	0.00	0.00	-2.86	-2.64	-2.64	-2.66	-2.65	-2.61	0.00	0.00	0.00	0.00	-4.66	-2.94	-2.79	-2.69
HG02379.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.78	0.00	0.00	-2.93	-2.64	-2.64	-2.72	-2.66	-2.71	0.00	0.00	0.00	0.00	0.00	-2.93	-2.83	-2.73
HG02380.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.77	-4.36	-4.66	-2.92	-2.67	-2.63	-2.71	-2.77	-2.70	0.00	-4.66	-4.66	0.00	0.00	-2.82	0.00	-2.69
HG02381.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.76	-2.80	-2.83	-3.07	-2.78	-2.84	-2.69	-2.81	-2.93	-3.26	-2.97	-2.86	0.00	-2.84	0.00	-2.82	-2.77
HG02382.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.81	0.00	0.00	-2.90	-2.69	-2.86	-2.72	-2.72	-2.90	-3.22	-2.89	0.00	-2.82	-2.81	-3.07	0.00	-2.76
HG02383.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.74	-2.71	-2.79	-2.97	-2.81	-2.82	-2.84	-2.97	-2.89	0.00	-2.92	-2.85	0.00	-2.81	-2.99	0.00	-2.70
HG02384.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.76	-4.70	0.00	-2.84	-2.63	-2.67	-2.68	-2.73	-2.71	0.00	0.00	0.00	0.00	0.00	-2.84	0.00	-2.71
HG02385.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.82	0.00	0.00	-2.87	-2.60	-2.64	-2.67	-2.71	-2.65	0.00	0.00	0.00	0.00	0.00	-2.81	0.00	-2.70
HG02386.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.89	-2.86	-2.89	-3.13	-2.61	-2.74	-2.76	-2.88	-2.74	0.00	-3.01	-2.96	0.00	-4.77	0.00	-2.65	-2.81
HG02387.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.85	0.00	0.00	-2.90	-2.68	-2.73	-2.69	-2.79	-2.97	-3.23	-2.99	-2.97	0.00	-2.93	0.00	-2.81	-2.78
HG02388.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.84	0.00	-4.24	-2.92	-2.66	-2.70	-2.71	-2.80	-2.92	-3.15	-3.05	0.00	-2.87	-2.87	-3.15	0.00	-2.74
HG02389.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.88	-2.88	-2.94	-3.12	-2.65	-2.78	-2.92	-2.81	-3.01	-3.29	-2.92	-2.99	-3.06	-2.91	-3.19	0.00	-2.81
HG02390.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.81	0.00	0.00	-2.79	-2.67	-2.69	-2.78	-2.84	-4.76	-3.23	-2.87	0.00	-2.72	-2.66	0.00	-4.76	-2.72
HG02391.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.72	-2.55	-2.58	-4.64	0.00	0.00	-2.61	-2.65	-2.61	-4.16	0.00	0.00	-4.64	-4.16	0.00	-2.55	-2.60
HG02392.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.87	0.00	0.00	-2.92	-2.77	-2.75	-2.75	-2.80	-2.89	-3.20	-3.03	-2.94	0.00	-2.86	-3.14	-4.77	-2.80
HG02394.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.80	0.00	-4.71	-2.89	-2.68	-2.66	-2.73	-2.75	-2.67	0.00	0.00	0.00	0.00	0.00	-3.21	-2.86	-2.77
HG02395.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.79	0.00	0.00	-2.84	-2.63	-2.68	-2.71	-2.80	-2.70	0.00	0.00	0.00	0.00	0.00	-3.11	-2.94	-2.70
HG02396.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.77	0.00	-4.70	-2.80	-2.63	-2.67	-2.72	-2.80	-2.68	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.71
HG02397.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.85	-2.74	-2.83	-3.04	-2.82	-2.84	-2.74	-2.79	-3.03	-3.22	-3.03	0.00	-2.84	-2.81	0.00	-2.84	-2.75
HG02398.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.78	0.00	-4.67	-2.84	-2.60	-2.61	-2.66	-2.79	-2.73	0.00	0.00	0.00	0.00	0.00	-2.94	-4.67	-2.71
HG02399.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.81	-2.74	-2.81	-3.08	-2.75	-2.75	-2.64	-2.71	-2.63	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.70
HG02401.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.79	0.00	0.00	-2.92	-2.67	-2.66	-2.70	-2.79	-2.90	-3.17	-3.00	0.00	-2.86	-2.80	0.00	-2.84	-2.72
HG02402.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.81	0.00	0.00	-2.81	-2.70	-2.70	-2.70	-2.77	-2.92	-3.21	-2.93	0.00	-2.82	-2.93	0.00	-2.88	-2.80
HG02406.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.77	0.00	0.00	-2.83	-2.74	-2.72	-2.71	-2.78	0.00	-3.16	-2.87	0.00	-2.71	-2.73	0.00	0.00	-2.82
HG02407.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.81	-2.77	-2.87	-3.06	-2.79	-2.84	-2.68	-2.69	-2.92	-3.19	-2.98	0.00	-2.88	-2.80	-2.99	0.00	-2.73
HG02408.mapped.ILLUMINA.bwa.CDX.exome.20130422	-2.52	-3.84	-3.66	-2.75	-2.48	-2.53	-2.59	-2.48	-2.50	-4.44	-3.74	0.00	-3.96	-3.54	-3.02	-2.71	-2.50
HG02409.mapped.ILLUMINA.bwa.CDX.exome.20120522	-2.89	0.00	-4.77	-2.79	-2.69	-2.75	-2.79	-2.79	0.00	-3.15	-2.74	-2.96	-2.90	-2.70	0.00	0.00	-2.75
HG02410.mapped.ILLUMINA.bwa.CDX.exome.20130422	-2.39	-4.11	0.00	-2.51	-2.45	-2.56	-2.57	-2.55	-2.41	0.00	-3.81	-3.81	0.00	-3.71	-3.07	-2.72	-2.45
HG02419.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.57	-2.79	-2.71	-4.67	-2.63	-2.62	-2.69	-2.69	-2.61	0.00	-2.77	-2.84	-2.85	-4.37	-3.13	0.00	-2.60
HG02420.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.56	0.00	-2.75	-2.95	-2.54	-2.63	-2.68	-2.60	-2.66	-3.53	-2.77	0.00	-2.71	-2.76	-3.12	-4.37	-2.55
HG02425.mapped.ILLUMINA.bwa.PEL.exome.20130422	-2.44	-2.73	-2.71	-2.76	-2.59	-2.69	-2.48	-2.47	-2.60	-3.29	-3.09	0.00	-2.80	-2.66	0.00	-2.62	-2.33
HG02427.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.48	0.00	0.00	-2.68	-2.53	-2.56	-2.57	-2.48	-2.48	0.00	0.00	0.00	0.00	-4.49	-3.07	-2.73	-2.47
HG02429.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.51	0.00	0.00	-2.57	-2.56	-2.55	-2.56	-2.48	-2.55	0.00	0.00	0.00	0.00	-4.18	-3.05	-2.70	-2.45
HG02433.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.53	0.00	-4.63	-2.63	-2.57	-2.62	-2.63	-2.56	-2.72	-3.43	-2.90	-4.63	-2.82	-2.69	0.00	-2.76	-2.53
HG02439.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.91	0.00	-2.71	-3.04	-2.57	-2.62	-2.59	-2.49	-2.58	0.00	-2.72	0.00	-2.70	0.00	-3.09	-4.47	-2.86
HG02442.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.52	0.00	-4.11	-2.71	-2.52	-2.56	-2.60	-2.59	-2.48	0.00	0.00	0.00	0.00	-4.28	-2.95	0.00	-2.46
HG02445.mapped.ILLUMINA.bwa.ACB.exome.20121211	-2.50	-4.58	-4.58	-2.71	-2.53	-2.55	-2.55	-2.49	-2.49	0.00	-4.58	-4.58	0.00	-4.58	-3.08	-2.74	-2.47
HG02449.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.64	0.00	0.00	-2.75	-2.45	-2.51	-2.57	-2.49	-2.48	0.00	0.00	0.00	0.00	-4.77	-2.59	0.00	-2.65
HG02450.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.71	-2.75	-2.75	-3.12	-2.47	-2.64	-2.59	-2.54	-2.55	0.00	-2.78	0.00	-2.74	0.00	0.00	-2.74	-2.85

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02455.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.81	0.00	-4.44	-2.82	-2.56	-2.55	-2.56	-2.60	-2.50	0.00	-3.84	0.00	-3.97	0.00	0.00	-2.55	-2.67
HG02461.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.58	0.00	-2.73	-2.90	-2.47	-2.55	-2.64	-2.58	-2.55	0.00	-2.70	-2.74	-2.88	0.00	-3.13	-2.74	-2.51
HG02462.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.54	0.00	-4.57	-2.52	-2.47	-2.56	-2.56	-2.62	-2.55	-4.57	0.00	-4.27	-4.57	-4.57	-2.93	-4.27	-2.47
HG02464.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.50	0.00	0.00	-2.50	-2.47	-2.50	-2.55	-2.55	-2.46	0.00	0.00	0.00	0.00	-4.48	0.00	-2.59	-2.49
HG02465.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.50	0.00	0.00	-2.62	-2.45	-2.49	-2.47	-2.53	-2.38	0.00	0.00	0.00	0.00	0.00	-2.94	-2.67	-2.40
HG02470.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.61	-2.62	-4.84	-3.05	-2.62	-2.60	-2.63	-2.78	-2.58	0.00	-2.73	-4.84	-2.62	-2.62	-2.92	0.00	-2.54
HG02471.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.62	-2.74	-2.69	-3.12	-2.44	-2.54	-2.58	-2.54	-2.46	0.00	-2.85	-2.71	-4.84	0.00	-2.94	-2.75	-2.65
HG02476.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.87	-2.81	-2.80	-3.28	-2.50	-2.55	-2.55	-2.53	-2.45	0.00	-2.82	-4.58	-2.79	-4.58	-2.98	-2.78	-2.69
HG02477.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.88	-2.52	-2.51	-4.43	-2.81	-2.70	-2.54	-2.53	-2.65	-3.52	-2.69	-2.53	0.00	-2.86	-2.98	0.00	-2.56
HG02479.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.30	0.00	0.00	-2.55	-2.46	-2.38	-2.34	-2.52	-2.39	-3.99	0.00	0.00	0.00	0.00	-2.95	-2.71	-2.24
HG02481.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.83	-2.82	-2.87	-3.57	-2.51	-2.61	-2.57	-2.56	-2.69	-3.68	-2.64	-2.74	-2.85	-2.72	-3.05	-4.05	-2.68
HG02484.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.26	-2.48	-2.69	-2.88	-2.72	-2.36	-2.29	-2.42	-2.32	0.00	-3.13	0.00	-2.97	0.00	-3.13	-2.78	-2.23
HG02485.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.46	-2.70	-2.74	-3.20	-2.33	-2.42	-2.33	-2.44	-2.59	-3.20	-2.66	-2.44	-2.98	-2.67	0.00	-2.87	-2.31
HG02489.mapped.ILLUMINA.bwa.ACB.exome.20120522	-2.72	-2.76	-2.73	-3.17	-2.43	-2.52	-2.59	-2.49	-2.46	0.00	-2.81	-2.70	-4.92	0.00	0.00	-2.52	-2.67
HG02490.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.55	-2.68	-2.76	-2.83	-2.56	-2.59	-2.70	-2.75	-2.69	0.00	-2.85	0.00	-2.73	-2.55	0.00	-2.77	-2.38
HG02491.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.60	-2.77	-2.74	-2.91	-2.53	-2.63	-2.69	-2.72	-4.58	-3.22	-2.67	-2.76	-2.72	-2.62	0.00	-4.58	-2.52
HG02493.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.95	-2.82	-2.80	-3.18	-2.63	-2.73	-2.70	-2.71	-4.58	-3.48	-2.56	-2.88	-2.75	-2.73	0.00	0.00	-2.79
HG02494.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.91	0.00	-4.89	-2.89	-2.62	-2.65	-2.61	-2.55	-2.77	-3.54	-2.82	0.00	-2.73	-2.79	0.00	-2.84	-2.85
HG02496.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.34	-3.92	0.00	-2.67	-2.36	-2.31	-2.34	-2.48	-2.30	0.00	0.00	0.00	0.00	0.00	-3.11	-2.61	-2.25
HG02497.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.38	0.00	-4.10	-2.58	-2.53	-2.31	-2.38	-2.50	-2.31	0.00	0.00	0.00	0.00	0.00	-3.26	-2.63	-2.26
HG02501.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.76	-4.49	-2.72	-3.14	-2.42	-2.53	-2.51	-2.60	-2.50	0.00	-2.83	0.00	-2.74	-4.49	-2.95	-2.80	-2.60
HG02502.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.73	-4.06	-3.88	-2.84	-2.50	-2.51	-2.43	-2.49	-2.38	0.00	-4.36	-4.06	-4.36	-4.36	-2.87	-2.68	-2.59
HG02505.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.69	-2.78	-2.80	-3.24	-2.43	-2.58	-2.50	-2.51	-2.32	-4.38	-2.84	-2.79	-4.08	0.00	0.00	-2.50	-2.63
HG02508.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.25	-2.55	-2.68	-2.73	-2.68	-2.58	-2.28	-2.40	-2.33	0.00	0.00	0.00	0.00	0.00	-2.94	0.00	-2.45
HG02511.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.24	-2.64	0.00	-2.82	-2.64	-2.21	-2.68	-2.66	-2.70	0.00	-2.74	0.00	-2.64	-2.48	-2.87	0.00	-2.18
HG02512.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.48	0.00	-4.57	-2.70	-2.54	-2.56	-2.46	-2.49	-2.50	0.00	-4.57	0.00	-4.57	0.00	-3.11	-2.65	-2.47
HG02513.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.47	-4.65	-4.05	-2.66	-2.62	-2.69	-2.62	-2.63	-2.77	-3.27	-2.98	-2.78	0.00	-2.67	0.00	-2.77	-2.54
HG02521.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.39	0.00	-4.61	-2.74	-2.55	-2.55	-2.58	-2.46	-2.46	0.00	0.00	0.00	-4.30	-4.61	-3.09	-2.71	-2.48
HG02522.mapped.ILLUMINA.bwa.KHV.exome.20120522	-2.61	-2.85	-2.78	-2.97	-2.52	-2.65	-2.69	-2.73	-2.72	-3.38	-2.71	-2.85	-2.89	-2.73	0.00	-2.87	-2.57
HG02536.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.73	0.00	-4.25	-2.99	-2.48	-2.40	-2.42	-2.55	-2.34	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.48
HG02537.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.65	0.00	-4.80	-2.81	-2.51	-2.55	-2.46	-2.52	-2.46	0.00	-4.80	0.00	-4.50	-4.10	-2.86	-4.10	-2.55
HG02541.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.79	-2.54	-2.50	-4.44	-4.75	0.00	-2.48	-2.44	-2.46	0.00	0.00	0.00	0.00	0.00	-2.94	-2.75	-2.63
HG02545.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.79	0.00	-2.74	-3.60	-2.48	-2.43	-2.43	-2.60	-2.43	-4.29	-2.79	0.00	-2.68	-3.99	-2.79	-4.29	-2.60
HG02546.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.83	0.00	0.00	-3.13	-2.49	-2.54	-2.36	-2.42	-2.44	-3.50	0.00	0.00	0.00	-3.98	-2.98	-2.85	-2.56
HG02549.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.91	-2.72	-2.74	-3.09	-2.52	-2.65	-2.58	-2.65	-2.63	0.00	-2.88	-2.78	0.00	-4.55	-2.90	-4.85	-2.76
HG02554.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.96	0.00	0.00	-2.84	-2.56	-2.67	-2.59	-2.60	-2.80	-3.31	-2.84	0.00	-2.82	-2.76	0.00	-2.89	-2.81
HG02555.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.99	-2.80	-2.87	-3.16	-2.67	-2.77	-2.73	-2.73	-2.82	-3.63	-2.66	-2.88	-2.82	-2.84	0.00	-2.89	-2.85
HG02557.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.85	0.00	-4.00	-2.88	-2.46	-2.42	-2.49	-2.56	-2.40	0.00	0.00	0.00	0.00	0.00	-2.65	-4.30	-2.49
HG02558.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.71	0.00	0.00	-3.03	-2.50	-2.50	-2.45	-2.62	-2.35	0.00	0.00	0.00	0.00	0.00	-2.75	-4.39	-2.56
HG02561.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.53	0.00	-2.67	-2.81	-2.59	-2.64	-2.57	-2.64	-2.49	0.00	-2.89	-2.75	0.00	-4.54	-2.99	-2.71	-2.43
HG02562.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.50	0.00	-4.21	-2.61	-2.44	-2.60	-2.56	-2.57	-2.47	0.00	-4.51	0.00	-4.03	-3.81	-2.98	-3.73	-2.47
HG02568.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.87	-4.84	-4.24	-2.75	-2.57	-2.48	-2.57	-2.63	-2.61	-4.36	-4.84	-4.54	-4.84	-4.36	-2.95	-4.84	-2.74
HG02570.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.59	-4.62	-4.14	-2.59	-2.48	-2.55	-2.65	-2.55	-2.58	0.00	-2.89	-2.65	-4.32	-4.62	-3.19	-2.71	-2.53
HG02571.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.52	0.00	-2.74	-2.85	-2.39	-2.53	-2.57	-2.65	-2.53	0.00	-2.93	0.00	-2.83	-4.55	-2.94	0.00	-2.39
HG02573.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.45	-2.69	-2.66	-2.71	-2.55	-2.55	-2.32	-2.60	-2.44	0.00	0.00	0.00	0.00	0.00	-2.96	0.00	-2.39
HG02574.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.46	0.00	-4.41	-2.59	-2.49	-2.51	-2.57	-2.46	-2.42	0.00	0.00	0.00	-4.41	-4.41	-3.09	-2.66	-2.38
HG02577.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.77	-4.36	-2.61	-3.11	-2.45	-2.51	-2.45	-2.49	-2.43	0.00	-2.81	0.00	-2.70	-4.36	-2.71	0.00	-2.56
HG02580.mapped.ILLUMINA.bwa.ACB.exome.20130415	-2.85	-4.79	-4.79	-2.88	-2.58	-2.58	-2.54	-2.59	-2.53	0.00	0.00	0.00	-4.79	-4.79	-2.89	-4.79	-2.69
HG02582.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.47	0.00	-4.01	-2.75	-2.51	-2.52	-2.50	-2.55	-2.43	0.00	-4.01	0.00	0.00	0.00	0.00	-2.57	-2.43
HG02583.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.61	-2.62	-2.63	-3.86	-2.66	-2.68	-2.62	-2.65	-2.59	-4.56	-2.84	-2.72	-4.08	-3.95	-2.98	0.00	-2.46
HG02585.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.54	-2.75	-2.79	-2.88	-2.51	-2.60	-2.58	-2.69	-2.58	0.00	-2.92	-2.75	0.00	0.00	-3.04	-4.57	-2.44
HG02586.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.51	0.00	-4.54	-2.51	-2.47	-2.52	-2.55	-2.51	-2.49	0.00	0.00	-4.54	0.00	-4.54	0.00	-2.45	-2.39
HG02588.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.48	-4.52	-4.52	-2.56	-2.49	-2.52	-2.54	-2.51	-2.43	0.00	0.00	0.00	0.00	0.00	-3.04	-2.66	-2.39
HG02589.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.60	-4.66	-4.06	-2.82	-2.60	-2.74	-2.68	-2.73	-2.71	0.00	-4.66	-4.66	-4.66	-4.26	-3.09	-4.66	-2.50
HG02594.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.60	-2.82	-2.82	-2.85	-2.55	-2.64	-2.62	-2.67	-2.55	0.00	-2.94	-2.77	0.00	-3.85	0.00	-2.48	-2.52
HG02595.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.56	0.00	-2.81	-2.88	-2.43	-2.58	-2.63	-2.52	-2.50	0.00	-2.81	0.00	-2.80	0.00	-3.05	-2.77	-2.43
HG02597.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.78	-2.73	-2.75	-3.40	-2.53	-2.53	-2.52	-2.55	-2.51	0.00	-3.02	-2.79	0.00	0.00	0.00	-2.64	-2.58
HG02600.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.56	0.00	0.00	-2.74	-2.53	-2.53	-2.59	-2.64	0.00	-3.17	-2.66	0.00	-2.65	-2.51	0.00	0.00	-2.51
HG02601.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.55	-2.61	-2.52	-4.14	-2.64	-2.65	-2.55	-2.70	-2.50	0.00	-2.99	-2.65	0.00	-4.44	0.00	-2.60	-2.43
HG02603.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.49	0.00	0.00	-2.51	-2.47	-2.48	-2.54	-2.57	-2.50	0.00	0.00	0.00	0.00	-4.15	0.00	-2.58	-2.39
HG02604.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.55	-4.23	-4.53	-2.62	-2.56	-2.58	-2.59	-2.57	-2.67	-3.27	-2.86	0.00	-2.84	-2.66	-3.10	0.00	-2.54
HG02610.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.62	-2.77	-2.76	-2.88	-2.46	-2.56	-2.61	-2.56	-2.50	0.00	-2.96	0.00	-2.78	-4.61	-3.06	-2.74	-2.49
HG02611.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.64	-2.67	-2.65	-4.57	-2.59	-2.64	-2.63	-2.61	-2.59	0.00	-2.70	-2.64	0.00	-4.57	-3.07	-2.86	-2.56
HG02613.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.54	-4.50	-2.72	-2.83	-2.69	-2.58	-2.59	-2.49	-2.62	-3.22	-2.89	0.00	-2.77	-2.63	-2.98	0.00	-2.42
HG02614.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.49	0.00	0.00	-2.53	-2.48	-2.48	-2.52	-2.60	-2.51	0.00	0.00	0.00	0.00	-4.42	-2.92	0.00	-2.37
HG02620.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.55	0.00	-4.53	-2.60	-2.54	-2.59	-2.47	-2.47	-2.45	-3.32	-4.53	0.00	-4.53	-4.53	-3.05	-2.76	-2.45
HG02621.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.54	-2.65	-4.45	-2.81	-2.62	-2.64	-2.66	-2.82	-2.57	0.00	-2.82	0.00	-2.72	-2.57	-3.09	-4.15	-2.44
HG02623.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.46	0.00	-4.04	-2.52	-2.49	-2.46	-2.52	-2.50	-2.45	0.00	0.00	0.00	0.00	0.00	-3.07	-2.69	-2.43
HG02624.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.58	-4.61	-2.79	-2.87	-2.41	-2.54	-2.62	-2.53	-2.55	0.00	-2.87	0.00	-2.81	-4.61	-3.10	-2.71	-2.44
HG02628.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.54	0.00	0.00	-2.69	-2.47	-2.59	-2.55	-2.54	-2.65	-3.16	-2.98	0.00	-2.85	-2.69	-3.02	-4.52	-2.54
HG02629.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.60	-2.74	-2.78	-2.86	-2.57	-2.60	-2.61	-2.61	-2.60	0.00	-2.90	-2.78	0.00	-4.57	-2.89	-4.57	-2.55
HG02634.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.51	0.00	-4.22	-2.66	-2.48	-2.46	-2.55	-2.53	-2.46	0.00	0.00	0.00	-4.52	-4.52	0.00	-2.44	-2.39
HG02635.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.53	-4.48	0.00	-2.51	-2.43	-2.55	-2.54	-2.56	-2.48	0.00	-4.48	-4.18	0.00	0.00	-3.01	-2.64	-2.47
HG02642.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.54	-2.70	-2.69	-2.79	-2.59	-2.62	-2.60	-2.44	-2.44	0.00	0.00	0.00	-4.49	-3.89	-2.96	-2.69	-2.40
HG02643.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.51	0.00	-4.36	-2.67	-2.40	-2.52	-2.55	-2.68	-2.52	0.00	-3.00	-2.82	0.00	0.00	-2.90	0.00	-2.39
HG02645.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.56	0.00	-4.51	-2.71	-2.42	-2.55	-2.62	-2.67	-2.54	0.00	-2.91	-2.72	0.00	0.00	-2.90	0.00	-2.51
HG02646.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.63	-2.78	-2.85	-2.85	-2.50	-2.60	-2.63	-2.46	-2.48	0.00	-2.98	-2.76	0.00	0.00	-3.20	-2.80	-2.55
HG02648.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.88	0.00	0.00	-2.79	-2.59	-2.61	-2.59	-2.49	-2.50	0.00	-4.82	0.00	-4.82	0.00	0.00	-2.50	-2.71
HG02649.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.88	-4.87	0.00	-2.92	-2.65	-2.66	-2.66	-2.60	-2.76	-3.49	-2.80	0.00	-2.80	-2.79	0.00	-2.83	-2.74
HG02651.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.81	-2.66	-2.71	-3.07	-2.70	-2.72	-2.72	-2.74	-2.72	0.00	-2.73	0.00	-2.73	-2.73	-3.08	-4.54	-2.72
HG02652.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.93	-2.51	-2.77	-4.91	-2.76	-2.81	-2.75	-2.84	-2.83	0.00	-2.58	-2.80	-2.74	-2.79	0.00	-2.83	-2.71
HG02654.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.52	0.00	-4.21	-2.68	-2.56	-2.58	-2.58	-2.63	-4.21	-3.19	-2.76	0.00	-2.65	-2.50	0.00	-4.51	-2.45
HG02655.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.51	-2.69	-4.42	-2.79	-2.55	-2.57	-2.62	-2.67	0.00	-3.24	-2.64	-4.42	-2.62	-2.46	0.00	-4.42	-2.47
HG02657.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.57	-2.79	-2.78	-2.90	-2.49	-2.65	-2.62	-2.60	-2.58	0.00	-3.01	-2.75	-4.20	0.00	-3.18	-2.76	-2.54
HG02658.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.43	-2.75	-2.74	-2.84	-2.66	-2.63	-2.57	-2.59	-2.72	-3.33	-2.91	0.00	-2.80	-2.61	0.00	-2.76	-2.46
HG02660.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.61	-2.67	-2.66	0.00	-2.63	-2.67	-2.67	-2.60	-2.65	-3.26	-2.63	-2.67	-2.90	-2.71	-3.21	0.00	-2.55
HG02661.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.44	0.00	-4.44	-2.50	-2.46	-2.52	-2.51	-2.60	-2.46	0.00	-4.14	0.00	0.00	0.00	0.00	-2.51	-2.41
HG02666.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.53	0.00	-2.75	-2.87	-2.45	-2.46	-2.68	-2.63	-2.56	0.00	-2.99	0.00	-2.87	-4.50	-2.97	-4.50	-2.45
HG02667.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.46	-4.44	0.00	-2.71	-2.43	-2.47	-2.50	-2.50	-2.49	0.00	0.00	-4.14	0.00	-4.44	-2.86	0.00	-2.43
HG02675.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.56	-2.78	-2.72	-2.91	-2.47	-2.59	-2.59	-2.57	-2.48	0.00	-2.87	-2.70	-4.52	-4.22	-3.03	-2.73	-2.48
HG02676.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.50	0.00	-4.46	-2.72	-2.44	-2.52	-2.56	-2.57	-2.50	0.00	0.00	0.00	-4.46	-4.16	-2.90	-4.46	-2.43
HG02678.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.44	-4.45	-4.45	-2.57	-2.50	-2.51	-2.57	-2.56	-2.50	0.00	0.00	-4.15	-4.15	0.00	-2.88	0.00	-2.40
HG02679.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.46	-2.73	-2.72	-2.77	-2.62	-2.54	-2.55	-2.44	-2.43	0.00	0.00	0.00	0.00	-4.46	-2.97	-2.72	-2.36
HG02681.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.89	-4.77	-4.77	-2.91	-2.57	-2.61	-2.57	-2.55	-2.71	-3.36	-2.81	0.00	-2.73	-2.73	0.00	-2.81	-2.75
HG02682.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.91	-2.68	-2.70	-3.05	-2.73	-2.73	-2.72	-2.77	-2.70	0.00	-2.75	0.00	-2.69	-2.70	-3.03	-4.28	-2.76
HG02684.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.53	-2.54	-2.57	-4.48	-2.60	-2.66	-2.68	-2.78	-2.62	0.00	-2.69	-2.74	-2.80	-2.63	0.00	-2.69	-2.46

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02685.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.53	-4.19	0.00	-2.70	-2.57	-2.57	-2.57	-2.62	-3.80	-3.11	-2.69	0.00	-2.60	-2.55	0.00	0.00	-2.50
HG02687.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.49	-2.64	-2.56	0.00	-2.64	-2.66	-2.67	-2.74	-4.19	-3.32	-2.66	0.00	-2.66	-2.53	0.00	-4.19	-2.47
HG02688.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.45	-2.77	-2.64	-2.75	-2.63	-2.56	-2.59	-2.50	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.33	-2.36
HG02690.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.73	0.00	-4.14	-3.01	-2.55	-2.61	-2.57	-2.56	-2.46	0.00	0.00	0.00	0.00	-4.74	-2.88	0.00	-2.70
HG02691.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.99	-2.84	-2.85	-3.22	-2.62	-2.73	-2.64	-2.63	-2.84	-3.40	-2.71	-2.86	-2.87	-2.93	-3.21	0.00	-2.93
HG02694.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.93	-2.72	-2.78	-3.37	-2.55	-2.61	-2.60	-2.64	-2.51	0.00	-2.91	-2.77	0.00	-4.07	0.00	-2.61	-2.68
HG02696.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.56	-2.78	-2.77	-2.87	-2.42	-2.65	-2.66	-2.72	-2.73	-3.36	-2.87	-2.82	-2.88	-2.73	0.00	-2.75	-2.52
HG02697.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.53	-2.57	-2.57	-4.00	-2.56	-2.62	-2.60	-2.62	-2.47	0.00	-2.89	-2.72	-4.48	-4.48	0.00	-2.61	-2.41
HG02699.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.83	0.00	-4.76	-2.94	-2.57	-2.64	-2.60	-2.54	-2.59	0.00	-4.76	0.00	0.00	-4.76	0.00	-2.45	-2.72
HG02700.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.79	-2.49	-2.52	0.00	-4.70	-4.70	-2.53	-2.39	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.68
HG02702.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.43	0.00	-4.35	-2.65	-2.49	-2.44	-2.56	-2.63	-2.44	0.00	0.00	-4.35	0.00	-4.05	-2.81	-4.35	-2.37
HG02703.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.47	0.00	-4.10	-2.73	-2.58	-2.48	-2.48	-2.57	-2.42	0.00	-4.40	-4.40	0.00	0.00	-2.81	0.00	-2.38
HG02715.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.59	-2.79	-2.78	-2.88	-2.47	-2.53	-2.63	-2.64	-2.57	0.00	-2.85	-2.69	-4.62	-4.32	-2.99	0.00	-2.53
HG02716.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.55	0.00	-2.70	-2.84	-2.59	-2.66	-2.47	-2.50	-2.44	-3.35	0.00	0.00	0.00	0.00	-3.14	-2.67	-2.44
HG02721.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.56	-2.78	-2.73	-4.07	-2.67	-2.59	-2.63	-2.69	-2.69	-3.27	-2.72	-2.78	-2.88	-2.68	-3.10	0.00	-2.52
HG02722.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.50	-2.74	-2.71	-2.80	-2.59	-2.56	-2.56	-2.53	-2.40	-4.38	0.00	0.00	0.00	-4.38	-3.15	-2.69	-2.36
HG02724.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.62	-2.66	-2.66	0.00	-2.57	-2.66	-2.66	-2.64	-4.29	-3.27	-2.63	-2.66	-2.70	-2.48	0.00	-4.11	-2.51
HG02725.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.43	0.00	0.00	-2.70	-2.48	-2.52	-2.52	-2.54	-2.47	0.00	-4.44	-4.14	0.00	0.00	-2.87	0.00	-2.43
HG02727.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.59	-2.63	-2.65	0.00	-2.64	-2.71	-2.65	-2.62	-2.75	-3.34	-2.70	-2.70	-2.88	-2.65	0.00	-2.77	-2.57
HG02728.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.59	-2.68	-2.65	-4.58	-2.55	-2.63	-2.64	-2.57	-2.73	-3.40	-2.72	-2.69	-2.87	-2.70	-3.13	0.00	-2.56
HG02731.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.79	-2.62	-2.76	0.00	-2.58	-2.60	-2.60	-2.67	-2.71	-3.42	-2.73	-2.81	-2.83	-2.85	0.00	-2.82	-2.68
HG02733.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.65	-2.59	-2.62	0.00	-2.64	-2.65	-2.66	-2.67	-2.75	-3.40	-2.67	-2.66	-2.83	-2.70	0.00	-2.73	-2.54
HG02734.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.51	-2.69	-2.64	-2.79	-2.61	-2.64	-2.70	-2.72	-4.49	-3.38	-2.68	-4.49	-2.58	-2.51	0.00	0.00	-2.44
HG02736.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.80	-2.70	-2.66	-3.05	-2.67	-2.71	-2.62	-2.45	-2.45	0.00	-4.77	-4.77	0.00	-4.77	-3.03	-2.72	-2.69
HG02737.mapped.ILLUMINA.bwa.PJL.exome.20130415	-3.00	-2.83	-2.85	-3.25	-2.60	-2.71	-2.67	-2.72	-2.84	-3.49	-2.67	-2.87	-2.86	-2.85	0.00	-2.91	-2.86
HG02756.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.50	-4.51	-4.51	-2.52	-2.46	-2.51	-2.51	-2.58	-2.53	0.00	0.00	0.00	0.00	0.00	-2.91	0.00	-2.43
HG02757.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.50	0.00	-4.52	-2.56	-2.53	-2.54	-2.51	-2.59	-2.43	0.00	0.00	0.00	0.00	-4.52	0.00	-2.42	-2.35
HG02759.mapped.ILLUMINA.bwa.GWD.exome.20130415	-3.00	-2.79	-2.66	0.00	-2.68	-2.68	-2.70	-2.61	-2.66	0.00	-2.64	-2.80	-2.79	0.00	-3.09	-2.87	-2.85
HG02760.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.91	-4.76	-2.52	0.00	-2.71	-2.76	-2.66	-2.74	-2.68	0.00	-2.61	0.00	-2.58	-2.70	-3.06	0.00	-2.72
HG02763.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.90	-2.67	-2.75	-3.27	-2.62	-2.55	-2.53	-2.53	-2.54	0.00	-2.83	-2.80	0.00	-4.09	-2.98	-4.57	-2.81
HG02768.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.62	0.00	-4.64	-2.64	-2.45	-2.61	-2.54	-2.56	-2.74	-3.32	-2.72	-4.64	-2.77	-2.69	-3.06	-4.04	-2.53
HG02769.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.45	-2.66	-2.71	-2.81	-2.64	-2.69	-2.53	-2.42	-2.43	0.00	0.00	-4.52	0.00	-4.22	-3.01	-2.67	-2.42
HG02771.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.42	0.00	-4.51	-2.67	-2.44	-2.49	-2.57	-2.57	-2.48	0.00	-4.51	0.00	0.00	0.00	-2.90	0.00	-2.41
HG02772.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.49	-2.74	-2.69	-2.76	-2.58	-2.62	-2.47	-2.63	-2.42	0.00	-4.17	0.00	0.00	0.00	-2.84	-4.47	-2.38
HG02774.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.86	-2.74	-2.78	-3.13	-2.73	-2.80	-2.62	-2.54	-2.73	-3.48	-2.77	0.00	-2.71	-2.78	-3.12	0.00	-2.75
HG02775.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.97	-2.74	-2.73	0.00	-2.75	-2.75	-2.71	-2.78	-4.19	-3.28	-2.51	-2.76	-2.74	-2.73	0.00	0.00	-2.92
HG02778.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.83	-4.06	0.00	-2.96	-2.54	-2.45	-2.51	-2.44	-2.45	0.00	-4.36	-4.36	-4.36	-3.88	-2.98	-2.74	-2.58
HG02780.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.78	-2.76	-4.04	-3.30	-2.51	-2.54	-2.55	-2.59	-2.68	-3.39	-2.88	0.00	-2.73	-2.67	0.00	-2.78	-2.61
HG02783.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.60	-2.74	-2.77	-2.86	-2.54	-2.60	-2.68	-2.63	-2.75	-3.33	-2.77	-2.77	-2.83	-2.74	0.00	-2.75	-2.56
HG02784.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.51	-2.56	-2.59	0.00	-2.67	-2.75	-2.57	-2.68	-2.43	0.00	-2.87	-2.77	0.00	-4.40	0.00	-2.54	-2.45
HG02786.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.59	-2.78	-2.74	-2.83	-2.49	-2.60	-2.63	-2.61	-2.59	0.00	-2.89	-2.74	-4.54	-4.54	-3.07	-2.67	-2.49
HG02787.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.65	-2.90	-2.85	-2.93	-2.46	-2.56	-2.60	-2.58	-2.78	-3.17	-2.70	-2.66	-2.93	-2.77	-3.21	-4.65	-2.61
HG02789.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.53	-2.73	-2.78	-2.89	-2.53	-2.53	-2.63	-2.62	-2.45	0.00	-2.96	-2.68	0.00	-4.48	-2.89	0.00	-2.53
HG02790.mapped.ILLUMINA.bwa.PJL.exome.20121211	-2.59	-2.70	-2.62	-4.26	-2.55	-2.61	-2.65	-2.72	-3.96	-3.22	-2.61	-2.66	-2.73	-2.61	0.00	0.00	-2.53
HG02792.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.87	-2.74	-2.72	-3.15	-2.79	-2.79	-2.66	-2.64	-2.78	-3.43	-2.74	-4.39	-2.83	-2.81	0.00	-2.79	-2.81
HG02793.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.99	-2.75	-2.74	-3.20	-2.55	-2.64	-2.62	-2.58	-2.64	0.00	-2.84	-2.81	-4.28	0.00	-3.14	-2.82	-2.83
HG02798.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.53	-4.31	0.00	-2.71	-2.45	-2.61	-2.65	-2.60	-2.55	0.00	-2.92	-2.75	0.00	-4.31	-2.96	0.00	-2.46
HG02799.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.55	-4.45	0.00	-2.73	-2.41	-2.50	-2.60	-2.50	-2.48	0.00	0.00	-4.45	0.00	-4.45	-3.03	-2.66	-2.39
HG02804.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.63	-2.75	-2.73	-2.86	-2.58	-2.58	-2.64	-2.68	-2.57	-4.62	-2.90	-4.62	-2.82	0.00	0.00	-2.44	-2.47
HG02805.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.44	-4.36	-2.67	-2.76	-2.63	-2.60	-2.52	-2.59	-2.42	0.00	0.00	-4.36	0.00	0.00	-2.93	0.00	-2.36
HG02807.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.53	-4.54	0.00	-2.51	-2.42	-2.58	-2.51	-2.55	-2.53	0.00	0.00	-4.54	0.00	-4.54	-3.14	-2.70	-2.38
HG02808.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.59	-2.69	-2.66	-4.63	-2.51	-2.63	-2.65	-2.73	-2.57	0.00	-2.77	-2.77	-2.86	-4.32	-2.97	0.00	-2.49
HG02810.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.47	0.00	-4.55	-2.68	-2.49	-2.55	-2.61	-2.46	-2.44	0.00	0.00	-4.55	0.00	-4.55	-3.02	-2.64	-2.41
HG02811.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.46	-2.77	-2.76	-2.88	-2.47	-2.53	-2.60	-2.54	-2.47	0.00	-2.89	-4.54	-2.83	-4.54	-3.09	-4.54	-2.56
HG02813.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.94	-2.79	-2.79	-2.88	-2.64	-2.49	-2.66	-2.73	-2.67	0.00	0.00	0.00	0.00	0.00	-2.98	0.00	-2.77
HG02814.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.94	-4.91	-2.86	-3.14	-2.58	-2.67	-2.64	-2.55	-2.53	0.00	-2.84	0.00	-2.79	0.00	-3.20	-2.79	-2.79
HG02816.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.78	-4.73	-4.73	-2.89	-2.55	-2.62	-2.60	-2.63	-2.53	0.00	0.00	0.00	0.00	0.00	-2.89	0.00	-2.62
HG02817.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.83	0.00	-4.84	-2.75	-2.49	-2.57	-2.57	-2.48	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.73
HG02819.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.44	-3.92	-2.61	-2.77	-2.56	-2.61	-2.51	-2.50	-2.53	0.00	-3.79	-4.09	-3.69	-3.55	-2.86	0.00	-2.43
HG02820.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.48	0.00	-4.10	-2.59	-2.45	-2.55	-2.57	-2.65	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.44
HG02836.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.94	0.00	-4.82	-2.79	-2.52	-2.59	-2.56	-2.67	-2.57	0.00	-4.82	0.00	-4.82	0.00	0.00	-2.61	-2.73
HG02837.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.89	0.00	-2.77	0.00	-2.76	-2.59	-2.52	-2.60	-2.51	0.00	-2.74	0.00	-2.71	0.00	-2.93	0.00	-2.69
HG02839.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.85	-2.65	-2.66	-3.07	-2.65	-2.71	-2.50	-2.62	0.00	-3.33	-2.71	-4.74	-2.68	-2.64	0.00	0.00	-2.84
HG02840.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.89	-2.72	-2.75	-3.07	-2.75	-2.76	-2.60	-2.52	-2.51	0.00	-4.41	0.00	-4.59	-4.29	0.00	-2.47	-2.73
HG02851.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.84	-4.41	-2.69	-3.09	-2.74	-2.73	-2.51	-2.45	-2.47	0.00	0.00	-4.29	0.00	0.00	-3.11	-2.72	-2.71
HG02852.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.95	-2.86	-2.85	-3.18	-2.59	-2.67	-2.67	-2.61	-2.60	0.00	-2.90	-2.85	0.00	-5.02	0.00	-2.63	-2.86
HG02854.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.55	-2.57	-2.53	-4.10	-2.64	-2.66	-2.57	-2.45	-2.48	0.00	-2.87	-2.63	-4.40	-4.40	-2.99	-2.69	-2.47
HG02855.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.56	-2.76	-2.73	-2.92	-2.51	-2.61	-2.56	-2.48	-2.47	0.00	-2.84	-2.71	0.00	-3.78	0.00	-2.47	-2.55
HG02860.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.87	0.00	0.00	-2.76	-2.54	-2.54	-2.52	-2.49	-2.57	0.00	0.00	0.00	0.00	0.00	-3.04	-2.75	-2.70
HG02861.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.82	-4.33	0.00	-2.75	-2.50	-2.39	-2.52	-2.59	-2.53	0.00	-4.51	0.00	-4.33	-4.51	-2.94	0.00	-2.75
HG02870.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.77	-4.22	-2.75	-3.10	-2.68	-2.71	-2.53	-2.59	-2.45	0.00	-2.79	-2.80	-4.52	-4.22	-2.73	-3.92	-2.56
HG02878.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.87	0.00	-4.77	-2.84	-2.53	-2.57	-2.52	-2.55	-2.47	0.00	0.00	0.00	-4.47	0.00	-2.88	0.00	-2.70
HG02879.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.85	0.00	-4.20	-2.93	-2.51	-2.53	-2.47	-2.59	-2.51	0.00	0.00	0.00	0.00	0.00	-2.92	0.00	-2.67
HG02881.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.98	-2.76	-2.78	-3.19	-2.52	-2.67	-2.69	-2.70	-2.60	0.00	-2.88	-2.76	-4.61	0.00	-3.04	0.00	-2.80
HG02882.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.79	-2.60	-2.61	-2.97	-2.59	-2.62	-2.46	-2.42	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.67	-2.75
HG02884.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.50	0.00	0.00	-2.71	-2.55	-2.58	-2.54	-2.52	-2.66	-3.52	-2.69	-2.69	-2.77	-2.65	-3.11	0.00	-2.54
HG02885.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.51	-4.41	0.00	-2.65	-2.50	-2.55	-2.51	-2.41	-2.52	-3.26	0.00	0.00	0.00	0.00	-2.89	-4.41	-2.52
HG02887.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.80	0.00	0.00	-2.88	-2.52	-2.57	-2.55	-2.59	-2.56	0.00	0.00	0.00	0.00	0.00	-2.98	0.00	-2.64
HG02888.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.86	0.00	-4.57	-2.90	-2.53	-2.59	-2.51	-2.57	-2.55	0.00	0.00	-4.87	0.00	-4.87	-2.94	0.00	-2.73
HG02890.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.57	-2.81	-2.72	-2.83	-2.61	-2.74	-2.61	-2.49	-2.67	-3.34	-2.91	-4.45	-2.79	-2.67	-3.07	0.00	-2.48
HG02891.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.52	-4.12	-2.68	-2.78	-2.53	-2.59	-2.57	-2.49	-2.55	0.00	-2.85	0.00	-2.72	-4.12	-2.93	-2.79	-2.45
HG02895.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.91	-2.79	-2.80	-3.12	-2.50	-2.66	-2.61	-2.60	-2.54	0.00	-2.84	-2.79	0.00	0.00	-3.19	-2.83	-2.79
HG02896.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.84	-4.14	-4.14	-2.73	-2.46	-2.58	-2.52	-2.62	-2.46	0.00	0.00	-4.54	0.00	0.00	-2.91	-4.36	-2.74
HG02922.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.54	-3.88	-4.18	-2.52	-2.53	-2.54	-2.51	-2.52	-2.49	0.00	0.00	0.00	0.00	-4.48	-2.93	-2.69	-2.42
HG02923.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.48	-4.50	0.00	-2.61	-2.48	-2.50	-2.50	-2.61	-2.43	0.00	0.00	0.00	0.00	-4.50	-2.88	0.00	-2.39
HG02938.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.95	-2.63	-2.68	-4.61	-2.68	-2.66	-2.66	-2.64	-2.60	0.00	-2.69	-2.64	-4.44	0.00	-3.13	-2.88	-2.83
HG02941.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.96	-2.87	-2.80	-3.24	-2.58	-2.70	-2.73	-2.66	-2.79	-3.42	-2.69	-2.91	-2.85	-2.81	0.00	-2.90	-2.85
HG02943.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.53	-4.05	-4.05	-2.58	-2.45	-2.55	-2.55	-2.49	-2.49	-4.53	-4.23	0.00	-3.93	-3.75	0.00	-2.41	-2.49
HG02944.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.60	-2.79	-2.75	-2.86	-2.46	-2.58	-2.61	-2.63	-2.57	0.00	-3.03	-2.74	0.00	0.00	-3.09	-2.82	-2.44
HG02946.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.91	0.00	-4.40	-2.86	-2.55	-2.61	-2.54	-2.57	-2.54	0.00	0.00	0.00	0.00	-4.88	-3.10	-2.76	-2.76
HG02947.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.87	0.00	0.00	-2.81	-2.56	-2.44	-2.55	-2.58	-2.56	0.00	0.00	0.00	-4.86	0.00	-2.93	-4.56	-2.72
HG02952.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.89	-4.83	-4.83	-2.88	-2.51	-2.58	-2.51	-2.48	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.69
HG02953.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.93	0.00	-4.43	-2.77	-2.50	-2.40	-2.56	-2.64	-2.58	0.00	0.00	0.00	0.00	0.00	-3.00	-4.43	-2.71
HG02968.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.86	-2.63	-2.69	-3.10	-2.69	-2.47	-2.60	-2.51	-2.52	0.00	-4.81	0.00	0.00	-4.81	-3.07	-2.81	-2.74
HG02970.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.86	-4.84	-4.54	-2.92	-2.57	-2.61	-2.56	-2.60	-2.55	0.00	0.00	-4.84	0.00	0.00	-3.01	0.00	-2.71
HG02971.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.94	-2.46	-2.74	-4.89	-2.78	-2.60	-2.62	-2.54	-2.62	-4.89	-2.84	-2.81	0.00	0.00	-3.12	-2.84	-2.82

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02973.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.45	-4.52	-4.52	-2.69	-2.47	-2.46	-2.55	-2.59	-2.48	0.00	-4.52	0.00	0.00	0.00	-2.94	0.00	-2.37
HG02974.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.49	0.00	-4.46	-2.62	-2.33	-2.48	-2.53	-2.54	-2.44	0.00	0.00	0.00	0.00	-4.46	-2.91	-4.46	-2.42
HG02976.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.79	0.00	-2.66	-2.99	-2.66	-2.64	-2.50	-2.58	-2.55	0.00	0.00	0.00	-4.81	0.00	-2.91	0.00	-2.62
HG02977.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.91	0.00	-2.82	-3.13	-2.64	-2.68	-2.64	-2.61	-2.65	0.00	-2.84	-4.94	-2.81	-4.94	-3.15	-2.86	-2.76
HG02979.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.77	0.00	-4.76	-2.87	-2.53	-2.55	-2.52	-2.56	-2.55	0.00	0.00	0.00	-4.76	0.00	-2.91	-4.16	-2.72
HG02981.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.87	0.00	0.00	-2.81	-2.49	-2.61	-2.58	-2.62	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.73
HG02982.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.87	-4.38	-2.73	-3.06	-2.52	-2.62	-2.65	-2.60	-2.64	0.00	-2.81	0.00	-2.79	0.00	-3.07	-2.83	-2.81
HG02983.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.89	-2.63	-2.61	-4.57	-2.73	-2.83	-2.61	-2.58	-2.58	0.00	-2.77	-2.75	-4.57	0.00	-3.09	-2.82	-2.75
HG03006.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.63	-2.74	-2.75	-2.87	-2.70	-2.72	-2.60	-2.63	-2.66	-3.30	-2.83	-3.96	-2.75	-2.71	0.00	-2.77	-2.51
HG03007.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.67	-2.77	-2.70	-2.95	-2.54	-2.65	-2.60	-2.59	-2.45	-3.48	-3.05	-2.77	-4.09	-4.56	0.00	-2.70	-2.58
HG03009.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.57	0.00	0.00	-2.62	-2.62	-2.54	-2.55	-2.56	-2.63	-3.07	-2.85	-2.75	0.00	-2.68	0.00	-2.73	-2.49
HG03012.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.51	-2.73	-2.73	-2.84	-2.65	-2.68	-2.54	-2.54	-2.68	-3.30	-2.89	-3.72	-2.73	-2.63	0.00	-2.72	-2.49
HG03015.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.80	-2.49	-2.51	0.00	0.00	-4.71	-2.63	-2.68	-2.63	0.00	-2.68	0.00	-2.63	-2.64	0.00	-2.75	-2.64
HG03016.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.85	-2.70	-2.70	-3.07	-2.72	-2.69	-2.57	-2.53	-2.60	0.00	0.00	0.00	0.00	-4.83	-3.05	-2.78	-2.74
HG03018.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.72	-2.70	-2.67	-3.13	-2.69	-2.69	-2.41	-2.59	-2.40	0.00	0.00	0.00	0.00	-3.86	0.00	-2.55	-2.52
HG03019.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.82	-2.50	-2.51	-4.39	-2.83	-2.71	-2.49	-2.53	-2.42	0.00	-2.93	-2.73	0.00	-4.39	-2.91	-2.87	-2.56
HG03021.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.88	0.00	-4.39	-3.05	-2.56	-2.51	-2.49	-2.57	-2.63	-3.79	-2.85	0.00	-2.73	-2.68	-2.90	-4.39	-2.54
HG03022.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.94	-2.64	-2.77	0.00	-2.68	-2.69	-2.48	-2.56	-2.66	-3.18	-2.91	0.00	-2.76	-2.60	0.00	-2.72	-2.57
HG03024.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.57	-2.69	-2.69	-2.92	-2.44	-2.50	-2.60	-2.54	-2.62	-3.35	-2.80	-2.79	-2.83	-2.72	-3.10	-4.46	-2.51
HG03025.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.52	-2.75	-2.59	-4.14	-2.46	-2.59	-2.59	-2.61	-2.71	-3.24	-2.62	-2.74	-2.66	-2.66	0.00	-4.44	-2.56
HG03027.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.52	-2.69	-2.70	-2.82	-2.64	-2.63	-2.48	-2.46	-2.46	0.00	0.00	-4.55	0.00	-4.55	-3.06	-2.68	-2.45
HG03028.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.57	0.00	-2.73	-2.79	-2.51	-2.55	-2.64	-2.64	-2.60	0.00	-2.98	0.00	-2.87	-4.58	-2.99	0.00	-2.49
HG03039.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.58	0.00	-2.76	-2.82	-2.48	-2.58	-2.58	-2.68	-2.53	0.00	-2.88	0.00	-2.90	0.00	-2.95	0.00	-2.46
HG03040.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.55	-2.65	-2.69	-2.77	-2.63	-2.63	-2.58	-2.51	-2.52	0.00	-4.26	0.00	0.00	-4.26	0.00	-2.43	-2.45
HG03045.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.50	-4.49	-2.61	-4.19	-2.57	-2.49	-2.58	-2.51	-2.46	0.00	-2.69	0.00	-2.75	0.00	-3.11	-2.72	-2.41
HG03046.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.61	-2.81	-2.73	-2.92	-2.49	-2.63	-2.66	-2.61	-2.53	0.00	-2.88	-2.74	-4.61	-4.31	-3.14	-2.81	-2.49
HG03048.mapped.ILLUMINA.bwa.GWD.exome.20121211	-2.55	-2.82	-2.68	-2.89	-2.51	-2.55	-2.60	-2.64	-2.53	0.00	-2.91	-2.73	0.00	0.00	-2.93	0.00	-2.42
HG03049.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.53	-2.78	-2.69	-2.85	-2.48	-2.61	-2.58	-2.64	-2.56	0.00	-2.89	-4.53	-2.86	0.00	-2.95	-4.23	-2.50
HG03052.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.59	-2.84	-2.87	-2.89	-2.51	-2.60	-2.62	-2.63	-2.73	-3.29	-2.88	-2.81	-2.95	-2.74	-3.22	-4.61	-2.52
HG03054.mapped.ILLUMINA.bwa.MSL.exome.20130415	-3.00	-2.88	-2.85	-2.86	-2.51	-2.76	-2.69	-2.78	-2.74	0.00	-2.90	-2.84	-4.94	-4.94	-2.99	0.00	-2.88
HG03055.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.84	0.00	-4.59	-2.93	-2.62	-2.63	-2.55	-2.62	-2.59	0.00	-4.89	0.00	-4.89	-4.89	0.00	-2.62	-2.75
HG03057.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.56	-2.83	-2.74	-2.90	-2.49	-2.64	-2.63	-2.69	-2.58	0.00	-2.90	-2.72	0.00	-4.34	-3.08	0.00	-2.55
HG03058.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.51	0.00	0.00	-2.67	-2.51	-2.48	-2.51	-2.48	-2.42	0.00	0.00	-4.42	0.00	0.00	-3.08	-2.73	-2.42
HG03060.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.93	-4.92	0.00	-2.98	-2.52	-2.67	-2.67	-2.59	-2.62	0.00	-2.82	-2.79	0.00	0.00	-3.10	-2.87	-2.81
HG03061.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.87	-2.71	-2.73	-3.08	-2.61	-2.69	-2.62	-2.64	-2.63	0.00	-2.78	-4.82	-2.74	-4.52	0.00	-2.73	-2.87
HG03063.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.88	-3.76	-3.98	-2.79	-2.53	-2.58	-2.56	-2.59	-2.56	0.00	-4.28	0.00	-4.76	0.00	0.00	-2.60	-2.71
HG03064.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.79	-2.66	-2.68	-3.08	-2.58	-2.71	-2.51	-2.41	-2.45	0.00	0.00	0.00	0.00	0.00	-2.87	-4.25	-2.69
HG03066.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.58	-2.61	-2.55	-3.97	-2.59	-2.67	-2.54	-2.47	-2.44	0.00	-2.91	-2.67	-4.15	-3.97	-2.95	-2.67	-2.51
HG03069.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.51	0.00	-4.43	-2.57	-2.42	-2.53	-2.52	-2.55	-2.47	-4.43	0.00	-4.13	-3.95	-4.13	-2.86	0.00	-2.44
HG03072.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.46	-4.36	-2.61	-2.76	-2.59	-2.58	-2.53	-2.57	-2.54	0.00	-2.83	0.00	-2.65	-2.56	-2.91	-4.36	-2.38
HG03073.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.80	0.00	-4.22	-2.93	-2.62	-2.61	-2.42	-2.61	-2.58	0.00	0.00	0.00	0.00	0.00	-2.94	-4.52	-2.72
HG03074.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.82	0.00	-4.50	-2.77	-2.44	-2.58	-2.55	-2.50	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.72	-2.76
HG03077.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.83	-4.82	0.00	-2.94	-2.58	-2.59	-2.53	-2.53	-2.57	-4.82	0.00	0.00	0.00	0.00	-3.03	-2.79	-2.74
HG03078.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.49	0.00	-4.53	-2.66	-2.45	-2.45	-2.57	-2.55	-2.48	0.00	0.00	0.00	0.00	-4.05	-2.95	-2.63	-2.45
HG03079.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.72	-2.52	-2.58	-2.88	-2.50	-2.58	-2.40	-2.45	-2.41	0.00	0.00	-4.61	0.00	0.00	0.00	-4.61	-4.61
HG03081.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.96	-2.81	-2.78	-3.18	-2.52	-2.67	-2.50	-2.63	-2.59	-3.43	-2.84	-4.90	-2.73	-4.59	0.00	-2.89	-2.96
HG03082.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.97	-2.83	-2.84	-3.13	-2.52	-2.72	-2.68	-2.73	-2.64	0.00	-2.80	0.00	-2.83	-4.95	-3.16	-2.89	-2.86
HG03084.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.54	-4.59	-2.62	0.00	-2.56	-2.59	-2.55	-2.65	-2.58	0.00	-2.71	0.00	-2.70	0.00	-2.97	-4.59	-2.45
HG03085.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.46	-2.73	-2.62	-2.81	-2.59	-2.56	-2.66	-2.70	-2.66	0.00	-2.78	-4.48	-2.77	-2.58	0.00	-2.68	-2.35
HG03086.mapped.ILLUMINA.bwa.MSL.exome.20130415	-3.04	-2.61	-2.55	0.00	-2.64	-2.64	-2.58	-2.66	-2.62	0.00	-2.77	-2.65	-4.67	0.00	-3.11	-2.81	-2.76
HG03088.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.86	0.00	0.00	-2.92	-2.54	-2.64	-2.54	-2.47	-2.49	0.00	-4.81	0.00	0.00	0.00	-3.08	-2.74	-2.75
HG03091.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.79	0.00	0.00	-2.80	-2.49	-2.61	-2.53	-2.59	-2.55	0.00	0.00	0.00	0.00	0.00	-2.97	-2.66	-2.68
HG03095.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.83	0.00	-4.30	-2.83	-2.56	-2.58	-2.58	-2.50	-2.56	0.00	0.00	-4.78	0.00	0.00	-3.03	-2.76	-2.73
HG03096.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.59	-2.61	-2.61	-4.12	-2.63	-2.67	-2.72	-2.74	-4.00	-3.30	-2.62	-2.72	-2.67	-2.55	0.00	0.00	-2.47
HG03097.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.43	0.00	-4.50	-2.66	-2.43	-2.47	-2.52	-2.45	-2.48	0.00	0.00	0.00	0.00	-4.03	-3.00	-4.20	-2.46
HG03099.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.53	-2.76	-2.63	-4.56	-2.63	-2.65	-2.53	-2.56	-2.47	0.00	-2.86	-4.56	-2.77	0.00	0.00	-2.56	-2.45
HG03100.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.57	-2.80	-2.84	-2.83	-2.50	-2.57	-2.59	-2.73	-2.55	0.00	-3.01	-2.78	0.00	-4.57	-2.99	0.00	-2.50
HG03103.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.75	0.00	-2.64	0.00	-2.59	-2.49	-2.48	-2.70	-4.75	0.00	-2.65	0.00	-2.62	-4.75	-2.92	0.00	-2.85
HG03105.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.79	0.00	-3.72	-2.93	-2.60	-2.56	-2.50	-2.62	-2.49	0.00	-4.19	-4.49	-3.95	0.00	-2.88	0.00	-2.70
HG03108.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.50	0.00	0.00	-2.60	-2.51	-2.34	-2.55	-2.62	-2.52	0.00	0.00	0.00	0.00	0.00	-2.94	0.00	-2.46
HG03109.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.57	-4.56	-4.56	-2.53	-2.40	-2.52	-2.63	-2.52	-2.50	0.00	0.00	0.00	-4.56	-4.08	-3.04	-2.70	-2.45
HG03111.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.86	-2.62	-2.61	-4.91	-2.76	-2.79	-2.61	-2.63	-2.57	0.00	-2.85	-2.78	0.00	0.00	0.00	-2.56	-2.82
HG03112.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.83	0.00	-4.18	-2.78	-2.53	-2.61	-2.57	-2.66	-2.55	0.00	0.00	0.00	0.00	-4.88	-2.90	-4.88	-2.74
HG03114.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.49	0.00	-4.55	-2.71	-2.51	-2.48	-2.55	-2.63	-2.47	0.00	0.00	0.00	0.00	0.00	-2.90	-4.55	-2.45
HG03115.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.52	-2.66	-2.75	-2.81	-2.61	-2.66	-2.66	-2.72	-2.62	0.00	-2.87	-4.55	-2.78	-2.58	-3.02	0.00	-2.44
HG03117.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.47	-2.64	-2.61	-2.84	-2.60	-2.56	-2.50	-2.51	-2.43	0.00	0.00	-4.38	-4.38	-4.38	0.00	-2.40	-2.41
HG03118.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.49	-4.41	-4.11	-2.60	-2.52	-2.53	-2.52	-2.44	-2.44	0.00	0.00	0.00	-4.41	-3.81	-2.96	-2.69	-2.47
HG03120.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.53	-4.22	0.00	-2.69	-2.46	-2.51	-2.57	-2.58	-2.46	0.00	0.00	0.00	0.00	0.00	-2.95	0.00	-2.43
HG03121.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.55	0.00	-2.76	-2.84	-2.55	-2.55	-2.58	-2.50	-2.55	0.00	-2.90	0.00	-2.78	-4.27	-3.03	0.00	-2.55
HG03123.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.43	-4.37	-4.37	-2.49	-2.43	-2.45	-2.43	-2.42	-2.46	0.00	0.00	0.00	0.00	-4.07	-3.07	-4.37	-2.47
HG03124.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.63	-2.73	-2.78	-2.91	-2.44	-2.60	-2.61	-2.63	-2.56	0.00	-3.03	-2.74	-4.06	0.00	-3.10	-2.73	-2.45
HG03126.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.97	-2.65	-2.74	-5.04	-2.66	-2.73	-2.72	-2.75	-2.75	0.00	-2.79	-2.71	0.00	-5.04	-3.10	0.00	-2.82
HG03127.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.87	-4.21	-4.21	-2.75	-2.57	-2.59	-2.52	-2.53	-2.56	0.00	-4.21	-4.91	0.00	-4.91	0.00	-2.76	-2.87
HG03129.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.45	0.00	0.00	-2.59	-2.36	-2.49	-2.53	-2.50	-2.46	0.00	0.00	0.00	0.00	0.00	-2.82	0.00	-2.38
HG03130.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.53	-4.13	-2.71	-2.92	-2.43	-2.51	-2.56	-2.57	-2.52	0.00	-2.85	-4.43	-2.78	0.00	-2.92	0.00	-2.44
HG03132.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.47	0.00	0.00	-2.55	-2.37	-2.46	-2.52	-2.50	-2.44	0.00	0.00	0.00	0.00	-4.15	-2.96	-2.68	-2.40
HG03133.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.45	-4.50	-3.90	-2.55	-2.45	-2.44	-2.48	-2.42	-2.44	0.00	0.00	-4.50	-4.50	0.00	-2.99	0.00	-2.50
HG03135.mapped.ILLUMINA.bwa.ESN.exome.20121211	-2.53	0.00	0.00	-2.59	-2.51	-2.54	-2.55	-2.55	-2.59	-3.30	-2.90	0.00	-2.88	-2.64	-3.05	0.00	-2.44
HG03136.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.52	-4.48	-2.72	-2.81	-2.45	-2.56	-2.60	-2.63	-2.59	0.00	-2.79	0.00	-2.78	-4.48	-2.91	-4.18	-2.47
HG03139.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.87	-4.89	-4.59	-2.79	-2.54	-2.62	-2.53	-2.61	-2.60	0.00	0.00	-4.89	-4.59	-4.89	-2.94	0.00	-2.74
HG03157.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.96	-2.79	-2.81	-3.12	-2.56	-2.67	-2.64	-2.65	-2.67	0.00	-2.83	0.00	-2.83	0.00	0.00	-2.86	-3.01
HG03159.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.50	-4.40	-3.92	-2.59	-2.43	-2.54	-2.58	-2.54	-2.53	0.00	-4.40	-4.10	-4.40	0.00	-2.86	0.00	-2.46
HG03160.mapped.ILLUMINA.bwa.ESN.exome.20130422	-2.48	-2.67	-2.69	-4.43	-2.66	-2.55	-2.55	-2.49	-2.51	0.00	-2.81	-4.13	-2.74	-4.13	-2.99	-2.73	-2.46
HG03162.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.50	-2.65	-2.62	-2.83	-2.59	-2.64	-2.59	-2.56	-2.54	0.00	-4.44	0.00	-3.74	-3.96	0.00	-2.45	-2.54
HG03163.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.46	-4.38	-4.08	-2.68	-2.47	-2.50	-2.56	-2.54	-2.49	0.00	-4.38	-4.08	0.00	0.00	-2.81	-4.08	-2.48
HG03166.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.90	-4.91	-4.61	-2.77	-2.50	-2.65	-2.61	-2.57	-2.59	0.00	-4.61	0.00	-4.91	-4.91	-3.13	-2.81	-2.78
HG03168.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.53	-3.79	-3.61	-2.69	-2.49	-2.50	-2.50	-2.54	-2.34	0.00	-3.91	-3.69	0.00	0.00	0.00	-2.60	-2.46
HG03169.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.48	-2.70	-4.09	-2.91	-2.59	-2.61	-2.68	-2.66	-2.60	0.00	-2.75	-4.09	-2.68	-2.58	-3.05	-4.09	-2.46
HG03172.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.50	-4.10	-3.56	-2.70	-2.46	-2.50	-2.54	-2.44	-2.53	0.00	-4.40	-4.10	-4.40	-3.92	-3.06	-2.74	-2.45
HG03175.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.93	0.00	-2.78	-3.10	-2.50	-2.65	-2.62	-2.66	-2.75	0.00	-2.81	0.00	-2.78	-4.93	-3.01	0.00	-2.74
HG03189.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.93	0.00	-2.76	-3.13	-2.56	-2.64	-2.59	-2.70	-2.58	0.00	-2.80	0.00	-2.75	-4.65	-3.00	0.00	-2.78
HG03190.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.90	0.00	-4.33	-2.81	-2.56	-2.62	-2.60	-2.60	-2.56	0.00	-4.93	0.00	0.00	-4.93	-2.98	0.00	-2.71
HG03193.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.94	-4.65	-4.95	-2.82	-2.58	-2.66	-2.61	-2.70	-2.59	0.00	-4.95	-4.95	-4.95	-4.65	-2.99	-4.65	-2.81
HG03195.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.44	0.00	0.00	-2.72	-2.46	-2.50	-2.50	-2.49	-2.51	-4.38	-4.38	-4.08	0.00	-3.91	-2.91	-3.91	-2.45
HG03196.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.53	-4.13	0.00	-2.74	-2.49	-2.49	-2.55	-2.46	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.46
HG03198.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.43	-2.43	-2.48	-4.02	-4.02	-3.84	-2.47	-2.39	-2.45	0.00	0.00	0.00	0.00	-4.32	0.00	-2.33	-2.35

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG03199.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.42	-2.59	-2.59	-2.72	-2.30	-3.04	-2.55	-2.48	0.00	0.00	-2.67	-2.57	0.00	0.00	-2.89	0.00	-2.48
HG03202.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.92	-2.70	-2.70	-3.05	-2.70	-2.68	-2.54	-2.51	-2.52	0.00	0.00	0.00	0.00	-4.81	-3.05	-2.77	-2.71
HG03209.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.96	-2.81	-2.81	-3.09	-2.69	-2.75	-2.65	-2.75	-2.67	0.00	-2.72	-2.70	0.00	-4.93	-3.07	0.00	-2.86
HG03212.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.86	0.00	-4.82	-2.76	-2.45	-2.57	-2.54	-2.48	-2.50	0.00	-4.82	0.00	0.00	0.00	0.00	-2.44	-2.69
HG03224.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.90	-2.81	-2.82	-3.19	-2.57	-2.68	-2.67	-2.73	-2.59	0.00	-2.88	-2.82	-4.95	-4.95	-3.12	0.00	-2.82
HG03225.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.85	0.00	-4.88	-2.91	-2.57	-2.57	-2.59	-2.63	-2.50	-4.88	0.00	-4.88	0.00	0.00	-2.99	0.00	-2.71
HG03228.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.97	-4.85	-4.85	-2.79	-2.64	-2.64	-2.58	-2.66	-4.55	-3.35	-2.66	0.00	-2.61	-2.64	0.00	0.00	-2.73
HG03229.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.75	-2.69	-2.66	-3.06	-2.72	-2.68	-2.52	-2.46	-2.43	0.00	-4.79	0.00	-4.49	-4.49	-3.11	-2.71	-2.66
HG03234.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.99	-2.72	-2.74	-5.00	-2.68	-2.73	-2.70	-2.75	-2.85	-3.62	-2.66	-2.60	-4.52	-2.85	0.00	-2.90	-2.89
HG03235.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.87	-4.90	0.00	-3.01	-2.66	-2.66	-2.61	-2.68	-2.77	-3.44	-2.79	-4.90	-2.77	-2.80	0.00	-2.80	-2.82
HG03237.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.82	-2.50	-2.56	0.00	-4.23	-4.14	-2.64	-2.75	-2.63	0.00	-2.72	-4.53	-2.65	-2.66	0.00	-2.76	-2.67
HG03238.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.93	-2.53	-2.66	0.00	-2.81	-2.84	-2.57	-2.64	-2.61	-3.39	-2.87	-2.79	-4.46	0.00	0.00	-2.69	-2.84
HG03240.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.53	-4.42	-4.12	-2.63	-2.49	-2.47	-2.55	-2.59	-2.52	0.00	0.00	-3.94	0.00	-4.42	-2.93	0.00	-2.44
HG03241.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.53	0.00	0.00	-2.56	-2.39	-2.54	-2.52	-2.45	-2.56	0.00	0.00	0.00	0.00	0.00	-3.08	-2.76	-2.49
HG03246.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.47	0.00	-4.33	-2.57	-2.35	-2.45	-2.49	-2.38	-2.42	0.00	0.00	0.00	0.00	0.00	-2.93	-4.03	-2.47
HG03247.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.50	-2.70	-2.65	-2.87	-2.40	-2.54	-2.54	-2.51	-2.37	0.00	-2.81	-4.40	-2.70	-4.40	0.00	-2.80	-2.54
HG03258.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.48	0.00	-2.70	-2.76	-2.54	-2.66	-2.54	-2.50	-2.44	0.00	0.00	0.00	0.00	-4.54	-3.14	-2.67	-2.36
HG03259.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.53	-2.81	-2.74	-2.82	-2.41	-2.56	-2.55	-2.72	-2.53	0.00	-2.90	-2.69	0.00	-4.54	-2.97	-4.54	-2.44
HG03265.mapped.ILLUMINA.bwa.ESN.exome.20130415	-3.01	-2.80	-2.77	-3.13	-2.59	-2.68	-2.65	-2.54	-2.60	0.00	-2.89	-2.82	-4.66	-4.66	-3.23	-2.87	-2.81
HG03267.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.87	0.00	-4.39	-2.78	-2.63	-2.44	-2.60	-2.65	-2.57	0.00	0.00	0.00	0.00	0.00	-2.99	-4.86	-2.74
HG03268.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.81	-4.51	-4.81	-2.71	-2.56	-2.52	-2.54	-2.43	-2.51	0.00	0.00	0.00	-4.81	-4.81	-3.02	0.00	-2.83
HG03270.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.96	-2.64	-2.85	-4.08	-2.73	-2.77	-2.80	-2.85	-3.69	-3.45	-2.50	-2.79	-2.73	-2.61	0.00	0.00	-2.84
HG03271.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.99	-2.83	-2.87	-3.16	-2.61	-2.64	-2.70	-2.66	-2.82	-3.64	-2.70	-2.90	-2.81	-2.85	-3.25	-4.68	-2.89
HG03279.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.86	-4.82	-4.51	-2.88	-2.55	-2.62	-2.55	-2.59	-2.56	0.00	-4.82	0.00	0.00	0.00	-2.95	-4.82	-2.68
HG03280.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.87	-4.82	-4.35	-2.81	-2.58	-2.60	-2.59	-2.52	-2.52	0.00	0.00	-4.82	0.00	-4.82	-3.05	-2.79	-2.74
HG03291.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.92	-2.68	-2.70	-3.01	-2.70	-2.69	-2.56	-2.62	-2.46	0.00	0.00	0.00	0.00	-4.47	0.00	-2.57	-2.73
HG03294.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.88	0.00	-2.71	-3.12	-2.69	-2.70	-2.70	-2.74	-2.70	0.00	-2.70	0.00	-2.73	-2.67	0.00	-2.72	-2.72
HG03295.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.99	-4.35	-2.82	-3.19	-2.57	-2.54	-2.64	-2.71	-2.72	0.00	-2.81	0.00	-2.86	-4.18	-3.05	-4.48	-2.82
HG03297.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.84	-4.87	-4.57	-2.89	-2.55	-2.56	-2.49	-2.61	-2.49	0.00	0.00	-4.87	0.00	-4.87	-2.95	0.00	-2.65
HG03298.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.87	-4.90	-4.60	-2.89	-2.53	-2.57	-2.52	-2.49	-2.41	0.00	-4.90	0.00	0.00	-4.90	-3.05	-2.71	-2.71
HG03300.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.78	-2.54	-2.54	0.00	-4.79	-4.49	-2.68	-2.70	-2.68	0.00	-2.65	0.00	-2.67	-2.67	0.00	-2.70	-2.68
HG03301.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.85	-2.65	-2.75	-3.02	-2.75	-2.79	-2.58	-2.52	-2.50	0.00	-4.79	-4.32	0.00	0.00	0.00	-2.46	-2.75
HG03303.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.86	-4.85	-2.71	-3.05	-2.71	-2.72	-2.50	-2.45	-2.47	0.00	-4.37	-4.85	0.00	-4.85	-3.05	-2.78	-2.67
HG03304.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.81	0.00	0.00	-2.92	-2.42	-2.59	-2.51	-2.62	-2.45	0.00	0.00	0.00	0.00	0.00	-2.86	-4.18	-2.72
HG03311.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.83	-2.66	-2.84	-3.23	-2.67	-2.61	-2.44	-2.49	-2.40	0.00	0.00	0.00	-4.44	-4.44	0.00	-2.46	-2.59
HG03313.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.78	-4.03	-4.21	-3.09	-2.44	-2.48	-2.48	-2.55	-2.42	0.00	0.00	-4.21	-4.51	0.00	0.00	-2.54	-2.59
HG03342.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.49	0.00	-4.41	-2.70	-2.39	-2.54	-2.54	-2.53	-2.45	0.00	0.00	0.00	0.00	-4.41	-2.89	-4.11	-2.48
HG03343.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.62	-2.77	-2.68	-2.86	-2.41	-2.58	-2.58	-2.54	-2.45	0.00	-2.84	-3.89	-2.80	-4.19	-3.10	-2.71	-2.53
HG03351.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.78	-2.67	-2.71	-3.14	-2.67	-2.64	-2.50	-2.58	-2.46	0.00	0.00	0.00	0.00	-4.54	-2.80	-4.23	-2.56
HG03352.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.93	-2.80	-2.82	-3.45	-2.57	-2.53	-2.62	-2.67	-2.51	0.00	-2.92	0.00	-2.85	-4.17	-3.20	-2.88	-2.68
HG03354.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.86	-4.74	-4.74	-2.87	-2.53	-2.57	-2.50	-2.54	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.69
HG03363.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.76	-2.72	-2.71	-3.19	-2.66	-2.69	-2.45	-2.46	-2.36	0.00	0.00	-4.39	0.00	-4.39	-2.92	-2.71	-2.60
HG03366.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.94	-2.82	-2.83	-3.13	-2.64	-2.67	-2.67	-2.60	-2.68	0.00	-2.89	-2.89	0.00	0.00	0.00	-2.53	-2.81
HG03367.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.97	-2.66	-2.78	-4.92	-2.87	-2.81	-2.76	-2.81	-2.74	0.00	-2.66	-4.44	-2.63	-2.82	0.00	-2.84	-2.75
HG03369.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.83	-2.86	-2.77	-3.37	-2.55	-2.47	-2.54	-2.63	-2.52	0.00	-3.12	-2.78	-4.48	0.00	-2.84	-4.48	-2.74
HG03370.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.85	-4.45	-4.15	-3.01	-2.49	-2.48	-2.47	-2.58	-2.37	0.00	-4.15	0.00	0.00	-3.98	-2.77	-3.85	-2.61
HG03372.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.73	-4.09	-4.39	-3.06	-2.52	-2.37	-2.55	-2.57	-2.43	0.00	0.00	-4.39	0.00	0.00	-2.74	-4.09	-2.62
HG03376.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.89	-2.72	-4.87	-3.08	-2.72	-2.76	-2.69	-2.73	-2.73	0.00	-2.80	-4.87	-2.72	-2.80	-3.08	0.00	-2.76
HG03378.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.81	-4.86	-4.17	-2.88	-2.54	-2.57	-2.57	-2.55	-2.50	0.00	-4.86	0.00	0.00	0.00	-2.88	0.00	-2.71
HG03380.mapped.ILLUMINA.bwa.MSL.exome.20130415	-3.01	-2.70	-2.73	0.00	-2.74	-2.73	-2.76	-2.79	-2.68	0.00	-2.73	-2.73	0.00	0.00	-3.09	-4.70	-2.82
HG03382.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.85	0.00	0.00	-2.76	-2.50	-2.60	-2.55	-2.61	-2.52	0.00	0.00	0.00	0.00	0.00	-2.93	0.00	-2.71
HG03385.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.97	-4.05	-4.41	-2.89	-2.57	-2.66	-2.63	-2.57	-2.54	0.00	-2.87	-2.86	0.00	0.00	-3.14	-2.82	-2.79
HG03388.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.94	-2.78	-2.81	-3.22	-2.56	-2.70	-2.58	-2.74	-2.61	0.00	-2.89	-2.85	-4.64	-4.64	-3.06	-4.64	-2.83
HG03391.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.53	-2.61	-2.56	-4.12	-2.63	-2.63	-2.60	-2.48	-2.50	-4.42	-2.86	-3.82	-2.81	0.00	-2.90	-4.12	-2.52
HG03394.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.79	-4.13	-4.43	-3.07	-2.56	-2.56	-2.49	-2.61	-2.39	0.00	-4.43	0.00	-4.43	0.00	-2.75	-4.43	-2.56
HG03397.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.54	-4.51	-4.03	-2.66	-2.55	-2.51	-2.51	-2.45	-2.42	0.00	-4.51	-4.21	-4.21	-4.51	-3.03	-2.67	-2.38
HG03401.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.90	0.00	0.00	-2.79	-2.48	-2.63	-2.58	-2.52	-2.50	0.00	0.00	0.00	0.00	0.00	-2.90	-2.79	-2.77
HG03410.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.91	0.00	-4.60	-2.76	-2.62	-2.61	-2.61	-2.61	-2.55	0.00	0.00	-4.60	0.00	-4.90	-2.94	0.00	-2.80
HG03419.mapped.ILLUMINA.bwa.MSL.exome.20130415	-3.05	-2.82	-2.89	-3.21	-2.59	-2.70	-2.63	-2.60	-2.72	-3.44	-2.90	-4.97	-2.87	-4.67	-3.20	-2.95	-2.85
HG03428.mapped.ILLUMINA.bwa.MSL.exome.20130415	-3.00	-2.83	-2.87	-3.16	-2.70	-2.65	-2.74	-2.73	-2.81	-3.55	-2.69	-2.82	-2.90	-2.90	0.00	-2.90	-2.92
HG03432.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.77	-2.53	-2.59	0.00	-2.57	-2.53	-2.48	-2.58	-2.42	0.00	-2.59	-2.71	-2.78	-4.42	0.00	0.00	-4.42
HG03433.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.87	0.00	0.00	-2.92	-2.53	-2.65	-2.61	-2.52	-2.56	0.00	0.00	0.00	0.00	0.00	-2.96	-2.75	-2.72
HG03436.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.57	-2.77	-2.74	-2.88	-2.47	-2.59	-2.63	-2.55	-2.56	0.00	-2.90	-2.72	0.00	0.00	-3.06	-2.79	-2.54
HG03437.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.48	-4.42	-2.63	-2.91	-2.49	-2.54	-2.57	-2.64	-2.53	0.00	-2.82	-3.94	-2.81	0.00	-2.87	0.00	-2.45
HG03439.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.93	-4.80	0.00	-2.73	-2.57	-2.61	-2.59	-2.51	-2.58	0.00	-4.80	-4.80	0.00	-4.80	-3.05	-2.82	-2.72
HG03442.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.86	-2.52	-2.60	-4.80	0.00	0.00	-2.70	-2.71	-2.64	0.00	-2.74	0.00	-2.72	-2.69	-3.01	0.00	-2.78
HG03445.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.89	-2.70	-2.68	-4.63	-2.84	-2.82	-2.67	-2.58	-2.52	0.00	-2.83	0.00	-2.82	-4.33	-3.11	-2.84	-2.81
HG03446.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.87	-2.71	-2.76	-3.07	-2.70	-2.76	-2.58	-2.51	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.74
HG03449.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.97	-4.25	-4.25	-3.04	-2.60	-2.72	-2.67	-2.70	-2.60	0.00	-2.87	-2.83	0.00	-4.65	-3.08	-4.35	-2.85
HG03451.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.55	-2.80	-2.74	-2.83	-2.47	-2.55	-2.63	-2.60	-2.52	0.00	-2.94	-2.77	0.00	-4.57	-3.06	-2.81	-2.48
HG03452.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.53	-4.20	-2.75	-2.90	-2.46	-2.43	-2.63	-2.60	-2.52	0.00	-3.01	0.00	-2.88	0.00	-2.95	-4.50	-2.47
HG03455.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.50	0.00	-3.81	-2.61	-2.53	-2.56	-2.56	-2.50	-2.48	0.00	-4.41	0.00	-4.41	-3.57	-2.98	-2.75	-2.48
HG03457.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.77	-2.55	-2.53	-4.56	-2.66	-2.79	-2.70	-2.79	-2.66	0.00	-2.64	-2.72	-2.67	-2.71	0.00	-2.92	-2.63
HG03458.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.43	-2.69	-2.63	-2.79	-2.58	-2.63	-2.56	-2.66	-2.57	0.00	-2.79	0.00	-2.68	-2.62	-3.05	-4.37	-2.37
HG03460.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.91	-2.82	-2.85	-3.18	-2.73	-2.74	-2.66	-2.74	-2.64	0.00	-2.65	-2.84	-2.87	-4.49	-3.08	-4.67	-2.82
HG03461.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.81	-4.50	-2.64	-2.97	-2.69	-2.71	-2.62	-2.76	-2.64	0.00	-2.71	-4.81	-2.65	-2.69	0.00	-2.69	-2.72
HG03464.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.55	0.00	-4.27	-2.59	-2.53	-2.50	-2.52	-2.47	-2.48	-3.37	0.00	-4.58	-4.58	-4.10	-3.06	-2.76	-2.44
HG03469.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.48	-2.79	-2.79	-2.88	-2.52	-2.53	-2.58	-2.68	-2.52	0.00	-2.86	-2.75	-4.59	-4.11	-3.02	-4.59	-2.47
HG03470.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.79	-2.69	-2.64	-3.06	-2.69	-2.68	-2.58	-2.46	-2.51	0.00	0.00	0.00	0.00	-4.78	-3.00	0.00	-2.86
HG03472.mapped.ILLUMINA.bwa.MSL.exome.20121211	-2.47	-2.72	-2.70	-2.78	-2.61	-2.67	-2.52	-2.44	-2.41	0.00	0.00	0.00	0.00	-4.44	-2.99	-2.66	-2.42
HG03473.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.84	-4.12	0.00	-2.91	-2.59	-2.66	-2.55	-2.63	-2.56	-4.82	0.00	0.00	0.00	0.00	-2.94	-4.82	-2.73
HG03476.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.47	0.00	0.00	-2.64	-2.45	-2.44	-2.49	-2.55	-2.44	0.00	0.00	0.00	-4.37	0.00	-2.85	-4.37	-2.42
HG03478.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.86	0.00	-4.10	-2.93	-2.64	-2.61	-2.56	-2.53	-2.58	0.00	0.00	-4.87	-4.40	-4.87	-3.07	-4.87	-2.87
HG03479.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.91	-2.68	-2.62	-4.87	-2.76	-2.78	-2.75	-2.82	-2.76	0.00	-2.59	-2.77	-2.77	-2.80	-3.10	0.00	-2.82
HG03484.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.48	-3.94	-3.47	-2.78	-2.52	-2.52	-2.55	-2.46	-2.49	0.00	-4.42	-3.94	0.00	-4.42	-2.93	-3.72	-2.47
HG03485.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.52	-2.77	-2.64	-2.85	-2.45	-2.55	-2.54	-2.48	-2.46	0.00	-2.79	-4.43	-2.74	-3.95	-2.95	-4.43	-2.61
HG03488.mapped.ILLUMINA.bwa.PJL.exome.20130422	-2.36	-2.49	-2.47	-4.51	-3.51	-3.81	-2.42	-2.51	-2.53	-3.28	-2.84	0.00	-2.79	-2.57	0.00	-2.61	-2.33
HG03490.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.70	0.00	0.00	-2.89	-2.49	-2.48	-2.44	-2.50	-2.42	0.00	0.00	0.00	-4.42	0.00	0.00	-2.51	-2.59
HG03491.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.77	-4.41	0.00	-2.98	-2.55	-2.45	-2.45	-2.51	-2.42	-4.41	-4.41	0.00	-4.11	-4.41	0.00	-2.53	-2.55
HG03499.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.82	-2.81	-2.76	-3.16	-2.51	-2.57	-2.49	-2.53	-2.50	-4.50	-3.02	-2.78	-4.50	-4.50	-3.02	-2.83	-2.65
HG03511.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.70	0.00	-4.14	-3.00	-2.46	-2.47	-2.45	-2.38	-2.47	0.00	0.00	0.00	0.00	0.00	-2.95	-4.14	-2.71
HG03514.mapped.ILLUMINA.bwa.ESN.exome.20130415	-3.00	-2.85	-2.67	-4.50	-2.60	-2.78	-2.72	-2.67	-2.73	-4.98	-2.67	-2.87	-2.85	-4.98	-3.20	-2.93	-2.86
HG03515.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.94	0.00	0.00	-2.85	-2.59	-2.58	-2.61	-2.59	-2.59	0.00	0.00	-4.39	-4.86	0.00	0.00	-2.61	-2.75
HG03517.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.90	-2.39	-2.53	-4.13	-2.80	-2.73	-2.59	-2.54	-2.72	-3.43	-2.67	-2.76	-2.78	-2.68	0.00	-2.94	-2.69
HG03518.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.67	0.00	-4.07	-2.98	-2.48	-2.46	-2.40	-2.53	-2.42	0.00	0.00	0.00	0.00	-4.37	0.00	-2.48	-2.57
HG03520.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.52	-3.53	-3.74	-2.63	-2.47	-2.53	-2.53	-2.57	-2.51	0.00	0.00	-4.44	0.00	0.00	-2.93	-3.59	-2.45

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG03521.mapped.ILLUMINA.bwa.ESN.exome.20130415	-2.58	0.00	-2.64	-2.87	-2.56	-2.51	-2.59	-2.64	-2.54	0.00	-2.88	0.00	-2.74	0.00	-2.92	0.00	-2.44
HG03538.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.54	-2.81	-2.70	-2.87	-2.46	-2.58	-2.60	-2.60	-2.58	0.00	-2.86	-2.78	-4.47	-4.47	-2.90	0.00	-2.50
HG03539.mapped.ILLUMINA.bwa.GWD.exome.20130415	-2.49	-2.65	-2.58	-2.77	-2.60	-2.66	-2.38	-2.55	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.49
HG03547.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.53	-2.69	-2.69	-2.83	-2.48	-2.53	-2.51	-2.59	-2.59	0.00	-2.84	-2.75	0.00	0.00	-2.95	0.00	-2.48
HG03548.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.46	-3.69	-3.91	-2.71	-2.46	-2.51	-2.44	-2.53	-2.45	0.00	-4.09	0.00	-3.91	-4.09	-2.86	-4.09	-2.44
HG03556.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.55	-4.20	0.00	-2.74	-2.57	-2.58	-2.59	-2.49	-2.57	0.00	0.00	0.00	0.00	0.00	-3.01	-2.65	-2.48
HG03557.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.48	-3.83	-2.54	0.00	-2.66	-2.67	-2.55	-2.51	-2.51	0.00	-2.76	-4.43	-2.77	0.00	-3.01	-2.67	-2.47
HG03558.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.71	-3.85	-4.15	-3.02	-2.54	-2.60	-2.52	-2.45	-2.43	-3.54	0.00	0.00	0.00	0.00	-3.00	-2.90	-2.60
HG03559.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.86	-2.69	-2.78	-3.24	-2.55	-2.60	-2.58	-2.58	-2.52	0.00	-2.97	-2.82	-4.16	-4.47	-3.02	-2.84	-2.63
HG03563.mapped.ILLUMINA.bwa.MSL.exome.20130422	-2.64	-2.71	-2.68	-2.86	-2.42	-2.61	-2.63	-2.53	-2.54	0.00	-2.87	0.00	-2.71	0.00	-2.97	-4.01	-2.55
HG03565.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.72	-4.42	0.00	-2.99	-2.47	-2.54	-2.44	-2.47	-2.39	0.00	0.00	0.00	0.00	-4.42	-2.94	-2.78	-2.60
HG03567.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.86	-4.42	-4.12	-3.12	-2.51	-2.53	-2.51	-2.48	-2.63	-3.34	-2.87	-4.42	-2.83	-2.69	-2.97	-4.42	-2.59
HG03571.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.87	-4.18	-4.31	-2.89	-2.56	-2.58	-2.55	-2.58	-2.57	0.00	0.00	-4.78	0.00	-4.78	-2.93	-4.78	-2.69
HG03572.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.37	-4.28	-2.53	-2.72	-2.48	-2.53	-2.55	-2.66	-2.50	0.00	-2.75	-3.80	-2.62	-2.54	0.00	-3.68	-2.45
HG03575.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.55	-2.71	-2.73	-2.93	-2.49	-2.59	-2.62	-2.60	-2.59	-4.48	-2.92	-4.00	-2.76	0.00	-3.06	-2.71	-2.52
HG03577.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.62	-4.27	-4.27	-2.63	-2.61	-2.63	-2.64	-2.51	-2.58	0.00	-2.87	-2.76	0.00	0.00	-3.09	-2.75	-2.60
HG03578.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.55	-2.75	-2.70	-2.99	-2.45	-2.58	-2.57	-2.56	-2.52	0.00	-2.96	-2.76	0.00	0.00	-3.05	-2.71	-2.53
HG03583.mapped.ILLUMINA.bwa.MSL.exome.20130415	-2.57	0.00	-2.68	-2.85	-2.46	-2.52	-2.56	-2.61	-2.52	0.00	-2.98	-4.41	-2.75	-4.11	-2.84	-4.41	-2.51
HG03585.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.46	-2.73	-2.61	-2.91	-2.62	-2.61	-2.50	-2.50	-2.44	0.00	0.00	0.00	0.00	0.00	-2.90	-2.64	-2.41
HG03589.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.58	-2.75	-2.71	-2.84	-2.63	-2.64	-2.54	-2.55	-2.61	-3.21	-2.74	0.00	-2.77	-2.63	0.00	-2.78	-2.49
HG03593.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.52	-2.77	-2.81	-2.87	-2.53	-2.63	-2.64	-2.61	-2.82	-3.21	-2.64	-2.80	-2.90	-2.75	0.00	-2.91	-2.62
HG03594.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.97	-2.65	-2.68	0.00	-2.81	-2.80	-2.68	-2.71	-2.83	-3.54	-2.72	-2.66	0.00	-2.82	0.00	-2.84	-2.80
HG03595.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.90	-2.67	-2.67	-4.97	-2.82	-2.80	-2.76	-2.81	-2.81	0.00	-2.61	-2.76	-2.81	-2.84	-3.17	0.00	-2.83
HG03598.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.84	-2.64	-2.87	0.00	-2.64	-2.56	-2.47	-2.61	-2.74	-3.39	-2.87	-2.90	-2.92	-2.86	0.00	-2.92	-2.71
HG03600.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.97	-2.75	-2.79	-3.13	-2.52	-2.68	-2.68	-2.64	-2.49	-4.79	-2.82	-2.75	-4.31	0.00	0.00	-2.68	-2.74
HG03603.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.94	-2.67	-2.68	-4.66	-2.63	-2.69	-2.64	-2.60	-2.65	0.00	-2.70	-2.66	0.00	-4.96	-3.14	-2.85	-2.78
HG03604.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.92	-3.88	-3.77	-2.94	-2.59	-2.63	-2.66	-2.54	-2.70	-3.52	-2.77	-3.80	-2.75	-2.77	-3.13	-4.88	-2.81
HG03607.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.92	-2.78	-2.80	-3.09	-2.57	-2.67	-2.66	-2.61	-2.68	0.00	-2.85	-2.83	-4.60	-4.30	-3.14	-2.85	-2.85
HG03611.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.83	-4.80	-4.32	-2.86	-2.59	-2.57	-2.61	-2.48	-2.54	0.00	-4.80	0.00	-4.80	-4.50	-2.99	-2.74	-2.72
HG03615.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.53	-2.67	-2.67	-2.82	-2.66	-2.65	-2.65	-2.67	-2.63	-4.47	-2.80	0.00	-2.71	-2.60	-2.95	-4.47	-2.47
HG03616.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.48	-2.66	-2.74	-2.80	-2.61	-2.65	-2.57	-2.55	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.47
HG03619.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.84	-2.54	-2.54	0.00	0.00	-4.96	-2.70	-2.77	-2.70	0.00	-2.79	0.00	-2.67	-2.77	0.00	-2.77	-2.72
HG03624.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.79	-4.25	-4.25	-3.09	-2.61	-2.55	-2.55	-2.59	-2.64	-3.44	-2.89	-4.55	-2.73	-2.74	0.00	-2.77	-2.66
HG03625.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.80	-4.15	-4.45	-3.13	-2.52	-2.52	-2.55	-2.59	-2.42	-4.45	-3.97	0.00	-3.75	-4.15	0.00	-2.64	-2.62
HG03629.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.73	-2.54	-4.53	-3.25	-2.45	-2.69	-2.67	-2.76	-2.69	0.00	-2.82	-2.71	-4.53	-2.66	0.00	-2.77	-2.61
HG03631.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.89	-2.70	-2.79	-3.35	-2.51	-2.59	-2.62	-2.63	-2.72	-3.44	-2.68	-2.62	0.00	-2.75	0.00	-2.84	-2.73
HG03634.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.94	-4.60	-4.29	-2.75	-2.58	-2.60	-2.54	-2.64	-2.55	0.00	-4.42	-4.90	0.00	-4.60	0.00	-2.61	-2.68
HG03636.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.69	-2.60	-2.78	-3.38	-2.61	-2.61	-2.46	-2.54	-2.40	0.00	0.00	0.00	-4.38	-3.90	-2.66	-4.38	-2.56
HG03640.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.78	-2.76	-4.15	-3.04	-2.58	-2.61	-2.48	-2.59	-2.66	-3.45	-2.85	-3.98	-2.84	-2.75	0.00	-2.87	-2.70
HG03642.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.63	-2.80	-2.72	-2.92	-2.56	-2.66	-2.68	-2.67	-2.75	-3.50	-2.73	-2.81	-2.81	-2.75	0.00	-2.73	-2.57
HG03643.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.50	-4.17	-4.00	-2.74	-2.51	-2.57	-2.56	-2.49	-2.50	-4.47	-3.77	-4.47	-4.00	-4.00	0.00	-2.56	-2.50
HG03644.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.67	-2.82	-2.81	-3.00	-2.54	-2.64	-2.66	-2.68	-2.59	-3.28	-2.80	-2.74	0.00	0.00	0.00	-2.69	-2.43
HG03645.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.99	-2.68	-2.72	-4.90	-2.71	-2.72	-2.70	-2.77	-4.30	-3.35	-2.50	-2.68	-2.72	-2.69	0.00	0.00	-2.87
HG03646.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.94	-2.75	-2.85	-3.18	-2.53	-2.69	-2.63	-2.72	-2.77	-3.39	-2.71	-2.68	-4.93	-2.82	0.00	-2.82	-2.87
HG03649.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.83	-2.59	-2.59	0.00	-2.58	-2.54	-2.53	-2.52	-2.50	0.00	-2.74	-2.59	0.00	-4.16	-3.03	-2.92	-2.65
HG03652.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.72	-2.37	-2.40	0.00	-3.71	-3.71	-2.49	-2.68	-2.48	0.00	-2.77	-2.66	0.00	-2.62	-2.79	-4.31	-2.43
HG03653.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.80	-3.85	0.00	-2.98	-2.45	-2.44	-2.46	-2.59	-2.37	0.00	-4.03	-4.33	0.00	0.00	-2.93	-2.72	-2.53
HG03660.mapped.ILLUMINA.bwa.PJL.exome.20130422	-2.39	-2.69	-2.62	-2.71	-2.55	-2.59	-2.60	-2.67	-2.54	0.00	-2.80	-4.21	-2.76	-2.60	0.00	-2.65	-2.32
HG03663.mapped.ILLUMINA.bwa.PJL.exome.20130422	-2.42	-2.55	-2.51	-4.27	-2.58	-2.65	-2.65	-2.71	-2.57	0.00	-2.60	-2.65	-2.71	-2.58	0.00	-2.70	-2.38
HG03667.mapped.ILLUMINA.bwa.PJL.exome.20130415	-3.05	-2.74	-2.76	-5.07	-2.72	-2.77	-2.74	-2.70	-2.89	-3.51	-2.66	-2.72	-2.91	-2.91	-3.18	0.00	-2.92
HG03668.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.95	-2.75	-2.79	-3.09	-2.54	-2.66	-2.65	-2.66	-2.61	0.00	-2.90	-2.83	0.00	0.00	-3.08	-4.68	-2.87
HG03672.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.80	-2.64	-2.70	-3.07	-2.69	-2.64	-2.55	-2.57	-2.52	0.00	0.00	-4.82	0.00	-4.52	0.00	-2.55	-2.72
HG03673.mapped.ILLUMINA.bwa.STU.exome.20130422	-2.61	-2.83	-2.75	-2.91	-2.54	-2.68	-2.61	-2.64	-2.79	-3.29	-2.79	-2.80	-2.86	-2.74	0.00	-2.74	-2.56
HG03679.mapped.ILLUMINA.bwa.STU.exome.20130422	-2.46	-4.01	-4.18	-2.73	-2.58	-2.51	-2.55	-2.40	-2.45	0.00	0.00	0.00	-4.18	-4.18	-3.14	-2.71	-2.47
HG03680.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.54	-3.69	-3.99	-2.69	-2.54	-2.55	-2.57	-2.46	-2.46	0.00	-4.46	-4.46	0.00	-4.16	-3.02	-2.68	-2.45
HG03681.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.48	-2.71	-2.75	-2.91	-2.48	-2.62	-2.66	-2.67	-2.59	-4.24	-3.08	-2.80	-4.54	-3.94	0.00	-2.65	-2.52
HG03684.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.48	-2.75	-2.62	-2.91	-2.60	-2.67	-2.64	-2.72	-3.95	-3.25	-2.66	0.00	-2.60	-2.51	0.00	-4.42	-2.43
HG03685.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.54	-2.70	-2.68	-2.94	-2.70	-2.73	-2.58	-2.53	-2.62	-3.36	-2.79	0.00	-2.69	-2.65	0.00	-2.80	-2.53
HG03686.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.81	-4.59	0.00	-2.82	-2.59	-2.65	-2.55	-2.51	-2.61	-4.89	-4.59	-4.41	-4.89	-4.41	-3.10	-2.76	-2.78
HG03687.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.97	-2.67	-2.71	0.00	-2.77	-2.86	-2.66	-2.77	-4.68	-3.31	-2.57	-2.84	-2.68	-2.67	0.00	0.00	-2.86
HG03689.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.94	-2.68	-2.70	0.00	-2.86	-2.85	-2.65	-2.63	-2.84	-3.54	-2.65	-2.80	-2.86	-2.85	-3.16	0.00	-2.82
HG03690.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.95	-2.80	-2.80	-3.13	-2.55	-2.69	-2.68	-2.60	-2.64	0.00	-2.85	-2.83	0.00	0.00	-3.13	-2.93	-2.82
HG03691.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.83	-2.67	-2.75	-3.04	-2.72	-2.78	-2.54	-2.49	-2.57	-4.84	0.00	0.00	-4.54	0.00	0.00	-2.43	-2.73
HG03692.mapped.ILLUMINA.bwa.STU.exome.20130422	-2.49	-2.70	-2.63	-2.85	-2.62	-2.65	-2.58	-2.53	-2.46	0.00	0.00	0.00	-3.86	-3.98	-3.12	-2.71	-2.48
HG03693.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.46	0.00	0.00	-2.57	-2.55	-2.53	-2.52	-2.49	-2.45	0.00	-3.97	0.00	-4.14	-3.97	0.00	-2.56	-2.43
HG03694.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.95	-2.76	-2.79	-3.13	-2.79	-2.81	-2.59	-2.65	-4.66	-3.31	-2.60	-2.78	-2.78	-2.65	0.00	0.00	-2.77
HG03695.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.77	-4.49	-4.79	-2.92	-2.57	-2.57	-2.56	-2.43	-2.46	0.00	0.00	0.00	-4.79	0.00	0.00	-2.44	-2.77
HG03696.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.76	0.00	0.00	-2.87	-2.51	-2.51	-2.53	-2.57	-2.46	0.00	0.00	0.00	0.00	-4.44	0.00	-2.57	-2.65
HG03697.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.99	-2.63	-2.65	-4.92	-2.82	-2.82	-2.64	-2.64	-2.80	-3.50	-2.66	-2.78	-2.74	-2.77	0.00	-2.91	-2.79
HG03698.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.89	-3.86	-3.78	-2.86	-2.55	-2.57	-2.54	-2.53	-2.48	-4.34	-3.70	-3.91	-4.12	-3.82	-3.08	-2.80	-2.69
HG03702.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.91	0.00	0.00	-2.92	-2.54	-2.60	-2.57	-2.60	-2.74	-3.36	-2.77	0.00	-2.69	-2.74	0.00	-2.83	-2.71
HG03703.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.87	-2.51	-2.67	-3.08	-2.69	-2.72	-2.52	-2.51	-2.55	0.00	-4.44	0.00	0.00	-4.44	-3.01	-2.75	-2.68
HG03705.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.87	-2.73	-2.78	-3.23	-2.53	-2.56	-2.58	-2.57	-2.68	-3.81	-2.73	-2.88	-2.92	-2.83	-3.13	-3.91	-2.71
HG03706.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.91	-2.71	-4.50	-3.14	-2.45	-2.57	-2.58	-2.60	-2.64	-3.54	-2.87	0.00	-2.77	-2.67	0.00	-2.81	-2.58
HG03708.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.98	-2.87	-2.85	-3.23	-2.57	-2.71	-2.65	-2.73	-2.77	-3.53	-2.68	-2.83	-2.85	-2.85	-3.22	-4.97	-2.91
HG03709.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.90	-4.39	-4.87	-3.00	-2.57	-2.59	-2.61	-2.52	-2.76	-3.44	-2.78	-4.57	-2.68	-2.76	-3.14	-4.57	-2.73
HG03711.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.99	-2.71	-2.66	-4.57	-2.66	-2.74	-2.66	-2.76	-2.85	-3.53	-2.65	-2.60	-5.05	-2.86	0.00	-2.91	-2.85
HG03713.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.52	-4.20	-3.60	-2.75	-2.51	-2.53	-2.56	-2.49	-2.48	0.00	0.00	-4.50	0.00	-3.90	0.00	-2.57	-2.42
HG03714.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.54	0.00	-3.88	-2.58	-2.54	-2.62	-2.61	-2.60	-2.63	-3.31	-2.90	-4.48	-2.75	-2.73	0.00	-2.68	-2.47
HG03715.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.58	-4.51	-4.51	-2.67	-2.57	-2.55	-2.60	-2.55	-2.72	-3.21	-2.87	-4.03	-2.79	-2.68	0.00	-2.74	-2.53
HG03716.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.51	-2.57	-2.53	-4.01	-2.70	-2.65	-2.68	-2.75	-3.58	-3.31	-2.60	-2.60	-2.74	-2.52	0.00	-3.88	-2.50
HG03717.mapped.ILLUMINA.bwa.ITU.exome.20130422	-2.52	-2.63	-2.69	-2.78	-2.69	-2.59	-2.55	-2.38	-2.44	0.00	0.00	-4.44	-4.44	0.00	0.00	-2.43	-2.49
HG03718.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.68	-2.38	-2.45	0.00	-3.83	-3.53	-2.57	-2.72	-2.52	0.00	-2.79	0.00	-2.67	-2.55	0.00	-2.60	-2.52
HG03720.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.46	-2.76	-2.70	-2.86	-2.47	-2.53	-2.50	-2.51	-2.48	0.00	-2.96	-2.70	-4.56	-4.56	-3.18	-2.83	-2.38
HG03722.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.50	0.00	0.00	-2.73	-2.52	-2.53	-2.53	-2.52	-2.49	0.00	0.00	0.00	0.00	-4.44	-2.91	-3.66	-2.41
HG03727.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.50	-2.70	-2.65	-2.79	-2.66	-2.61	-2.70	-2.75	-3.98	-3.31	-2.66	0.00	-2.57	-2.57	0.00	-4.46	-2.49
HG03729.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.48	-3.71	-4.01	-2.61	-2.54	-2.60	-2.53	-2.52	-2.48	0.00	-3.89	-3.64	0.00	-3.71	0.00	-2.43	-2.48
HG03730.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.52	0.00	-4.42	-2.75	-2.51	-2.47	-2.58	-2.58	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.45
HG03731.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.57	-2.72	-2.74	-2.89	-2.65	-2.71	-2.59	-2.53	-2.66	-3.38	-2.88	0.00	-2.75	-2.65	-3.14	0.00	-2.49
HG03733.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.84	-4.46	-4.63	-2.93	-2.58	-2.59	-2.55	-2.49	-2.53	0.00	-4.63	-4.63	0.00	-4.93	-3.09	-2.78	-2.75
HG03736.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.81	0.00	-4.88	-2.81	-2.52	-2.50	-2.47	-2.47	-2.53	0.00	0.00	-4.88	0.00	0.00	0.00	-2.56	-2.68
HG03738.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.92	-2.74	-2.72	-3.13	-2.75	-2.84	-2.60	-2.61	-2.74	-3.42	-2.85	0.00	-2.76	-2.78	0.00	-2.85	-2.74
HG03740.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.56	-2.74	-2.70	-2.86	-2.67	-2.69	-2.57	-2.61	-2.67	-3.23	-2.95	0.00	-2.78	-2.67	0.00	-2.70	-2.53
HG03741.mapped.ILLUMINA.bwa.STU.exome.20130422	-2.61	-2.75	-2.73	-3.15	-2.51	-2.67	-2.64	-2.56	-2.56	-4.55	-3.02	-2.69	0.00	-4.07	-3.08	-2.75	-2.55
HG03742.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.86	-2.67	-2.70	-2.98	-2.72	-2.68	-2.71	-2.78	-2.65	0.00	-2.80	-4.74	-2.68	-2.66	-3.04	-4.74	-2.72
HG03743.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.53	0.00	-4.18	-2.81	-2.55	-2.58	-2.51	-2.53	0.00	-3.16	-2.74	-2.57	-3.70	-2.52	0.00	-4.48	-2.50

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG03744.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.94	-2.55	-2.76	0.00	-2.59	-2.60	-2.55	-2.61	-2.59	0.00	-2.82	-2.76	0.00	0.00	-3.15	-2.82	-2.81
HG03745.mapped.ILLUMINA.bwa.STU.exome.20130415	-3.00	-2.83	-2.86	-3.12	-2.57	-2.67	-2.66	-2.64	-2.83	-3.49	-2.76	-2.68	0.00	-2.86	0.00	-2.91	-2.84
HG03746.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.49	-2.72	-2.63	-2.80	-2.66	-2.67	-2.67	-2.83	-2.57	0.00	-2.92	0.00	-2.71	-2.61	0.00	-2.76	-2.44
HG03750.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.56	-2.81	-2.71	-2.94	-2.51	-2.63	-2.61	-2.57	-2.56	0.00	-2.97	-2.77	-4.51	-4.04	0.00	-2.54	-2.53
HG03752.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.99	-2.67	-2.67	0.00	-2.82	-2.82	-2.63	-2.65	-2.76	-3.50	-2.64	-2.79	-2.80	-2.86	0.00	-2.84	-2.83
HG03753.mapped.ILLUMINA.bwa.STU.exome.20130415	-3.03	-2.73	-2.75	-5.08	-2.67	-2.73	-2.70	-2.66	-2.83	-3.57	-2.62	-2.72	-2.85	-2.88	-3.25	-4.48	-2.86
HG03754.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.52	-3.97	-3.85	-2.58	-2.57	-2.57	-2.60	-2.55	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.45
HG03755.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.43	-2.50	-2.54	0.00	-2.62	-2.64	-2.70	-2.74	-3.78	-3.26	-2.59	-2.45	-2.59	-2.46	0.00	-4.08	-2.37
HG03756.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.53	-2.71	-2.70	-4.16	-2.63	-2.67	-2.69	-2.57	-2.69	-3.41	-2.69	-2.71	-2.85	-2.80	-3.15	0.00	-2.58
HG03757.mapped.ILLUMINA.bwa.STU.exome.20130422	-2.60	-2.72	-2.74	-2.88	-2.48	-2.61	-2.69	-2.63	-2.57	-4.56	-2.86	-2.76	0.00	0.00	-2.99	-3.60	-2.53
HG03760.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.95	-2.64	-2.68	-4.48	-2.60	-2.59	-2.61	-2.62	-2.83	-3.45	-2.68	-2.55	-4.96	0.00	0.00	-2.89	-2.96
HG03762.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.90	-4.10	0.00	-3.12	-2.49	-2.51	-2.53	-2.59	-2.36	0.00	-4.40	-4.40	-4.10	0.00	0.00	-2.54	-2.54
HG03765.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.88	-2.79	-2.78	-3.42	-2.61	-2.67	-2.82	-2.66	-4.53	-3.21	-2.63	-2.85	-2.67	-2.57	0.00	-3.93	-2.74
HG03767.mapped.ILLUMINA.bwa.PJL.exome.20130415	-2.88	-4.24	-4.24	-3.05	-2.63	-2.58	-2.58	-2.64	-4.06	-3.31	-2.64	0.00	-2.66	-2.54	0.00	-3.84	-2.63
HG03770.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.53	-2.69	-2.71	-2.78	-2.68	-2.71	-2.55	-2.56	-2.56	-3.35	0.00	0.00	0.00	0.00	0.00	-2.59	-2.52
HG03771.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.47	-3.75	0.00	-2.57	-2.54	-2.53	-2.58	-2.60	-2.51	0.00	-4.45	-3.98	0.00	-4.45	-3.07	-2.68	-2.44
HG03772.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.64	-2.76	-2.79	-2.91	-2.54	-2.66	-2.64	-2.73	-2.70	-3.29	-2.73	-2.77	-2.80	-2.74	0.00	-2.86	-2.58
HG03773.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.50	-2.74	-2.70	-2.81	-2.64	-2.68	-2.59	-2.40	-2.48	0.00	0.00	0.00	0.00	0.00	-3.01	-2.66	-2.46
HG03774.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.90	-2.71	-2.73	-3.39	-2.48	-2.53	-2.53	-2.61	-2.47	-4.39	-3.13	-2.67	-4.39	-3.91	0.00	-2.63	-2.60
HG03775.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.58	-2.58	-2.60	-3.82	-2.73	-2.70	-2.63	-2.56	-2.58	0.00	-2.85	-2.72	-3.91	-4.04	-3.12	-2.67	-2.55
HG03777.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.88	-4.04	-4.18	-2.98	-2.64	-2.67	-2.60	-2.59	-2.71	-3.44	-2.78	-4.41	-2.76	-2.76	0.00	-2.83	-2.74
HG03778.mapped.ILLUMINA.bwa.ITU.exome.20130415	-3.00	-2.84	-2.87	-3.16	-2.56	-2.67	-2.66	-2.64	-2.82	-3.50	-2.70	-2.70	-3.80	-2.84	0.00	-2.89	-2.81
HG03779.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.95	-2.62	-2.68	-4.86	-2.81	-2.78	-2.64	-2.61	-2.78	-3.35	-2.61	-2.83	-2.76	-2.79	0.00	-2.86	-2.80
HG03780.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.71	-4.51	-4.21	-3.12	-2.60	-2.61	-2.59	-2.47	-2.77	-3.44	-2.84	-4.51	-2.74	-2.72	0.00	-2.81	-2.64
HG03781.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.56	0.00	0.00	-2.72	-2.52	-2.59	-2.59	-2.52	-2.62	-3.34	-2.97	-2.72	-4.49	-2.69	-3.07	-4.18	-2.53
HG03782.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.87	-3.52	-3.69	-2.79	-2.57	-2.64	-2.57	-2.65	-2.70	-3.44	-2.75	-3.56	-2.77	-2.73	0.00	-2.83	-2.72
HG03784.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.55	-3.72	-4.50	-2.73	-2.55	-2.58	-2.60	-2.55	-2.63	-3.27	-2.91	-4.02	-2.77	-2.68	-3.04	-3.90	-2.55
HG03785.mapped.ILLUMINA.bwa.ITU.exome.20130415	-3.00	-2.72	-2.68	0.00	-2.67	-2.75	-2.56	-2.65	-2.81	-3.23	-2.59	-2.68	-2.80	-2.85	0.00	-2.93	-2.85
HG03786.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.42	-2.67	-2.77	-2.88	-2.65	-2.64	-2.51	-2.50	-2.46	0.00	0.00	0.00	-3.72	0.00	0.00	-2.43	-2.47
HG03787.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.51	-2.67	-2.67	-2.83	-2.66	-2.70	-2.64	-2.65	-2.58	-4.46	-2.91	-4.46	-2.73	-2.65	-2.97	-4.16	-2.43
HG03788.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.61	0.00	0.00	-2.79	-2.57	-2.58	-2.67	-2.61	-2.69	-3.28	-2.93	0.00	-2.78	-2.69	0.00	-2.77	-2.49
HG03789.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.50	-2.77	-2.77	-2.85	-2.50	-2.67	-2.65	-2.60	-2.68	-3.27	-2.71	-2.65	0.00	-2.71	0.00	-2.85	-2.56
HG03790.mapped.ILLUMINA.bwa.ITU.exome.20130415	-3.03	-2.86	-2.85	-3.22	-2.48	-2.65	-2.62	-2.58	-2.70	-3.51	-2.62	-2.71	-4.31	0.00	-3.19	-2.93	-2.87
HG03792.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.73	-4.78	-4.47	-2.85	-2.59	-2.59	-2.52	-2.49	-2.53	0.00	-4.78	0.00	-4.78	-4.78	-3.02	-2.74	-2.69
HG03793.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.51	-2.70	-2.73	-2.89	-2.68	-2.71	-2.62	-2.71	-2.63	-3.27	-2.88	-4.25	-2.79	-2.70	0.00	-2.79	-2.59
HG03796.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.52	-4.46	-3.99	-2.73	-2.48	-2.53	-2.56	-2.58	-2.49	-4.16	0.00	0.00	0.00	-4.16	-3.07	-2.70	-2.44
HG03800.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.45	-2.82	-2.74	-2.92	-2.47	-2.59	-2.61	-2.50	-2.61	-4.58	-2.85	-2.73	0.00	-3.88	-3.09	-2.76	-2.52
HG03802.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.59	-2.58	-2.56	-4.53	-2.72	-2.74	-2.65	-2.61	-2.67	-3.42	-2.72	-2.65	0.00	-2.73	0.00	-2.77	-2.56
HG03803.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.60	-2.72	0.00	-2.92	-2.49	-2.60	-2.62	-2.63	-2.67	-3.28	-2.92	0.00	-2.86	-2.67	0.00	-2.73	-2.55
HG03805.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.93	-2.75	-2.79	-3.12	-2.73	-2.81	-2.65	-2.66	-4.56	-3.25	-2.67	0.00	-2.63	-2.65	0.00	-4.86	-2.77
HG03808.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.95	-2.81	-2.80	-3.20	-2.56	-2.69	-2.66	-2.70	-2.66	0.00	-2.82	-2.80	0.00	-4.94	0.00	-2.68	-2.80
HG03809.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.85	-2.60	-2.65	-4.59	-2.76	-2.77	-2.65	-2.57	-2.74	-3.37	-2.61	-2.81	-2.76	-2.77	-3.10	0.00	-2.86
HG03812.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.47	-4.37	-4.07	-2.54	-2.49	-2.52	-2.52	-2.54	-2.48	-4.37	-4.07	-4.07	-4.07	-4.07	0.00	-2.52	-2.43
HG03814.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.69	-4.69	-4.69	-2.73	-2.55	-2.52	-2.49	-2.47	-2.52	0.00	-4.08	-4.39	-4.69	-4.69	-3.01	-2.69	-2.63
HG03815.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.42	0.00	-4.05	-2.60	-2.64	-2.64	-2.64	-2.65	-4.05	-3.21	-2.68	0.00	-2.62	-2.64	0.00	0.00	-2.53
HG03817.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.38	0.00	0.00	-2.62	-2.52	-2.54	-2.52	-2.42	-2.42	0.00	-4.09	0.00	-4.39	-4.09	-3.07	-2.68	-2.44
HG03821.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.79	-2.74	-2.67	-3.18	-2.74	-2.71	-2.48	-2.52	-2.47	0.00	-3.80	0.00	-4.50	-4.20	0.00	-2.57	-2.60
HG03823.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.95	-2.77	-2.75	-3.15	-2.58	-2.74	-2.67	-2.71	-2.84	-3.48	-2.66	-2.84	-2.81	-2.80	0.00	-2.86	-2.85
HG03824.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.81	-2.64	-2.67	-3.05	-2.68	-2.72	-2.68	-2.73	-4.74	-3.38	-2.59	0.00	-2.58	-2.61	0.00	-4.44	-2.76
HG03826.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.92	-2.79	-2.84	-3.16	-2.57	-2.73	-2.71	-2.70	-4.89	-3.38	-2.66	-2.62	0.00	-2.74	0.00	0.00	-2.88
HG03829.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.90	-2.61	-2.68	0.00	-2.72	-2.75	-2.73	-2.76	-2.75	-4.79	-2.57	-2.72	-2.74	-2.71	-3.03	0.00	-2.80
HG03830.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.87	-2.69	-2.77	-3.02	-2.45	-2.59	-2.61	-2.62	-2.58	0.00	-2.79	-2.74	-4.52	-4.82	0.00	-2.65	-2.79
HG03832.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.77	-4.02	0.00	-2.98	-2.51	-2.57	-2.52	-2.54	-2.58	-4.72	-4.72	-4.24	-4.42	-4.42	-2.88	0.00	-2.68
HG03833.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.92	-2.82	-2.82	-3.20	-2.63	-2.74	-2.69	-2.71	-4.69	-3.40	-2.61	-2.82	-2.71	-2.70	0.00	-4.99	-2.87
HG03836.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.73	-4.72	-4.72	-2.72	-2.58	-2.54	-2.51	-2.44	-2.56	-4.72	0.00	0.00	0.00	0.00	-3.01	-2.71	-2.67
HG03837.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.82	-2.71	-2.72	-3.09	-2.71	-2.73	-2.60	-2.66	-4.18	-3.24	-2.57	-2.72	-2.73	-2.63	0.00	0.00	-2.75
HG03838.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.60	-2.67	-2.69	-4.35	-2.63	-2.64	-2.62	-2.66	-2.55	0.00	-2.79	-2.70	0.00	-4.65	0.00	-2.69	-2.55
HG03844.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.62	-2.73	-2.75	-2.96	-2.51	-2.60	-2.68	-2.66	-3.83	-3.17	-2.65	-2.76	-2.66	-2.60	0.00	0.00	-2.55
HG03846.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.41	0.00	0.00	-2.51	-2.43	-2.44	-2.43	-2.47	-2.39	0.00	0.00	0.00	-4.53	-4.23	-3.03	-2.73	-2.34
HG03848.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.30	-2.47	-2.44	-4.17	-3.57	-4.17	-2.41	-2.36	-2.46	0.00	-3.78	-3.70	-3.78	-3.36	0.00	-2.36	-2.28
HG03849.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.41	-2.73	-2.71	-2.80	-2.61	-2.70	-2.58	-2.51	-2.47	0.00	-4.14	0.00	0.00	0.00	0.00	-2.55	-2.44
HG03850.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.82	-2.61	-2.62	-4.48	-2.64	-2.64	-2.58	-2.61	-3.88	-3.25	-2.54	-2.87	-2.65	-2.57	0.00	-4.00	-2.68
HG03851.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.47	-2.64	-2.61	-4.35	-2.53	-2.59	-2.57	-2.64	-2.67	-3.27	-2.66	-2.61	-2.94	-2.70	0.00	-2.69	-2.49
HG03854.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.91	-2.73	-2.72	-3.08	-2.77	-2.75	-2.62	-2.68	-2.66	-3.46	-2.78	0.00	-2.69	-2.76	0.00	-2.72	-2.76
HG03856.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.48	-2.78	-2.76	-2.82	-2.45	-2.59	-2.61	-2.52	-2.65	-3.45	-2.76	-2.80	-2.87	-2.66	-3.12	0.00	-2.37
HG03857.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.89	0.00	-4.55	-2.97	-2.63	-2.63	-2.60	-2.67	-2.73	-3.49	-2.79	0.00	-2.76	-2.73	0.00	-2.77	-2.76
HG03858.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.55	-3.66	-3.80	-2.76	-2.54	-2.58	-2.65	-2.63	-2.63	-3.30	-2.90	-3.90	-2.75	-2.68	0.00	-2.86	-2.50
HG03861.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.77	-4.69	-4.39	-2.85	-2.52	-2.56	-2.52	-2.50	-2.51	-4.69	-4.39	0.00	0.00	-4.69	0.00	-2.41	-2.66
HG03862.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.58	-2.78	-2.69	-2.93	-2.50	-2.63	-2.62	-2.69	-2.58	0.00	-2.99	-2.75	0.00	-4.53	0.00	-2.65	-2.56
HG03863.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.88	-2.71	-2.77	-3.04	-2.71	-2.74	-2.61	-2.55	-2.73	-3.41	-2.71	-4.49	-2.67	-2.72	0.00	-2.79	-2.74
HG03864.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.41	0.00	-4.45	-2.72	-2.48	-2.53	-2.55	-2.52	-2.58	-3.30	-2.78	0.00	-2.74	-2.60	0.00	-4.15	-2.56
HG03866.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.88	-4.12	-4.42	-2.96	-2.56	-2.54	-2.45	-2.52	-2.66	-3.19	-3.02	0.00	-2.77	-2.74	-2.93	0.00	-2.58
HG03867.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.45	0.00	-4.08	-2.62	-2.46	-2.48	-2.55	-2.58	-2.59	-3.18	-2.86	0.00	-2.83	-2.59	0.00	-2.74	-2.37
HG03868.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.75	-4.41	-3.63	-2.90	-2.52	-2.52	-2.44	-2.56	-2.44	0.00	-4.11	-4.41	-4.11	-3.93	0.00	-2.61	-2.62
HG03869.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.64	-2.83	-2.71	-3.00	-2.54	-2.65	-2.61	-2.60	-2.72	-3.31	-2.79	-2.82	-2.77	-2.76	0.00	-2.82	-2.58
HG03870.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.43	-4.59	-4.11	-2.69	-2.44	-2.44	-2.46	-2.52	-2.58	-3.34	-2.88	-4.59	-2.76	-2.67	0.00	-2.79	-2.38
HG03871.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.69	-2.37	-2.37	-3.98	-3.81	-3.59	-3.51	-3.51	-3.68	-4.28	-2.51	-4.28	-2.41	-2.35	0.00	0.00	-2.48
HG03872.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.42	-4.56	-4.25	-2.62	-2.47	-2.44	-2.47	-2.51	-2.62	-3.48	-2.89	-4.56	-2.81	-2.61	0.00	-2.80	-2.34
HG03873.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.93	-2.71	-2.79	-3.14	-2.58	-2.62	-2.62	-2.60	-2.83	-3.53	-2.67	-2.71	0.00	-2.84	-3.14	-4.84	-2.83
HG03874.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.49	-2.69	-2.66	-2.84	-2.63	-2.69	-2.64	-2.72	-3.67	-3.37	-2.62	0.00	-2.60	-2.49	0.00	0.00	-2.46
HG03875.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.88	-4.57	-4.87	-2.99	-2.65	-2.66	-2.63	-2.55	-2.72	-3.34	-2.79	0.00	-2.75	-2.76	0.00	-2.84	-2.79
HG03882.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.52	-3.88	-4.18	-2.53	-2.55	-2.54	-2.54	-2.51	-2.54	-4.18	-3.70	-3.88	-4.00	-4.18	-3.08	-2.73	-2.47
HG03884.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.63	-2.71	-2.80	-2.93	-2.57	-2.66	-2.67	-2.67	-2.76	-3.46	-2.81	-2.78	-2.83	-2.76	0.00	-2.79	-2.60
HG03885.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.55	-2.69	-2.65	-2.84	-2.65	-2.68	-2.67	-2.69	-3.96	-3.33	-2.65	-2.66	-2.78	-2.54	0.00	0.00	-2.50
HG03886.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.54	0.00	-4.52	-2.72	-2.54	-2.63	-2.61	-2.62	-3.83	-3.09	-2.72	0.00	-2.64	-2.59	0.00	-4.22	-2.52
HG03887.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.57	-2.76	-2.71	-2.84	-2.74	-2.73	-2.56	-2.54	-2.70	-3.30	-2.95	0.00	-2.76	-2.67	-3.10	0.00	-2.57
HG03888.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.64	-2.67	-2.64	-4.58	-2.63	-2.68	-2.67	-2.72	-2.81	-3.50	-2.68	-2.64	-2.85	-2.75	0.00	-2.78	-2.60
HG03890.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.46	-4.59	0.00	-2.67	-2.50	-2.51	-2.52	-2.58	-2.57	-3.27	-2.92	0.00	-2.74	-2.63	0.00	-2.75	-2.36
HG03894.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.80	-4.06	-3.63	-3.00	-2.55	-2.57	-2.51	-2.55	-2.65	-3.63	-2.90	0.00	-2.77	-2.74	-3.00	-3.83	-2.72
HG03895.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.38	-2.69	-2.62	-2.76	-2.62	-2.53	-2.58	-2.75	-2.53	-4.19	-2.90	0.00	-2.69	-2.53	0.00	-2.80	-2.30
HG03896.mapped.ILLUMINA.bwa.STU.exome.20130422	-2.54	-4.15	-3.85	-2.58	-2.53	-2.53	-2.60	-2.58	-2.47	0.00	-3.85	-3.98	0.00	-4.15	0.00	-2.55	-2.43
HG03897.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.52	-2.59	-2.55	0.00	-2.70	-2.64	-2.51	-2.55	-2.62	-3.25	-2.63	-2.75	-2.76	-2.68	0.00	-2.76	-2.41
HG03898.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.60	-2.79	-2.77	-2.92	-2.52	-2.61	-2.64	-2.58	-2.71	-3.50	-2.78	-2.78	-2.81	-2.73	-3.15	0.00	-2.57
HG03899.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.86	0.00	-4.88	-2.92	-2.58	-2.56	-2.57	-2.50	-2.55	-4.58	0.00	0.00	-4.58	-4.28	-3.06	-2.75	-2.71
HG03900.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.58	0.00	-4.57	-2.72	-2.59	-2.59	-2.57	-2.51	-2.69	-3.39	-2.90	0.00	-2.83	-2.69	-3.09	-3.96	-2.53
HG03902.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.42	-2.73	-2.64	-2.82	-2.64	-2.61	-2.53	-2.50	-2.50	0.00	-3.77	0.00	-4.37	-3.89	0.00	-2.51	-2.46

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG03905.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.55	-2.62	-2.57	-4.44	-2.69	-2.66	-2.60	-2.53	-2.66	-3.36	-2.75	-2.75	-2.79	-2.66	-3.06	-3.96	-2.48
HG03907.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.92	-2.59	-2.77	-3.13	-2.44	-2.70	-2.54	-2.56	-2.60	-4.86	-2.78	-2.77	-4.56	-3.86	-3.10	-2.81	-2.82
HG03908.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.91	-2.78	-2.83	-3.19	-2.59	-2.71	-2.68	-2.72	-4.91	-3.36	-2.59	-2.86	-2.65	-2.54	0.00	0.00	-2.79
HG03910.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.37	-2.71	-2.64	-2.92	-2.59	-2.70	-2.57	-2.43	-2.61	-3.25	-2.87	0.00	-2.75	-2.60	0.00	-2.76	-2.46
HG03911.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.54	0.00	-4.49	-2.62	-2.55	-2.56	-2.59	-2.63	-2.71	-3.29	-2.91	-4.49	-2.69	-2.65	0.00	-2.62	-2.49
HG03913.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.90	-2.83	-2.83	-3.24	-2.58	-2.74	-2.65	-2.67	-2.81	-3.57	-2.64	-2.83	-2.84	-2.88	0.00	-2.89	-2.80
HG03914.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.97	-2.77	-2.78	-3.16	-2.55	-2.72	-2.61	-2.62	-2.62	0.00	-2.85	-2.76	-4.41	-4.89	0.00	-2.71	-2.75
HG03916.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.50	-2.66	-2.60	-2.83	-2.59	-2.59	-2.53	-2.47	-2.51	-4.39	-4.39	0.00	0.00	0.00	-2.92	-2.62	-2.40
HG03917.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.82	-2.72	-2.77	-3.07	-2.79	-2.82	-2.66	-2.52	-2.71	-3.38	-2.79	0.00	-2.72	-2.81	0.00	-2.83	-2.76
HG03919.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.57	-2.62	-2.56	-3.98	-2.57	-2.63	-2.60	-2.56	-2.56	0.00	-2.80	-2.61	0.00	0.00	-3.14	-2.71	-2.56
HG03920.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.88	0.00	-4.43	-2.79	-2.60	-2.65	-2.54	-2.58	-2.58	0.00	-4.43	0.00	-4.91	0.00	0.00	-2.50	-2.71
HG03922.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.86	-3.84	-3.93	-2.93	-2.57	-2.63	-2.56	-2.52	-2.42	0.00	-4.14	-3.99	-4.84	-4.84	0.00	-2.63	-2.74
HG03925.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.87	-2.66	-2.69	-3.02	-2.68	-2.73	-2.56	-2.49	-2.43	0.00	0.00	0.00	-4.82	0.00	-3.04	-2.74	-2.73
HG03926.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.90	0.00	0.00	-3.00	-2.61	-2.66	-2.60	-2.56	-2.75	-3.45	-2.77	0.00	-2.73	-2.77	0.00	-2.80	-2.74
HG03928.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.51	-4.07	-4.07	-2.56	-2.41	-2.47	-2.49	-2.46	-2.47	0.00	0.00	-3.90	-4.07	-4.07	-2.91	-2.74	-2.45
HG03931.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.54	-2.83	-2.68	-2.89	-2.55	-2.69	-2.54	-2.62	-2.66	-3.25	-2.87	0.00	-2.68	-2.64	0.00	-2.72	-2.49
HG03934.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.36	-2.67	-2.63	-2.85	-2.60	-2.60	-2.71	-2.69	-2.59	0.00	-2.83	0.00	-2.72	-2.59	0.00	-2.69	-2.49
HG03937.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.52	-2.77	-2.71	-2.87	-2.46	-2.55	-2.56	-2.58	-2.56	-4.45	-2.85	-2.65	-4.15	-4.45	-2.97	-4.45	-2.52
HG03940.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.80	0.00	0.00	-2.74	-2.60	-2.60	-2.59	-2.50	-2.57	0.00	0.00	0.00	0.00	-4.49	-3.02	-2.71	-2.74
HG03941.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.89	-4.44	0.00	-3.01	-2.58	-2.58	-2.58	-2.58	-2.69	-3.42	-2.74	-4.74	-2.67	-2.73	0.00	-2.77	-2.66
HG03943.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.37	-2.43	-2.45	-4.33	0.00	-4.03	-3.43	-4.33	-3.73	-4.33	-2.52	0.00	-2.41	-2.35	0.00	-3.73	-2.32
HG03944.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.80	-2.61	-2.71	-3.34	-2.70	-2.64	-2.46	-2.51	-2.48	0.00	-4.42	-4.42	-3.94	-3.64	0.00	-2.58	-2.54
HG03945.mapped.ILLUMINA.bwa.STU.exome.20130415	-3.03	-4.67	-4.50	-3.05	-2.45	-2.68	-2.58	-2.58	-2.63	-3.47	-2.94	-2.86	0.00	-4.97	0.00	-2.77	-2.85
HG03947.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.49	-2.78	-2.78	-2.90	-2.47	-2.52	-2.52	-2.57	-2.78	-3.44	-2.80	-2.76	-2.87	-2.67	0.00	-2.75	-2.41
HG03948.mapped.ILLUMINA.bwa.STU.exome.20130422	-2.62	-2.89	-2.76	-2.93	-2.50	-2.62	-2.67	-2.68	-2.75	-3.31	-2.79	-2.81	-2.93	-2.69	0.00	-2.84	-2.55
HG03949.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.51	-2.90	-2.82	-2.90	-2.38	-2.50	-2.52	-2.52	-2.56	-3.74	-2.76	-2.63	0.00	-4.64	-3.18	-2.82	-2.50
HG03950.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.62	-2.82	-2.79	-2.93	-2.55	-2.63	-2.68	-2.73	-2.75	-3.33	-2.82	-2.65	0.00	-2.75	0.00	-2.82	-2.53
HG03951.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.98	-2.78	-2.82	-3.14	-2.57	-2.69	-2.74	-2.61	-2.82	-3.56	-2.68	-2.85	-2.80	-2.85	0.00	-2.88	-2.85
HG03953.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.49	-2.73	-2.70	-2.84	-2.59	-2.67	-2.55	-2.57	-2.63	-3.26	-2.91	0.00	-2.94	-2.56	0.00	-2.72	-2.36
HG03955.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.83	-2.58	-2.54	0.00	-4.57	-4.88	-2.59	-2.59	-2.68	-3.36	-2.73	-4.88	-2.72	-2.73	0.00	-2.76	-2.73
HG03960.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.40	-3.77	-3.64	-2.55	-2.46	-2.49	-2.52	-2.60	0.00	-3.05	-2.67	-3.77	-2.68	-2.50	0.00	-4.07	-2.38
HG03963.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.59	-2.67	-2.79	-2.87	-2.45	-2.54	-2.56	-2.51	-2.66	-3.29	-2.75	-2.81	-2.85	-2.68	0.00	-2.79	-2.45
HG03965.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.86	-4.69	-4.39	-3.04	-2.63	-2.72	-2.67	-2.74	-2.56	-3.56	-2.91	0.00	-2.82	-2.84	0.00	-2.68	-2.81
HG03967.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.90	-2.75	-2.73	-3.09	-2.76	-2.76	-2.73	-2.78	-4.17	-3.40	-2.60	0.00	-2.57	-2.58	0.00	0.00	-2.76
HG03968.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.45	-2.76	-2.67	-2.77	-2.46	-2.53	-2.53	-2.62	-2.34	0.00	-2.89	-2.75	0.00	0.00	0.00	-2.57	-2.40
HG03969.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.86	-4.35	-3.65	-3.07	-2.51	-2.50	-2.47	-2.58	-2.48	0.00	0.00	0.00	-4.05	0.00	0.00	-2.51	-2.58
HG03971.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.95	-2.82	-2.83	-3.25	-2.60	-2.72	-2.62	-2.46	-2.59	-3.46	-2.88	-2.88	-3.66	-3.83	0.00	-2.58	-2.84
HG03973.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.78	-2.66	-2.67	-3.01	-2.70	-2.73	-2.56	-2.48	-2.55	-4.78	0.00	0.00	-4.78	0.00	-2.98	-2.78	-2.72
HG03974.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.97	-2.78	-2.81	-3.22	-2.58	-2.72	-2.72	-2.77	-2.82	-3.54	-2.65	-2.88	-2.85	-2.77	0.00	-2.86	-2.81
HG03976.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.87	-2.66	-2.68	-3.04	-2.68	-2.76	-2.67	-2.71	-2.71	0.00	-2.72	-4.76	-2.67	-2.70	-3.04	-4.46	-2.73
HG03977.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.95	-2.68	-2.70	0.00	-2.62	-2.63	-2.55	-2.56	-2.85	-3.41	-2.61	-2.62	-2.94	-2.85	-3.16	-4.08	-2.76
HG03978.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.46	-4.51	-4.20	-2.75	-2.58	-2.57	-2.62	-2.52	-2.72	-3.33	-2.91	0.00	-2.78	-2.69	0.00	-2.78	-2.52
HG03985.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.87	-2.65	-2.70	-3.29	-2.67	-2.74	-2.41	-2.52	-2.49	0.00	0.00	0.00	0.00	-3.90	-3.05	-2.79	-2.53
HG03986.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.60	-2.73	-2.77	-2.90	-2.51	-2.60	-2.66	-2.56	-2.73	-3.46	-2.73	-2.70	0.00	-2.72	0.00	-2.84	-2.58
HG03989.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.89	-2.74	-2.80	-3.34	-2.57	-2.61	-2.59	-2.66	-2.67	-3.67	-2.65	-2.80	-2.83	-2.76	0.00	-2.81	-2.70
HG03990.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.90	-2.66	-2.94	-3.52	-2.56	-2.55	-2.53	-2.52	-2.42	-4.47	-2.84	-2.77	-4.47	-4.47	-3.04	-2.91	-2.64
HG03991.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.86	0.00	-4.48	-3.11	-2.56	-2.50	-2.58	-2.56	-3.57	-3.22	-2.59	-4.48	-2.60	-2.54	0.00	-4.00	-2.58
HG03995.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.79	0.00	-4.83	-2.75	-2.52	-2.51	-2.53	-2.59	-2.52	-4.83	-4.83	-4.83	-4.83	-4.83	0.00	-2.59	-2.71
HG03998.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.87	-2.76	-2.78	-3.42	-2.45	-2.53	-2.56	-2.63	-3.77	-3.39	-2.67	-2.54	0.00	-2.66	0.00	-4.47	-2.71
HG03999.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.95	-2.77	-2.77	-3.19	-2.56	-2.69	-2.69	-2.68	-2.77	-3.39	-2.69	-2.83	-2.82	-2.78	0.00	-2.80	-2.80
HG04001.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.72	-2.67	-2.75	-3.33	-2.60	-2.58	-2.47	-2.47	-2.43	-4.33	0.00	-3.73	-3.85	-4.03	0.00	-2.46	-2.48
HG04002.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.91	-2.74	-2.74	-3.11	-2.52	-2.68	-2.66	-2.65	-2.59	0.00	-2.80	-2.76	0.00	0.00	0.00	-2.69	-2.83
HG04003.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.89	-4.02	-4.02	-3.39	-2.46	-2.56	-2.53	-2.59	-3.80	-3.32	-2.65	-2.71	-2.90	-2.67	0.00	-4.50	-2.77
HG04006.mapped.ILLUMINA.bwa.STU.exome.20130422	-2.47	-2.81	-2.72	-2.96	-2.57	-2.65	-2.63	-2.66	-3.55	-3.23	-2.65	-2.65	-2.90	-2.59	0.00	-4.55	-2.57
HG04014.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.39	-2.77	-2.77	-2.90	-2.40	-2.53	-2.54	-2.48	-2.43	0.00	-3.06	-2.75	0.00	-4.57	-3.01	-2.75	-2.37
HG04015.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.49	-2.60	-2.55	0.00	-2.53	-2.60	-2.59	-2.62	-2.69	-3.28	-2.73	-2.57	-2.85	-2.64	0.00	-2.73	-2.45
HG04017.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.79	-4.45	-4.45	-2.86	-2.50	-2.60	-2.54	-2.49	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.44	-2.65
HG04018.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.85	0.00	-4.32	-2.79	-2.56	-2.61	-2.58	-2.51	-2.68	-3.41	-2.81	-2.74	0.00	-2.72	0.00	-2.77	-2.71
HG04019.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.37	-3.60	-3.90	-2.53	-2.34	-2.44	-2.45	-2.56	-2.45	0.00	-4.50	-3.72	-4.50	0.00	0.00	-2.44	-2.33
HG04020.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.37	-3.90	-4.13	-2.69	-2.44	-2.44	-2.51	-2.54	-2.56	-3.37	-2.93	-4.60	-2.78	-2.62	0.00	-2.68	-2.37
HG04022.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.40	0.00	0.00	-2.52	-2.40	-2.48	-2.41	-2.46	-2.36	0.00	0.00	0.00	0.00	-4.53	0.00	-2.47	-2.36
HG04023.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.84	-2.83	-2.79	-3.55	-2.50	-2.55	-2.53	-2.61	-2.66	-3.50	-2.69	-2.77	-2.74	-2.78	0.00	-2.91	-2.67
HG04025.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.35	-2.49	-2.47	0.00	-3.67	-4.03	-2.65	-2.67	-4.03	-3.31	-2.65	-4.21	-2.48	-2.36	0.00	-4.03	-2.28
HG04026.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.81	-2.68	-2.70	-3.08	-2.51	-2.65	-2.63	-2.67	-2.62	-4.77	-2.85	-2.76	0.00	-4.77	0.00	-2.64	-2.74
HG04029.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.49	-2.59	-2.54	-4.30	-2.71	-2.71	-2.50	-2.63	-2.69	-3.22	-2.77	-2.69	-2.86	-2.64	0.00	-2.72	-2.40
HG04033.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.47	-2.77	-2.81	-2.89	-2.46	-2.53	-2.51	-2.54	-2.69	-3.14	-2.77	-2.73	-2.91	-2.67	-3.11	-3.94	-2.51
HG04035.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.42	-2.55	-2.51	-4.10	-2.63	-2.63	-2.65	-2.74	-3.80	-3.24	-2.53	-2.49	-2.87	-2.45	0.00	-3.74	-2.37
HG04038.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.87	-4.36	-4.36	-3.04	-2.52	-2.49	-2.49	-2.63	-4.36	-3.25	-2.57	-2.71	-2.73	-2.49	0.00	-3.76	-2.58
HG04039.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.80	0.00	0.00	-2.99	-2.51	-2.48	-2.50	-2.50	-2.56	-3.56	-2.80	0.00	-2.75	-2.72	0.00	-2.78	-2.63
HG04042.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.50	-2.59	-2.57	-4.15	-2.63	-2.67	-2.49	-2.61	-2.65	-3.30	-2.70	-2.74	-2.87	-2.64	0.00	-2.86	-2.44
HG04047.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.80	-2.65	-2.73	-3.17	-2.68	-2.66	-2.69	-2.72	-2.55	0.00	-2.92	0.00	-2.73	-2.65	-2.92	-4.42	-2.61
HG04054.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.85	-3.87	-3.78	-3.05	-2.56	-2.51	-2.52	-2.56	-2.47	-4.48	-4.48	-4.18	0.00	0.00	-2.80	-4.00	-2.58
HG04056.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.82	-4.46	-3.86	-3.01	-2.66	-2.55	-2.51	-2.55	-2.71	-3.42	-2.99	-4.46	-2.88	-2.83	0.00	-2.87	-2.62
HG04059.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.91	-2.63	-2.67	-4.56	-2.62	-2.63	-2.59	-2.65	-2.69	-3.60	-2.69	-2.61	0.00	-2.87	0.00	-2.88	-2.70
HG04060.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.83	-2.66	-2.70	-3.17	-2.74	-2.67	-2.66	-2.84	-2.66	-4.52	-2.94	-2.75	-4.52	-2.71	0.00	-2.84	-2.59
HG04061.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.80	-2.53	-2.59	0.00	-2.69	-2.72	-2.51	-2.55	-2.46	0.00	-3.00	-2.73	-4.50	-4.20	-2.98	-2.74	-2.58
HG04062.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.78	0.00	-4.19	-2.92	-2.57	-2.52	-2.50	-2.50	-2.69	-3.45	-2.86	0.00	-2.81	-2.74	0.00	-2.78	-2.67
HG04063.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.33	-2.78	-2.65	-2.80	-2.64	-2.54	-2.57	-2.64	-2.57	0.00	-2.91	0.00	-2.73	-2.55	-3.00	0.00	-2.31
HG04070.mapped.ILLUMINA.bwa.ITU.exome.20130415	-3.03	-2.69	-2.86	-3.24	-2.60	-2.78	-2.69	-2.77	-4.69	-3.35	-2.57	-2.92	-2.73	-2.74	0.00	-4.69	-2.89
HG04075.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.91	-2.79	-2.82	-3.16	-2.54	-2.68	-2.65	-2.60	-2.53	0.00	-2.89	-2.82	-4.93	-4.93	0.00	-2.55	-2.86
HG04076.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.75	-2.56	-2.69	-3.14	-2.68	-2.61	-2.65	-2.82	-2.68	0.00	-2.85	0.00	-2.75	-2.68	0.00	-2.75	-2.47
HG04080.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.80	-2.76	-2.67	-3.42	-2.52	-2.56	-2.49	-2.57	-2.47	0.00	-2.97	-2.77	0.00	-4.12	-2.94	-2.86	-2.56
HG04090.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.70	-2.54	-2.58	-3.08	-2.63	-2.70	-2.57	-2.73	-2.50	0.00	-2.82	-4.01	-2.85	-2.63	0.00	-2.76	-2.51
HG04093.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.53	-2.54	-2.53	0.00	-2.71	-2.65	-2.50	-2.57	-2.66	-3.37	-2.69	-2.67	-2.83	-2.59	0.00	-2.70	-2.42
HG04094.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.94	-2.65	-2.71	-3.31	-2.53	-2.61	-2.44	-2.50	-2.40	0.00	-3.05	-2.80	0.00	-4.39	0.00	-2.64	-2.60
HG04096.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.90	-2.76	-2.79	-3.18	-2.73	-2.75	-2.60	-2.66	-4.44	-3.18	-2.61	0.00	-2.59	-2.66	0.00	0.00	-2.73
HG04098.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.94	-2.65	-2.69	-3.03	-2.70	-2.74	-2.53	-2.55	-2.51	0.00	0.00	-4.84	-4.36	0.00	0.00	-2.61	-2.68
HG04099.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.57	-2.58	-2.58	-3.78	-2.48	-2.53	-2.57	-2.62	-2.78	-3.51	-2.65	-2.56	-2.91	-2.66	0.00	-2.87	-2.45
HG04100.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.89	-2.79	-2.80	-3.14	-2.60	-2.75	-2.71	-2.65	-2.81	-3.53	-2.65	-4.84	-2.81	-2.85	-3.15	-4.84	-2.82
HG04106.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.34	-3.88	-3.68	-2.61	-2.49	-2.51	-2.51	-2.55	-2.67	-3.37	-3.03	-2.68	-4.58	-2.62	0.00	-2.68	-2.40
HG04107.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.47	-2.57	-2.59	-3.90	-2.63	-2.50	-2.58	-2.59	-2.64	-3.30	-2.70	-2.55	0.00	-2.70	0.00	-2.80	-2.42
HG04118.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.79	-2.51	-2.59	-4.46	-2.72	-2.81	-2.49	-2.57	-2.66	-3.25	-2.76	-2.74	-2.89	-2.72	0.00	-2.78	-2.62
HG04131.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.87	-2.81	-2.75	-3.14	-2.68	-2.72	-2.75	-2.81	-3.60	-3.60	-2.65	0.00	-2.59	-2.53	0.00	-3.74	-2.63
HG04134.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.79	-4.12	-3.82	-2.94	-2.44	-2.53	-2.44	-2.58	-2.37	0.00	-3.94	-3.82	-3.94	-3.82	-2.75	0.00	-2.55
HG04140.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.89	-4.50	-4.20	-3.08	-2.55	-2.52	-2.50	-2.48	-2.43	-4.50	0.00	0.00	-4.50	0.00	-2.89	-2.67	-2.61
HG04141.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.90	0.00	-3.77	-2.87	-2.50	-2.50	-2.52	-2.51	-2.47	-4.47	-3.99	-4.16	-4.47	-4.47	-2.85	-2.80	-2.65

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG04144.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.92	-4.56	-4.17	-2.78	-2.59	-2.62	-2.54	-2.63	-2.75	-3.18	-2.81	-4.87	-2.78	-2.78	0.00	-2.80	-2.72
HG04146.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.53	0.00	0.00	-2.60	-2.54	-2.54	-2.53	-2.60	-2.64	-3.24	-2.82	0.00	-2.72	-2.62	0.00	-2.73	-2.48
HG04152.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.99	-2.58	-2.61	-4.71	-2.78	-2.84	-2.62	-2.71	-2.76	-3.26	-2.68	-2.83	-2.78	-2.82	0.00	-2.85	-2.77
HG04153.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.90	-2.70	-2.71	-3.07	-2.77	-2.72	-2.56	-2.53	-2.51	-4.71	-4.71	-5.01	-4.53	-4.31	-3.08	-2.78	-2.66
HG04155.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.94	-2.77	-2.80	-3.10	-2.57	-2.70	-2.64	-2.61	-2.61	0.00	-2.82	-2.83	0.00	-4.67	-3.21	-2.88	-2.80
HG04156.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.81	-2.63	-4.54	-3.05	-2.40	-2.59	-2.47	-2.60	-2.77	-3.28	-2.70	0.00	-2.72	-2.71	0.00	-2.76	-2.63
HG04158.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.84	-2.81	-2.76	-3.18	-2.52	-2.60	-2.53	-2.62	-2.55	0.00	-2.93	-2.88	0.00	0.00	-2.84	-4.28	-2.67
HG04159.mapped.ILLUMINA.bwa.BEB.exome.20130422	-2.58	-2.77	-2.76	-2.89	-2.51	-2.60	-2.67	-2.60	-2.70	-3.35	-2.81	-2.73	-2.90	-2.71	0.00	-2.74	-2.55
HG04161.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.95	-5.03	0.00	-2.94	-2.59	-2.62	-2.60	-2.57	-2.77	-3.26	-2.84	-4.73	-2.77	-2.79	-3.16	0.00	-2.74
HG04162.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.80	-3.89	-3.95	-2.87	-2.53	-2.54	-2.53	-2.57	-2.56	-4.80	-4.10	-4.50	0.00	-4.20	-2.92	-4.20	-2.70
HG04164.mapped.ILLUMINA.bwa.BEB.exome.20130415	-3.00	-2.68	-2.72	-4.99	-2.71	-2.89	-2.76	-2.74	-2.84	-3.56	-2.58	-2.74	-2.81	-2.89	0.00	-2.87	-2.93
HG04171.mapped.ILLUMINA.bwa.BEB.exome.20130415	-3.06	0.00	-4.70	-2.92	-2.56	-2.67	-2.56	-2.58	-2.71	-3.40	-2.92	-2.89	0.00	-4.70	0.00	-2.62	-2.87
HG04173.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.72	-3.99	-4.17	-3.17	-2.51	-2.51	-2.50	-2.44	-2.43	-4.47	0.00	-4.47	-4.17	-4.47	0.00	-2.57	-2.56
HG04176.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.82	-2.75	-2.71	-3.07	-2.72	-2.75	-2.60	-2.60	-2.52	-4.84	0.00	0.00	0.00	-4.36	0.00	-2.46	-2.74
HG04177.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.91	-2.72	-2.74	-4.89	-2.76	-2.77	-2.76	-2.79	-2.77	-4.89	-2.66	-2.80	-2.79	-2.82	0.00	-2.77	-2.71
HG04180.mapped.ILLUMINA.bwa.BEB.exome.20130415	-3.00	-2.65	-2.72	0.00	-2.67	-2.72	-2.69	-2.74	-2.82	-3.52	-2.59	-2.72	-2.80	-2.83	0.00	-2.87	-2.88
HG04182.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.83	-2.75	-2.93	-3.30	-2.53	-2.66	-2.62	-2.61	-2.54	0.00	-2.88	-2.81	0.00	-4.53	-2.81	-4.53	-2.66
HG04183.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.80	-2.66	-2.74	-3.29	-2.56	-2.59	-2.59	-2.60	-2.53	0.00	-2.92	-2.82	0.00	0.00	-2.93	-3.09	-2.65
HG04185.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.87	-2.72	-2.77	-3.40	-2.53	-2.58	-2.59	-2.56	-2.53	-4.60	-2.91	-2.77	-4.60	-3.90	-3.00	-2.87	-2.68
HG04186.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.67	-2.57	-2.71	-3.00	-2.58	-3.97	-2.54	-2.76	-2.51	0.00	-3.97	-3.80	-3.80	0.00	0.00	-2.73	-2.45
HG04188.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.95	-2.76	-2.77	-3.07	-2.54	-2.68	-2.64	-2.71	-2.62	0.00	-2.78	-2.78	-4.29	-4.42	0.00	-2.72	-2.80
HG04189.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.89	-4.54	-4.24	-2.94	-2.64	-2.65	-2.61	-2.71	-2.74	-3.44	-2.73	-4.37	-2.77	-2.71	0.00	-2.81	-2.77
HG04194.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.93	-2.63	-2.61	-4.93	-2.79	-2.86	-2.63	-2.61	-2.77	-3.50	-2.63	-2.81	-2.81	-2.83	0.00	-2.82	-2.80
HG04195.mapped.ILLUMINA.bwa.BEB.exome.20130415	-2.86	-4.75	-4.15	-2.84	-2.50	-2.51	-2.54	-2.49	-2.50	0.00	-4.75	0.00	0.00	-4.45	0.00	-2.52	-2.64
HG04198.mapped.ILLUMINA.bwa.ITU.exome.20130415	-3.03	-2.82	-2.86	-3.17	-2.60	-2.73	-2.70	-2.67	-2.60	0.00	-2.90	-2.85	0.00	0.00	-3.23	-2.87	-2.86
HG04200.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.96	-2.68	-2.68	0.00	-2.81	-2.83	-2.68	-2.59	-2.80	-3.38	-2.63	-2.83	-2.82	-2.84	-3.15	-4.65	-2.78
HG04202.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.93	-2.78	-2.82	-3.13	-2.56	-2.72	-2.64	-2.62	-2.68	0.00	-2.88	-2.83	0.00	-4.92	0.00	-2.57	-2.82
HG04206.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.91	-4.41	-4.19	-2.90	-2.56	-2.62	-2.62	-2.60	-2.55	-4.59	-4.19	-4.29	-4.29	-4.19	0.00	-2.83	-2.80
HG04209.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.95	-2.85	-2.87	-3.20	-2.60	-2.67	-2.69	-2.65	-2.81	-3.45	-2.63	-2.86	-2.81	-2.88	-3.26	-4.49	-2.81
HG04210.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.90	0.00	-4.93	-2.92	-2.55	-2.56	-2.53	-2.50	-2.52	0.00	0.00	0.00	0.00	0.00	-2.98	-4.45	-2.76
HG04211.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.83	-2.75	-2.73	-3.14	-2.78	-2.73	-2.54	-2.62	-2.48	-4.93	-4.15	-4.08	0.00	-4.45	0.00	-2.57	-2.69
HG04212.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.90	-4.88	-4.58	-2.96	-2.60	-2.69	-2.62	-2.64	-2.75	-3.42	-2.81	0.00	-2.77	-2.80	-3.10	0.00	-2.77
HG04214.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.91	-2.79	-2.78	-3.08	-2.76	-2.66	-2.62	-2.64	-2.73	-3.51	-2.82	0.00	-2.73	-2.81	0.00	-2.81	-2.76
HG04216.mapped.ILLUMINA.bwa.ITU.exome.20130415	-3.14	-2.85	-2.86	-5.18	-2.67	-2.76	-2.71	-2.65	-2.94	-3.52	-2.66	-2.60	-4.40	-2.97	-3.33	-4.88	-3.00
HG04219.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.93	-2.70	-2.77	-3.17	-2.85	-2.83	-2.66	-2.67	0.00	-3.27	-2.62	0.00	-2.65	-2.65	0.00	0.00	-2.79
HG04222.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.81	0.00	-4.74	-2.94	-2.59	-2.63	-2.62	-2.65	-2.73	-3.46	-4.44	-3.97	-2.69	-2.74	0.00	-2.77	-2.76
HG04225.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.94	-2.86	-2.85	-3.15	-2.61	-2.73	-2.75	-2.72	-2.81	-3.53	-2.70	-2.88	-2.86	-2.83	0.00	-2.83	-2.84
HG04227.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.82	-3.89	-4.19	-2.94	-2.56	-2.59	-2.55	-2.59	-2.52	0.00	-4.19	-4.79	0.00	-4.49	-3.02	-2.74	-2.69
HG04229.mapped.ILLUMINA.bwa.STU.exome.20130415	-2.83	-2.61	-2.72	-4.49	-2.65	-2.61	-2.62	-2.64	-2.60	0.00	-2.83	-2.73	0.00	0.00	0.00	-2.64	-2.78
HG04235.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.83	-2.69	-2.71	-3.12	-2.71	-2.76	-2.56	-2.45	-2.49	0.00	0.00	0.00	0.00	-4.81	-3.08	-2.72	-2.67
HG04238.mapped.ILLUMINA.bwa.ITU.exome.20130415	-2.81	-4.81	-4.81	-2.76	-2.57	-2.63	-2.56	-2.50	-2.58	0.00	0.00	0.00	0.00	0.00	-3.02	-2.77	-2.78
HG04239.mapped.ILLUMINA.bwa.ITU.exome.20130415	-3.02	-2.76	-2.85	-3.19	-2.58	-2.71	-2.68	-2.76	-2.83	-3.55	-2.65	-2.87	-2.78	-2.83	0.00	-2.86	-2.88
NA06984.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.72	-2.84	-2.86	-3.08	-2.59	-2.64	-2.70	-2.77	-2.85	-3.50	-2.77	-2.91	-3.05	-2.82	0.00	-2.92	-2.59
NA06985.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.27	-2.61	-2.64	-3.00	-2.64	-2.57	-2.21	-2.45	-2.34	-4.04	0.00	0.00	0.00	0.00	-3.09	-2.64	-2.20
NA06986.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.50	-2.70	-2.62	0.00	0.00	0.00	-2.64	-2.53	-2.54	0.00	0.00	0.00	0.00	-4.80	0.00	-2.46	-2.48
NA06989.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.62	-2.85	-2.80	-3.00	-2.76	-2.82	-2.66	-2.75	-2.88	-3.64	-3.02	0.00	-2.87	-2.82	0.00	-2.85	-2.66
NA06994.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.64	0.00	0.00	-2.83	-2.44	-2.48	-2.37	-2.38	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.37	-2.63
NA07000.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.30	-2.61	0.00	-4.09	-2.42	-2.30	-2.37	-2.48	-2.55	-3.24	-2.83	0.00	-2.75	-2.51	0.00	-2.61	-2.25
NA07037.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.76	0.00	0.00	-2.89	-2.68	-2.68	-2.69	-2.75	-2.72	0.00	0.00	0.00	0.00	0.00	0.00	-2.62	-2.71
NA07048.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.54	-2.80	-2.80	-3.08	-2.73	-2.75	-2.63	-2.54	-2.51	0.00	0.00	0.00	0.00	0.00	-3.22	-2.88	-2.48
NA07051.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.68	-2.85	-2.90	-3.07	-2.57	-2.66	-2.70	-2.79	-2.81	-3.68	-2.96	-2.71	0.00	-2.89	0.00	-2.97	-2.61
NA07056.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.33	-2.61	-2.71	-2.96	-2.55	-2.41	-2.24	-2.52	-2.26	0.00	0.00	0.00	0.00	0.00	0.00	-2.29	-2.15
NA07347.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.58	0.00	0.00	-2.79	-2.57	-2.56	-2.64	-2.70	-2.62	0.00	0.00	0.00	0.00	-4.74	0.00	-2.62	-2.63
NA07357.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.27	-4.03	0.00	-2.69	-2.42	-2.33	-2.27	-2.50	-2.33	0.00	0.00	0.00	0.00	0.00	0.00	-2.28	-2.26
NA10847.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.62	-2.66	0.00	-3.09	-2.42	-2.54	-2.55	-2.61	0.00	-3.48	-2.57	-2.74	-2.72	-2.56	0.00	0.00	-2.61
NA10851.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.33	0.00	0.00	-2.61	-2.38	-2.31	-2.26	-2.35	-2.33	0.00	0.00	0.00	0.00	0.00	0.00	-2.29	-2.25
NA11829.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.31	-2.71	-2.54	-2.75	-2.69	-2.60	-2.32	-2.47	-2.44	0.00	0.00	0.00	-4.09	0.00	-2.77	0.00	-2.20
NA11830.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.22	-2.31	-2.32	-3.96	0.00	0.00	-2.26	-2.59	-2.30	0.00	0.00	0.00	0.00	0.00	-2.75	0.00	-2.16
NA11831.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.23	-2.69	-2.56	-2.85	-2.80	-2.50	-2.38	-2.38	-2.32	0.00	0.00	0.00	0.00	0.00	-3.05	-2.75	-2.17
NA11832.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.29	-2.62	-2.64	-2.81	-2.40	-2.42	-2.29	-2.57	-2.34	0.00	-2.88	-2.53	-4.11	-4.11	0.00	-2.48	-2.22
NA11840.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.70	0.00	0.00	-2.68	-2.50	-2.56	-2.53	-2.59	-2.63	-4.06	-2.78	0.00	-2.68	-2.64	0.00	-2.70	-2.67
NA11843.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.58	0.00	-4.25	-2.65	-2.57	-2.57	-2.57	-2.64	-2.53	0.00	-4.55	-4.55	0.00	0.00	0.00	-2.66	-2.54
NA11881.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.31	-2.62	-2.54	-2.75	-2.65	-2.67	-2.31	-2.43	-2.37	0.00	0.00	-4.12	-4.12	0.00	-2.70	0.00	-2.27
NA11892.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.85	-2.77	-2.79	0.00	-2.76	-2.79	-2.85	-2.85	-2.75	0.00	-2.92	-2.83	0.00	0.00	-3.24	-2.97	-2.82
NA11893.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.78	0.00	0.00	-2.79	-2.64	-2.72	-2.72	-2.82	-2.72	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.73
NA11894.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.80	-2.74	-2.79	-3.09	-2.84	-2.89	-2.73	-2.87	-2.66	0.00	0.00	0.00	0.00	0.00	0.00	-2.69	-2.74
NA11918.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.54	-4.84	-4.84	-2.80	-2.62	-2.57	-2.70	-2.54	-2.63	0.00	0.00	0.00	-4.84	0.00	-3.39	-2.85	-2.56
NA11919.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.61	-4.60	-4.30	-2.91	-2.65	-2.68	-2.65	-2.65	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.59
NA11920.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.54	-2.84	-2.82	-3.10	-2.79	-2.79	-2.68	-2.60	-2.56	0.00	0.00	0.00	0.00	0.00	-3.34	-2.90	-2.53
NA11930.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.72	-2.68	-2.70	0.00	-2.85	-2.81	-2.69	-2.73	-2.89	-3.50	-2.78	-2.90	-2.96	-2.87	0.00	-2.93	-2.61
NA11931.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.91	-2.87	-2.89	-3.13	-2.72	-2.79	-2.79	-2.91	-3.13	-3.32	-2.92	-2.81	0.00	-2.98	0.00	-3.00	-2.86
NA11932.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.87	-2.87	-2.96	-3.15	-2.69	-2.84	-2.80	-2.81	-3.09	-3.33	-2.87	-2.99	-2.93	-2.94	0.00	-2.96	-2.84
NA11933.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.86	0.00	0.00	-2.74	-2.64	-2.64	-2.74	-2.69	-2.73	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.77
NA11992.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.35	-2.50	-2.50	-2.82	-2.66	-2.54	-2.27	-2.42	-2.65	-3.62	-2.84	0.00	-2.75	-2.45	0.00	-2.63	-2.29
NA11994.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.31	0.00	-4.17	-2.68	-2.49	-2.46	-2.32	-2.60	-3.87	-3.13	-2.66	0.00	-2.48	-2.38	0.00	0.00	-2.34
NA11995.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.20	0.00	-3.89	-2.78	-2.53	-2.25	-2.35	-2.51	-2.78	-3.41	-2.89	-3.89	-3.05	-2.49	0.00	-2.71	-2.16
NA12003.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.22	-2.61	-2.70	-3.24	-2.94	-2.52	-2.31	-2.73	-2.32	0.00	0.00	0.00	0.00	-3.54	0.00	-2.56	-2.16
NA12004.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.25	-2.49	-2.55	-2.76	-2.60	-2.60	-2.36	-2.34	-2.25	0.00	0.00	0.00	0.00	-3.66	0.00	-2.41	-2.20
NA12005.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.45	-2.54	-2.55	-2.98	-2.71	-2.70	-2.34	-2.35	-2.54	-3.28	-3.05	0.00	-2.67	-2.62	0.00	-2.67	-2.19
NA12006.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.23	-2.36	-2.33	-4.10	-2.80	-2.54	-2.24	-2.54	-2.25	0.00	-2.92	-2.62	0.00	-4.10	0.00	-2.35	-2.19
NA12043.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.49	-2.77	-2.68	-3.17	-2.65	-2.48	-2.42	-2.60	-2.57	-3.35	-2.85	-2.71	-2.85	-2.63	0.00	-2.82	-2.32
NA12044.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.28	-2.61	-2.59	-2.79	-2.77	-2.71	-2.32	-2.44	-2.62	-2.99	-2.82	0.00	-2.75	-2.46	-2.99	0.00	-2.26
NA12045.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.57	-2.85	-2.80	-2.99	-2.72	-2.72	-2.63	-2.72	-2.53	0.00	0.00	0.00	0.00	-4.71	-3.22	-2.94	-2.49
NA12046.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.32	-2.80	-2.64	-2.91	-2.37	-2.35	-2.29	-2.50	-2.41	0.00	-2.94	-2.64	0.00	0.00	0.00	-2.39	-2.26
NA12058.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.62	0.00	0.00	-2.78	-2.63	-2.68	-2.73	-2.63	-2.79	-3.57	-2.98	-4.38	-2.87	-2.78	0.00	-2.88	-2.65
NA12144.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.30	0.00	0.00	-2.47	-2.45	-2.32	-2.28	-2.46	-2.33	0.00	-3.78	0.00	0.00	-4.08	0.00	-2.38	-2.30
NA12154.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.25	0.00	0.00	-2.62	-2.40	-2.32	-2.30	-2.40	-2.64	-3.27	-2.89	0.00	-2.67	-2.61	0.00	-2.70	-2.32
NA12155.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.32	-2.67	-2.55	-2.85	-2.67	-2.59	-2.35	-2.52	-2.43	0.00	0.00	0.00	0.00	0.00	-3.09	-2.74	-2.28
NA12156.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.28	0.00	0.00	-2.71	-2.52	-2.27	-2.40	-2.55	-2.59	-3.36	-2.79	0.00	-2.59	-2.66	0.00	-2.60	-2.24
NA12234.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.36	0.00	0.00	-2.49	-2.39	-2.50	-2.30	-2.61	-2.51	-3.24	-3.03	0.00	-2.66	-2.51	0.00	-2.76	-2.34
NA12249.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.60	0.00	0.00	-2.68	-2.51	-2.48	-2.50	-2.49	-2.70	-3.76	-2.78	0.00	-2.78	-2.60	0.00	-2.73	-2.54
NA12272.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.62	0.00	0.00	-2.75	-2.49	-2.52	-2.55	-2.53	-2.59	-3.59	-2.71	-4.63	-2.73	-2.62	0.00	-2.66	-2.63
NA12273.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.65	0.00	0.00	-2.79	-2.45	-2.46	-2.49	-2.47	-2.35	0.00	0.00	0.00	0.00	-4.51	0.00	-2.49	-2.53
NA12275.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.84	-2.70	-2.70	0.00	-2.70	-2.71	-2.64	-2.62	-2.91	-3.68	-2.66	-2.70	-2.84	-2.82	0.00	-2.87	-2.80
NA12282.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.60	0.00	0.00	-2.93	-2.50	-2.48	-2.58	-2.51	-2.32	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.64
NA12283.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.57	-2.56	-2.56	-2.96	-2.59	-2.61	-2.46	-2.44	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.50

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA12286.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.65	0.00	0.00	-2.66	-2.50	-2.52	-2.51	-2.44	-2.41	0.00	0.00	0.00	0.00	0.00	-2.83	-2.61	-2.64
NA12287.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.82	0.00	-4.74	-2.80	-2.72	-2.79	-2.76	-2.93	-3.02	-3.26	-3.08	0.00	-2.90	-2.82	0.00	-2.96	-2.86
NA12340.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.62	-4.61	-4.61	-2.66	-2.55	-2.65	-2.70	-2.66	-2.81	-3.57	-3.05	0.00	-2.81	-2.81	-3.36	0.00	-2.51
NA12341.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.57	0.00	0.00	-2.71	-2.52	-2.55	-2.62	-2.65	-2.58	0.00	0.00	0.00	-4.52	0.00	-3.35	-2.85	-2.43
NA12342.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.59	0.00	-4.23	-2.62	-2.50	-2.63	-2.64	-2.57	-2.60	0.00	0.00	0.00	0.00	0.00	-3.30	-2.72	-2.55
NA12347.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.81	-2.81	-2.85	-3.04	-2.79	-2.87	-2.72	-2.73	-2.76	-4.72	0.00	0.00	0.00	0.00	-3.12	-2.91	-2.80
NA12348.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.80	-4.79	0.00	-3.01	-2.73	-2.82	-2.78	-2.83	0.00	-3.22	-2.85	-2.93	-2.89	-2.77	0.00	0.00	-2.87
NA12383.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.90	-2.89	-2.95	-3.21	-2.72	-2.79	-2.84	-2.98	0.00	-3.25	-2.77	-2.96	-2.82	-2.84	0.00	0.00	-2.85
NA12399.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.54	-2.81	-2.75	-2.95	-2.73	-2.77	-2.61	-2.62	-2.50	0.00	0.00	0.00	0.00	-4.68	0.00	-2.58	-2.54
NA12400.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.54	0.00	-4.28	-2.73	-2.54	-2.55	-2.57	-2.61	-2.52	0.00	0.00	0.00	-4.58	0.00	-2.95	-4.11	-2.48
NA12413.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.86	0.00	0.00	-2.94	-2.75	-2.77	-2.77	-2.85	-2.98	-3.31	-3.08	-2.94	0.00	-2.91	0.00	-2.91	-2.76
NA12414.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.30	0.00	0.00	-2.54	-2.38	-2.39	-2.30	-2.54	-2.25	0.00	0.00	0.00	0.00	0.00	-3.19	-2.62	-2.29
NA12489.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.31	0.00	0.00	-2.66	-2.38	-2.29	-2.26	-2.37	-2.24	0.00	0.00	0.00	0.00	0.00	-2.87	-2.51	-2.23
NA12546.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.87	0.00	0.00	-2.85	-2.72	-2.80	-2.78	-2.80	-2.98	-3.27	-3.12	-3.03	0.00	-2.94	-3.11	0.00	-2.83
NA12716.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.74	-4.68	0.00	-2.78	-2.57	-2.56	-2.54	-2.61	-2.73	-3.99	-2.80	0.00	-2.77	-2.66	0.00	-2.66	-2.71
NA12717.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.61	0.00	0.00	-2.69	-2.46	-2.51	-2.51	-2.46	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.57
NA12718.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.71	-2.70	-2.67	-3.03	-2.45	-2.57	-2.60	-2.60	-2.53	0.00	-2.76	-2.73	0.00	0.00	0.00	-2.55	-2.68
NA12748.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.58	-2.80	-2.74	-2.85	-2.67	-2.71	-2.60	-2.74	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.51
NA12749.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.82	0.00	0.00	-2.76	-2.66	-2.71	-2.76	-2.80	-2.71	0.00	0.00	-4.71	0.00	0.00	0.00	-2.59	-2.82
NA12750.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.83	-2.73	-2.78	-3.10	-2.74	-2.79	-2.59	-2.58	-2.52	0.00	-4.81	-4.34	-4.51	-4.51	-3.08	-2.87	-2.71
NA12751.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.61	0.00	0.00	-2.79	-2.46	-2.48	-2.44	-2.53	-2.35	0.00	0.00	-4.62	0.00	0.00	0.00	-2.47	-2.57
NA12760.mapped.ILLUMINA.bwa.CEU.exome.20120522	-2.65	-2.63	-2.69	-3.00	-2.61	-2.64	-2.50	-2.54	-2.35	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.63
NA12761.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.64	-2.49	-2.50	-4.57	0.00	-4.27	-2.53	-2.56	0.00	-3.46	-2.54	0.00	-2.55	-2.46	0.00	0.00	-2.61
NA12762.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.25	-2.46	-2.59	-2.95	-2.65	-2.55	-2.36	-2.53	-2.27	0.00	0.00	0.00	0.00	-4.03	0.00	-2.41	-2.16
NA12763.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.81	-2.76	-2.79	-3.09	-2.54	-2.61	-2.70	-2.68	-2.56	0.00	-2.88	-2.82	0.00	0.00	-3.03	-2.88	-2.74
NA12775.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.87	-2.71	-2.74	0.00	-2.99	-2.96	-2.70	-2.81	-3.12	-3.16	-2.99	-2.94	-2.99	-2.90	-3.26	-4.80	-2.88
NA12776.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.74	-2.76	-2.81	-3.08	-2.87	-2.90	-2.70	-2.80	-2.67	-4.75	0.00	0.00	0.00	0.00	-3.13	-2.81	-2.70
NA12777.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.80	0.00	0.00	-3.11	-2.64	-2.68	-2.73	-2.74	-2.67	0.00	0.00	0.00	0.00	-4.76	-3.15	-2.90	-2.71
NA12778.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.85	0.00	0.00	-2.80	-2.66	-2.75	-2.70	-2.84	-2.97	-3.31	-3.14	0.00	-2.84	-2.92	-3.26	-4.79	-2.78
NA12812.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.39	-2.67	-2.60	-2.92	-2.49	-2.41	-2.42	-2.63	-2.37	0.00	-2.87	-2.55	0.00	0.00	0.00	-2.49	-2.26
NA12813.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.40	-2.41	-2.46	0.00	-2.66	-2.51	-2.34	-2.49	-2.55	-3.82	-2.58	-2.39	0.00	-2.50	0.00	-2.54	-2.45
NA12814.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.27	0.00	0.00	-2.74	-2.42	-2.33	-2.34	-2.52	-2.46	-3.04	-2.72	0.00	-2.68	-2.70	0.00	-2.55	-2.32
NA12815.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.29	-2.68	-2.82	-2.80	-2.48	-2.31	-2.34	-2.58	-2.57	-3.34	-2.60	-2.66	-2.89	-2.68	0.00	-2.76	-2.28
NA12827.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.67	-2.68	-2.79	-2.97	-2.72	-2.78	-2.82	-2.95	0.00	-3.15	-3.03	0.00	-2.86	-2.75	0.00	0.00	-2.85
NA12828.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.85	0.00	0.00	-2.81	-2.69	-2.71	-2.77	-2.83	-2.92	-3.20	-3.03	0.00	-3.02	-2.87	0.00	-2.87	-2.83
NA12829.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.66	-2.81	-2.81	-3.03	-2.57	-2.69	-2.72	-2.70	0.00	-3.31	-2.70	-2.81	-2.74	-2.68	0.00	0.00	-2.64
NA12830.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.52	0.00	-4.55	-2.64	-2.57	-2.53	-2.58	-2.61	-2.56	0.00	-4.55	0.00	0.00	0.00	-3.23	-2.82	-2.51
NA12842.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.56	-2.85	-2.79	-3.06	-2.73	-2.76	-2.70	-2.61	-2.69	0.00	0.00	-4.86	0.00	-4.56	0.00	-2.50	-2.52
NA12843.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.48	0.00	-4.23	-2.69	-2.50	-2.58	-2.57	-2.63	-2.52	0.00	0.00	-4.53	0.00	-4.53	0.00	-2.50	-2.52
NA12872.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.48	-2.61	-2.98	-2.98	-2.85	-2.45	-2.33	-2.51	-2.53	-3.33	-2.85	0.00	-2.88	-2.66	0.00	-2.80	-2.30
NA12873.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.33	0.00	-3.78	-2.55	-2.54	-2.39	-2.34	-2.49	-2.33	0.00	0.00	0.00	0.00	0.00	-3.00	-2.70	-2.26
NA12874.mapped.ILLUMINA.bwa.CEU.exome.20130415	-2.29	0.00	0.00	-2.61	-2.48	-2.29	-2.37	-2.46	-2.32	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.20
NA12878.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.65	-2.91	-2.85	-3.07	-2.56	-2.72	-2.78	-2.82	-2.83	-3.41	-2.85	-2.88	-2.89	-2.84	0.00	-2.94	-2.63
NA12889.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.50	-2.85	-2.86	-3.01	-2.72	-2.71	-2.67	-2.60	-2.58	0.00	0.00	0.00	-4.83	0.00	0.00	-2.65	-2.60
NA12890.mapped.ILLUMINA.bwa.CEU.exome.20121211	-2.37	-2.66	-2.59	-2.86	-2.68	-2.65	-2.44	-2.44	-2.39	0.00	0.00	0.00	0.00	0.00	-3.03	-2.72	-2.30
NA18486.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.53	-2.80	0.00	-2.99	-2.70	-2.81	-2.82	-2.85	-2.79	0.00	-2.88	0.00	-2.79	-2.71	0.00	-2.83	-2.48
NA18488.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.55	0.00	0.00	-2.93	-2.71	-2.60	-2.68	-2.69	-2.59	0.00	0.00	0.00	0.00	-4.35	-3.19	-2.78	-2.52
NA18489.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.58	0.00	-2.84	-3.05	-2.55	-2.59	-2.69	-2.71	-2.59	0.00	-3.01	0.00	-2.94	0.00	-3.03	0.00	-2.60
NA18498.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.44	-2.68	-2.71	-2.90	-2.65	-2.64	-2.48	-2.63	-2.46	0.00	0.00	-4.37	0.00	0.00	0.00	-2.42	-2.35
NA18499.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.57	-2.75	-2.74	-3.02	-2.72	-2.80	-2.66	-2.48	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.48
NA18501.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.55	-4.68	-4.68	-2.75	-2.56	-2.61	-2.61	-2.63	-2.58	0.00	0.00	0.00	0.00	0.00	-3.01	0.00	-2.57
NA18502.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.35	-2.44	-2.55	-2.96	-2.58	-2.48	-2.26	-2.30	-2.35	0.00	0.00	-3.69	0.00	-4.17	-2.81	-2.44	-2.28
NA18504.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.54	0.00	0.00	-2.69	-2.53	-2.56	-2.63	-2.68	-2.60	0.00	0.00	0.00	0.00	-4.67	-3.00	-4.67	-2.55
NA18505.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.38	-3.82	-2.54	-3.05	-2.39	-2.30	-2.34	-2.37	-2.43	0.00	-2.78	0.00	-2.65	-4.30	-2.92	-2.60	-2.39
NA18507.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.28	-4.09	-3.79	-2.77	-2.36	-2.25	-2.25	-2.56	-2.51	-3.19	-2.68	0.00	-2.62	-2.55	-2.95	0.00	-2.26
NA18508.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.46	-2.59	-2.62	-3.03	-2.45	-2.39	-2.46	-2.33	-2.38	-4.37	-3.05	-2.64	-4.07	-4.07	-2.95	-2.63	-2.40
NA18510.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.57	0.00	-4.79	-2.70	-2.53	-2.56	-2.63	-2.65	-2.53	0.00	0.00	0.00	-4.79	-4.79	-3.26	-2.90	-2.52
NA18511.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.78	-2.80	-2.81	-3.12	-2.61	-2.76	-2.67	-2.78	-2.77	0.00	-2.98	-2.99	0.00	0.00	-3.09	0.00	-2.92
NA18516.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.64	-2.58	-2.86	-2.97	-2.59	-2.67	-2.72	-2.73	-2.66	0.00	-3.05	-2.88	0.00	0.00	-3.15	0.00	-2.65
NA18517.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.82	-2.76	-2.78	-3.07	-2.79	-2.90	-2.69	-2.69	-2.66	0.00	0.00	0.00	0.00	0.00	-3.16	-2.80	-2.78
NA18519.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.58	0.00	0.00	-2.76	-2.52	-2.54	-2.54	-2.71	-2.54	0.00	-4.56	0.00	0.00	0.00	-3.07	0.00	-2.49
NA18520.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.52	0.00	-4.73	-2.73	-2.56	-2.53	-2.63	-2.62	-2.58	0.00	0.00	0.00	0.00	-4.73	-2.99	0.00	-2.51
NA18522.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.47	-2.86	-2.83	-3.04	-2.72	-2.74	-2.80	-2.78	-2.75	0.00	-3.07	0.00	-2.86	-2.73	-3.06	0.00	-2.47
NA18523.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.94	-2.76	-2.78	0.00	-2.80	-2.84	-2.83	-2.82	-2.84	0.00	-2.92	-2.85	0.00	0.00	0.00	-2.71	-2.85
NA18525.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.29	0.00	0.00	-2.64	-2.37	-2.29	-2.31	-2.57	-2.39	0.00	0.00	0.00	0.00	-3.77	-2.96	-2.90	-2.27
NA18526.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.77	0.00	0.00	-2.76	-2.65	-2.71	-2.75	-2.86	-2.79	0.00	0.00	0.00	0.00	0.00	-3.11	-3.02	-2.71
NA18528.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.34	0.00	0.00	-2.64	-2.40	-2.39	-2.39	-2.54	-2.36	0.00	0.00	0.00	-4.15	0.00	0.00	-2.35	-2.28
NA18530.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.84	0.00	0.00	-2.89	-2.67	-2.70	-2.70	-2.77	-2.75	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.73
NA18531.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.28	0.00	0.00	-2.70	-2.35	-2.26	-2.32	-2.46	-2.58	-3.04	-2.78	0.00	-2.78	-2.45	-3.26	-3.74	-2.16
NA18532.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.86	0.00	0.00	-2.90	-2.62	-2.75	-2.74	-2.92	-2.77	0.00	0.00	0.00	0.00	-4.85	-2.99	0.00	-2.72
NA18533.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.47	0.00	-4.25	-2.79	-2.54	-2.52	-2.55	-2.54	-2.50	0.00	0.00	-4.55	-4.55	-4.25	-2.90	0.00	-2.48
NA18534.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.69	0.00	0.00	-2.86	-2.64	-2.67	-2.71	-2.79	-2.70	0.00	0.00	0.00	0.00	0.00	-2.87	0.00	-2.75
NA18535.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.57	0.00	0.00	-2.86	-2.65	-2.63	-2.75	-2.66	-4.91	-3.40	-2.87	-2.63	0.00	-2.64	0.00	0.00	-2.60
NA18536.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.86	0.00	0.00	-3.01	-2.74	-2.85	-2.75	-2.79	-2.94	-3.25	-3.07	-2.93	0.00	-2.90	-3.19	0.00	-2.83
NA18537.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.81	-2.77	-2.74	-3.01	-2.79	-2.90	-2.95	-3.18	-3.10	0.00	-3.16	0.00	-2.92	-2.94	-3.22	0.00	-2.70
NA18538.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.63	-2.83	-2.82	-3.03	-2.78	-2.78	-2.74	-2.62	-2.75	-3.50	-3.01	-2.87	-4.76	-2.81	-3.28	-4.76	-2.57
NA18539.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.60	-4.65	0.00	-2.85	-2.55	-2.60	-2.70	-2.60	-2.73	-3.35	-2.99	0.00	-2.76	-2.69	0.00	-2.75	-2.50
NA18541.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.63	-4.64	-4.64	-2.71	-2.64	-2.65	-2.68	-2.58	-2.75	-3.38	-3.08	0.00	-2.75	-2.77	-3.08	0.00	-2.57
NA18542.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.91	-3.03	-3.06	-3.16	-2.67	-2.87	-2.77	-2.77	-3.09	-3.21	-2.84	-3.04	-2.95	-3.01	-3.23	-4.93	-2.93
NA18543.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.73	0.00	0.00	-2.74	-2.68	-2.70	-2.70	-2.72	-2.69	-4.72	0.00	0.00	0.00	0.00	-3.09	-2.93	-2.80
NA18544.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.87	0.00	0.00	-2.99	-2.77	-2.68	-2.73	-2.80	-3.05	-3.22	-2.95	-2.80	0.00	-2.97	-3.29	0.00	-2.89
NA18545.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.78	0.00	0.00	-2.77	-2.68	-2.67	-2.67	-2.76	-2.72	0.00	-4.41	0.00	-4.71	0.00	-3.07	-2.91	-2.68
NA18546.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.84	0.00	0.00	-2.97	-2.74	-2.68	-2.76	-2.81	-2.96	-3.24	-3.03	0.00	-2.92	-2.93	0.00	-2.86	-2.77
NA18547.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.93	0.00	0.00	-2.96	-2.64	-2.72	-2.76	-3.01	-3.09	-3.25	-3.14	0.00	-2.92	-2.88	-3.12	0.00	-2.73
NA18548.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.81	0.00	0.00	-2.93	-2.60	-2.69	-2.70	-2.70	-2.63	0.00	0.00	0.00	0.00	0.00	-3.03	-2.84	-2.74
NA18549.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.76	-2.74	-2.75	-3.03	-2.78	-2.80	-2.71	-2.74	-2.71	0.00	0.00	0.00	0.00	0.00	-3.11	-2.81	-2.66
NA18550.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.90	0.00	-4.80	-2.92	-2.73	-2.80	-2.78	-2.89	-2.82	0.00	0.00	0.00	0.00	0.00	-3.26	-3.20	-2.81
NA18552.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.91	0.00	0.00	-3.03	-2.75	-2.81	-2.77	-2.86	-3.08	-3.38	-3.28	-3.09	0.00	-2.98	0.00	-3.24	-2.83
NA18553.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.53	0.00	0.00	-2.81	-2.53	-2.68	-2.64	-2.66	-2.57	0.00	0.00	0.00	0.00	-4.61	-2.95	0.00	-2.54
NA18555.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.86	0.00	0.00	-3.00	-2.68	-2.70	-2.74	-2.76	-2.72	0.00	0.00	0.00	0.00	0.00	-3.14	-2.89	-2.78
NA18557.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.83	0.00	0.00	-2.90	-2.67	-2.67	-2.74	-2.71	-2.68	0.00	0.00	0.00	0.00	0.00	-3.01	-2.83	-2.74
NA18558.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.81	0.00	0.00	-2.87	-2.70	-2.72	-2.72	-2.97	-2.76	0.00	0.00	0.00	0.00	0.00	-2.95	0.00	-2.72
NA18559.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.79	-2.81	-2.89	-3.04	-2.83	-2.92	-2.78	-2.83	-2.99	-3.32	-3.04	0.00	-2.89	-2.89	-3.12	0.00	-2.79
NA18560.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.54	0.00	0.00	-2.90	-2.53	-2.63	-2.67	-2.71	-2.54	0.00	0.00	0.00	0.00	0.00	-3.23	0.00	-2.51
NA18561.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.81	0.00	0.00	-2.99	-2.77	-2.75	-2.72	-2.82	0.00	-3.16	-2.88	0.00	-2.75	-2.73	0.00	0.00	-2.78
NA18562.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.80	0.00	0.00	-2.94	-2.62	-2.65	-2.71	-2.81	-2.71	0.00	-4.42	0.00	0.00	-4.42	-2.91	0.00	-2.74

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA18563.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.80	0.00	0.00	-2.92	-2.73	-2.72	-2.76	-2.81	-2.98	-3.31	-3.14	-2.90	0.00	-2.88	-3.17	0.00	-2.82
NA18564.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.82	0.00	0.00	-2.90	-2.67	-2.70	-2.77	-2.86	-2.97	-3.23	-3.18	-2.95	0.00	-2.88	0.00	-3.05	-2.78
NA18565.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.59	-2.83	-2.87	-3.13	-2.77	-2.81	-2.69	-2.68	-2.86	-3.63	-3.04	0.00	-2.90	-2.78	0.00	-2.92	-2.52
NA18566.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.81	0.00	0.00	-2.70	-2.63	-2.71	-2.69	-2.98	-2.75	0.00	0.00	0.00	0.00	0.00	-2.92	0.00	-2.74
NA18567.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.59	-2.79	-2.74	-2.98	-2.75	-2.79	-2.70	-2.64	-2.58	0.00	0.00	0.00	0.00	0.00	-3.21	-2.80	-2.56
NA18570.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.78	0.00	0.00	-2.69	-2.62	-2.62	-2.72	-2.88	-2.70	0.00	0.00	0.00	0.00	-4.64	-2.89	0.00	-2.71
NA18571.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.77	0.00	0.00	-2.84	-2.61	-2.65	-2.63	-2.81	-2.68	0.00	0.00	0.00	0.00	0.00	-2.85	0.00	-2.71
NA18572.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.81	0.00	0.00	-2.85	-2.68	-2.68	-2.74	-2.87	-2.99	-3.31	-3.15	0.00	-2.84	-2.88	-3.07	0.00	-2.77
NA18573.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.73	0.00	0.00	-2.75	-2.53	-2.72	-2.79	-2.84	-2.88	0.00	0.00	0.00	0.00	-2.72	0.00	-2.74	-2.59
NA18574.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.58	0.00	0.00	-2.83	-2.57	-2.57	-2.65	-2.66	-2.55	0.00	0.00	0.00	0.00	0.00	-3.03	0.00	-2.60
NA18577.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.75	0.00	0.00	-2.97	-2.69	-2.71	-2.76	-2.83	-2.74	0.00	0.00	0.00	0.00	0.00	-2.98	0.00	-2.77
NA18579.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.77	-4.83	0.00	-2.98	-2.73	-2.72	-2.72	-2.85	-2.77	0.00	0.00	0.00	0.00	0.00	-2.93	0.00	-2.75
NA18582.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.87	-2.92	-2.92	-3.21	-2.70	-2.81	-2.83	-2.91	-2.84	0.00	-3.07	-2.99	0.00	0.00	-3.22	0.00	-3.02
NA18591.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.95	-2.82	-2.76	-3.11	-2.49	-2.68	-2.56	-2.53	-2.77	-3.31	-2.83	-2.67	-4.29	-2.73	-3.07	0.00	-2.71
NA18592.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.80	-2.76	-2.87	-3.08	-2.86	-2.84	-2.93	-3.20	-3.04	0.00	-3.14	-2.94	0.00	-2.92	-3.19	0.00	-2.66
NA18593.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.76	0.00	0.00	-2.90	-2.51	-2.67	-2.66	-2.82	-2.72	0.00	0.00	0.00	0.00	0.00	-2.91	-4.69	-2.75
NA18595.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.82	0.00	0.00	-2.87	-2.61	-2.70	-2.75	-2.78	-2.76	0.00	0.00	0.00	0.00	0.00	-2.93	0.00	-2.73
NA18596.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.91	0.00	0.00	-2.85	-2.79	-2.82	-2.75	-2.73	-3.01	-3.15	-3.11	0.00	-2.98	-2.99	-3.18	0.00	-2.88
NA18597.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.76	0.00	0.00	-2.91	-2.66	-2.65	-2.70	-2.74	-2.70	0.00	0.00	0.00	0.00	-4.39	-2.90	0.00	-2.75
NA18599.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.81	0.00	0.00	-2.92	-2.66	-2.74	-2.63	-2.80	-2.71	0.00	0.00	0.00	0.00	-4.64	-2.86	0.00	-2.70
NA18602.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.77	0.00	0.00	-2.91	-2.66	-2.68	-2.68	-2.94	-2.74	0.00	0.00	0.00	0.00	0.00	-2.88	0.00	-2.76
NA18603.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.80	-2.85	-2.85	-3.06	-2.82	-2.93	-2.75	-2.73	-2.96	-3.25	-3.10	0.00	-2.94	-2.82	-3.16	0.00	-2.77
NA18605.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.80	-2.75	-2.80	-3.11	-2.83	-2.87	-2.70	-2.81	-2.98	-3.23	-3.13	0.00	-2.88	-2.84	-3.04	0.00	-2.75
NA18606.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.89	0.00	0.00	-3.00	-2.73	-2.74	-2.77	-2.88	-3.02	-3.32	-3.02	0.00	-2.95	-2.92	-3.12	0.00	-2.77
NA18608.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.89	0.00	0.00	-2.95	-2.66	-2.68	-2.72	-2.74	-2.91	-3.20	-3.02	0.00	-2.84	-2.85	-3.11	0.00	-2.74
NA18609.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.73	-2.70	-2.75	-2.97	-2.77	-2.81	-2.77	-3.03	-2.91	0.00	-2.94	0.00	-2.77	-2.77	0.00	-2.74	-2.64
NA18610.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.89	-2.82	-2.88	-3.13	-2.64	-2.76	-2.83	-2.93	-2.82	-4.78	-3.19	-2.97	0.00	0.00	0.00	-2.67	-2.81
NA18611.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.70	0.00	0.00	-2.81	-2.62	-2.62	-2.67	-2.88	-2.76	-4.62	0.00	0.00	-4.62	-4.62	-2.91	-2.76	-2.66
NA18612.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.93	-4.80	0.00	-2.83	-2.72	-2.76	-2.81	-2.80	-3.06	-3.30	-3.04	0.00	-2.92	-2.91	-3.11	0.00	-2.84
NA18613.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.86	-2.81	-2.86	-3.08	-2.85	-2.82	-2.85	-3.05	-3.06	0.00	-3.04	-2.97	-4.71	-2.83	0.00	-2.83	-2.72
NA18614.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.36	-4.22	0.00	-2.70	-2.46	-2.37	-2.36	-2.59	-2.60	-3.44	-2.92	0.00	-2.80	-2.51	-3.07	0.00	-2.33
NA18615.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.18	0.00	0.00	-2.53	-2.53	-2.29	-2.21	-2.48	-2.35	0.00	0.00	0.00	0.00	0.00	-2.60	0.00	-2.15
NA18616.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.59	-4.77	-4.77	-2.82	-2.55	-2.62	-2.67	-2.64	-2.56	0.00	0.00	0.00	0.00	0.00	-3.23	-2.89	-2.55
NA18617.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.29	0.00	0.00	-2.65	-2.37	-2.27	-2.18	-2.33	-2.32	0.00	0.00	0.00	0.00	0.00	0.00	-2.32	-2.30
NA18618.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.35	0.00	-4.11	-2.68	-2.63	-2.32	-2.34	-2.45	-2.77	-3.11	-3.03	0.00	-2.68	-2.51	0.00	-2.58	-2.26
NA18619.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.19	-4.03	0.00	-2.62	-2.69	-2.13	-2.37	-2.48	-2.42	0.00	0.00	0.00	0.00	0.00	-3.03	-2.50	-2.17
NA18620.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.85	0.00	0.00	-2.91	-2.68	-2.73	-2.72	-2.90	-3.00	-3.26	-3.16	0.00	-2.91	-2.82	-3.15	-4.74	-2.76
NA18621.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.83	0.00	0.00	-2.92	-2.58	-2.71	-2.70	-2.79	-2.76	0.00	0.00	0.00	0.00	0.00	-3.09	-2.89	-2.77
NA18622.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.80	0.00	0.00	-2.88	-2.67	-2.70	-2.67	-2.78	-2.65	0.00	-4.42	0.00	0.00	0.00	-3.07	-2.85	-2.74
NA18623.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.83	-4.83	-4.83	-2.94	-2.70	-2.69	-2.74	-2.88	-2.76	0.00	0.00	0.00	0.00	-4.52	-2.87	0.00	-2.77
NA18624.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.75	0.00	0.00	-2.88	-2.60	-2.68	-2.67	-2.75	-2.74	0.00	0.00	-4.62	0.00	0.00	-2.97	-2.82	-2.66
NA18625.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.31	0.00	0.00	-2.66	-2.51	-2.36	-2.30	-2.46	-2.54	-3.11	-2.81	0.00	-2.76	-2.60	-2.94	0.00	-2.28
NA18626.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.35	0.00	-3.93	-2.64	-2.49	-2.37	-2.41	-2.49	-2.54	-3.33	-3.00	0.00	-2.61	-2.60	-3.06	0.00	-2.37
NA18627.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.36	-2.67	-2.54	-2.88	-2.71	-2.53	-2.24	-2.40	-2.31	-4.11	-4.11	-3.81	-4.11	-3.64	-2.88	-2.61	-2.24
NA18628.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.31	0.00	-4.09	-2.56	-2.43	-2.32	-2.33	-2.45	-2.34	0.00	0.00	0.00	0.00	-4.09	-2.79	0.00	-2.17
NA18629.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.81	0.00	0.00	-2.96	-2.59	-2.43	-2.57	-2.56	-2.66	-3.50	-2.92	-4.50	-2.73	-2.81	-3.00	-4.50	-2.70
NA18630.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.12	0.00	0.00	-2.69	-2.46	-2.24	-2.31	-2.51	-2.17	0.00	0.00	0.00	0.00	0.00	-3.06	-2.69	-2.27
NA18631.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.57	-2.76	-2.78	-2.97	-2.75	-2.76	-2.64	-2.65	-2.74	-3.33	-3.09	-2.79	0.00	-2.70	-3.20	-4.76	-2.50
NA18632.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.96	-2.93	-2.98	-3.18	-2.72	-2.80	-2.90	-2.88	-3.04	-3.35	-2.90	-2.84	0.00	-2.92	0.00	-3.05	-2.87
NA18633.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.79	0.00	0.00	-2.84	-2.66	-2.67	-2.72	-2.81	-2.77	0.00	0.00	0.00	0.00	0.00	-2.82	0.00	-2.74
NA18634.mapped.ILLUMINA.bwa.CHB.exome.20120522	-2.65	0.00	0.00	-2.80	-2.61	-2.67	-2.65	-2.68	-2.80	-3.30	-2.98	0.00	-2.92	-2.76	-3.26	0.00	-2.59
NA18635.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.78	0.00	0.00	-2.89	-2.64	-2.73	-2.66	-2.78	-2.74	0.00	0.00	0.00	0.00	0.00	-3.05	-2.99	-2.70
NA18636.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.80	-2.77	-2.88	-3.03	-2.86	-2.91	-2.72	-2.80	-2.77	0.00	0.00	-4.76	0.00	0.00	-3.13	-2.83	-2.76
NA18637.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.80	-4.72	0.00	-2.94	-2.68	-2.79	-2.75	-2.88	-3.08	-3.17	-3.19	-2.92	0.00	-2.92	-3.19	0.00	-2.70
NA18638.mapped.ILLUMINA.bwa.CHB.exome.20121211	-2.60	-2.82	-2.80	-3.10	-2.85	-2.84	-2.74	-2.74	-2.83	-3.65	-3.11	-2.84	0.00	-2.84	-3.39	-4.77	-2.61
NA18639.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.16	0.00	0.00	-2.62	-2.47	-2.21	-2.24	-2.46	-2.33	0.00	0.00	0.00	0.00	0.00	0.00	-3.41	-2.16
NA18640.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.34	0.00	0.00	-2.63	-2.44	-2.41	-2.37	-2.55	-2.32	0.00	0.00	0.00	0.00	0.00	-2.82	0.00	-2.21
NA18641.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.36	-2.72	-2.65	-3.02	-2.82	-2.50	-2.34	-2.50	-2.63	-3.47	-3.05	0.00	-2.78	-2.57	-2.96	0.00	-2.26
NA18642.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.28	0.00	-4.11	-2.60	-2.61	-2.31	-2.34	-2.41	-2.64	-3.33	-3.20	-2.76	0.00	-2.56	-2.96	-4.11	-2.26
NA18643.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.26	-2.60	-2.62	-2.65	-2.88	-2.49	-2.56	-2.65	-2.48	0.00	-3.00	0.00	-2.69	-2.52	-2.85	0.00	-2.23
NA18644.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.82	-4.15	0.00	-2.96	-2.53	-2.56	-2.48	-2.53	-2.54	0.00	0.00	-4.45	-4.15	-4.45	-2.78	-4.15	-2.60
NA18645.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.20	0.00	0.00	-2.85	-2.45	-2.19	-2.33	-2.43	-2.29	0.00	0.00	0.00	0.00	-4.00	-2.62	0.00	-2.27
NA18646.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.84	-4.56	-4.56	-3.03	-2.61	-2.59	-2.56	-2.64	-2.71	-3.36	-2.90	-4.56	-2.81	-2.77	0.00	-2.82	-2.66
NA18647.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.47	-3.75	0.00	-2.67	-2.60	-2.59	-2.41	-2.57	-2.62	-3.35	-3.09	0.00	-2.90	-2.84	-3.05	-3.75	-2.41
NA18648.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.86	-4.42	-4.42	-2.98	-2.45	-2.53	-2.48	-2.60	-2.48	0.00	0.00	-4.12	0.00	-4.42	-2.71	-3.82	-2.59
NA18740.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.44	0.00	0.00	-2.61	-2.44	-2.38	-2.33	-2.52	-2.66	-3.61	-3.05	0.00	-2.84	-2.66	-2.98	0.00	-2.33
NA18745.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.24	0.00	0.00	-2.54	-2.43	-2.36	-2.27	-2.66	-2.33	0.00	0.00	0.00	0.00	-4.01	-2.66	0.00	-2.24
NA18747.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.35	0.00	0.00	-2.60	-2.39	-2.32	-2.28	-2.42	-2.33	0.00	0.00	0.00	0.00	-4.16	-3.20	-2.67	-2.26
NA18748.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.42	0.00	0.00	-2.77	-2.60	-2.41	-2.37	-2.64	-2.79	-3.87	-3.06	-2.63	0.00	-2.64	-3.22	-4.17	-2.25
NA18749.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.36	0.00	0.00	-2.75	-2.54	-2.36	-2.34	-2.52	-2.32	0.00	0.00	0.00	-4.18	0.00	0.00	-2.39	-2.27
NA18757.mapped.ILLUMINA.bwa.CHB.exome.20130415	-2.31	-4.05	-3.75	-2.59	-2.38	-2.29	-2.33	-2.67	-2.34	0.00	0.00	0.00	0.00	0.00	-2.87	0.00	-2.24
NA18853.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.60	0.00	-2.84	-3.12	-2.54	-2.69	-2.74	-2.73	-2.67	0.00	-2.96	-2.86	0.00	-4.51	-3.04	0.00	-2.62
NA18856.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.57	-2.79	-2.67	0.00	-2.71	-2.77	-2.83	-2.92	-2.73	0.00	-2.74	0.00	-2.69	-2.70	0.00	-2.87	-2.60
NA18858.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.82	-2.80	-2.82	-3.02	-2.79	-2.85	-2.72	-2.73	-2.70	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.72
NA18861.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.76	0.00	0.00	-2.99	-2.56	-2.73	-2.73	-2.84	-2.76	0.00	0.00	0.00	0.00	0.00	-3.10	-2.83	-2.76
NA18864.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.91	-2.79	-2.80	-3.18	-2.58	-2.70	-2.69	-2.68	-2.68	-4.92	-2.84	-2.83	-4.92	-4.92	-3.01	-4.44	-2.84
NA18865.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.86	-4.48	-4.78	-2.73	-2.43	-2.64	-2.54	-2.58	-2.49	0.00	0.00	0.00	0.00	0.00	-2.95	0.00	-2.73
NA18867.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.54	0.00	-4.93	-2.92	-2.62	-2.63	-2.72	-2.58	-2.63	0.00	0.00	0.00	-4.93	-4.46	0.00	-2.53	-2.60
NA18868.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.62	0.00	-2.80	-3.08	-2.55	-2.70	-2.75	-2.71	-2.71	0.00	-2.91	0.00	-2.90	0.00	-3.06	0.00	-2.62
NA18870.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.49	0.00	0.00	-2.86	-2.48	-2.54	-2.53	-2.52	-2.51	0.00	0.00	-4.71	0.00	-4.71	-3.07	0.00	-2.60
NA18871.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.67	-2.83	-2.74	-2.97	-2.59	-2.70	-2.70	-2.69	-2.58	0.00	-2.91	0.00	-2.85	-4.66	-3.27	0.00	-2.74
NA18873.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.57	-2.96	-2.85	-3.09	-2.57	-2.67	-2.59	-2.61	-2.64	0.00	-3.11	-2.78	0.00	-4.81	0.00	-2.98	-2.70
NA18874.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.63	0.00	0.00	-2.72	-2.59	-2.43	-2.64	-2.82	-2.63	0.00	-4.58	0.00	0.00	-4.28	-3.18	0.00	-2.56
NA18876.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.99	-2.79	-2.81	-3.10	-2.55	-2.68	-2.64	-2.53	-2.64	0.00	-2.88	-2.82	0.00	0.00	-3.12	-2.87	-2.81
NA18877.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.88	0.00	-4.54	-2.75	-2.53	-2.60	-2.51	-2.54	-2.50	0.00	0.00	-4.84	0.00	-4.84	-2.93	0.00	-2.63
NA18878.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.83	-4.83	-4.53	-2.88	-2.52	-2.54	-2.43	-2.53	-2.51	0.00	0.00	0.00	-4.83	0.00	-2.83	0.00	-2.65
NA18879.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.98	-2.87	-2.90	-3.24	-2.70	-2.76	-2.67	-2.64	-2.87	-3.55	-2.70	-2.92	-2.87	-2.91	-3.27	-5.07	-2.83
NA18881.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.95	-2.64	-2.67	-4.02	-2.73	-2.81	-2.66	-2.55	-2.53	-3.96	-2.83	-2.75	0.00	-3.91	0.00	-2.79	-2.80
NA18907.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.80	0.00	0.00	-2.93	-2.54	-2.72	-2.74	-2.75	-2.74	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.77
NA18908.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.56	-2.75	-2.72	-2.95	-2.69	-2.69	-2.63	-2.52	-2.50	0.00	0.00	0.00	0.00	-4.36	0.00	-2.41	-2.49
NA18909.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.90	-2.87	-2.98	-3.11	-2.67	-2.76	-2.83	-2.83	-2.79	0.00	-3.07	-2.96	0.00	0.00	-3.17	-3.04	-2.87
NA18910.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.55	-2.82	-2.65	0.00	-2.72	-2.72	-2.78	-2.79	-2.73	0.00	-2.72	0.00	-2.68	-2.74	-3.16	-4.70	-2.57
NA18912.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.54	-2.82	-2.82	-2.95	-2.74	-2.78	-2.77	-2.77	-2.76	0.00	-3.03	0.00	-2.91	-2.70	-3.20	0.00	-2.51
NA18915.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.84	0.00	-4.49	-2.76	-2.56	-2.60	-2.56	-2.64	-2.52	0.00	0.00	-4.49	0.00	-4.79	-2.90	-4.32	-2.69
NA18916.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.34	-4.29	0.00	-3.98	0.00	0.00	-2.46	-2.49	-4.29	0.00	0.00	0.00	0.00	0.00	-2.94	0.00	-2.68
NA18917.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.66	0.00	-2.47	0.00	-2.68	-2.64	-2.55	-2.54	-2.48	0.00	-2.82	0.00	-2.74	0.00	-2.75	0.00	-2.64

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA18923.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.69	0.00	0.00	-2.90	-2.54	-2.55	-2.55	-2.52	-2.54	0.00	0.00	0.00	0.00	0.00	-2.70	0.00	-2.67
NA18924.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.59	0.00	0.00	-2.66	-2.41	-2.49	-2.49	-2.52	-2.45	0.00	0.00	0.00	0.00	0.00	-2.65	0.00	-2.65
NA18933.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.51	-2.57	-2.52	-2.90	-2.53	-2.36	-2.48	-2.34	-2.29	0.00	0.00	0.00	0.00	0.00	-2.98	0.00	-2.69
NA18934.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.69	-2.68	-2.68	-2.98	-2.46	-2.51	-2.54	-2.57	-2.45	0.00	-2.80	-2.75	0.00	-4.66	-2.79	0.00	-2.55
NA18939.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.25	0.00	0.00	-2.61	-2.52	-2.31	-2.33	-2.45	-2.63	-3.49	-3.01	0.00	-2.79	-2.51	-3.09	-3.61	-2.26
NA18940.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.78	0.00	0.00	-2.72	-2.66	-2.68	-2.75	-2.78	-2.66	0.00	0.00	0.00	0.00	0.00	-3.06	-2.88	-2.73
NA18941.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.32	0.00	0.00	-2.55	-2.41	-2.38	-2.29	-2.63	-2.39	0.00	0.00	-4.09	0.00	0.00	-2.84	0.00	-2.22
NA18942.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.79	0.00	0.00	-2.93	-2.67	-2.66	-2.71	-2.78	-2.71	0.00	0.00	0.00	0.00	0.00	-2.87	0.00	-2.71
NA18943.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.84	0.00	0.00	-2.86	-2.74	-2.75	-2.76	-2.83	-2.99	-3.28	-3.09	-2.92	-4.80	-2.88	0.00	-2.95	-2.80
NA18944.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.79	0.00	-4.74	-2.95	-2.66	-2.73	-2.75	-2.88	-2.91	-3.27	-3.04	-2.92	0.00	-2.84	-3.16	0.00	-2.76
NA18945.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.80	0.00	0.00	-2.91	-2.62	-2.65	-2.67	-2.76	-2.68	0.00	0.00	0.00	0.00	0.00	-3.07	-2.89	-2.76
NA18946.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.26	-4.12	0.00	-2.65	-2.36	-2.38	-2.28	-2.55	-2.28	0.00	-3.82	0.00	0.00	0.00	-2.74	0.00	-2.22
NA18947.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.79	-4.67	0.00	-2.87	-2.62	-2.65	-2.66	-2.77	-2.70	0.00	0.00	0.00	0.00	0.00	-3.10	-2.82	-2.69
NA18948.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.89	-2.80	-2.91	-3.10	-2.91	-2.96	-2.75	-2.84	-3.06	-3.23	-2.85	0.00	-2.69	-2.78	0.00	-2.95	-2.79
NA18949.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.92	0.00	0.00	-3.02	-2.75	-2.71	-2.74	-2.80	-2.95	-3.21	-2.88	0.00	-2.76	-2.93	-3.25	0.00	-2.81
NA18950.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.51	0.00	-4.56	-2.92	-2.60	-2.64	-2.67	-2.69	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.63	-2.62
NA18951.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.63	0.00	-4.58	-2.58	-2.46	-2.52	-2.56	-2.92	0.00	0.00	0.00	0.00	-4.58	-4.58	0.00	-4.58	-2.76
NA18952.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.93	-2.87	-4.82	-3.09	-2.67	-2.81	-2.80	-2.88	-3.00	-3.27	-2.87	-2.95	-2.97	-2.91	-3.19	0.00	-2.81
NA18953.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.53	0.00	0.00	-2.92	-2.57	-2.60	-2.64	-2.56	-2.77	-3.45	-3.01	0.00	-2.90	-2.78	-3.30	0.00	-2.73
NA18954.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.28	0.00	-4.11	-2.88	-2.49	-2.31	-2.28	-2.50	-2.58	-3.42	-2.97	-2.53	0.00	-2.47	-2.97	-4.11	-2.26
NA18956.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.31	0.00	0.00	-2.57	-2.53	-2.41	-2.36	-2.48	-2.64	-3.26	-2.96	0.00	-2.82	-2.64	0.00	-2.61	-2.35
NA18957.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.23	0.00	0.00	-2.71	-2.33	-2.30	-2.22	-2.29	-2.26	0.00	0.00	0.00	-3.94	-3.46	-3.10	-2.60	-2.22
NA18959.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.50	0.00	0.00	-2.76	-2.54	-2.61	-2.69	-2.66	-2.60	0.00	0.00	-4.81	0.00	0.00	-2.99	0.00	-2.54
NA18960.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.52	-4.90	0.00	-2.79	-2.57	-2.61	-2.69	-2.60	-2.55	0.00	0.00	0.00	0.00	0.00	-3.25	-2.87	-2.55
NA18961.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.55	0.00	-4.73	-2.89	-2.55	-2.66	-2.66	-2.56	-2.78	-3.37	-2.94	-2.76	0.00	-2.78	-3.12	0.00	-2.57
NA18962.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.31	0.00	0.00	-2.59	-2.49	-2.27	-2.35	-2.42	-2.31	0.00	0.00	0.00	0.00	-4.01	-2.59	0.00	-2.20
NA18963.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.36	0.00	-4.19	-2.62	-2.45	-2.28	-2.32	-2.47	-2.32	0.00	0.00	0.00	0.00	0.00	-2.89	-2.52	-2.28
NA18964.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.52	0.00	-4.84	-2.86	-2.67	-2.63	-2.68	-2.65	-2.59	0.00	0.00	0.00	0.00	0.00	-3.00	0.00	-2.58
NA18965.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.28	0.00	0.00	-2.60	-2.40	-2.41	-2.39	-2.44	-2.32	0.00	0.00	0.00	0.00	0.00	-2.71	0.00	-2.26
NA18966.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.63	0.00	0.00	-2.72	-2.47	-2.52	-2.51	-2.51	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.61
NA18967.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.53	-2.63	-2.60	-2.86	-2.62	-2.62	-2.53	-2.49	-2.38	0.00	0.00	0.00	0.00	0.00	-2.74	-4.58	-2.60
NA18968.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.60	-4.56	-4.56	-2.80	-2.45	-2.50	-2.49	-2.44	-2.27	0.00	0.00	0.00	0.00	0.00	-2.84	-2.65	-2.66
NA18969.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.64	0.00	0.00	-2.86	-2.38	-2.55	-2.51	-2.47	-2.39	0.00	0.00	0.00	0.00	0.00	-2.93	-2.73	-2.63
NA18970.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.60	-4.26	-4.56	-2.78	-2.49	-2.51	-2.48	-2.52	-2.35	0.00	0.00	0.00	0.00	0.00	-2.72	0.00	-2.55
NA18971.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.64	0.00	0.00	-2.64	-2.43	-2.46	-2.51	-2.57	-2.46	0.00	0.00	0.00	0.00	-4.68	0.00	-2.56	-2.60
NA18972.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.53	0.00	0.00	-2.61	-2.46	-2.47	-2.45	-2.54	-2.42	0.00	0.00	0.00	0.00	0.00	-3.09	-2.79	-2.61
NA18973.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.72	0.00	0.00	-2.91	-2.58	-2.58	-2.58	-2.53	-2.66	-3.79	-2.85	-2.72	-4.39	-2.66	-2.95	0.00	-2.66
NA18974.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.68	0.00	0.00	-2.84	-2.46	-2.53	-2.54	-2.49	-2.37	0.00	0.00	0.00	0.00	-4.60	-2.70	0.00	-2.61
NA18975.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.74	0.00	0.00	-2.87	-2.54	-2.59	-2.59	-2.49	-2.62	-3.75	-2.79	0.00	-2.77	-2.62	-2.93	0.00	-2.55
NA18976.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.70	0.00	-4.66	-2.92	-2.59	-2.59	-2.63	-2.61	-2.72	-3.82	-2.74	0.00	-2.70	-2.66	0.00	-2.74	-2.68
NA18977.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.35	-3.94	-4.24	-2.66	-2.38	-2.29	-2.36	-2.41	-2.29	0.00	-3.64	-4.24	0.00	0.00	-2.73	0.00	-2.35
NA18978.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.29	0.00	0.00	-2.62	-2.49	-2.23	-2.19	-2.56	-2.29	0.00	0.00	0.00	0.00	0.00	-2.66	0.00	-2.22
NA18979.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.44	0.00	0.00	-2.76	-2.61	-2.45	-2.55	-2.42	-2.74	-3.26	-2.96	0.00	-2.82	-2.82	0.00	-2.99	-2.27
NA18980.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.37	0.00	0.00	-2.76	-2.46	-2.38	-2.31	-2.45	-2.55	-3.30	-2.82	-2.54	0.00	-2.45	-3.10	-4.30	-2.36
NA18981.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.60	0.00	-4.67	-2.71	-2.47	-2.53	-2.51	-2.51	-2.50	0.00	0.00	0.00	0.00	0.00	-2.84	-2.82	-2.58
NA18982.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.54	0.00	0.00	-2.90	-2.58	-2.62	-2.65	-2.61	-2.60	0.00	0.00	0.00	0.00	-4.81	-2.96	0.00	-2.53
NA18983.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.58	0.00	0.00	-2.85	-2.65	-2.70	-2.76	-2.67	-2.75	-3.49	-2.90	-2.79	0.00	-2.79	0.00	-2.90	-2.62
NA18984.mapped.ILLUMINA.bwa.JPT.exome.20121211	-2.55	-4.33	-4.63	-2.83	-2.61	-2.64	-2.64	-2.55	-2.64	-3.38	-2.89	-2.72	0.00	-2.70	-3.10	0.00	-2.56
NA18985.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.49	0.00	0.00	-2.60	-2.43	-2.50	-2.56	-2.57	-2.48	0.00	0.00	0.00	0.00	-3.97	-2.93	-4.45	-2.40
NA18986.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.57	0.00	-4.72	-2.73	-2.55	-2.56	-2.66	-2.60	-2.72	-3.46	-2.97	0.00	-2.85	-2.74	-3.15	-4.72	-2.57
NA18987.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.62	0.00	-4.67	-2.71	-2.41	-2.48	-2.44	-2.50	-2.48	0.00	0.00	0.00	0.00	-4.67	-2.91	-2.77	-2.54
NA18988.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.54	0.00	0.00	-2.72	-2.51	-2.58	-2.59	-2.55	-2.52	0.00	0.00	0.00	0.00	0.00	-3.17	-2.67	-2.49
NA18989.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.59	-2.89	-2.82	-3.00	-2.73	-2.77	-2.64	-2.59	-2.65	0.00	0.00	0.00	0.00	-4.79	-3.02	0.00	-2.54
NA18990.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.70	0.00	-4.71	-2.89	-2.51	-2.56	-2.57	-2.62	0.00	-3.60	-2.55	-2.78	-2.78	-2.53	0.00	-4.71	-2.68
NA18991.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.69	0.00	0.00	-2.86	-2.54	-2.56	-2.56	-2.65	-2.72	-3.82	-2.81	0.00	-2.71	-2.69	0.00	-2.79	-2.62
NA18992.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.28	-2.62	-2.55	-2.76	-2.84	-2.57	-2.33	-2.46	-2.27	0.00	0.00	0.00	0.00	0.00	-3.11	-2.41	-2.21
NA18993.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.32	0.00	0.00	-2.53	-2.51	-2.48	-2.37	-2.36	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.28
NA18994.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.25	0.00	-4.02	-2.64	-2.42	-2.27	-2.26	-2.46	-2.36	0.00	0.00	0.00	0.00	-4.02	-2.68	-4.02	-2.23
NA18995.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.50	0.00	0.00	-2.62	-2.49	-2.30	-2.44	-2.49	0.00	-3.16	-2.66	0.00	-2.62	-2.45	0.00	-4.00	-2.33
NA18997.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.33	-2.72	-2.72	-2.84	-2.76	-2.59	-2.32	-2.54	-2.37	0.00	0.00	0.00	-4.02	0.00	-3.41	-2.81	-2.34
NA18998.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.34	0.00	0.00	-2.71	-2.44	-2.31	-2.28	-2.44	-2.31	0.00	0.00	0.00	0.00	-4.16	-3.04	-2.65	-2.31
NA18999.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.56	0.00	-4.82	-2.91	-2.62	-2.60	-2.72	-2.61	-2.61	0.00	0.00	0.00	-4.82	-4.82	-3.06	0.00	-2.53
NA19000.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.60	0.00	-4.92	-2.91	-2.59	-2.64	-2.71	-2.61	-2.85	-3.58	-3.03	-2.85	0.00	-2.84	-3.23	-4.92	-2.57
NA19001.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.35	0.00	0.00	-2.79	-2.50	-2.42	-2.32	-2.72	-2.69	-3.46	-2.99	-2.67	0.00	-2.55	-3.22	0.00	-2.35
NA19002.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.25	0.00	-3.72	-2.76	-2.39	-2.22	-2.24	-2.45	-2.35	0.00	0.00	0.00	0.00	0.00	-2.60	0.00	-2.26
NA19003.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.60	-2.82	0.00	-3.00	-2.52	-2.64	-2.68	-2.68	-4.70	-3.33	-2.76	-2.65	0.00	-2.69	0.00	0.00	-2.56
NA19004.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.56	0.00	0.00	-2.84	-2.62	-2.66	-2.68	-2.51	-2.57	0.00	0.00	0.00	0.00	-4.74	-3.11	-2.76	-2.56
NA19005.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.26	0.00	-4.09	-2.65	-2.46	-2.29	-2.28	-2.42	-2.39	0.00	0.00	-4.09	0.00	0.00	-2.64	0.00	-2.18
NA19006.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.85	-4.99	-4.99	-2.84	-2.57	-2.60	-2.51	-2.55	-2.47	0.00	-4.69	-4.99	-4.69	-4.99	-3.13	-2.81	-2.69
NA19007.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.61	-2.91	-2.90	-3.17	-2.58	-2.63	-2.73	-2.71	-2.61	0.00	-3.09	-2.78	0.00	-4.97	-3.23	-3.20	-2.59
NA19009.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.34	0.00	-4.01	-2.63	-2.43	-2.27	-2.34	-2.65	-2.29	0.00	0.00	0.00	0.00	-4.01	-2.93	-2.75	-2.19
NA19010.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.30	0.00	0.00	-2.67	-2.39	-2.30	-2.24	-2.43	-2.32	0.00	0.00	0.00	0.00	0.00	-2.57	-3.90	-2.29
NA19011.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.83	-4.18	-4.96	-2.96	-2.48	-2.59	-2.56	-2.63	-2.57	0.00	0.00	-4.96	-4.66	0.00	-2.91	0.00	-2.72
NA19012.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.62	-2.94	-2.94	-3.15	-2.61	-2.70	-2.81	-2.74	-2.86	-3.64	-2.93	-2.86	-2.98	-2.87	-3.36	0.00	-2.66
NA19017.mapped.ILLUMINA.bwa.LWK.exome.20121211	-2.54	-4.51	-4.51	-2.76	-2.57	-2.54	-2.54	-2.66	-2.67	-3.37	-2.88	0.00	-2.79	-2.66	0.00	-2.74	-2.42
NA19019.mapped.ILLUMINA.bwa.LWK.exome.20121211	-2.56	0.00	-4.44	-2.54	-2.49	-2.52	-2.59	-2.54	-2.47	-3.23	-4.44	0.00	-4.44	-4.44	-3.04	-2.65	-2.49
NA19020.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.24	-2.68	0.00	-2.85	-2.66	-2.48	-2.55	-2.68	0.00	-3.38	-2.39	0.00	-2.42	-2.25	0.00	-4.08	-2.25
NA19023.mapped.ILLUMINA.bwa.LWK.exome.20121211	-2.47	0.00	-3.94	-2.72	-2.53	-2.57	-2.47	-2.41	-2.44	0.00	0.00	-3.94	0.00	-4.11	-2.94	0.00	-2.50
NA19024.mapped.ILLUMINA.bwa.LWK.exome.20121211	-2.60	-2.73	-2.74	-2.91	-2.45	-2.60	-2.64	-2.54	-2.54	-4.54	-2.93	-2.78	0.00	-4.06	-3.11	-2.76	-2.53
NA19025.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.87	-2.71	-2.66	-3.07	-2.73	-2.78	-2.64	-2.84	-2.72	0.00	-2.71	0.00	-2.68	-2.68	-3.10	0.00	-2.68
NA19026.mapped.ILLUMINA.bwa.LWK.exome.20121211	-2.46	-2.66	-2.70	-2.79	-2.58	-2.57	-2.52	-2.55	-2.49	0.00	0.00	-4.44	-4.44	0.00	-2.85	-4.44	-2.38
NA19027.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.51	-2.73	0.00	-2.95	-2.58	-2.46	-2.55	-2.57	-2.92	-3.67	-2.97	-2.72	-2.87	-2.79	-3.55	0.00	-2.36
NA19028.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.18	-2.44	0.00	-2.93	-2.72	-2.50	-2.48	-2.63	-2.63	0.00	-2.89	0.00	-2.57	-2.56	0.00	-2.44	-2.21
NA19030.mapped.ILLUMINA.bwa.LWK.exome.20121211	-2.51	0.00	-4.43	-2.52	-2.45	-2.46	-2.46	-2.53	-2.54	-3.25	-2.94	-4.43	-2.79	-2.55	0.00	0.00	-2.48
NA19031.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.32	-2.72	-2.56	-3.24	-2.44	-2.33	-2.32	-2.49	-2.60	-3.24	-2.59	0.00	-2.48	-2.52	0.00	-2.78	-2.34
NA19035.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.34	0.00	0.00	-2.37	-2.41	-2.27	-2.19	-2.37	-2.26	0.00	0.00	0.00	0.00	0.00	0.00	-2.76	-2.36
NA19036.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.26	-4.08	0.00	-2.63	-2.46	-2.29	-2.35	-2.55	-2.32	0.00	-3.12	0.00	-2.60	0.00	-2.66	0.00	-2.37
NA19037.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.83	-2.67	-2.66	-3.14	-2.69	-2.70	-2.54	-2.61	-2.55	0.00	-4.55	-4.85	0.00	0.00	-3.03	-2.76	-2.68
NA19038.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.31	-2.70	-2.66	-2.87	-2.59	-2.68	-2.26	-2.52	-2.34	0.00	0.00	0.00	0.00	0.00	0.00	-2.40	-2.22
NA19041.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.32	-2.26	-2.64	0.00	0.00	0.00	-2.54	-2.77	-4.07	-3.29	-2.52	0.00	-2.41	-2.29	0.00	0.00	-2.25
NA19042.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.92	-2.68	-2.74	-3.11	-2.78	-2.74	-2.68	-2.79	-2.72	0.00	-2.75	-4.86	-2.74	-2.72	0.00	-2.80	-2.70
NA19043.mapped.ILLUMINA.bwa.LWK.exome.20121211	-2.49	-2.68	-3.98	-2.79	-2.59	-2.49	-2.58	-2.63	-2.49	0.00	0.00	0.00	0.00	-3.98	-2.87	-4.46	-2.42
NA19054.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.62	0.00	0.00	-2.76	-2.56	-2.60	-2.67	-2.69	-2.58	0.00	0.00	0.00	0.00	0.00	-2.99	0.00	-2.58
NA19055.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.54	0.00	-4.62	-2.78	-2.53	-2.57	-2.65	-2.56	-2.50	0.00	0.00	0.00	0.00	0.00	-3.18	-2.74	-2.53
NA19056.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.53	0.00	-4.79	-2.92	-2.65	-2.65	-2.66	-2.60	-2.51	0.00	0.00	-4.79	0.00	0.00	-3.04	-2.85	-2.59
NA19057.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.70	0.00	-4.70	-2.89	-2.65	-2.63	-2.72	-2.71	-2.76	-3.70	-3.01	0.00	-2.90	-2.75	-3.28	0.00	-2.65

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA19058.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.61	0.00	-4.74	-2.88	-2.59	-2.68	-2.70	-2.60	-2.73	-3.36	-2.89	0.00	-2.83	-2.76	-3.16	0.00	-2.59
NA19059.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.60	0.00	0.00	-2.84	-2.55	-2.62	-2.60	-2.61	-2.60	0.00	0.00	0.00	0.00	-4.64	-2.98	0.00	-2.54
NA19060.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.56	0.00	-4.95	-2.87	-2.57	-2.56	-2.71	-2.62	-2.83	-3.59	-3.00	-2.87	0.00	-2.80	-3.23	0.00	-2.53
NA19062.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.52	0.00	0.00	-2.75	-2.54	-2.52	-2.63	-2.59	-4.26	-3.28	-2.90	0.00	-2.78	-2.68	-3.24	0.00	-2.69
NA19063.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.60	0.00	-4.89	-2.76	-2.63	-2.54	-2.71	-2.71	-2.87	-3.48	-2.98	0.00	-2.96	-2.80	0.00	-2.87	-2.58
NA19064.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.64	0.00	0.00	-2.84	-2.58	-2.59	-2.63	-2.68	-2.72	-3.41	-3.09	-2.81	0.00	-2.76	-3.19	0.00	-2.53
NA19065.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.54	0.00	-3.27	-2.78	-2.58	-2.59	-2.55	-2.59	-2.57	0.00	0.00	0.00	0.00	0.00	0.00	-2.95	-2.52
NA19066.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.56	-2.84	0.00	-3.01	-2.53	-2.60	-2.64	-2.57	-2.56	0.00	-2.95	-2.77	0.00	-4.79	-3.20	-4.79	-2.73
NA19067.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.62	0.00	0.00	-2.91	-2.57	-2.57	-2.65	-2.66	-2.58	0.00	0.00	-4.71	0.00	-4.41	-3.13	-2.83	-2.57
NA19068.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.54	0.00	0.00	-2.84	-2.56	-2.63	-2.67	-2.64	-2.64	0.00	0.00	0.00	0.00	-4.46	-3.00	-4.76	-2.56
NA19070.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.45	0.00	0.00	-2.79	-2.55	-2.60	-2.67	-2.64	-2.54	0.00	0.00	0.00	0.00	0.00	-3.15	-2.83	-2.50
NA19072.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.60	0.00	-4.32	-2.82	-2.45	-2.46	-2.49	-2.46	-2.43	0.00	0.00	0.00	0.00	0.00	-2.96	-2.68	-2.60
NA19074.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.68	-2.65	-2.61	-3.00	-2.61	-2.65	-2.68	-2.71	-2.67	0.00	-2.81	-2.69	0.00	-2.56	0.00	-2.70	-2.62
NA19075.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.69	0.00	0.00	-2.85	-2.51	-2.54	-2.54	-2.50	-2.41	0.00	0.00	0.00	0.00	0.00	-2.69	0.00	-2.64
NA19076.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.65	0.00	0.00	-2.75	-2.47	-2.52	-2.49	-2.51	-2.47	0.00	0.00	0.00	0.00	0.00	-2.89	-2.75	-2.61
NA19077.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.63	0.00	0.00	-2.80	-2.52	-2.48	-2.51	-2.48	-2.36	0.00	0.00	0.00	0.00	-4.56	-2.83	-2.66	-2.59
NA19078.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.81	-4.48	0.00	-2.93	-2.59	-2.68	-2.62	-2.70	-2.61	-4.78	-4.78	-4.78	-4.78	-4.78	-2.97	0.00	-2.68
NA19079.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.64	-2.66	-2.68	-3.04	-2.63	-2.65	-2.50	-2.50	-2.62	-3.64	-2.77	-2.72	0.00	-2.65	-2.87	0.00	-2.61
NA19080.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.69	0.00	0.00	-2.98	-2.58	-2.57	-2.56	-2.46	-2.62	-3.69	-2.74	0.00	-2.72	-2.65	-2.92	0.00	-2.68
NA19081.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.64	-2.58	-2.62	-2.97	-2.66	-2.57	-2.50	-2.43	-2.38	0.00	0.00	0.00	0.00	0.00	-2.85	-2.72	-2.56
NA19082.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.63	0.00	0.00	-2.88	-2.50	-2.55	-2.52	-2.43	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.38	-2.59
NA19083.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.55	0.00	0.00	-2.66	-2.50	-2.52	-2.52	-2.44	-2.44	0.00	0.00	0.00	-4.59	0.00	-2.91	-2.77	-2.60
NA19084.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.68	0.00	0.00	-2.90	-2.46	-2.50	-2.52	-2.53	-2.69	-3.86	-2.69	-2.73	0.00	-2.61	0.00	-2.74	-2.62
NA19085.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.57	-2.67	-2.69	-3.01	-2.68	-2.70	-2.54	-2.53	-2.60	-3.78	-2.71	0.00	-2.74	-2.63	0.00	-2.82	-2.71
NA19086.mapped.ILLUMINA.bwa.JPT.exome.20130422	-2.32	0.00	0.00	-2.60	-2.52	-2.31	-2.27	-2.34	-2.24	0.00	0.00	0.00	0.00	-4.04	-3.19	-2.48	-2.30
NA19087.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.84	0.00	0.00	-2.79	-2.70	-2.70	-2.73	-2.80	-3.00	-3.22	-3.06	0.00	-2.91	-2.79	-3.24	0.00	-2.76
NA19088.mapped.ILLUMINA.bwa.JPT.exome.20120522	-2.73	-2.73	-2.88	-2.95	-2.77	-2.83	-2.70	-2.86	-2.71	0.00	0.00	0.00	0.00	0.00	-2.89	0.00	-2.68
NA19089.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.84	0.00	-4.67	-2.88	-2.49	-2.59	-2.55	-2.62	-2.55	0.00	0.00	0.00	0.00	-4.97	-2.96	0.00	-2.67
NA19090.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.88	0.00	-4.92	-2.85	-2.57	-2.61	-2.52	-2.63	-2.56	0.00	0.00	-4.92	0.00	-4.62	0.00	-2.60	-2.66
NA19091.mapped.ILLUMINA.bwa.JPT.exome.20130415	-2.90	0.00	0.00	-2.79	-2.65	-2.70	-2.61	-2.63	-2.85	-3.33	-2.85	-5.00	-2.75	-2.81	0.00	-2.86	-2.77
NA19092.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.46	0.00	-4.35	-2.83	-2.49	-2.60	-2.58	-2.59	-2.48	0.00	0.00	0.00	0.00	0.00	-3.07	0.00	-2.50
NA19093.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.53	0.00	0.00	-2.90	-2.60	-2.60	-2.65	-2.60	-2.60	0.00	0.00	-4.67	0.00	0.00	-2.98	0.00	-2.52
NA19095.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.24	0.00	0.00	-2.60	-2.47	-2.17	-2.34	-2.47	-2.40	-3.87	-3.87	0.00	0.00	0.00	-2.83	-4.17	-2.23
NA19096.mapped.ILLUMINA.bwa.YRI.exome.20130422	-2.32	0.00	0.00	-2.55	-2.62	-2.52	-2.26	-2.73	-2.36	0.00	0.00	0.00	0.00	0.00	-3.14	0.00	-2.47
NA19098.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.73	-2.68	-2.73	-3.06	-2.42	-2.50	-2.55	-2.58	-2.48	0.00	-2.82	-2.79	-4.74	0.00	-2.95	-2.82	-2.63
NA19099.mapped.ILLUMINA.bwa.YRI.exome.20130422	-2.32	0.00	0.00	-2.64	-2.30	-2.25	-2.21	-2.28	-2.27	0.00	-4.21	0.00	0.00	-3.90	-2.55	-4.21	-2.44
NA19102.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.56	0.00	-4.79	-2.74	-2.49	-2.61	-2.68	-2.53	-2.58	0.00	0.00	0.00	0.00	-4.49	-3.08	-2.85	-2.58
NA19107.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.83	-2.78	-2.86	-3.14	-2.85	-2.89	-2.70	-2.81	-2.96	-3.17	-3.06	0.00	-2.93	-2.88	-3.03	0.00	-2.80
NA19108.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.85	-2.87	-2.86	-3.22	-2.64	-2.81	-2.84	-2.83	-2.76	-4.80	-3.09	0.00	-2.92	-4.80	0.00	-2.75	-2.80
NA19113.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.33	0.00	0.00	-2.53	-2.64	-2.38	-2.39	-2.51	-2.38	0.00	0.00	0.00	0.00	0.00	-2.74	0.00	-2.27
NA19114.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.83	0.00	0.00	-2.98	-2.69	-2.80	-2.72	-2.74	-2.94	-3.25	-3.11	0.00	-2.83	-2.82	-3.11	0.00	-2.76
NA19116.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.59	-2.87	-2.90	-3.00	-2.74	-2.78	-2.65	-2.63	-2.59	0.00	-3.01	-2.83	0.00	-4.35	-3.18	-2.87	-2.53
NA19117.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.19	-2.48	-2.67	-3.07	-2.67	-2.51	-2.29	-2.48	-2.32	-4.07	0.00	0.00	0.00	-4.07	-2.89	-2.49	-2.28
NA19118.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.31	0.00	-2.34	-3.88	-2.88	-2.53	-2.30	-2.45	-2.29	0.00	-2.86	0.00	-2.73	0.00	-2.88	-2.67	-2.34
NA19119.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.67	-2.62	-2.63	-2.92	-2.58	-2.62	-2.67	-2.67	-2.56	0.00	-2.67	0.00	-2.64	-2.58	0.00	-2.68	-2.60
NA19121.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.41	0.00	0.00	-2.58	-2.49	-2.35	-2.23	-2.43	-2.48	0.00	0.00	-4.10	0.00	0.00	0.00	-3.02	-2.46
NA19129.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.81	0.00	-2.87	-3.03	-2.69	-2.77	-2.77	-2.79	-2.80	0.00	-3.05	0.00	-2.83	0.00	-3.20	-2.91	-2.84
NA19130.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.68	-3.00	-2.95	-3.04	-2.73	-2.72	-2.66	-2.57	-2.59	0.00	0.00	0.00	-4.97	-4.67	-3.13	-2.94	-2.62
NA19131.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.64	-2.71	-2.68	-3.09	-2.60	-2.50	-2.54	-2.56	-2.45	0.00	0.00	0.00	0.00	0.00	-2.74	0.00	-2.62
NA19137.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.69	-2.52	-2.53	-4.12	-3.64	-4.12	-3.52	-3.95	-3.95	-4.42	-2.59	0.00	-2.59	-2.56	0.00	-4.12	-2.60
NA19138.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.62	0.00	0.00	-2.76	-2.47	-2.52	-2.51	-2.56	-2.47	0.00	0.00	0.00	0.00	0.00	-2.71	0.00	-2.60
NA19141.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.68	-2.54	-2.70	0.00	-2.65	-2.66	-2.72	-2.84	-2.65	0.00	-2.49	-2.68	-2.72	-2.72	0.00	-2.70	-2.65
NA19143.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.68	-2.61	-2.61	-2.94	-2.65	-2.71	-2.65	-2.67	-2.58	0.00	-2.78	0.00	-2.68	-2.61	-2.91	0.00	-2.63
NA19144.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.79	-2.63	-2.66	-4.79	-2.60	-2.59	-2.65	-2.67	-2.79	-3.71	-2.56	-2.80	-2.68	-2.74	0.00	-2.84	-2.71
NA19146.mapped.ILLUMINA.bwa.YRI.exome.20130422	-2.26	-2.75	-2.63	-3.07	-2.70	-2.49	-2.57	-2.73	-2.51	0.00	-2.94	0.00	-2.76	-2.63	-2.91	0.00	-2.26
NA19147.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.83	-2.76	-4.43	-3.06	-2.82	-2.80	-2.91	-3.03	-2.88	0.00	-2.96	0.00	-2.85	-2.89	-3.08	0.00	-2.80
NA19149.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.26	0.00	-2.58	-2.91	-2.47	-2.36	-2.29	-2.45	-2.38	0.00	-2.94	0.00	-2.81	0.00	-2.86	-2.73	-2.26
NA19152.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.69	0.00	0.00	-2.91	-2.41	-2.53	-2.60	-2.46	-2.45	0.00	-2.74	-2.69	0.00	-4.65	0.00	-2.40	-2.67
NA19153.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.58	0.00	0.00	-2.69	-2.51	-2.51	-2.54	-2.45	-2.46	0.00	-4.65	0.00	0.00	0.00	-2.93	-2.70	-2.56
NA19159.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.55	0.00	0.00	-2.86	-2.42	-2.52	-2.50	-2.38	-2.44	0.00	0.00	0.00	0.00	0.00	-2.80	-2.78	-2.59
NA19160.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.65	0.00	0.00	-2.68	-2.37	-2.54	-2.55	-2.56	-2.43	0.00	0.00	0.00	0.00	0.00	-2.70	0.00	-2.58
NA19171.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.61	-2.66	-2.63	-2.97	-2.62	-2.68	-2.54	-2.50	-2.46	0.00	0.00	0.00	0.00	0.00	-2.91	-2.74	-2.61
NA19172.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.62	-2.93	-2.89	-3.11	-2.61	-2.70	-2.74	-2.78	-2.66	0.00	-3.17	-2.86	0.00	0.00	-3.13	0.00	-2.63
NA19175.mapped.ILLUMINA.bwa.YRI.exome.20130422	-2.42	-4.01	-4.01	-2.68	-2.45	-2.33	-2.36	-2.50	-2.30	0.00	0.00	0.00	0.00	0.00	-2.83	0.00	-2.32
NA19184.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.25	0.00	-2.55	-2.90	-2.98	-2.52	-2.46	-2.72	-2.50	0.00	-2.94	0.00	-2.83	-2.62	-2.90	0.00	-2.19
NA19185.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.36	0.00	0.00	-2.58	-2.58	-2.16	-2.41	-2.54	-2.38	0.00	0.00	0.00	0.00	0.00	-3.07	-2.65	-2.26
NA19189.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.80	0.00	0.00	-2.74	-2.59	-2.75	-2.76	-2.78	-2.72	0.00	0.00	0.00	0.00	0.00	-2.87	0.00	-2.75
NA19190.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.79	0.00	0.00	-2.75	-2.71	-2.57	-2.73	-2.79	-2.77	0.00	0.00	0.00	0.00	0.00	-2.95	0.00	-2.81
NA19197.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.62	-2.54	-2.55	0.00	-2.71	-2.68	-2.58	-2.52	-2.38	0.00	-2.72	-2.73	0.00	0.00	0.00	-2.42	-2.64
NA19198.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.64	0.00	0.00	-2.66	-2.44	-2.45	-2.47	-2.45	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.57
NA19200.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.65	-2.64	-2.68	-2.96	-2.44	-2.54	-2.55	-2.50	-2.47	0.00	-2.80	-2.73	-4.75	0.00	-2.96	-2.75	-2.61
NA19201.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.64	0.00	0.00	-2.86	-2.48	-2.50	-2.49	-2.44	-2.43	0.00	0.00	0.00	0.00	0.00	-2.79	-2.58	-2.67
NA19204.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.58	-2.59	0.00	-2.91	-2.57	-2.62	-2.60	-2.67	-2.58	0.00	-2.79	0.00	-2.66	-2.59	0.00	-2.60	-2.64
NA19206.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.66	0.00	0.00	-2.67	-2.43	-2.58	-2.53	-2.53	-2.55	0.00	0.00	0.00	0.00	0.00	-2.84	-2.74	-2.58
NA19207.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.66	-2.65	-2.73	-3.06	-2.46	-2.57	-2.56	-2.58	-2.50	0.00	-2.84	-2.75	0.00	0.00	-2.96	-2.82	-2.66
NA19209.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.62	0.00	0.00	-2.69	-2.37	-2.54	-2.53	-2.44	-2.52	0.00	0.00	0.00	0.00	0.00	-2.86	-2.64	-2.59
NA19210.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.69	0.00	0.00	-2.70	-2.56	-2.59	-2.62	-2.49	-2.39	0.00	-2.83	-2.68	-4.67	0.00	-2.94	-2.70	-2.67
NA19213.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.64	0.00	-4.30	-2.83	-2.64	-2.49	-2.72	-2.80	-2.63	0.00	0.00	0.00	0.00	-4.78	-3.07	0.00	-2.63
NA19214.mapped.ILLUMINA.bwa.YRI.exome.20130422	-2.15	0.00	0.00	-2.47	-2.43	-2.24	-2.22	-2.33	-2.29	0.00	0.00	0.00	0.00	0.00	-2.93	0.00	-2.29
NA19222.mapped.ILLUMINA.bwa.YRI.exome.20130422	-2.44	-2.79	-2.63	-2.82	-2.52	-2.44	-2.43	-2.60	-2.42	0.00	-2.95	-2.72	0.00	-4.00	-2.82	-4.00	-2.28
NA19223.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.64	0.00	0.00	-2.66	-2.47	-2.53	-2.56	-2.52	-2.53	0.00	0.00	0.00	-4.64	0.00	-2.86	-2.69	-2.60
NA19225.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.82	-4.41	0.00	-2.74	-2.62	-2.69	-2.66	-2.85	-2.71	0.00	0.00	0.00	0.00	0.00	-2.91	0.00	-2.71
NA19235.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.53	0.00	-4.93	-2.83	-2.51	-2.59	-2.68	-2.61	-2.58	0.00	0.00	0.00	0.00	0.00	-3.25	-2.88	-2.52
NA19236.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.58	-2.81	-2.77	-2.97	-2.76	-2.70	-2.82	-2.84	-2.78	0.00	-2.88	-4.72	-2.86	-2.78	-3.13	-4.72	-2.58
NA19238.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.76	-2.73	-4.79	-3.08	-2.73	-2.73	-2.71	-2.73	-2.65	0.00	-2.73	-4.79	-2.75	-2.71	-2.84	-4.49	-2.66
NA19239.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.81	-3.98	-3.56	-3.08	-2.56	-2.55	-2.55	-2.59	-2.39	0.00	-4.46	-4.46	-4.46	-4.46	-2.82	-2.80	-2.63
NA19240.mapped.ILLUMINA.bwa.YRI.exome.20130415	-2.84	-2.67	-3.90	-3.10	-2.70	-2.63	-2.73	-2.88	-2.60	0.00	-2.90	-4.38	-2.81	-2.64	-2.70	-4.38	-2.62
NA19247.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.58	0.00	0.00	-2.88	-2.62	-2.64	-2.71	-2.56	-2.62	0.00	0.00	-4.82	0.00	-4.52	-3.25	-2.78	-2.54
NA19248.mapped.ILLUMINA.bwa.YRI.exome.20120522	-2.51	0.00	-2.70	-2.91	-2.64	-2.70	-2.73	-2.99	-2.77	0.00	-2.82	0.00	-2.79	-2.65	0.00	-2.82	-2.45
NA19256.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.87	0.00	-2.92	-3.07	-2.73	-2.75	-2.77	-2.77	-2.80	0.00	-3.07	0.00	-2.90	0.00	-3.21	-2.91	-2.79
NA19257.mapped.ILLUMINA.bwa.YRI.exome.20121211	-2.92	-2.75	-2.80	0.00	-2.80	-2.80	-2.80	-2.95	-2.80	-4.82	-2.88	-2.83	0.00	0.00	0.00	-2.79	-2.84
NA19307.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.36	-2.66	-2.57	-2.80	-2.63	-2.60	-2.53	-2.82	-2.60	0.00	-2.98	0.00	-2.68	-2.62	-3.08	0.00	-2.21
NA19308.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.22	-2.14	-2.24	0.00	-2.69	-2.48	0.00	0.00	-3.79	0.00	-2.56	0.00	-2.14	-2.26	0.00	0.00	-2.22
NA19309.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.14	-2.52	-2.45	-2.80	-2.68	-2.42	-2.52	-2.66	-2.61	0.00	-2.77	0.00	-2.64	-2.57	-2.96	0.00	-2.13
NA19310.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.26	-2.61	0.00	-2.93	-2.50	-2.57	-2.63	-2.76	-2.53	0.00	-2.85	0.00	-2.59	-2.59	-3.09	0.00	-2.17
NA19311.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.62	-2.55	-2.63	-2.89	-2.56	-2.57	-2.56	-2.63	-2.55	0.00	-2.75	0.00	-2.63	-2.58	-2.89	0.00	-2.52

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA19312.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.31	-2.64	-2.51	-2.71	-2.70	-2.67	-2.74	-2.65	-2.59	0.00	-2.82	0.00	-2.78	-2.65	0.00	-2.57	-2.24
NA19313.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.66	-2.64	-2.64	-2.94	-2.61	-2.59	-2.55	-2.52	-2.49	0.00	0.00	0.00	0.00	-4.63	-2.74	0.00	-2.58
NA19314.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.30	-2.52	-2.73	-2.70	-2.50	-2.38	-2.25	-2.39	-2.27	0.00	-2.98	-3.98	-2.68	0.00	0.00	0.00	0.00
NA19315.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.62	0.00	0.00	-2.84	-2.48	-2.48	-2.51	-2.40	-2.46	0.00	0.00	0.00	0.00	0.00	-2.80	-2.67	-2.55
NA19316.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.69	-2.42	-2.62	0.00	-2.56	-2.57	-2.56	-2.57	-2.54	0.00	-2.66	-2.59	0.00	0.00	-2.78	0.00	-2.67
NA19317.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.63	0.00	0.00	-2.76	-2.40	-2.46	-2.40	-2.50	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.68	-2.55
NA19318.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.63	0.00	0.00	-2.92	-2.49	-2.56	-2.55	-2.50	-2.48	0.00	-2.74	-2.72	0.00	0.00	-2.94	-2.69	-2.60
NA19319.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.65	0.00	-2.49	0.00	-2.60	-2.62	-2.60	-2.68	-2.58	0.00	-2.51	0.00	-2.48	-2.55	0.00	-2.75	-2.59
NA19320.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.87	-4.95	-4.95	-2.83	-2.58	-2.60	-2.51	-2.55	-2.58	0.00	0.00	-4.95	-4.65	0.00	-2.89	-4.65	-2.67
NA19321.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.62	0.00	0.00	-2.65	-2.38	-2.45	-2.53	-2.50	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.44	-2.56
NA19323.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.58	-3.93	-4.23	-2.68	-2.51	-2.64	-2.61	-2.65	-2.63	-3.39	-2.95	-3.84	-2.83	-2.67	-3.03	0.00	-2.53
NA19324.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.73	0.00	-4.65	-2.66	-2.40	-2.51	-2.52	-2.42	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.36	-2.60
NA19327.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.54	0.00	0.00	-2.61	-2.31	-2.49	-2.50	-2.40	-2.41	0.00	0.00	0.00	0.00	0.00	-2.92	0.00	-2.68
NA19328.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.59	0.00	-2.64	-2.93	-2.35	-2.51	-2.48	-2.45	-2.40	0.00	-2.82	0.00	-2.70	-4.70	0.00	-2.67	-2.65
NA19331.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.57	-2.37	-2.45	0.00	-4.89	0.00	-2.45	-2.51	-2.37	0.00	0.00	0.00	0.00	0.00	-2.77	0.00	-2.49
NA19332.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.61	-2.80	-2.80	-2.95	-2.54	-2.63	-2.88	-2.81	-2.65	0.00	-2.76	0.00	-2.69	-2.79	-3.15	-4.68	-2.62
NA19334.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.62	-2.72	-2.73	-4.80	-2.82	-2.81	-2.69	-2.72	-2.64	0.00	-3.00	-2.86	0.00	-4.50	-3.06	0.00	-2.60
NA19338.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.60	-2.83	-2.77	-2.99	-2.50	-2.64	-2.70	-2.68	-2.66	0.00	-3.00	-2.79	0.00	-4.37	-2.99	0.00	-2.54
NA19346.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.52	0.00	0.00	-2.71	-2.60	-2.62	-2.64	-2.56	-2.60	0.00	0.00	0.00	0.00	0.00	-2.99	0.00	-2.60
NA19347.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.49	-2.74	-2.65	0.00	-2.79	-2.78	-2.63	-2.60	-2.61	0.00	-3.05	0.00	-2.92	0.00	-3.21	0.00	-2.72
NA19350.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.58	0.00	0.00	-2.72	-2.52	-2.55	-2.62	-2.64	-2.57	0.00	0.00	0.00	0.00	-4.69	0.00	-2.74	-2.72
NA19351.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.29	0.00	-4.09	-2.73	-2.65	-2.27	-2.23	-2.48	-2.26	0.00	0.00	0.00	0.00	0.00	-3.01	-2.65	-2.18
NA19355.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.27	-2.30	-2.25	-4.02	-2.67	-2.51	-2.24	-2.38	-2.28	0.00	-2.97	-2.54	0.00	0.00	0.00	-2.76	-2.41
NA19360.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.38	-2.56	-2.46	0.00	-2.54	-2.27	-2.39	-2.48	-2.31	0.00	-2.63	-2.60	-2.59	0.00	-3.06	-2.74	-2.28
NA19372.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.29	-2.64	-4.03	-2.80	-2.69	-2.39	-2.59	-2.64	-2.39	0.00	-2.78	0.00	-2.69	-2.45	0.00	-2.43	-2.23
NA19374.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.44	0.00	0.00	-2.76	-2.41	-2.34	-2.29	-2.47	-2.51	-3.19	-3.19	0.00	-2.80	0.00	0.00	-2.64	-2.30
NA19375.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.31	0.00	0.00	-2.58	-2.35	-2.29	-2.32	-2.38	-2.23	0.00	0.00	0.00	0.00	0.00	-3.02	0.00	-2.50
NA19376.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.32	-2.52	-2.90	-2.77	-2.50	-2.31	-2.38	-2.42	-2.38	0.00	-3.20	-4.05	-2.56	0.00	0.00	-2.62	-2.59
NA19377.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.39	-2.51	-2.59	-2.83	-2.78	-2.46	-2.31	-2.48	-2.29	0.00	0.00	0.00	0.00	0.00	-2.68	0.00	-2.25
NA19378.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.65	-2.83	-2.71	-2.90	-2.51	-2.61	-2.60	-2.68	-2.56	0.00	-2.84	-2.72	0.00	-4.55	-3.10	-2.74	-2.53
NA19379.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.34	-2.52	-2.68	-2.88	-2.47	-2.34	-2.48	-2.49	-2.43	0.00	-2.99	-2.78	0.00	0.00	-2.99	-2.59	-2.26
NA19380.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.54	0.00	0.00	-2.79	-2.43	-2.48	-2.37	-2.44	-2.39	0.00	0.00	0.00	0.00	-4.64	-2.71	0.00	-2.56
NA19383.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.27	0.00	0.00	-2.57	-2.39	-2.32	-2.29	-2.46	-2.36	0.00	-4.03	0.00	0.00	0.00	-2.78	-4.03	-2.18
NA19384.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.28	-2.54	-2.53	-2.88	-2.62	-2.44	-2.28	-2.36	-2.32	0.00	0.00	-4.11	-4.11	-4.11	0.00	-2.40	-2.18
NA19385.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.62	-2.61	-2.64	-2.91	-2.61	-2.56	-2.66	-2.70	-2.57	0.00	-2.69	0.00	-2.66	-2.59	-2.88	0.00	-2.67
NA19390.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.24	-2.59	-2.63	-2.86	-2.61	-2.54	-2.45	-2.80	-2.50	0.00	-3.01	0.00	-2.65	-2.54	0.00	-2.63	-2.30
NA19391.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.36	0.00	-2.73	-2.73	-2.69	-2.59	-2.44	-2.66	-2.37	0.00	-3.08	0.00	-2.99	0.00	0.00	-2.51	-2.25
NA19393.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.23	0.00	0.00	-2.57	-2.58	-2.40	-2.33	-2.53	-2.40	0.00	-3.00	-4.11	-2.91	-4.11	-2.97	-2.97	-2.36
NA19394.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.44	0.00	0.00	-2.72	-2.49	-2.40	-2.28	-2.59	-2.31	0.00	0.00	0.00	0.00	0.00	-2.88	-2.84	-2.37
NA19395.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.31	0.00	0.00	-2.58	-2.42	-2.34	-2.40	-2.54	-2.23	0.00	0.00	0.00	0.00	0.00	-2.71	0.00	-2.23
NA19397.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.27	-2.59	-2.51	-2.88	-2.39	-2.31	-2.33	-2.51	-2.55	-3.48	-2.83	-2.62	-3.01	-2.53	0.00	0.00	-2.49
NA19399.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.38	-4.22	-2.84	-3.01	-2.48	-2.45	-2.34	-2.50	-2.38	0.00	-2.94	0.00	-2.75	0.00	-2.72	-4.22	-2.39
NA19401.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.29	0.00	-2.34	0.00	-2.41	-2.34	-2.26	-2.50	-2.36	0.00	-2.56	0.00	-2.45	0.00	0.00	-2.94	-2.36
NA19403.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.27	0.00	0.00	-2.71	-2.60	-2.42	-2.37	-2.34	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.27
NA19404.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.18	0.00	0.00	-2.40	-2.63	-2.61	-2.52	-2.53	-2.48	0.00	-3.14	0.00	-2.57	-2.37	0.00	-2.47	-2.17
NA19428.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.29	0.00	-2.78	-2.93	-2.47	-2.32	-2.24	-2.42	-2.44	0.00	-2.93	0.00	-2.62	0.00	-2.90	-2.64	-2.34
NA19429.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.36	-2.69	-2.78	-2.96	-2.53	-2.35	-2.31	-2.45	-2.27	0.00	-3.10	0.00	-2.99	0.00	-3.06	0.00	-2.47
NA19430.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.39	0.00	0.00	-2.64	-2.44	-2.36	-2.37	-2.41	-2.37	0.00	0.00	0.00	0.00	-4.00	-2.62	0.00	-2.26
NA19431.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.29	0.00	0.00	-2.72	-2.50	-2.29	-2.35	-2.51	-2.33	0.00	0.00	0.00	0.00	0.00	-3.22	-2.74	-2.30
NA19434.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.33	0.00	0.00	-2.73	-2.53	-2.41	-2.22	-2.46	-2.31	-3.62	0.00	0.00	0.00	0.00	0.00	-2.40	-2.20
NA19435.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.40	0.00	0.00	-2.50	-2.46	-2.38	-2.34	-2.49	-2.33	0.00	0.00	0.00	0.00	0.00	-2.92	0.00	-2.29
NA19436.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.39	0.00	0.00	-2.68	-2.56	-2.49	-2.41	-2.49	-2.35	0.00	0.00	0.00	0.00	0.00	-3.34	-2.94	-2.32
NA19437.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.24	0.00	0.00	-2.55	-2.41	-2.22	-2.27	-2.48	-2.51	-3.08	-2.91	0.00	-2.77	-2.47	0.00	0.00	-2.46
NA19438.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.33	-3.98	0.00	-2.70	-2.43	-2.44	-2.31	-2.48	-2.34	0.00	0.00	0.00	0.00	0.00	-2.68	-3.98	-2.30
NA19439.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.44	-2.67	-2.63	-3.14	-2.49	-2.41	-2.38	-2.51	-2.44	0.00	-3.00	0.00	-2.92	-4.18	0.00	-2.59	-2.36
NA19440.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.37	0.00	0.00	-2.49	-2.74	-2.41	-2.43	-2.67	-2.34	0.00	0.00	0.00	-3.99	0.00	-3.04	-2.74	-2.36
NA19443.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.35	-2.61	-2.64	-2.86	-2.64	-2.74	-2.43	-2.69	-2.63	-3.14	-3.01	0.00	-2.86	-2.62	0.00	-2.68	-2.32
NA19445.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.30	0.00	-4.08	-2.53	-2.71	-2.40	-2.32	-2.45	-2.28	0.00	0.00	0.00	-4.08	0.00	-3.12	-2.75	-2.30
NA19446.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.33	0.00	0.00	-2.74	-2.54	-2.35	-2.35	-2.58	-2.33	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.37
NA19448.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.48	0.00	0.00	-2.61	-2.39	-2.40	-2.43	-2.48	-2.38	0.00	0.00	0.00	0.00	0.00	-3.13	-2.80	-2.34
NA19449.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.37	-2.60	-2.68	-2.77	-2.77	-2.60	-2.49	-2.61	-2.54	0.00	-2.95	0.00	-2.79	-2.75	-2.92	0.00	-2.21
NA19451.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.29	0.00	0.00	-2.53	-2.53	-2.37	-2.27	-2.56	-2.35	0.00	0.00	0.00	0.00	0.00	-2.80	0.00	-2.28
NA19452.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.29	0.00	0.00	-2.64	-2.47	-2.36	-2.25	-2.44	-2.55	-3.21	-2.88	0.00	-2.80	-2.66	-2.94	0.00	-2.24
NA19454.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.57	-4.22	0.00	-2.78	-2.54	-2.58	-2.65	-2.65	-4.22	-3.09	-2.69	0.00	-2.59	-2.55	0.00	-4.52	-2.52
NA19455.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.34	0.00	-4.20	-2.71	-2.47	-2.47	-2.41	-2.40	-2.39	0.00	-3.16	0.00	-2.74	-4.20	-3.12	-4.20	-2.46
NA19456.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.38	-2.39	-2.37	-3.99	-2.74	-2.55	-2.30	-2.42	-2.26	0.00	-3.09	0.00	-2.59	0.00	-2.85	0.00	-2.42
NA19457.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.55	0.00	0.00	-2.72	-2.47	-2.45	-2.46	-2.53	-2.39	0.00	0.00	0.00	0.00	0.00	-2.76	0.00	-2.55
NA19461.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.39	0.00	-3.64	-2.62	-2.46	-2.28	-2.37	-2.48	-2.33	0.00	0.00	0.00	0.00	-4.12	-2.78	0.00	-2.32
NA19462.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.14	-2.56	-2.74	-2.69	-2.71	-2.86	-2.58	-2.71	-2.46	0.00	-3.34	0.00	-2.80	-2.58	-3.04	0.00	-2.27
NA19463.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.40	-2.64	-2.73	-2.86	-2.70	-2.66	-2.43	-2.59	-2.39	0.00	0.00	0.00	0.00	0.00	-3.20	-2.76	-2.26
NA19466.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.36	-2.60	-2.88	-2.76	-2.70	-2.60	-2.30	-2.51	-2.31	0.00	0.00	0.00	0.00	0.00	0.00	-2.28	-2.21
NA19467.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.38	0.00	-2.60	-2.92	-2.44	-2.35	-2.37	-2.53	-2.35	0.00	-3.62	-2.73	0.00	0.00	-3.14	-2.70	-2.35
NA19468.mapped.ILLUMINA.bwa.LWK.exome.20130422	-2.39	-2.43	-2.61	0.00	-2.40	-2.32	-2.39	-2.48	-2.37	0.00	-2.86	0.00	-2.46	0.00	0.00	-2.84	-2.53
NA19471.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.67	0.00	-2.85	-3.13	-2.55	-2.64	-2.90	-2.57	-2.68	0.00	-3.02	0.00	-2.94	-4.85	-3.03	0.00	-2.61
NA19472.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.62	0.00	-2.78	-2.97	-2.62	-2.63	-2.71	-2.70	-2.63	0.00	-2.98	0.00	-2.92	0.00	-3.26	-2.83	-2.66
NA19473.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.82	-2.83	-2.87	0.00	0.00	0.00	-2.98	-3.16	-3.02	0.00	-3.32	0.00	-2.99	-2.99	-3.45	0.00	-2.80
NA19474.mapped.ILLUMINA.bwa.LWK.exome.20120522	-2.53	-2.77	-2.75	-2.99	-2.66	-2.71	-2.67	-2.56	-2.59	0.00	0.00	0.00	0.00	0.00	-3.16	-2.82	-2.56
NA19475.mapped.ILLUMINA.bwa.LWK.exome.20130415	-2.90	-2.75	-2.79	-3.10	-2.82	-2.78	-2.74	-2.86	-2.80	0.00	-2.83	0.00	-2.79	-2.79	0.00	-2.84	-2.72
NA19625.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.60	-2.79	-2.83	-3.04	-2.57	-2.60	-2.72	-2.73	-2.61	0.00	-3.09	-2.82	0.00	-4.77	-3.37	-3.01	-2.58
NA19648.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.64	-2.77	-2.90	0.00	-2.60	-2.63	-2.74	-2.75	-4.32	-3.46	-2.68	0.00	-2.83	-2.57	0.00	0.00	-2.57
NA19649.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.59	0.00	-4.58	-2.81	-2.49	-2.51	-2.61	-2.61	-2.56	0.00	0.00	0.00	0.00	0.00	-3.21	-2.90	-2.50
NA19651.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.67	-2.88	-2.89	-3.10	-2.59	-2.68	-2.71	-2.71	-2.65	0.00	-3.02	-2.79	0.00	0.00	-3.35	-2.88	-2.56
NA19652.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.56	-2.68	-2.78	-2.85	-2.80	-2.77	-2.58	-2.69	-2.57	0.00	0.00	-4.54	0.00	0.00	0.00	-2.49	-2.48
NA19654.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.59	-2.83	-2.86	-2.97	-2.55	-2.61	-2.66	-2.75	-2.63	0.00	-2.98	-2.83	0.00	0.00	-3.18	0.00	-2.58
NA19655.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.57	0.00	0.00	-2.77	-2.57	-2.53	-2.60	-2.67	-2.53	0.00	0.00	0.00	0.00	0.00	-3.28	-2.77	-2.51
NA19657.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.54	0.00	0.00	-2.74	-2.54	-2.62	-2.60	-2.69	-2.54	0.00	-4.55	0.00	0.00	0.00	0.00	-2.65	-2.55
NA19658.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.54	-2.73	-2.76	-2.94	-2.74	-2.72	-2.69	-2.63	-2.58	0.00	0.00	0.00	0.00	0.00	-3.25	-2.77	-2.53
NA19660.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.61	-2.81	-2.73	-2.95	-2.84	-2.78	-2.57	-2.59	-2.74	-3.47	-2.96	-2.77	0.00	-2.79	-3.41	0.00	-2.48
NA19661.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.60	0.00	0.00	-2.69	-2.58	-2.58	-2.66	-2.69	-2.75	-3.46	-2.97	0.00	-2.82	-2.75	0.00	-2.86	-2.52
NA19663.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.66	-2.83	-2.94	-3.10	-2.50	-2.54	-2.68	-2.77	-2.70	0.00	-2.83	0.00	-2.74	-4.66	0.00	-2.71	-2.58
NA19664.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.62	-2.93	-2.88	-2.95	-2.55	-2.68	-2.67	-2.79	-4.63	-3.30	-2.64	-2.71	-2.99	-2.65	0.00	0.00	-2.57
NA19669.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.62	-2.80	0.00	-2.89	-2.51	-2.63	-2.64	-2.69	-2.87	-3.34	-3.01	-4.54	-2.91	-2.75	0.00	-2.85	-2.50
NA19670.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.63	0.00	-4.57	-2.70	-2.55	-2.61	-2.62	-2.77	-2.83	-3.61	-2.92	0.00	-2.83	-2.80	0.00	-2.91	-2.51
NA19675.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.58	0.00	-4.23	-2.70	-2.49	-2.55	-2.59	-2.59	-2.53	0.00	0.00	0.00	0.00	0.00	-3.25	-2.78	-2.53
NA19676.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.63	-2.91	-2.92	-2.97	-2.60	-2.68	-2.73	-2.81	-2.82	-3.53	-2.74	-2.83	-2.94	-2.88	0.00	-2.92	-2.56
NA19678.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.60	0.00	0.00	-2.63	-2.50	-2.59	-2.58	-2.69	-2.56	0.00	0.00	0.00	0.00	-4.55	-3.32	-2.89	-2.50

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA19679.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.60	-2.84	-2.89	-3.10	-2.53	-2.66	-2.67	-2.81	-2.65	0.00	-3.04	-2.80	0.00	0.00	0.00	-2.68	-2.58
NA19681.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.52	0.00	-4.56	-2.71	-2.52	-2.61	-2.57	-2.68	-2.55	0.00	0.00	0.00	0.00	0.00	-3.44	-2.77	-2.57
NA19682.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.47	0.00	0.00	-2.82	-2.48	-2.61	-2.60	-2.72	-2.53	0.00	-4.60	-4.60	0.00	0.00	-3.14	-2.80	-2.55
NA19684.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.56	-2.79	-2.81	-2.87	-2.73	-2.85	-2.61	-2.68	-2.74	-3.35	-2.95	0.00	-2.90	-2.70	0.00	-2.94	-2.60
NA19685.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.67	-4.24	0.00	-2.64	-2.55	-2.54	-2.59	-2.65	-2.51	0.00	0.00	0.00	0.00	-4.24	-3.18	-2.87	-2.51
NA19700.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.45	-2.80	-2.71	-2.97	-2.74	-2.72	-2.57	-2.63	-2.53	0.00	0.00	0.00	0.00	-4.22	0.00	-2.63	-2.53
NA19701.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.50	-2.73	-2.76	-2.86	-2.80	-2.77	-2.64	-2.60	-2.54	0.00	0.00	-4.26	-4.56	-4.56	0.00	-2.59	-2.56
NA19703.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.51	-2.78	-2.72	-2.81	-2.68	-2.71	-2.58	-2.63	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.45
NA19704.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.53	0.00	0.00	-2.68	-2.51	-2.62	-2.67	-2.61	-2.52	0.00	0.00	0.00	0.00	-4.08	0.00	-2.53	-2.52
NA19707.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.49	0.00	0.00	-2.66	-2.51	-2.60	-2.64	-2.68	-2.60	0.00	0.00	0.00	0.00	0.00	-3.41	-2.83	-2.51
NA19711.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.65	-2.87	-2.80	-3.11	-2.48	-2.68	-2.65	-2.73	-2.62	0.00	-2.92	-2.94	0.00	-4.57	-3.29	-2.98	-2.51
NA19712.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.46	-2.49	-2.66	0.00	0.00	0.00	-2.80	-2.91	-2.65	0.00	-2.92	0.00	-2.78	-2.64	0.00	-2.76	-2.43
NA19713.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.55	0.00	-4.05	-2.68	-2.47	-2.61	-2.59	-2.68	-2.56	0.00	0.00	0.00	0.00	-4.05	-2.97	-4.53	-2.45
NA19716.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.52	-2.76	-2.76	-2.87	-2.74	-2.71	-2.57	-2.64	-2.49	0.00	-4.51	-4.51	-4.51	-4.51	-3.19	-2.83	-2.45
NA19717.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.64	-4.60	-4.60	-2.79	-2.59	-2.65	-2.66	-2.71	-4.00	-3.22	-2.75	-4.30	-2.73	-2.60	0.00	-4.12	-2.52
NA19719.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.49	0.00	-4.53	-2.63	-2.51	-2.57	-2.63	-2.68	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.53
NA19720.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.56	0.00	0.00	-2.68	-2.57	-2.62	-2.62	-2.68	-2.85	-3.60	-3.01	0.00	-2.89	-2.80	-3.20	0.00	-2.55
NA19722.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.55	-2.71	-2.80	-2.93	-2.77	-2.79	-2.62	-2.63	-2.55	0.00	0.00	0.00	0.00	0.00	-3.24	-2.84	-2.52
NA19723.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.66	-2.79	0.00	-2.91	-2.54	-2.55	-2.51	-2.68	-2.88	-3.60	-3.04	0.00	-2.87	-2.80	0.00	-2.93	-2.50
NA19725.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.54	0.00	0.00	-2.68	-2.56	-2.53	-2.59	-2.59	-2.59	0.00	0.00	0.00	0.00	-4.53	-3.27	-2.92	-2.49
NA19726.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.56	0.00	-4.55	-2.63	-2.52	-2.56	-2.62	-2.65	-2.47	0.00	0.00	0.00	0.00	-4.55	0.00	-2.61	-2.46
NA19728.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.72	-2.79	-2.77	-3.14	-2.53	-2.64	-2.57	-2.48	-2.76	-3.66	-2.70	-2.82	-2.84	-2.81	-3.07	0.00	-2.68
NA19729.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.56	0.00	0.00	-2.77	-2.48	-2.48	-2.48	-2.48	-2.43	0.00	0.00	0.00	0.00	0.00	-2.65	0.00	-2.62
NA19731.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.63	0.00	-2.69	-2.95	-2.42	-2.49	-2.55	-2.56	-2.51	0.00	-2.71	0.00	-2.74	0.00	-2.76	0.00	-2.65
NA19732.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.61	0.00	0.00	-2.96	-2.54	-2.49	-2.55	-2.45	-2.67	-3.50	-2.77	0.00	-2.70	-2.62	-2.84	0.00	-2.66
NA19734.mapped.ILLUMINA.bwa.MXL.exome.20130422	-2.30	0.00	0.00	-2.75	-2.49	-2.41	-2.36	-2.56	-2.37	0.00	0.00	0.00	0.00	0.00	-2.89	-2.65	-2.34
NA19735.mapped.ILLUMINA.bwa.MXL.exome.20130422	-2.45	-2.71	-2.76	-3.00	-2.59	-2.50	-2.42	-2.59	-2.59	-3.43	-2.81	-2.73	-2.88	-2.68	0.00	-2.93	-2.36
NA19740.mapped.ILLUMINA.bwa.MXL.exome.20130415	-2.36	0.00	0.00	-2.48	-2.47	-2.28	-2.25	-2.41	-2.33	0.00	0.00	0.00	-4.17	-4.17	0.00	-2.38	-2.28
NA19741.mapped.ILLUMINA.bwa.MXL.exome.20130422	-2.23	-2.64	-2.51	-2.68	-2.81	-2.47	-2.51	-2.59	-2.52	0.00	-2.91	0.00	-2.78	-2.38	0.00	-2.61	-2.15
NA19746.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.64	0.00	0.00	-2.84	-2.47	-2.49	-2.55	-2.49	-2.57	-3.65	-2.73	-2.66	0.00	-2.66	-2.89	0.00	-2.56
NA19747.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.66	0.00	0.00	-2.87	-2.51	-2.56	-2.57	-2.56	-2.64	-3.61	-2.73	0.00	-2.73	-2.63	0.00	-2.68	-2.63
NA19749.mapped.ILLUMINA.bwa.MXL.exome.20130415	-2.85	-4.39	-4.87	-2.91	-2.64	-2.68	-2.65	-2.65	-2.78	-3.64	-2.96	-4.56	-2.84	-2.83	0.00	-2.87	-2.73
NA19750.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.60	-2.55	-2.62	-2.92	-2.61	-2.61	-2.48	-2.46	-2.43	0.00	0.00	0.00	0.00	0.00	-2.74	0.00	-2.50
NA19752.mapped.ILLUMINA.bwa.MXL.exome.20130422	-2.29	-4.12	0.00	-2.72	-2.54	-2.27	-2.31	-2.34	-2.67	-3.17	-3.22	0.00	-2.82	-2.62	0.00	-2.45	-2.28
NA19755.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.77	-2.71	-2.76	-3.08	-2.50	-2.56	-2.58	-2.56	-2.71	-3.83	-2.62	-2.74	-2.82	-2.72	-2.99	0.00	-2.62
NA19756.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.70	-2.74	-2.77	-3.09	-2.51	-2.58	-2.64	-2.58	-2.73	-3.89	-2.58	-2.74	-2.78	-2.71	-3.01	0.00	-2.71
NA19758.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.68	0.00	-4.35	-2.72	-2.59	-2.54	-2.53	-2.49	-2.66	-4.04	-2.75	0.00	-2.79	-2.64	-2.88	0.00	-2.63
NA19759.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.60	0.00	-4.64	-2.90	-2.45	-2.46	-2.47	-2.44	-2.35	0.00	0.00	0.00	0.00	0.00	-2.82	-2.62	-2.60
NA19761.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.61	0.00	0.00	-2.85	-2.51	-2.46	-2.51	-2.53	-2.43	0.00	0.00	0.00	0.00	-4.57	-2.64	0.00	-2.57
NA19762.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.62	-2.73	-2.64	-3.01	-2.66	-2.67	-2.44	-2.57	-2.73	-4.10	-2.89	0.00	-2.72	-2.59	0.00	-2.82	-2.50
NA19764.mapped.ILLUMINA.bwa.MXL.exome.20130415	-2.31	0.00	0.00	-2.66	-2.55	-2.31	-2.40	-2.41	-2.69	-3.40	-2.87	0.00	-2.72	-2.66	-3.10	0.00	-2.24
NA19770.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.65	-2.78	-2.74	-3.09	-2.48	-2.59	-2.57	-2.63	-2.87	-3.89	-2.70	-2.74	-2.79	-2.69	0.00	-2.87	-2.60
NA19771.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.68	0.00	0.00	-2.87	-2.49	-2.53	-2.57	-2.59	0.00	-3.52	-2.69	-2.81	-2.80	-2.55	0.00	0.00	-2.58
NA19773.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.70	0.00	-4.24	-2.71	-2.43	-2.52	-2.46	-2.59	-2.44	0.00	0.00	0.00	0.00	0.00	-2.97	-2.71	-2.51
NA19774.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.60	0.00	0.00	-2.78	-2.45	-2.49	-2.47	-2.44	-2.37	0.00	0.00	0.00	0.00	0.00	-2.87	-2.71	-2.51
NA19776.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.68	-2.70	-2.72	-2.98	-2.62	-2.65	-2.58	-2.59	-2.66	-3.83	-2.79	0.00	-2.68	-2.66	0.00	-2.78	-2.61
NA19777.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.65	0.00	0.00	-2.63	-2.53	-2.53	-2.53	-2.44	-2.39	0.00	0.00	0.00	0.00	-4.59	0.00	-2.53	-2.63
NA19779.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.63	0.00	-4.58	-2.80	-2.51	-2.51	-2.52	-2.57	-2.44	0.00	0.00	0.00	0.00	0.00	-2.75	0.00	-2.59
NA19780.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.61	0.00	0.00	-2.77	-2.44	-2.50	-2.51	-2.52	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.59
NA19782.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.62	0.00	0.00	-2.95	-2.58	-2.49	-2.48	-2.45	-2.42	0.00	0.00	0.00	0.00	0.00	-2.64	0.00	-2.56
NA19783.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.67	-2.66	-2.67	-3.00	-2.64	-2.68	-2.50	-2.57	-2.67	-3.99	-2.82	0.00	-2.71	-2.64	0.00	-2.71	-2.52
NA19785.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.62	-4.41	-4.72	-2.88	-2.44	-2.54	-2.48	-2.42	-2.60	-3.94	-2.72	0.00	-2.65	-2.62	-2.84	0.00	-2.66
NA19786.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.64	0.00	0.00	-2.72	-2.40	-2.50	-2.55	-2.51	-2.46	0.00	0.00	-4.68	0.00	0.00	-2.84	-2.72	-2.63
NA19788.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.59	-2.64	-2.64	-2.91	-2.58	-2.66	-2.48	-2.46	-2.46	0.00	0.00	0.00	0.00	0.00	-2.88	-2.73	-2.60
NA19789.mapped.ILLUMINA.bwa.MXL.exome.20120522	-2.55	0.00	0.00	-2.59	-2.38	-2.56	-2.57	-2.69	-2.53	0.00	0.00	0.00	-4.51	-2.54	0.00	-2.61	-2.52
NA19792.mapped.ILLUMINA.bwa.MXL.exome.20121211	-2.58	-4.47	0.00	-2.74	-2.51	-2.55	-2.50	-2.62	-2.79	-3.17	-2.97	0.00	-2.84	-2.64	0.00	-2.62	-2.51
NA19794.mapped.ILLUMINA.bwa.MXL.exome.20130422	-2.32	-2.48	-2.47	0.00	0.00	0.00	-2.39	-2.52	-2.31	0.00	0.00	0.00	0.00	0.00	-3.18	-2.77	-2.28
NA19795.mapped.ILLUMINA.bwa.MXL.exome.20130415	-2.36	0.00	-4.11	-2.61	-2.61	-2.38	-2.35	-2.52	-2.34	0.00	0.00	0.00	0.00	0.00	-2.97	-3.11	-2.31
NA19818.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.56	-2.72	-2.73	-2.89	-2.69	-2.72	-2.62	-2.65	-2.57	0.00	0.00	0.00	0.00	-4.55	-2.99	0.00	-2.38
NA19819.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.55	-4.59	0.00	-2.72	-2.43	-2.56	-2.60	-2.66	-2.61	0.00	0.00	0.00	0.00	0.00	-3.19	0.00	-2.57
NA19834.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.51	-4.51	0.00	-2.63	-2.75	-4.21	-2.74	-2.80	-2.65	0.00	-2.89	0.00	-2.88	-2.65	0.00	-2.79	-2.49
NA19835.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.72	-2.91	-2.82	-3.01	-2.55	-2.69	-2.67	-2.78	-2.86	-3.59	-2.86	-2.95	-2.88	-2.88	-3.37	0.00	-2.61
NA19900.mapped.ILLUMINA.bwa.ASW.exome.20121211	-2.57	0.00	-4.62	-2.82	-2.49	-2.61	-2.62	-2.68	-2.59	0.00	-3.00	0.00	-2.78	-4.31	-2.99	0.00	-2.52
NA19901.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.57	0.00	-4.55	-2.62	-2.55	-2.62	-2.59	-2.70	-2.59	0.00	0.00	0.00	0.00	-4.55	0.00	-2.59	-2.50
NA19904.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.52	0.00	-4.54	-2.76	-2.61	-2.53	-2.52	-2.65	-2.57	0.00	0.00	0.00	0.00	0.00	-2.97	-4.54	-2.48
NA19908.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.59	-2.77	-2.79	-2.90	-2.68	-2.51	-2.59	-2.64	-2.57	0.00	0.00	-4.55	0.00	0.00	-3.32	-2.87	-2.48
NA19909.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.50	-2.73	-2.68	-2.89	-2.71	-2.68	-2.76	-2.77	-2.73	0.00	-2.85	-4.50	-2.77	-2.77	0.00	-2.72	-2.46
NA19913.mapped.ILLUMINA.bwa.ASW.exome.20130415	-2.84	-2.69	-2.71	-3.04	-2.67	-2.77	-2.49	-2.57	-2.54	0.00	0.00	0.00	-4.86	0.00	-2.92	0.00	-2.64
NA19914.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.58	-2.81	-2.81	-2.84	-2.60	-2.60	-2.58	-2.65	-2.52	0.00	-2.95	-4.57	-2.86	0.00	-3.29	-4.57	-2.67
NA19916.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.61	0.00	0.00	-2.76	-2.58	-2.60	-2.64	-2.65	-2.53	0.00	-4.56	-4.56	0.00	-4.26	-3.10	-2.81	-2.54
NA19917.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.63	-2.86	-2.84	-2.89	-2.53	-2.69	-2.63	-2.71	-2.58	0.00	-2.94	-2.83	0.00	0.00	-3.35	-2.90	-2.53
NA19920.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.51	-2.76	-2.70	-2.93	-2.64	-2.69	-2.73	-2.98	-2.76	0.00	-2.78	0.00	-2.77	-2.70	0.00	-2.75	-2.49
NA19921.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.56	-2.66	-2.64	0.00	-2.76	-2.88	-2.66	-2.69	-2.89	-3.56	-2.80	-2.84	-2.86	-2.76	0.00	-2.87	-2.58
NA19922.mapped.ILLUMINA.bwa.ASW.exome.20130415	-2.38	-2.97	-2.73	-2.97	-2.58	-2.45	-2.53	-2.67	-2.30	0.00	-3.09	-2.71	0.00	0.00	-2.94	-4.09	-2.26
NA19923.mapped.ILLUMINA.bwa.ASW.exome.20130415	-2.30	0.00	0.00	-2.53	-2.69	-2.56	-2.34	-2.69	-2.50	-3.05	-3.23	0.00	-2.61	-2.75	0.00	-2.83	-2.35
NA19982.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.70	-2.70	-3.01	0.00	-2.61	-2.66	-2.72	-2.90	-4.69	-3.41	-2.65	-2.72	-2.76	-2.67	0.00	-4.69	-2.59
NA19984.mapped.ILLUMINA.bwa.ASW.exome.20130422	-2.29	0.00	0.00	-2.65	-2.53	-2.34	-2.28	-2.42	-2.61	-3.31	-2.94	0.00	-2.83	-2.52	-2.97	-4.08	-2.24
NA19985.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.58	-4.23	0.00	-2.83	-2.37	-2.55	-2.52	-2.56	-2.50	0.00	0.00	0.00	0.00	0.00	-2.73	0.00	-2.56
NA20126.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.79	-2.64	-2.66	0.00	-2.64	-2.62	-2.68	-2.62	-2.77	-3.79	-2.57	-2.62	-2.78	-2.75	0.00	-2.82	-2.77
NA20127.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.67	0.00	-4.62	-2.75	-2.50	-2.43	-2.56	-2.56	-2.73	-3.71	-2.82	0.00	-2.73	-2.64	0.00	-2.72	-2.70
NA20274.mapped.ILLUMINA.bwa.ASW.exome.20130415	-3.20	-2.91	-2.88	-3.25	-2.68	-2.80	-2.76	-2.79	-2.71	0.00	-3.03	-3.00	-5.12	0.00	-3.31	-3.05	-2.89
NA20276.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.73	-2.67	-2.69	-3.01	-2.46	-2.54	-2.57	-2.56	-2.42	0.00	-2.85	-2.72	0.00	0.00	-2.79	0.00	-2.63
NA20278.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.67	0.00	0.00	-2.95	-2.46	-2.58	-2.57	-2.52	-2.67	-3.60	-2.78	0.00	-2.78	-2.70	-2.93	0.00	-2.63
NA20281.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.67	0.00	0.00	-2.82	-2.54	-2.51	-2.55	-2.51	-2.46	0.00	0.00	0.00	0.00	0.00	-2.98	-2.77	-2.59
NA20282.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.59	-2.56	-2.62	-2.95	-2.65	-2.61	-2.64	-2.69	-2.59	0.00	-2.76	0.00	-2.63	-2.59	-2.91	0.00	-2.57
NA20287.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.70	-2.72	-2.70	-3.08	-2.45	-2.57	-2.59	-2.48	-2.54	0.00	-2.80	-2.76	0.00	0.00	-2.98	-2.83	-2.70
NA20289.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.59	0.00	-4.56	-2.79	-2.45	-2.48	-2.37	-2.41	-2.36	0.00	-4.56	0.00	0.00	0.00	0.00	-2.68	-2.67
NA20291.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.71	-2.74	-2.71	-3.10	-2.46	-2.53	-2.56	-2.66	-2.42	0.00	-2.87	0.00	-2.78	0.00	-2.94	-2.87	-2.65
NA20294.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.57	0.00	0.00	-2.84	-2.62	-2.69	-2.71	-2.67	-2.60	0.00	-2.66	0.00	-2.66	-2.58	-2.91	0.00	-2.59
NA20296.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.70	-2.72	-2.74	-3.11	-2.49	-2.61	-2.61	-2.59	-2.55	0.00	-2.88	-2.79	0.00	0.00	0.00	-2.51	-2.70
NA20298.mapped.ILLUMINA.bwa.ASW.exome.20130415	-2.20	0.00	0.00	-2.52	-2.45	-2.30	-2.20	-2.42	-2.39	0.00	0.00	0.00	0.00	0.00	-2.74	0.00	-2.22
NA20299.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.65	0.00	0.00	-2.86	-2.48	-2.55	-2.54	-2.56	-2.70	-3.99	-2.79	0.00	-2.71	-2.67	0.00	-2.74	-2.59
NA20314.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.68	0.00	0.00	-2.90	-2.60	-2.54	-2.61	-2.58	-2.71	-3.69	-2.74	-4.69	-2.73	-2.64	-2.92	0.00	-2.65
NA20317.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.64	-2.69	-2.71	-3.08	-2.68	-2.70	-2.58	-2.59	-2.53	0.00	-2.74	-2.69	0.00	0.00	-2.81	-4.65	-2.63
NA20318.mapped.ILLUMINA.bwa.ASW.exome.20130415	-3.12	-5.11	-4.51	-3.09	-2.66	-2.80	-2.71	-2.82	-2.66	0.00	-3.12	-3.00	0.00	-5.11	-3.36	-3.01	-2.86
NA20320.mapped.ILLUMINA.bwa.ASW.exome.20130415	-3.09	-4.83	-4.65	-2.95	-2.73	-2.74	-2.63	-2.78	-2.69	0.00	0.00	0.00	0.00	0.00	-3.30	-2.97	-2.82

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA20321.mapped.ILLUMINA.bwa.ASW.exome.20130415	-3.07	-2.76	-2.85	-3.22	-2.92	-2.89	-2.63	-2.64	-2.62	0.00	0.00	-5.09	0.00	0.00	-3.31	-2.98	-2.80
NA20322.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.64	-2.63	-2.63	-3.01	-2.69	-2.61	-2.52	-2.42	-2.42	0.00	0.00	0.00	0.00	0.00	-2.80	-2.65	-2.62
NA20332.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.73	-2.77	-2.78	-3.07	-2.56	-2.57	-2.61	-2.64	-2.76	-4.11	-2.68	-2.64	-4.81	-2.78	-3.01	0.00	-2.68
NA20334.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.59	-4.63	-4.63	-2.88	-2.36	-2.48	-2.52	-2.48	-2.48	0.00	0.00	0.00	0.00	0.00	-2.93	-2.76	-2.58
NA20336.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.67	-2.73	-2.74	-3.01	-2.47	-2.57	-2.57	-2.59	-2.54	0.00	-2.82	-2.72	0.00	0.00	-2.79	0.00	-2.67
NA20339.mapped.ILLUMINA.bwa.ASW.exome.20130415	-2.24	-2.60	0.00	-2.78	-2.63	-2.53	-2.62	-2.86	-2.53	0.00	-2.92	0.00	-2.73	-2.54	-3.03	0.00	-2.24
NA20340.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.81	-2.70	-2.67	-3.04	-2.48	-2.62	-2.61	-2.55	-2.44	0.00	-2.73	0.00	-2.76	0.00	-2.96	-2.75	-2.72
NA20341.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.69	0.00	-4.73	-2.89	-2.49	-2.55	-2.60	-2.59	-2.77	-3.78	-2.62	-2.77	-2.74	-2.70	0.00	-2.73	-2.71
NA20342.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.59	-2.65	-2.61	-2.91	-2.67	-2.64	-2.68	-2.72	-2.55	0.00	-2.71	0.00	-2.70	-2.66	-2.78	0.00	-2.53
NA20344.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.64	0.00	0.00	-2.64	-2.46	-2.56	-2.49	-2.44	-2.46	0.00	0.00	0.00	0.00	0.00	-2.87	-2.62	-2.67
NA20346.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.71	-2.72	-2.71	-3.07	-2.47	-2.64	-2.64	-2.51	-2.56	0.00	-2.87	-2.73	0.00	0.00	-2.96	-2.79	-2.75
NA20348.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.57	0.00	0.00	-2.75	-2.38	-2.45	-2.55	-2.50	-2.43	0.00	0.00	0.00	-4.65	0.00	-2.84	-2.73	-2.51
NA20351.mapped.ILLUMINA.bwa.ASW.exome.20130415	-2.44	0.00	0.00	-2.71	-2.47	-2.42	-2.34	-2.55	-2.45	0.00	-2.84	0.00	-2.80	0.00	-2.75	-3.90	-2.32
NA20355.mapped.ILLUMINA.bwa.ASW.exome.20130415	-3.18	-2.87	-2.93	-3.29	-2.72	-2.78	-2.71	-2.84	-2.78	0.00	-3.04	-2.98	-5.14	0.00	-3.26	-4.66	-2.91
NA20356.mapped.ILLUMINA.bwa.ASW.exome.20120522	-2.75	-2.67	-2.62	0.00	-2.62	-2.61	-2.61	-2.59	-2.56	0.00	-2.62	-2.62	0.00	0.00	-2.75	0.00	-2.70
NA20357.mapped.ILLUMINA.bwa.ASW.exome.20130422	-2.35	0.00	-3.77	-2.60	-2.37	-2.33	-2.37	-2.46	-2.31	0.00	-4.07	0.00	-4.07	0.00	-2.93	-2.73	-2.27
NA20359.mapped.ILLUMINA.bwa.ASW.exome.20130422	-2.36	0.00	0.00	-2.66	-2.55	-2.35	-2.29	-2.54	-2.45	-4.04	0.00	0.00	0.00	0.00	-3.09	-2.76	-2.28
NA20362.mapped.ILLUMINA.bwa.ASW.exome.20130415	-2.78	-2.66	-2.78	-3.22	-2.66	-2.68	-2.41	-2.52	-2.44	0.00	0.00	-4.45	0.00	-4.45	-2.73	-3.97	-2.51
NA20412.mapped.ILLUMINA.bwa.ASW.exome.20130415	-2.28	-2.65	-2.61	-2.97	-2.90	-2.48	-2.26	-2.48	-2.57	-3.35	-3.00	0.00	-2.58	-2.70	0.00	-2.60	-2.18
NA20502.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.27	-4.21	0.00	-2.65	-2.55	-2.42	-2.33	-2.42	-2.63	-3.17	-2.95	-2.47	-4.21	-2.53	0.00	-2.46	-2.26
NA20503.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.43	-2.67	-2.77	-2.88	-2.55	-2.48	-2.38	-2.62	-4.20	-3.02	-2.58	-2.74	-2.60	-2.46	0.00	0.00	-2.34
NA20504.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.31	0.00	0.00	-2.69	-2.39	-2.32	-2.31	-2.45	-2.26	0.00	0.00	0.00	0.00	0.00	-3.05	-2.69	-2.20
NA20505.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.28	-2.71	-2.68	-3.08	-2.39	-2.31	-2.28	-2.52	-2.85	-3.30	-2.71	-2.36	0.00	-2.68	0.00	-2.68	-2.31
NA20506.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.34	-2.50	-2.56	-2.96	-2.73	-2.43	-2.47	-2.53	-2.82	0.00	-2.76	0.00	-2.62	-2.42	0.00	-2.58	-2.22
NA20507.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.26	-3.91	0.00	-2.66	-2.53	-2.33	-2.29	-2.44	-2.27	0.00	0.00	-4.22	0.00	0.00	-2.89	-2.58	-2.30
NA20508.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.39	-2.70	-2.68	-2.84	-2.56	-2.38	-2.37	-2.56	-2.58	-3.25	-2.86	-2.53	0.00	-2.60	0.00	-2.59	-2.34
NA20509.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.56	-2.68	-2.75	-2.89	-2.50	-2.34	-2.34	-2.47	-2.71	-3.17	-2.58	-2.51	-2.87	-2.67	-3.05	0.00	-2.47
NA20510.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.45	-2.60	-2.59	-4.29	-2.36	-2.30	-2.36	-2.38	-2.60	-3.24	-2.58	-2.59	-2.62	-2.61	0.00	-2.65	-2.40
NA20511.mapped.ILLUMINA.bwa.TSI.exome.20130415	-3.06	-4.81	-4.81	-3.00	-2.70	-2.75	-2.66	-2.71	-2.64	0.00	0.00	0.00	0.00	0.00	0.00	-2.72	-2.84
NA20512.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.32	-2.41	-2.48	0.00	-2.51	-2.32	-2.37	-2.44	-2.45	0.00	-2.70	-2.39	0.00	0.00	0.00	-2.33	-2.32
NA20513.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.35	-2.54	-2.74	-2.78	-2.61	-2.42	-2.31	-2.60	-4.06	-3.06	-2.49	-2.64	-2.45	-2.33	0.00	0.00	-2.29
NA20514.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.39	-2.59	-2.73	-2.99	-2.43	-2.40	-2.43	-2.44	-2.64	-3.55	-2.62	-2.58	-2.78	-2.56	0.00	-2.75	-2.31
NA20515.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.29	0.00	0.00	-2.68	-2.46	-2.34	-2.45	-2.66	-2.66	-3.35	-3.04	0.00	-2.80	-2.54	-2.92	0.00	-2.29
NA20516.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.29	-2.64	-2.57	-2.81	-2.65	-2.51	-2.26	-2.47	-2.28	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.27
NA20517.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.36	0.00	0.00	-2.58	-2.46	-2.33	-2.34	-2.51	-2.62	-3.27	-3.06	0.00	-2.67	-2.74	0.00	-2.64	-2.38
NA20518.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.34	-2.79	-2.68	-2.81	-2.66	-2.56	-2.45	-2.46	-2.58	-3.21	-2.79	0.00	-2.73	-2.65	0.00	-2.77	-2.30
NA20519.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.31	-2.61	-2.54	-2.99	-2.67	-2.67	-2.24	-2.44	-2.33	0.00	0.00	0.00	0.00	0.00	0.00	-2.23	-2.24
NA20520.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.35	-3.88	0.00	-2.59	-2.37	-2.37	-2.27	-2.52	-2.29	0.00	-4.18	0.00	0.00	-4.18	-2.76	-4.18	-2.35
NA20521.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.36	0.00	0.00	-2.54	-2.50	-2.28	-2.28	-2.51	-2.31	0.00	0.00	0.00	-4.02	0.00	0.00	-2.40	-2.24
NA20522.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.48	0.00	-4.12	-2.69	-2.59	-2.37	-2.38	-2.46	-2.62	-3.42	-3.08	0.00	-2.73	-2.56	-2.98	0.00	-2.22
NA20524.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.43	-2.70	-2.67	-2.86	-2.53	-2.44	-2.36	-2.50	-2.72	-3.16	-2.81	-2.56	0.00	-2.74	0.00	-2.86	-2.32
NA20525.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.53	-3.86	0.00	-2.82	-2.38	-2.30	-2.37	-2.39	-2.68	-3.12	-2.52	-2.80	-2.82	-2.68	0.00	-2.67	-2.38
NA20526.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.22	0.00	-4.11	-2.59	-2.33	-2.21	-2.23	-2.38	-2.33	0.00	-3.81	-3.81	0.00	-3.81	-2.79	-2.47	-2.25
NA20527.mapped.ILLUMINA.bwa.TSI.exome.20130422	-2.38	-2.55	-2.57	-2.91	-2.65	-2.50	-2.46	-2.66	-3.71	-3.34	-2.55	-2.51	-2.56	-2.31	0.00	0.00	-2.25
NA20528.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.29	0.00	0.00	-2.73	-2.43	-2.26	-2.28	-2.45	-2.32	0.00	0.00	0.00	0.00	-4.20	0.00	-2.29	-2.28
NA20529.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.47	-4.32	0.00	-2.81	-2.36	-2.33	-2.34	-2.30	-2.34	-3.47	-3.04	-2.56	0.00	0.00	-2.98	-2.65	-2.42
NA20530.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.39	-2.60	-2.60	-2.92	-2.82	-2.60	-2.34	-2.58	-2.42	0.00	-4.00	-4.00	0.00	0.00	-2.92	-2.56	-2.23
NA20531.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.24	-2.65	-2.72	-2.84	-2.65	-2.55	-2.31	-2.44	-2.68	-3.40	-2.78	0.00	-2.68	-2.56	-2.95	-3.88	-2.29
NA20532.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.26	-2.68	-2.66	-2.75	-2.73	-2.50	-2.28	-2.57	-2.35	0.00	0.00	0.00	0.00	0.00	0.00	-2.26	-2.19
NA20533.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.33	0.00	0.00	-2.70	-2.52	-2.21	-2.30	-2.41	-2.27	0.00	0.00	0.00	-4.08	0.00	-2.82	-2.57	-2.19
NA20534.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.37	-2.51	-2.69	-3.04	-2.30	-2.34	-2.33	-2.49	-2.56	-3.36	-2.53	-2.57	-2.67	-2.54	-2.96	-4.27	-2.41
NA20535.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.33	-4.27	0.00	-2.68	-2.50	-2.38	-2.30	-2.49	-2.61	-3.16	-2.91	-4.27	-2.74	-2.60	0.00	-2.81	-2.31
NA20536.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.29	0.00	-3.68	-2.53	-2.42	-2.29	-2.39	-2.37	-2.37	0.00	0.00	0.00	0.00	0.00	-3.26	-2.80	-2.33
NA20538.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.36	-2.57	-2.63	-2.93	-2.51	-2.42	-2.39	-2.45	-2.68	-3.21	-2.60	-2.42	-4.29	-2.60	-3.04	0.00	-2.33
NA20539.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.27	-3.71	0.00	-2.58	-2.45	-2.27	-2.37	-2.27	-2.61	-3.40	-2.73	0.00	-2.71	-2.56	0.00	-2.68	-2.19
NA20540.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.26	-2.77	-2.69	-2.87	-2.68	-2.60	-2.39	-2.35	-2.35	0.00	0.00	0.00	0.00	0.00	0.00	-2.34	-2.24
NA20541.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.24	-2.60	0.00	-2.93	-2.61	-2.57	-2.25	-2.30	-2.33	0.00	0.00	0.00	-4.13	0.00	-2.93	-2.70	-2.20
NA20542.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.81	-2.71	-2.70	0.00	-2.88	-2.87	-2.78	-2.85	0.00	-3.15	-2.66	-2.75	-2.93	-2.71	0.00	-4.71	-2.78
NA20543.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.82	-2.88	-2.90	-3.13	-2.63	-2.77	-2.76	-2.87	-2.75	0.00	-3.06	-2.93	-4.82	0.00	0.00	-2.72	-2.85
NA20544.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.76	0.00	-2.83	-3.05	-2.81	-2.80	-2.67	-2.73	-2.69	0.00	-4.70	-4.70	0.00	-4.70	-3.02	-2.79	-2.68
NA20581.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.87	-2.88	-2.94	-3.23	-2.75	-2.79	-2.83	-2.93	0.00	-3.30	-2.75	-2.88	-3.07	-2.79	0.00	-4.55	-2.84
NA20582.mapped.ILLUMINA.bwa.TSI.exome.20120522	-2.77	0.00	0.00	-2.76	-2.65	-2.68	-2.70	-2.84	-2.72	0.00	0.00	0.00	0.00	0.00	-3.15	-2.87	-2.79
NA20585.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.79	0.00	-4.74	-2.74	-2.64	-2.83	-2.68	-2.75	-2.63	0.00	0.00	-4.74	0.00	0.00	0.00	-2.63	-2.74
NA20586.mapped.ILLUMINA.bwa.TSI.exome.20120522	-2.77	-2.75	-2.82	-3.03	-2.80	-2.83	-2.70	-2.70	-2.74	-4.66	0.00	0.00	0.00	0.00	0.00	-2.47	-2.73
NA20587.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.53	0.00	0.00	-2.72	-2.54	-2.63	-2.60	-2.61	-2.69	-3.32	-2.90	0.00	-2.77	-2.63	0.00	-2.68	-2.50
NA20588.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.90	-2.71	-2.76	-4.74	-2.94	-2.86	-2.78	-2.86	-2.96	-3.24	-2.83	-2.79	0.00	-2.88	0.00	-2.85	-2.77
NA20589.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.73	0.00	0.00	-2.90	-2.63	-2.65	-2.67	-2.79	-2.69	0.00	0.00	0.00	0.00	0.00	-3.06	-2.81	-2.72
NA20752.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.78	0.00	0.00	-2.79	-2.60	-2.67	-2.69	-2.74	-2.66	0.00	0.00	0.00	-4.73	0.00	0.00	-2.59	-2.71
NA20753.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.72	0.00	-4.77	-2.80	-2.58	-2.68	-2.74	-2.77	-2.76	0.00	0.00	0.00	0.00	0.00	-3.11	-2.83	-2.78
NA20754.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.78	-2.77	0.00	-2.97	-2.58	-2.71	-2.69	-2.75	-2.70	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.73
NA20755.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.88	-2.66	-2.73	0.00	0.00	0.00	-2.72	-2.76	-4.69	-3.15	-2.73	0.00	-2.63	-2.68	0.00	0.00	-2.79
NA20756.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.93	-2.88	-2.98	-3.21	-2.70	-2.81	-2.84	-2.93	-3.02	-3.30	-2.94	-2.85	-4.87	-2.96	0.00	-2.99	-2.87
NA20757.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.84	0.00	0.00	-2.90	-2.61	-2.71	-2.71	-2.72	-2.61	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.77
NA20758.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.81	-2.73	-2.86	-3.00	-2.86	-2.86	-2.85	-2.96	-2.90	0.00	-2.98	0.00	-2.86	-2.80	0.00	-2.88	-2.72
NA20759.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.84	0.00	0.00	-2.75	-2.68	-2.74	-2.81	-2.90	-3.21	-3.21	-3.18	0.00	-2.88	-2.89	0.00	-2.95	-2.74
NA20760.mapped.ILLUMINA.bwa.TSI.exome.20120522	-2.85	-2.83	-2.91	-3.18	-2.66	-2.77	-2.78	-2.85	-2.75	0.00	-3.10	-2.93	0.00	0.00	-3.18	-3.05	-2.69
NA20761.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.80	0.00	-4.62	-2.87	-2.62	-2.68	-2.68	-2.72	-2.80	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.73
NA20762.mapped.ILLUMINA.bwa.TSI.exome.20130415	-3.11	-2.93	-2.86	-3.32	-2.66	-2.74	-2.68	-2.80	-2.73	0.00	-3.04	-2.96	0.00	-4.85	-3.28	-3.13	-2.87
NA20763.mapped.ILLUMINA.bwa.TSI.exome.20130415	-3.23	-2.66	-2.80	0.00	-2.84	-2.87	-2.79	-2.86	-2.99	-3.45	-2.75	-2.75	-5.24	-3.03	0.00	-3.08	-2.94
NA20764.mapped.ILLUMINA.bwa.TSI.exome.20130415	-3.13	-3.67	-4.05	-2.95	-2.67	-2.69	-2.66	-2.75	-2.93	-3.37	-2.91	-3.73	-2.94	-2.89	-3.33	-4.53	-2.84
NA20765.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.86	-2.84	0.00	-3.11	-2.64	-2.80	-2.79	-2.85	-3.12	-3.35	-3.07	0.00	-2.93	-2.91	0.00	-2.98	-2.78
NA20766.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.70	-2.74	-2.69	0.00	-2.59	-2.64	-2.74	-2.74	-2.92	-3.65	-2.69	-2.69	-3.00	-2.85	0.00	-2.99	-2.58
NA20767.mapped.ILLUMINA.bwa.TSI.exome.20130415	-3.05	-2.65	-2.67	-5.13	-2.91	-2.88	-2.66	-2.68	-2.63	0.00	-2.97	-2.88	-4.83	0.00	0.00	-2.64	-2.81
NA20768.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.48	-4.53	0.00	-2.72	-2.53	-2.50	-2.60	-2.61	-2.51	0.00	-4.53	0.00	0.00	0.00	0.00	-2.60	-2.53
NA20769.mapped.ILLUMINA.bwa.TSI.exome.20120522	-2.58	0.00	-4.60	-2.70	-2.60	-2.55	-2.55	-2.66	-2.58	-4.60	0.00	0.00	0.00	0.00	-3.32	-2.94	-2.54
NA20770.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.66	-2.86	-2.85	-2.95	-2.58	-2.62	-2.68	-2.71	-2.65	-4.63	-2.96	-2.84	-4.33	0.00	0.00	-2.63	-2.58
NA20771.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.50	0.00	-4.26	-2.78	-2.52	-2.60	-2.61	-2.61	-2.57	0.00	-4.56	0.00	-4.56	0.00	-3.24	-2.89	-2.52
NA20772.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.50	-2.70	-2.67	-2.90	-2.69	-2.78	-2.55	-2.59	-2.62	0.00	-4.56	0.00	0.00	0.00	0.00	-2.52	-2.45
NA20773.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.66	-2.73	-2.66	-4.70	-2.66	-2.71	-2.76	-2.67	-2.67	0.00	-2.80	-2.68	0.00	-4.39	0.00	-2.61	-2.62
NA20774.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.70	-2.84	-2.91	-2.98	-2.56	-2.71	-2.63	-2.80	-2.82	-3.54	-2.83	-2.85	-2.93	-2.80	0.00	-2.94	-2.55
NA20775.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.51	-2.84	-2.79	-2.95	-2.80	-2.81	-2.65	-2.77	-4.58	-3.26	-2.70	0.00	-2.67	-2.54	0.00	0.00	-2.51
NA20778.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.59	-2.80	-2.82	-2.97	-2.51	-2.59	-2.61	-2.76	-2.65	0.00	-2.97	-2.83	0.00	0.00	-3.23	-2.88	-2.57
NA20783.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.62	-2.84	-2.89	-2.95	-2.58	-2.61	-2.67	-2.72	-2.53	0.00	-2.98	-2.84	0.00	0.00	-3.46	-2.82	-2.56
NA20785.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.68	0.00	0.00	-2.70	-2.60	-2.65	-2.66	-2.76	-2.88	-3.55	-3.01	0.00	-2.90	-2.84	0.00	-2.88	-2.55
NA20786.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.65	-2.70	-2.71	0.00	-2.64	-2.66	-2.74	-2.75	-2.97	-3.54	-2.75	-2.59	0.00	-2.88	0.00	-3.06	-2.65
NA20787.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.56	0.00	0.00	-2.71	-2.51	-2.53	-2.62	-2.68	-2.68	0.00	0.00	0.00	0.00	-4.57	0.00	-2.55	-2.49

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA20790.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.46	0.00	0.00	-2.59	-2.52	-2.53	-2.62	-2.75	-2.57	0.00	0.00	-4.52	0.00	0.00	0.00	-2.63	-2.46
NA20792.mapped.ILLUMINA.bwa.TSI.exome.20120522	-2.50	-4.55	-4.55	-2.75	-2.55	-2.59	-2.60	-2.64	-2.57	0.00	0.00	0.00	0.00	-4.25	-3.14	-2.85	-2.48
NA20795.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.50	-2.81	-2.79	-2.94	-2.78	-2.82	-2.60	-2.59	-2.60	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.50
NA20796.mapped.ILLUMINA.bwa.TSI.exome.20120522	-2.48	-4.77	-4.77	-2.90	-2.62	-2.60	-2.64	-2.72	-2.68	-3.47	-3.10	0.00	-2.81	-2.75	0.00	-2.86	-2.51
NA20797.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.45	-2.54	-2.50	0.00	0.00	0.00	-2.53	-2.52	-2.46	0.00	0.00	0.00	-4.43	0.00	0.00	-2.50	-2.39
NA20798.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.62	0.00	-4.67	-2.87	-2.63	-2.58	-2.66	-2.69	-2.50	0.00	0.00	0.00	-4.67	-4.67	0.00	-2.59	-2.46
NA20799.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.58	-2.82	-2.72	-2.99	-2.72	-2.76	-2.66	-2.65	-2.57	0.00	0.00	0.00	0.00	0.00	-3.18	-2.83	-2.56
NA20800.mapped.ILLUMINA.bwa.TSI.exome.20120522	-2.58	0.00	0.00	-2.97	-2.62	-2.58	-2.64	-2.56	-2.52	0.00	0.00	0.00	0.00	-4.64	0.00	-2.55	-2.54
NA20801.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.68	0.00	0.00	-2.85	-2.65	-2.67	-2.72	-2.65	-2.78	-3.44	-3.02	0.00	-2.90	-2.82	0.00	-2.96	-2.64
NA20802.mapped.ILLUMINA.bwa.TSI.exome.20120522	-2.62	0.00	-4.72	-2.80	-2.59	-2.67	-2.72	-2.63	-2.65	0.00	0.00	0.00	0.00	0.00	-3.28	-2.91	-2.61
NA20803.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.63	0.00	-4.76	-2.80	-2.62	-2.61	-2.68	-2.76	-2.75	-3.42	-3.03	0.00	-2.88	-2.79	0.00	-2.84	-2.52
NA20804.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.69	-2.91	-2.95	-3.13	-2.61	-2.63	-2.76	-2.79	-2.87	-3.72	-2.92	-2.68	0.00	-2.85	0.00	-2.98	-2.67
NA20805.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.56	0.00	0.00	-2.80	-2.60	-2.63	-2.64	-2.69	-2.60	0.00	0.00	0.00	0.00	-4.72	0.00	-2.66	-2.48
NA20806.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.63	0.00	0.00	-2.73	-2.64	-2.66	-2.73	-2.62	-2.84	-3.48	-3.06	0.00	-2.90	-2.76	0.00	-2.91	-2.60
NA20807.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.60	-2.69	-2.66	-2.96	-2.66	-2.63	-2.53	-2.53	-2.50	0.00	0.00	0.00	0.00	0.00	-2.78	-4.58	-2.59
NA20808.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.63	0.00	0.00	-2.95	-2.48	-2.54	-2.55	-2.54	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.57
NA20809.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.63	0.00	0.00	-2.93	-2.51	-2.53	-2.51	-2.42	-2.36	0.00	0.00	0.00	0.00	-4.62	0.00	-2.39	-2.53
NA20810.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.76	-2.79	-2.79	-3.07	-2.52	-2.62	-2.68	-2.64	-2.75	-3.87	-2.59	-2.78	-2.86	-2.72	-3.04	0.00	-2.71
NA20811.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.82	-2.77	-2.74	-3.16	-2.53	-2.62	-2.60	-2.64	-2.71	-3.73	-2.69	-2.66	0.00	-2.74	0.00	-2.80	-2.77
NA20812.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.69	-2.69	-2.67	-3.01	-2.48	-2.52	-2.57	-2.63	-2.54	0.00	-2.76	-2.75	0.00	0.00	0.00	-2.56	-2.62
NA20813.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.72	-2.76	-2.77	-3.08	-2.54	-2.56	-2.61	-2.72	-2.81	-4.13	-2.68	-2.83	-2.81	-2.75	0.00	-2.86	-2.68
NA20814.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.73	-2.73	-2.77	-3.09	-2.50	-2.62	-2.61	-2.55	-2.76	-3.98	-2.66	-2.64	0.00	-2.75	0.00	-2.74	-2.70
NA20815.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.62	-2.69	-2.72	-3.11	-2.65	-2.70	-2.55	-2.42	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.60
NA20818.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.73	-4.91	-4.91	-2.84	-2.45	-2.52	-2.58	-2.50	-2.53	-3.80	-2.88	-2.79	0.00	-4.91	-3.02	-2.81	-2.78
NA20819.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.72	-2.70	-2.73	-3.06	-2.44	-2.55	-2.57	-2.59	0.00	-3.75	-2.50	-2.65	-2.72	-2.49	0.00	0.00	-2.63
NA20821.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.78	0.00	-4.44	-2.86	-2.57	-2.55	-2.52	-2.57	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.71
NA20822.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.91	0.00	-4.86	-2.97	-2.66	-2.68	-2.67	-2.56	-2.73	-3.48	-2.84	-4.86	-2.76	-2.73	0.00	-2.80	-2.76
NA20826.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.67	-2.66	-2.64	-2.99	-2.66	-2.66	-2.50	-2.58	-2.45	0.00	0.00	-4.79	0.00	-4.79	0.00	-2.52	-2.64
NA20827.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.71	-2.42	-2.48	0.00	-3.31	-3.37	-2.52	-2.68	-2.47	0.00	-2.68	0.00	-2.85	-2.57	0.00	-2.74	-2.40
NA20828.mapped.ILLUMINA.bwa.TSI.exome.20121211	-2.58	-2.69	-2.69	-2.96	-2.60	-2.69	-2.55	-2.48	-2.41	0.00	0.00	0.00	0.00	0.00	-2.92	-2.74	-2.60
NA20832.mapped.ILLUMINA.bwa.TSI.exome.20130415	-2.89	-4.48	0.00	-2.91	-2.57	-2.56	-2.55	-2.62	-2.62	-3.48	-2.90	-4.48	-2.78	-2.74	-2.88	0.00	-2.64
NA20845.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.42	-2.78	-2.71	-2.85	-2.70	-2.56	-2.60	-2.62	-2.57	0.00	-4.66	0.00	0.00	-4.66	0.00	-2.59	-2.47
NA20846.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.59	-4.47	0.00	-2.72	-2.65	-2.66	-2.72	-2.62	-2.79	-3.52	-2.95	0.00	-2.87	-2.77	0.00	-2.87	-2.55
NA20847.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.57	-2.79	-2.76	-2.87	-2.56	-2.60	-2.62	-2.64	-2.61	0.00	-2.95	-2.91	0.00	0.00	0.00	-2.65	-2.60
NA20849.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.60	-2.78	-2.70	-2.91	-2.68	-2.76	-2.59	-2.67	-2.74	-3.40	-2.94	-4.70	-2.83	-2.71	0.00	-2.83	-2.52
NA20850.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.55	-2.69	-2.63	-4.38	-2.71	-2.65	-2.59	-2.67	-2.58	0.00	-2.88	-2.80	0.00	-4.68	0.00	-2.60	-2.51
NA20851.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.62	-2.81	-2.81	-2.93	-2.58	-2.71	-2.73	-2.67	-2.75	-3.48	-2.79	-2.85	-2.87	-2.76	-3.28	-4.78	-2.59
NA20852.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.54	0.00	-4.67	-2.57	-2.59	-2.60	-2.61	-2.54	-2.58	0.00	0.00	-4.67	0.00	-4.37	-3.13	-2.74	-2.48
NA20853.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.60	-2.65	-2.69	0.00	-2.79	-2.78	-2.69	-2.68	-2.76	-3.46	-2.82	-2.81	-2.89	-2.78	0.00	-2.80	-2.54
NA20854.mapped.ILLUMINA.bwa.GIH.exome.20121211	-2.58	-2.84	-2.82	-2.95	-2.56	-2.72	-2.71	-2.71	-2.78	-3.51	-2.82	-2.90	-2.84	-2.81	0.00	-2.90	-2.58
NA20856.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.51	-2.84	-2.82	-3.01	-2.63	-2.71	-2.77	-2.63	-2.79	-3.47	-2.83	-2.83	-2.91	-2.83	-3.16	0.00	-2.61
NA20858.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.56	-2.60	-2.64	0.00	0.00	-2.56	-2.63	-2.61	-2.54	0.00	0.00	-4.70	0.00	-4.40	0.00	-2.57	-2.41
NA20859.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.60	-2.82	-2.79	-2.99	-2.57	-2.65	-2.70	-2.63	-2.67	0.00	-2.95	-2.85	-4.75	-4.75	-3.21	-2.88	-2.55
NA20861.mapped.ILLUMINA.bwa.GIH.exome.20121211	-2.56	-2.67	-2.69	-4.76	-2.78	-2.82	-2.72	-2.70	-2.75	-3.40	-2.81	-2.68	-4.76	-2.79	0.00	-2.91	-2.56
NA20862.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.53	-4.43	-4.26	-2.82	-2.59	-2.65	-2.64	-2.63	-4.26	-3.34	-2.76	-2.78	-2.84	-2.61	0.00	0.00	-2.54
NA20863.mapped.ILLUMINA.bwa.GIH.exome.20121211	-2.69	-2.71	-2.79	-3.04	-2.74	-2.84	-2.64	-2.73	-2.72	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.74
NA20864.mapped.ILLUMINA.bwa.GIH.exome.20121211	-2.78	0.00	0.00	-2.94	-2.57	-2.65	-2.73	-2.75	-2.65	0.00	0.00	0.00	0.00	0.00	0.00	-2.63	-2.76
NA20866.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.47	-2.58	-2.54	-4.34	-4.34	-2.68	-2.57	-2.57	-2.51	0.00	0.00	-4.64	0.00	-4.34	0.00	-2.58	-2.42
NA20867.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.87	-2.77	-2.76	0.00	-2.65	-2.79	-2.78	-2.85	0.00	-3.22	-2.66	-2.77	-2.88	-2.73	0.00	0.00	-2.84
NA20868.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.85	-2.76	-2.88	-3.11	-2.79	-2.76	-2.81	-2.96	0.00	-3.24	-2.82	0.00	-2.68	-2.65	0.00	0.00	-2.71
NA20869.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.55	-2.69	-2.73	-2.87	-2.68	-2.70	-2.74	-2.75	-4.19	-3.52	-2.72	0.00	-2.66	-2.56	0.00	0.00	-2.49
NA20870.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.62	-2.67	-2.68	-4.45	-2.61	-2.72	-2.67	-2.69	-2.65	0.00	-2.76	-2.73	-4.45	-4.28	0.00	-2.69	-2.60
NA20871.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.47	0.00	-4.74	-2.67	-2.62	-2.68	-2.64	-2.70	-4.74	-3.25	-2.81	-4.74	-2.70	-2.63	0.00	-4.74	-2.53
NA20872.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.57	0.00	-4.73	-2.79	-2.59	-2.69	-2.69	-2.59	-2.82	-3.38	-2.97	0.00	-2.88	-2.77	0.00	-2.84	-2.54
NA20874.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.62	-2.70	-2.69	-4.45	-2.74	-2.79	-2.72	-2.66	-2.78	-3.52	-2.82	-2.73	0.00	-2.73	0.00	-2.83	-2.62
NA20875.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.54	-2.73	-2.74	-2.90	-2.66	-2.73	-2.60	-2.58	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.64	-2.43
NA20876.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.57	-2.81	-2.80	-2.89	-2.73	-2.73	-2.61	-2.68	-2.76	-3.39	-2.91	0.00	-2.85	-2.76	0.00	-2.83	-2.52
NA20877.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.51	0.00	-4.65	-2.73	-2.53	-2.57	-2.59	-2.54	-2.55	-4.65	0.00	0.00	-4.65	-4.35	-3.19	-2.87	-2.48
NA20878.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.49	-2.69	-2.72	-2.82	-2.67	-2.69	-2.67	-2.76	-2.63	0.00	-2.85	0.00	-2.76	-2.63	0.00	-2.69	-2.44
NA20881.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.56	0.00	-4.37	-2.61	-2.67	-2.58	-2.55	-2.59	-2.55	0.00	0.00	-4.67	0.00	-4.67	0.00	-2.50	-2.48
NA20882.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.50	-2.53	-2.35	0.00	-2.77	-2.75	-2.40	-2.55	-2.55	-3.41	-2.54	-2.38	0.00	-2.53	0.00	-2.85	-2.38
NA20884.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.37	-2.59	-2.66	-2.98	-2.46	-2.33	-2.41	-2.45	-2.59	-3.34	-2.69	-2.67	-2.69	-2.62	0.00	-2.62	-2.31
NA20885.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.54	0.00	0.00	-2.78	-2.53	-2.56	-2.59	-2.64	-2.51	0.00	0.00	0.00	0.00	-4.36	0.00	-2.64	-2.45
NA20886.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.55	-2.78	-2.75	-2.89	-2.72	-2.71	-2.58	-2.48	-2.53	0.00	-4.69	-4.69	0.00	-4.69	0.00	-2.47	-2.46
NA20887.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.62	-2.85	-2.86	-2.91	-2.58	-2.67	-2.71	-2.67	-4.17	-3.29	-2.75	-2.82	-2.76	-2.64	0.00	-4.47	-2.52
NA20888.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.55	-2.73	-2.72	-2.97	-2.68	-2.70	-2.67	-2.75	-2.71	0.00	-2.93	0.00	-2.82	-2.59	0.00	-2.70	-2.45
NA20889.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.63	-2.85	-2.84	-2.99	-2.58	-2.63	-2.69	-2.70	-2.82	-3.35	-2.78	-2.88	-2.85	-2.80	0.00	-2.88	-2.59
NA20890.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.60	0.00	-4.04	-2.89	-2.52	-2.64	-2.68	-2.60	-2.67	-3.58	-3.01	-2.90	-4.81	0.00	-3.22	-2.91	-2.67
NA20891.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.56	-4.69	-4.21	-2.63	-2.56	-2.60	-2.63	-2.61	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.63	-2.52
NA20892.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.49	-2.71	-2.73	-2.88	-2.69	-2.69	-2.57	-2.59	-2.50	0.00	0.00	-4.65	0.00	-4.65	0.00	-2.57	-2.49
NA20893.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.43	0.00	-4.29	-2.74	-2.58	-2.57	-2.62	-2.49	-2.42	0.00	0.00	0.00	0.00	-4.59	0.00	-2.46	-2.50
NA20894.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.46	-2.74	-2.70	-2.92	-2.75	-2.71	-2.70	-2.80	-4.67	-3.31	-2.75	0.00	-2.62	-2.58	0.00	-4.67	-2.51
NA20895.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.43	-2.79	-2.71	-2.89	-2.71	-2.72	-2.71	-2.76	-2.71	0.00	-2.92	0.00	-2.76	-2.68	0.00	-2.73	-2.50
NA20896.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.53	-2.61	-2.73	-4.66	-2.69	-2.68	-2.62	-2.50	-2.54	0.00	0.00	-4.66	0.00	-4.66	0.00	-2.56	-2.50
NA20897.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.53	-4.43	-4.25	-2.64	-2.61	-2.62	-2.65	-2.62	-2.75	-3.43	-2.95	-4.73	-2.87	-2.75	0.00	-2.81	-2.51
NA20898.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.64	-2.84	-2.78	-2.88	-2.54	-2.63	-2.61	-2.60	-2.60	0.00	-2.97	-2.82	-4.75	-4.45	0.00	-2.66	-2.58
NA20899.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.39	-2.44	-2.45	-4.54	-4.24	-3.94	-3.94	-4.24	-4.24	0.00	-2.64	0.00	-2.52	-2.37	0.00	-4.54	-2.37
NA20900.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.93	-2.76	-2.84	-3.09	-2.56	-2.68	-2.65	-2.77	-2.80	-3.39	-2.77	-2.71	0.00	-2.84	0.00	-2.86	-2.80
NA20901.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.55	-2.87	-2.84	-3.01	-2.63	-2.71	-2.69	-2.75	-4.18	-3.35	-2.70	-2.85	-2.81	-2.65	0.00	0.00	-2.61
NA20902.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.54	-4.41	0.00	-2.67	-2.60	-2.60	-2.67	-2.67	-4.23	-3.30	-2.76	0.00	-2.75	-2.59	0.00	-4.71	-2.50
NA20903.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.54	0.00	-4.24	-2.65	-2.58	-2.62	-2.60	-2.66	-4.42	-3.21	-2.77	0.00	-2.71	-2.59	0.00	0.00	-2.53
NA20904.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.46	-4.38	0.00	-2.80	-2.54	-2.59	-2.64	-2.49	-2.52	0.00	-4.68	-4.68	-4.68	-4.20	-3.16	-2.74	-2.50
NA20905.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.57	-2.68	-2.67	-4.69	-2.65	-2.72	-2.66	-2.71	-2.60	0.00	-2.76	-2.61	0.00	-4.69	0.00	-2.67	-2.62
NA20906.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.63	-2.85	-2.87	-2.97	-2.55	-2.70	-2.75	-2.71	-2.75	-3.52	-2.79	-2.82	-2.81	-2.79	0.00	-2.84	-2.54
NA20908.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.59	-2.78	-2.74	-2.99	-2.55	-2.65	-2.66	-2.57	-2.64	0.00	-2.96	-2.87	0.00	0.00	-3.20	-2.85	-2.56
NA20910.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.54	-4.39	0.00	-2.73	-2.56	-2.60	-2.58	-2.55	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.69	-2.42
NA20911.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.60	-2.77	-4.72	-2.84	-2.53	-2.64	-2.66	-2.66	-2.75	-3.40	-2.96	-4.12	-2.84	-2.78	0.00	-2.83	-2.51
NA21086.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.53	0.00	-4.67	-2.67	-2.55	-2.61	-2.62	-2.54	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.44
NA21087.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.55	-2.75	-2.76	-2.86	-2.64	-2.70	-2.73	-2.78	-4.63	-3.45	-2.71	0.00	-2.64	-2.51	0.00	0.00	-2.46
NA21088.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.55	0.00	-4.41	-2.78	-2.56	-2.64	-2.66	-2.62	-2.74	-3.35	-2.96	0.00	-2.91	-2.74	0.00	-2.82	-2.55
NA21089.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.62	-2.68	0.00	-3.07	-2.40	-2.49	-2.56	-2.61	-2.65	-3.64	-2.85	0.00	-2.73	-2.68	0.00	-2.75	-2.59
NA21090.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.57	0.00	0.00	-2.70	-2.46	-2.46	-2.49	-2.47	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.48	-2.52
NA21091.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.55	-2.64	-2.62	-2.99	-2.64	-2.66	-2.65	-2.79	0.00	-3.62	-2.59	0.00	-2.49	-2.42	0.00	0.00	-2.52
NA21092.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.51	-2.42	-2.37	0.00	0.00	-4.33	-2.56	-2.68	-2.55	0.00	-2.68	0.00	-2.56	-2.52	0.00	-2.64	-2.48
NA21093.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.49	-4.60	-4.60	-2.66	-2.53	-2.59	-2.56	-2.47	-2.52	0.00	0.00	0.00	0.00	-4.30	0.00	-2.59	-2.49
NA21094.mapped.ILLUMINA.bwa.GIH.exome.20121211	-2.65	-2.71	-2.68	-3.05	-2.48	-2.60	-2.53	-2.57	-2.53	0.00	-2.80	-2.74	0.00	-4.74	0.00	-2.58	-2.68

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA21095.mapped.ILLUMINA.bwa.GIH.exome.20121211	-2.56	-2.83	-2.75	-2.89	-2.49	-2.65	-2.68	-2.64	-2.60	0.00	-2.92	-2.83	-4.67	-4.37	0.00	-2.51	-2.55
NA21097.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.45	-2.31	-2.26	0.00	0.00	0.00	-4.62	0.00	0.00	0.00	-2.42	0.00	-2.32	-2.27	0.00	0.00	-2.34
NA21098.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.60	-2.44	-2.46	0.00	-2.62	-2.63	-2.45	-2.51	-2.49	0.00	-2.86	-2.68	0.00	-4.72	-2.93	-2.73	-2.53
NA21099.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.73	-2.69	-2.72	-3.08	-2.45	-2.54	-2.58	-2.62	-2.68	-3.69	-2.61	-2.69	-2.73	-2.68	0.00	-2.79	-2.62
NA21100.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.58	-2.50	-2.57	0.00	-2.61	-2.61	-2.66	-2.72	0.00	-3.46	-2.41	-2.61	-2.52	-2.45	0.00	0.00	-2.55
NA21101.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.64	-2.56	-2.54	0.00	-2.70	-2.68	-2.53	-2.64	-2.68	-3.74	-2.60	-2.67	-2.76	-2.64	0.00	-2.78	-2.61
NA21102.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.58	0.00	-4.72	-2.73	-2.44	-2.44	-2.42	-2.46	-2.41	0.00	0.00	-4.72	0.00	0.00	-2.95	-2.65	-2.56
NA21103.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.58	0.00	0.00	-2.84	-2.45	-2.43	-2.45	-2.41	-2.37	0.00	0.00	0.00	0.00	0.00	0.00	-2.37	-2.52
NA21104.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.29	-2.65	-2.58	-2.97	-2.65	-2.55	-2.27	-2.41	-2.29	0.00	0.00	0.00	0.00	0.00	-3.53	-2.55	-2.18
NA21105.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.33	-2.62	-4.17	-2.63	-2.49	-2.33	-2.21	-2.35	-2.40	-3.22	0.00	0.00	0.00	0.00	0.00	-2.48	-2.32
NA21106.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.32	-2.72	0.00	-2.64	-2.49	-2.33	-2.24	-2.51	-2.67	-3.28	-3.01	0.00	-2.72	-2.52	0.00	-2.64	-2.18
NA21107.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.30	-2.64	-2.81	-2.97	-2.41	-2.31	-2.31	-2.41	-2.55	-3.33	-2.59	-2.64	-2.85	-2.50	-3.06	0.00	-2.24
NA21108.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.27	0.00	0.00	-2.71	-2.39	-2.29	-2.33	-2.33	-2.36	0.00	0.00	0.00	0.00	-4.14	0.00	-2.30	-2.23
NA21109.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.23	-2.48	-2.47	-3.15	-2.52	-2.46	-2.39	-2.65	-2.60	0.00	-2.65	0.00	-2.54	-2.43	0.00	-2.41	-2.18
NA21110.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.35	0.00	0.00	-2.59	-2.46	-2.43	-2.29	-2.41	-2.55	-3.43	-2.83	0.00	-2.66	-2.63	-3.13	0.00	-2.31
NA21111.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.30	0.00	0.00	-2.54	-2.46	-2.28	-2.24	-2.43	-2.28	0.00	0.00	0.00	0.00	0.00	0.00	-2.29	-2.19
NA21112.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.30	-2.74	-2.74	-2.99	-2.54	-2.53	-2.28	-2.37	0.00	-2.99	-2.54	0.00	-2.46	-2.29	0.00	0.00	-2.22
NA21113.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.24	0.00	-3.96	-2.71	-2.37	-2.26	-2.28	-2.40	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.27	-2.14
NA21114.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.53	-2.66	-2.64	-4.65	-2.70	-2.77	-2.64	-2.54	-2.55	0.00	-2.89	-2.77	0.00	0.00	-3.16	-2.79	-2.55
NA21115.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.22	-2.60	-2.77	-2.95	-2.73	-2.48	-2.39	-2.51	-2.31	0.00	0.00	0.00	0.00	0.00	-3.01	-2.60	-2.28
NA21116.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.32	0.00	0.00	-2.75	-2.52	-2.39	-2.41	-2.53	-2.45	-3.55	-3.00	0.00	-2.73	-2.62	-3.25	0.00	-2.30
NA21117.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.32	-2.63	-2.79	-2.86	-2.59	-2.63	-2.33	-2.52	-2.52	-3.29	-3.07	0.00	-2.74	-2.62	0.00	-2.69	-2.32
NA21118.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.26	0.00	0.00	-2.70	-2.50	-2.30	-2.47	-2.47	-2.80	-3.48	-2.91	-4.08	-2.70	-2.59	-3.30	0.00	-2.28
NA21119.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.25	0.00	0.00	-2.39	-2.58	-2.16	-2.37	-2.43	-2.33	0.00	0.00	0.00	0.00	-4.01	-3.01	-2.50	-2.26
NA21120.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.29	0.00	0.00	-2.64	-2.37	-2.29	-2.42	-2.40	-2.59	-3.21	-3.21	0.00	-2.57	-2.60	-3.08	-3.98	-2.24
NA21122.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.27	-2.59	-2.47	-2.82	-2.71	-2.46	-2.26	-2.49	-2.33	0.00	0.00	0.00	-4.05	-4.05	0.00	-2.36	-2.27
NA21123.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.25	-2.52	-2.55	-3.06	-2.50	-2.36	-2.33	-2.53	-2.70	-3.20	-2.76	-2.68	-2.80	-2.70	0.00	-2.64	-2.34
NA21124.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.51	-2.56	-2.53	-4.48	-2.57	-2.63	-2.63	-2.79	-4.18	-3.30	-2.57	-2.73	-2.65	-2.53	0.00	0.00	-2.47
NA21125.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.18	-2.68	-2.64	-2.94	-2.56	-2.68	-2.48	-2.70	0.00	-3.07	-2.64	0.00	-2.42	-2.34	0.00	0.00	-2.19
NA21126.mapped.ILLUMINA.bwa.GIH.exome.20121211	-2.48	-2.60	-2.58	0.00	-2.59	-2.59	-2.59	-2.54	-2.54	0.00	-2.81	-2.70	0.00	-4.19	-3.00	-2.68	-2.38
NA21127.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.81	-2.63	-2.62	0.00	0.00	0.00	-2.61	-2.49	-2.70	-3.41	-2.76	0.00	-2.76	-2.75	0.00	-2.77	-2.74
NA21128.mapped.ILLUMINA.bwa.GIH.exome.20130415	-3.14	-2.96	-2.94	-3.33	-2.73	-2.79	-2.72	-2.83	-2.98	-3.59	-2.78	-2.92	-2.99	-3.02	0.00	-3.06	-2.82
NA21129.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.50	-2.66	-2.76	-2.75	-2.57	-2.68	-2.54	-2.59	-2.48	0.00	-4.40	-4.10	0.00	-4.40	-2.84	0.00	-2.41
NA21130.mapped.ILLUMINA.bwa.GIH.exome.20130415	-3.22	-3.00	-2.95	-3.41	-2.65	-2.79	-2.64	-2.75	-2.85	-3.58	-2.93	-2.81	-4.94	-5.24	0.00	-2.89	-2.95
NA21133.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.99	-2.78	-2.81	-3.21	-2.53	-2.70	-2.66	-2.60	-2.70	0.00	-2.87	-2.79	0.00	-4.91	-3.16	-2.89	-2.81
NA21135.mapped.ILLUMINA.bwa.GIH.exome.20130415	-2.99	-2.64	-2.67	0.00	-2.83	-2.84	-2.79	-2.85	0.00	-3.34	-2.55	-2.69	-2.77	-2.72	0.00	-4.93	-2.84
NA21137.mapped.ILLUMINA.bwa.GIH.exome.20120522	-2.42	0.00	0.00	-2.75	-2.55	-2.59	-2.62	-2.59	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.43
NA21141.mapped.ILLUMINA.bwa.GIH.exome.20121211	-2.74	-2.74	-2.80	-3.03	-2.83	-2.81	-2.63	-2.74	-2.71	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.69
NA21142.mapped.ILLUMINA.bwa.GIH.exome.20121211	-2.75	-4.70	-4.70	-2.76	-2.65	-2.71	-2.68	-2.77	-2.69	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.71
NA21143.mapped.ILLUMINA.bwa.GIH.exome.20121211	-2.85	0.00	0.00	-2.77	-2.67	-2.69	-2.73	-2.78	-2.96	-3.22	-3.03	0.00	-2.89	-2.87	0.00	-2.86	-2.76
NA21144.mapped.ILLUMINA.bwa.GIH.exome.20121211	-2.83	-2.77	-2.77	-4.83	-2.78	-2.80	-2.78	-2.88	-3.03	-3.34	-2.76	-2.80	-2.97	-2.97	0.00	-2.95	-2.82
TCGA-02-0003-10A-01D-1490-08_GBM	-2.54	0.00	0.00	-2.79	-2.57	-2.58	-2.66	-2.51	-2.61	0.00	0.00	0.00	0.00	-4.64	0.00	-2.41	-2.58
TCGA-02-0033-10A-01D-1490-08_GBM	-2.57	-2.71	-2.77	-2.96	-2.66	-2.64	-2.74	-2.69	-2.68	0.00	-2.82	-4.64	-2.74	-2.68	-3.05	-4.34	-2.51
TCGA-02-0047-10A-01D-1490-08_GBM	-2.49	-2.74	-2.72	-2.95	-2.70	-2.76	-2.64	-2.48	-2.54	0.00	0.00	0.00	0.00	0.00	-3.02	-2.69	-2.60
TCGA-02-0055-10A-01D-1490-08_GBM	-2.55	-2.77	-2.70	-2.95	-2.70	-2.75	-2.65	-2.47	-2.60	0.00	0.00	0.00	0.00	-4.61	-3.05	-2.73	-2.53
TCGA-02-2470-10A-01D-1494-08_GBM	-2.57	0.00	-4.70	-2.83	-2.61	-2.70	-2.67	-2.69	-2.79	-3.34	-2.92	0.00	-2.83	-2.76	0.00	-2.78	-2.56
TCGA-02-2483-10A-01D-1494-08_GBM	-2.62	-4.36	0.00	-2.94	-2.62	-2.59	-2.70	-2.62	-4.67	-3.22	-2.73	0.00	-2.72	-2.64	0.00	0.00	-2.60
TCGA-02-2485-10A-01D-1494-08_GBM	-2.55	0.00	-4.02	-2.68	-2.54	-2.56	-2.68	-2.43	-2.49	0.00	0.00	0.00	-4.62	0.00	0.00	-2.51	-2.50
TCGA-02-2486-10A-01D-1494-08_GBM	-2.49	-2.62	-2.61	-4.12	-3.90	-4.29	-2.55	-2.52	-2.52	0.00	0.00	-4.29	0.00	-4.29	-2.91	-4.60	-2.48
TCGA-05-4244-10A-01D-1105-08_LUAD	-2.59	-2.72	-2.72	-2.95	-2.65	-2.72	-2.63	-2.61	-2.68	-3.38	-2.90	0.00	-2.79	-2.70	0.00	-2.77	-2.53
TCGA-05-4249-10A-01D-1105-08_LUAD	-2.52	0.00	0.00	-2.79	-2.53	-2.52	-2.59	-2.49	-2.56	0.00	0.00	0.00	0.00	-4.58	0.00	-2.64	-2.52
TCGA-05-4250-10A-01D-1105-08_LUAD	-2.53	0.00	0.00	-2.67	-2.54	-2.50	-2.61	-2.61	-2.48	0.00	0.00	0.00	0.00	-4.28	0.00	-2.49	-2.55
TCGA-05-4382-10A-01D-1265-08_LUAD	-2.60	-2.74	-2.72	-2.95	-2.65	-2.68	-2.64	-2.62	-2.73	-3.39	-2.92	0.00	-2.83	-2.70	-3.18	-4.59	-2.56
TCGA-05-4384-10A-01D-1753-08_LUAD	-2.45	0.00	0.00	-2.63	-2.48	-2.41	-2.50	-2.57	-2.49	0.00	0.00	0.00	0.00	-4.42	0.00	-2.57	-2.31
TCGA-05-4389-10A-01D-1265-08_LUAD	-2.63	-2.90	-2.80	-3.00	-2.51	-2.59	-2.71	-2.71	-4.22	-3.22	-2.74	-2.69	-2.89	-2.63	0.00	0.00	-2.59
TCGA-05-4390-10A-01D-1753-08_LUAD	-2.51	0.00	-4.48	-2.62	-2.56	-2.52	-2.45	-2.52	-2.72	-3.27	-2.99	0.00	-2.88	-2.63	0.00	-2.84	-2.46
TCGA-05-4395-10A-01D-1265-08_LUAD	-2.46	-4.58	0.00	-2.67	-2.53	-2.53	-2.57	-2.54	-2.51	0.00	-4.58	-4.58	-4.58	-4.58	0.00	-2.58	-2.50
TCGA-05-4396-10A-01D-1855-08_LUAD	-2.50	-4.68	-4.68	-2.80	-2.46	-2.59	-2.56	-2.60	-2.82	-3.34	-2.78	-2.75	-2.89	-2.78	0.00	-2.87	-2.59
TCGA-05-4397-10A-01D-1265-08_LUAD	-2.50	0.00	0.00	-2.82	-2.49	-2.50	-2.54	-2.54	-2.58	0.00	0.00	0.00	-4.58	-4.58	0.00	-2.63	-2.47
TCGA-05-4398-10A-01D-1265-08_LUAD	-2.41	0.00	0.00	-2.70	-2.47	-2.55	-2.62	-2.55	-2.52	0.00	0.00	-4.59	-4.59	0.00	-2.90	0.00	-2.51
TCGA-05-4402-10A-01D-1265-08_LUAD	-2.39	-4.51	0.00	-2.72	-2.46	-2.61	-2.63	-2.58	-2.56	0.00	0.00	0.00	0.00	-2.55	-3.03	0.00	-2.56
TCGA-05-4403-10A-01D-1265-08_LUAD	-2.57	-2.65	-2.69	-4.64	-2.66	-2.66	-2.61	-2.57	-2.80	-3.36	-2.78	-2.70	-2.79	-2.75	0.00	-2.79	-2.56
TCGA-05-4405-10A-01D-1855-08_LUAD	-2.43	0.00	-4.57	-2.75	-2.55	-2.61	-2.59	-2.51	-2.46	0.00	-4.57	0.00	0.00	0.00	-3.17	-2.73	-2.47
TCGA-05-4410-10A-01D-1855-08_LUAD	-2.36	-2.70	-2.71	-2.88	-2.69	-2.67	-2.55	-2.51	-2.49	0.00	0.00	0.00	0.00	0.00	-3.01	-2.73	-2.47
TCGA-05-4415-10A-01D-1855-08_LUAD	-2.47	0.00	0.00	-2.67	-2.52	-2.66	-2.52	-2.47	-2.55	0.00	0.00	0.00	0.00	-4.55	0.00	-2.43	-2.49
TCGA-05-4417-10A-01D-1855-08_LUAD	-2.50	-2.73	-2.73	-2.84	-2.40	-2.71	-2.70	-2.76	-4.58	-3.30	-2.63	-2.57	0.00	-2.55	0.00	0.00	-2.61
TCGA-05-4418-10A-01D-1265-08_LUAD	-2.62	-2.86	-2.80	-3.01	-2.53	-2.66	-2.70	-2.70	-2.75	-3.41	-2.81	-2.78	-2.84	-2.76	0.00	-2.95	-2.61
TCGA-05-4420-10A-01D-1265-08_LUAD	-2.56	0.00	0.00	-2.71	-2.55	-2.60	-2.61	-2.66	-2.67	-3.44	-2.97	0.00	-2.81	-2.71	0.00	-2.77	-2.56
TCGA-05-4422-10A-01D-1265-08_LUAD	-2.50	-2.68	-2.70	-2.96	-2.61	-2.66	-2.59	-2.56	-2.48	0.00	0.00	0.00	0.00	-4.29	0.00	-2.60	-2.49
TCGA-05-4424-10A-01D-1855-08_LUAD	-2.41	0.00	-4.58	-2.56	-2.53	-2.56	-2.60	-2.60	-2.46	0.00	0.00	0.00	0.00	-4.27	0.00	-2.62	-2.50
TCGA-05-4425-10A-01D-1753-08_LUAD	-2.44	-2.63	-2.57	-2.81	-2.63	-2.66	-2.50	-2.51	-2.52	0.00	0.00	-4.15	0.00	-4.45	0.00	-2.47	-2.37
TCGA-05-4426-10A-01D-1265-08_LUAD	-2.59	-2.72	-2.67	-4.69	-2.57	-2.65	-2.68	-2.71	-4.21	-3.29	-2.66	-2.58	-2.86	-2.64	0.00	-4.69	-2.60
TCGA-05-4427-10A-01D-1855-08_LUAD	-2.45	-2.63	-2.68	-2.76	-2.61	-2.65	-2.58	-2.46	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.39
TCGA-05-4430-10A-01D-1265-08_LUAD	-2.57	0.00	-4.34	-2.86	-2.59	-2.61	-2.62	-2.69	-2.66	-3.39	-2.94	0.00	-2.77	-2.67	0.00	-2.77	-2.60
TCGA-05-4432-10A-01D-1265-08_LUAD	-2.50	-4.11	0.00	-2.85	-2.51	-2.57	-2.62	-2.47	-2.45	0.00	-4.29	-3.98	-4.29	-3.89	0.00	-2.51	-2.51
TCGA-05-4433-10A-01D-1855-08_LUAD	-2.58	-2.71	-2.74	-2.84	-2.50	-2.60	-2.57	-2.65	-2.66	0.00	-2.92	-2.77	0.00	-4.59	0.00	-2.64	-2.56
TCGA-05-4434-10A-01D-1265-08_LUAD	-2.44	0.00	-4.64	-2.69	-2.55	-2.59	-2.62	-2.66	-2.70	-3.28	-2.97	0.00	-2.76	-2.66	0.00	-2.81	-2.54
TCGA-05-5423-10A-01D-1625-08_LUAD	-2.45	0.00	0.00	-2.64	-2.48	-2.53	-2.49	-2.54	-2.51	0.00	0.00	0.00	-4.03	0.00	0.00	-2.53	-2.42
TCGA-05-5425-10A-01D-1625-08_LUAD	-2.38	-4.52	-4.52	-2.63	-2.48	-2.51	-2.52	-2.54	-2.40	0.00	0.00	0.00	0.00	-4.52	0.00	-2.50	-2.44
TCGA-05-5428-10A-01D-1625-08_LUAD	-2.51	0.00	-4.23	-2.63	-2.49	-2.54	-2.49	-2.59	-2.61	-3.41	-3.01	0.00	-2.80	-2.69	0.00	-2.74	-2.43
TCGA-05-5429-10A-01D-1625-08_LUAD	-2.48	-2.66	-2.64	-2.87	-2.69	-2.66	-2.44	-2.52	-2.47	0.00	0.00	0.00	0.00	-4.48	0.00	-2.48	-2.38
TCGA-05-5715-10A-01D-1625-08_LUAD	-2.49	-2.69	-2.68	-2.91	-2.71	-2.61	-2.53	-2.62	-2.67	-3.36	-2.94	-4.54	-2.75	-2.62	0.00	-2.85	-2.44
TCGA-06-0119-10A-01D-1490-08_GBM	-2.58	-4.60	-4.30	-2.82	-2.55	-2.61	-2.62	-2.61	-2.71	-3.40	-2.91	-4.12	-2.75	-2.70	0.00	-2.73	-2.52
TCGA-06-0122-10A-01D-1490-08_GBM	-2.57	-2.71	-2.68	-2.96	-2.68	-2.67	-2.62	-2.51	-2.58	0.00	-4.58	0.00	0.00	-4.27	-3.04	-2.71	-2.51
TCGA-06-0124-10A-01D-1490-08_GBM	-2.66	-2.82	-2.67	-3.01	-2.79	-2.80	-2.64	-2.62	-2.78	-3.32	-2.83	-4.68	-2.72	-2.81	0.00	-2.84	-2.66
TCGA-06-0125-10A-01D-1490-08_GBM	-2.61	-2.76	-2.78	-3.02	-2.53	-2.65	-2.65	-2.57	-2.67	-4.65	-2.89	-2.77	-4.35	-4.65	0.00	-2.55	-2.58
TCGA-06-0126-10A-01D-1490-08_GBM	-2.63	-2.76	-2.74	-2.92	-2.76	-2.77	-2.65	-2.53	-2.74	-3.36	-2.87	-2.75	-4.59	-2.68	0.00	-2.81	-2.58
TCGA-06-0128-10A-01D-1490-08_GBM	-2.58	-4.60	0.00	-2.85	-2.55	-2.58	-2.67	-2.59	-2.48	0.00	-4.60	-4.60	0.00	-4.12	0.00	-2.60	-2.51
TCGA-06-0129-10A-01D-1490-08_GBM	-2.56	-2.83	-2.80	-2.96	-2.57	-2.67	-2.67	-2.56	-2.75	-3.42	-2.84	-2.76	-2.86	-2.78	-3.19	0.00	-2.66
TCGA-06-0130-10A-01D-1490-08_GBM	-2.58	-2.66	-2.75	-2.95	-2.66	-2.64	-2.65	-2.55	-2.51	0.00	0.00	-4.58	0.00	0.00	-3.06	-2.75	-2.53
TCGA-06-0132-10A-01D-1491-08_GBM	-2.60	-2.75	-2.73	-2.98	-2.68	-2.68	-2.63	-2.52	-2.62	0.00	0.00	-4.59	-4.59	-4.59	0.00	-2.62	-2.58
TCGA-06-0137-10A-01D-1490-08_GBM	-2.58	-2.74	-2.70	-2.94	-2.67	-2.70	-2.61	-2.61	-2.54	0.00	0.00	0.00	0.00	0.00	-2.84	-4.10	-2.56
TCGA-06-0139-10A-01D-1490-08_GBM	-2.65	-2.84	-2.80	-3.04	-2.57	-2.66	-2.68	-2.64	-2.79	-3.48	-2.83	-2.67	0.00	-2.76	0.00	-2.84	-2.60
TCGA-06-0140-10A-01D-1490-08_GBM	-2.54	0.00	0.00	-2.64	-2.55	-2.56	-2.61	-2.64	-2.48	-4.56	0.00	0.00	-4.26	-4.56	0.00	-2.61	-2.50
TCGA-06-0141-10A-01D-1490-08_GBM	-2.53	-2.79	-2.77	-3.08	-2.72	-2.74	-2.57	-2.57	-2.73	-3.20	-3.06	-2.69	0.00	-2.66	0.00	-2.88	-2.53
TCGA-06-0142-10A-01D-1490-08_GBM	-2.53	-2.86	-2.82	-3.03	-2.59	-2.72	-2.71	-2.62	-2.77	-3.44	-2.78	-2.83	-2.87	-2.79	0.00	-2.80	-2.62

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-06-0145-10A-01D-1490-08_GBM	-2.50	0.00	-4.55	-2.78	-2.50	-2.56	-2.58	-2.61	-2.55	0.00	0.00	0.00	0.00	-4.55	0.00	-2.58	-2.50
TCGA-06-0151-10A-01D-1491-08_GBM	-2.67	0.00	0.00	-2.97	-2.67	-2.66	-2.70	-2.55	-2.85	-3.29	-2.94	0.00	-2.90	-2.77	0.00	-2.79	-2.66
TCGA-06-0152-10A-01D-1492-08_GBM	-2.67	0.00	-4.66	-2.90	-2.64	-2.70	-2.75	-2.70	-2.78	-3.34	-2.88	0.00	-2.81	-2.84	0.00	-2.72	-2.66
TCGA-06-0154-10A-01D-1491-08_GBM	-2.70	-2.91	-2.83	-3.01	-2.75	-2.88	-2.73	-2.72	-2.77	-3.40	-2.93	-4.48	-2.85	-2.86	0.00	-2.90	-2.75
TCGA-06-0155-10A-01D-1492-08_GBM	-2.59	-2.73	-2.74	-2.97	-2.69	-2.66	-2.63	-2.59	-2.58	0.00	0.00	-4.63	0.00	0.00	-3.11	-2.75	-2.54
TCGA-06-0157-10A-01D-1491-08_GBM	-2.64	-4.64	-4.64	-2.96	-2.61	-2.68	-2.70	-2.48	-2.56	0.00	0.00	-4.64	0.00	0.00	0.00	-2.45	-2.61
TCGA-06-0158-10A-01D-1491-08_GBM	-2.52	0.00	0.00	-2.76	-2.55	-2.65	-2.69	-2.66	-4.27	-3.23	-2.84	0.00	-2.72	-2.52	0.00	-4.57	-2.66
TCGA-06-0165-10A-01D-1491-08_GBM	-2.65	0.00	-4.67	-2.75	-2.69	-2.64	-2.71	-2.72	-2.74	-3.37	-2.92	-4.67	-2.84	-2.74	0.00	-2.77	-2.66
TCGA-06-0166-10A-01D-1491-08_GBM	-2.60	-2.79	-2.74	-2.92	-2.65	-2.73	-2.67	-2.61	-2.62	0.00	0.00	-4.61	-4.61	-4.61	-2.93	0.00	-2.65
TCGA-06-0167-10A-01D-1491-08_GBM	-2.53	-4.32	0.00	-2.87	-2.58	-2.65	-2.61	-2.54	-2.60	0.00	-4.63	-4.63	0.00	0.00	-3.00	-2.71	-2.59
TCGA-06-0168-10A-01D-1491-08_GBM	-2.68	-4.66	0.00	-3.03	-2.64	-2.69	-2.71	-2.66	-2.82	-3.32	-2.92	0.00	-2.90	-2.71	0.00	-2.75	-2.68
TCGA-06-0169-10A-01D-1490-08_GBM	-2.58	-4.60	-3.90	-2.68	-2.57	-2.63	-2.63	-2.56	-2.52	0.00	0.00	-4.60	-4.60	-4.60	-3.06	-2.73	-2.57
TCGA-06-0171-10A-01D-1491-08_GBM	-2.64	-2.84	0.00	-3.04	-2.55	-2.71	-2.74	-2.56	-2.78	-3.39	-2.88	0.00	-2.84	-2.77	-3.17	0.00	-2.71
TCGA-06-0173-10B-01D-1491-08_GBM	-2.71	-2.84	-2.77	-3.05	-2.59	-2.66	-2.74	-2.54	-2.62	0.00	-3.01	-2.80	0.00	0.00	-3.15	-2.80	-2.63
TCGA-06-0174-10B-01D-1491-08_GBM	-2.67	-2.69	-2.64	0.00	-2.64	-2.64	-2.72	-2.74	-2.80	-3.35	-2.75	-2.63	0.00	-2.73	0.00	-2.81	-2.56
TCGA-06-0178-10B-01D-1491-08_GBM	-2.58	0.00	0.00	-2.86	-2.59	-2.61	-2.69	-2.51	-2.63	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.60
TCGA-06-0184-10B-01D-1491-08_GBM	-2.55	-2.79	-2.79	-3.04	-2.74	-2.75	-2.72	-2.65	-4.36	-3.28	-2.81	0.00	-2.73	-2.69	0.00	-4.36	-2.65
TCGA-06-0185-10B-01D-1491-08_GBM	-2.51	0.00	0.00	-2.69	-2.60	-2.64	-2.70	-2.43	-2.57	0.00	0.00	0.00	0.00	-4.60	-3.06	-2.73	-2.58
TCGA-06-0187-10B-01D-1491-08_GBM	-2.58	-2.75	-2.73	-2.98	-2.71	-2.74	-2.69	-2.57	-2.51	0.00	0.00	0.00	-4.62	0.00	-3.05	-2.72	-2.57
TCGA-06-0188-10B-01D-1491-08_GBM	-2.63	0.00	-4.33	-2.84	-2.66	-2.66	-2.69	-2.61	-2.56	0.00	0.00	0.00	0.00	-4.64	-3.10	-2.73	-2.60
TCGA-06-0189-10A-01D-1491-08_GBM	-2.46	-2.75	-2.77	-2.82	-2.73	-2.69	-2.67	-2.60	-2.59	0.00	-4.59	0.00	0.00	-3.99	-2.90	-3.55	-2.59
TCGA-06-0190-10B-01D-1491-08_GBM	-2.69	-2.88	-2.81	-3.03	-2.57	-2.70	-2.74	-2.64	-2.87	-3.48	-2.84	-2.81	-2.86	-2.79	-3.27	-4.20	-2.61
TCGA-06-0192-10A-01D-1492-08_GBM	-2.64	-2.83	-2.82	-3.01	-2.49	-2.62	-2.72	-2.51	-2.59	0.00	-2.89	-2.72	0.00	-4.69	0.00	-2.47	-2.66
TCGA-06-0195-10A-01D-1491-08_GBM	-2.48	0.00	-4.19	-2.79	-2.52	-2.72	-2.70	-2.73	-2.64	0.00	0.00	0.00	0.00	-2.63	0.00	-2.65	-2.58
TCGA-06-0209-10A-01D-1491-08_GBM	-2.44	0.00	-4.31	-2.71	-2.58	-2.61	-2.66	-2.62	-2.64	0.00	-4.61	0.00	0.00	0.00	-3.06	-2.74	-2.56
TCGA-06-0210-10A-01D-1491-08_GBM	-2.60	-4.66	-4.19	-2.74	-2.66	-2.71	-2.74	-2.66	-2.73	-3.43	-2.88	-2.75	-4.36	-2.78	0.00	-2.78	-2.57
TCGA-06-0211-10A-01D-1491-08_GBM	-2.66	0.00	0.00	-2.90	-2.63	-2.63	-2.67	-2.60	-2.66	0.00	0.00	0.00	0.00	-4.63	0.00	-2.62	-2.64
TCGA-06-0213-10A-01D-1491-08_GBM	-2.49	0.00	0.00	-2.69	-2.55	-2.64	-2.67	-2.60	-2.61	0.00	0.00	0.00	-4.57	-4.57	-2.84	-4.57	-2.62
TCGA-06-0214-10A-01D-1491-08_GBM	-2.65	-2.84	-2.82	-3.06	-2.75	-2.83	-2.73	-2.64	-2.80	-3.39	-2.95	0.00	-2.81	-2.76	0.00	-2.80	-2.67
TCGA-06-0216-10A-01D-1492-08_GBM	-2.56	-4.10	0.00	-2.69	-2.59	-2.62	-2.64	-2.43	-2.56	-4.57	-4.57	0.00	0.00	-4.57	0.00	-2.41	-2.57
TCGA-06-0219-10A-01D-1491-08_GBM	-2.51	0.00	-4.33	-2.72	-2.64	-2.64	-2.65	-2.65	-2.55	0.00	-4.63	-4.03	-4.63	0.00	0.00	-2.49	-2.59
TCGA-06-0221-10A-01D-1491-08_GBM	-2.68	-2.88	-2.86	-3.06	-2.66	-2.74	-2.81	-2.65	-2.82	-3.41	-2.83	-2.81	-2.88	-2.81	0.00	-2.80	-2.70
TCGA-06-0237-10A-01D-1491-08_GBM	-2.74	-2.85	-2.90	-3.00	-2.59	-2.76	-2.76	-2.67	-2.79	-3.50	-2.92	-2.69	0.00	-2.81	-3.22	-4.23	-2.68
TCGA-06-0238-10A-01D-1492-08_GBM	-2.61	-2.76	-2.76	-2.99	-2.70	-2.71	-2.67	-2.61	-2.57	0.00	0.00	-4.62	-4.62	0.00	0.00	-2.58	-2.60
TCGA-06-0240-10A-01D-1491-08_GBM	-2.67	0.00	0.00	-2.96	-2.64	-2.70	-2.74	-2.54	-2.76	-3.42	-2.95	0.00	-2.81	-2.77	0.00	-2.75	-2.65
TCGA-06-0241-10A-01D-1491-08_GBM	-2.65	-2.72	-2.72	-4.65	-2.76	-2.72	-2.68	-2.68	-2.56	-4.65	-2.96	-2.74	0.00	-4.65	0.00	-2.58	-2.61
TCGA-06-0644-10A-01D-1492-08_GBM	-2.72	-2.80	-2.73	0.00	-2.79	-2.87	-2.75	-2.60	-2.76	-3.30	-2.80	-2.74	0.00	-2.81	-3.16	0.00	-2.66
TCGA-06-0645-10A-01D-1492-08_GBM	-2.62	-2.76	-2.75	-2.94	-2.71	-2.78	-2.72	-2.53	-2.55	0.00	0.00	-4.61	-4.31	0.00	-3.12	-2.69	-2.64
TCGA-06-0646-10A-01D-1492-08_GBM	-2.65	-2.75	-2.74	-2.94	-2.71	-2.69	-2.70	-2.54	-2.54	0.00	0.00	-4.60	0.00	0.00	0.00	-2.48	-2.61
TCGA-06-0648-10A-01D-1492-08_GBM	-2.49	-4.61	-4.31	-2.73	-2.58	-2.64	-2.66	-2.51	-2.69	0.00	0.00	0.00	0.00	-4.61	0.00	-2.46	-2.60
TCGA-06-0649-10A-01D-1492-08_GBM	-2.57	-2.78	-2.75	-2.99	-2.50	-2.64	-2.68	-2.49	-2.57	0.00	-2.85	-2.71	0.00	-4.35	0.00	-2.63	-2.64
TCGA-06-0650-10A-01D-1696-08_GBM	-2.39	-2.66	-2.69	-2.79	-2.62	-2.63	-2.55	-2.49	-2.48	0.00	-4.49	-4.49	0.00	0.00	-3.05	-2.74	-2.44
TCGA-06-0686-10A-01D-1492-08_GBM	-2.49	-4.64	0.00	-2.70	-2.51	-2.59	-2.64	-2.50	-2.61	0.00	0.00	-4.64	0.00	-4.34	0.00	-2.42	-2.52
TCGA-06-0743-10A-01D-1492-08_GBM	-2.64	-2.81	-2.85	-3.03	-2.55	-2.69	-2.72	-2.65	-2.61	0.00	-2.94	-2.81	0.00	0.00	0.00	-2.63	-2.60
TCGA-06-0744-10A-01D-1492-08_GBM	-2.54	-2.64	-2.59	-3.89	-4.29	-3.82	-2.64	-2.49	-2.71	-3.45	-2.82	-4.59	-2.81	-2.65	-3.09	-4.59	-2.56
TCGA-06-0745-10A-01D-1492-08_GBM	-2.62	-4.38	-4.38	-2.78	-2.59	-2.63	-2.74	-2.53	-2.81	-3.45	-2.95	-4.68	-2.82	-2.80	0.00	-2.73	-2.59
TCGA-06-0747-10A-01D-1492-08_GBM	-2.60	-2.72	-2.75	-2.93	-2.67	-2.69	-2.66	-2.51	-2.51	0.00	0.00	-4.58	0.00	0.00	-3.04	-2.70	-2.55
TCGA-06-0749-10A-01D-1492-08_GBM	-2.61	-4.68	-4.37	-2.94	-2.60	-2.68	-2.66	-2.61	-2.77	-3.35	-2.88	0.00	-2.84	-2.71	-3.17	-4.68	-2.63
TCGA-06-0750-10A-01D-1492-08_GBM	-2.68	-2.89	-2.86	-3.09	-2.59	-2.70	-2.79	-2.60	-2.84	-3.41	-2.75	-2.67	0.00	-2.85	0.00	-2.85	-2.66
TCGA-06-0875-10A-01D-1492-08_GBM	-2.64	-2.80	-2.76	-3.02	-2.50	-2.64	-2.70	-2.70	-2.64	0.00	-2.98	-2.73	0.00	0.00	-2.96	-4.70	-2.58
TCGA-06-0876-10A-01D-1492-08_GBM	-2.60	-2.83	-2.81	-2.97	-2.72	-2.74	-2.66	-2.55	-2.76	-3.30	-2.79	0.00	-2.85	-2.75	-3.07	-4.62	-2.59
TCGA-06-0877-10A-01D-1492-08_GBM	-2.67	-2.72	-2.78	-4.72	-2.73	-2.79	-2.71	-2.53	-2.83	-3.40	-2.77	-2.83	-2.84	-2.79	0.00	-2.77	-2.64
TCGA-06-0878-10A-01D-1492-08_GBM	-2.68	0.00	-4.20	-3.00	-2.65	-2.64	-2.61	-2.58	-2.73	-3.40	-2.84	0.00	-2.82	-2.70	-3.12	-4.38	-2.66
TCGA-06-0879-10A-01D-1492-08_GBM	-2.65	-2.85	-2.82	-2.98	-2.50	-2.66	-2.71	-2.55	-2.69	0.00	-2.87	-2.81	0.00	-4.70	0.00	-2.47	-2.63
TCGA-06-0881-10A-01D-1492-08_GBM	-2.62	-2.78	-2.82	-2.98	-2.51	-2.67	-2.72	-2.66	-2.63	0.00	-2.94	-2.72	0.00	0.00	-2.98	-4.69	-2.62
TCGA-06-0882-10A-01D-1492-08_GBM	-2.52	-4.31	-4.01	-2.85	-2.60	-2.59	-2.60	-2.59	-2.51	0.00	-4.61	-4.61	-4.61	0.00	0.00	-2.53	-2.58
TCGA-06-0939-10A-01D-1353-08_GBM	-2.57	-2.87	-2.77	-3.07	-2.48	-2.61	-2.66	-2.59	-2.77	-3.37	-2.83	-2.74	-2.88	-2.78	0.00	-2.83	-2.56
TCGA-06-1804-10A-01D-1696-08_GBM	-2.50	-2.73	-2.59	-2.80	-2.60	-2.65	-2.51	-2.44	-2.46	0.00	0.00	0.00	0.00	-4.19	-2.99	-2.71	-2.41
TCGA-06-1806-10B-01D-1845-08_GBM	-2.50	0.00	0.00	-2.63	-2.56	-2.56	-2.60	-2.53	-2.52	0.00	0.00	0.00	0.00	-4.59	-3.06	-2.74	-2.48
TCGA-06-2557-10A-01D-1494-08_GBM	-2.52	0.00	-4.25	-2.66	-2.47	-2.52	-2.54	-2.39	-2.56	0.00	0.00	0.00	0.00	-4.07	-3.06	0.00	-2.59
TCGA-06-2558-10A-01D-1494-08_GBM	-2.49	-2.80	-2.76	-2.99	-2.57	-2.62	-2.64	-2.70	-2.65	0.00	-2.97	-2.78	0.00	0.00	-2.95	-4.20	-2.56
TCGA-06-2559-10A-01D-1494-08_GBM	-2.55	-4.60	-4.60	-2.80	-2.55	-2.55	-2.61	-2.50	-2.53	0.00	0.00	0.00	0.00	-4.60	-3.10	-2.70	-2.57
TCGA-06-2561-10A-01D-1494-08_GBM	-2.59	0.00	0.00	-2.90	-2.59	-2.59	-2.65	-2.68	-2.77	-3.34	-2.97	-2.70	-4.66	-2.76	0.00	-2.80	-2.60
TCGA-06-2562-10A-01D-1494-08_GBM	-2.53	0.00	-4.30	-2.77	-2.58	-2.53	-2.60	-2.53	-2.57	0.00	0.00	0.00	-4.13	-4.30	-2.96	-4.30	-2.49
TCGA-06-2563-10A-01D-1494-08_GBM	-2.64	-4.39	-4.39	-2.75	-2.58	-2.65	-2.70	-2.57	-2.71	-3.35	-2.94	0.00	-2.86	-2.70	-3.12	-4.21	-2.56
TCGA-06-2564-10A-01D-1494-08_GBM	-2.64	-2.86	-2.82	-3.02	-2.58	-2.69	-2.72	-2.62	-2.79	-3.44	-2.84	-2.79	-2.87	-2.81	-3.18	-4.74	-2.62
TCGA-06-2565-10A-01D-1494-08_GBM	-2.62	-2.51	-2.72	0.00	-2.68	-2.70	-2.73	-2.74	-4.01	-3.29	-2.65	-2.78	-2.71	-2.57	0.00	0.00	-2.54
TCGA-06-2567-10A-01D-1494-08_GBM	-2.47	-2.59	-2.53	0.00	-4.09	-4.27	-2.57	-2.43	-2.45	0.00	0.00	0.00	0.00	-4.57	-3.00	-2.70	-2.47
TCGA-06-2569-10A-01D-1494-08_GBM	-2.56	-2.76	-2.75	-2.94	-2.71	-2.72	-2.66	-2.57	-2.73	-3.33	-2.86	-4.63	-2.77	-2.66	0.00	-2.79	-2.52
TCGA-06-2570-10A-01D-1495-08_GBM	-2.51	-4.30	-4.30	-2.66	-2.47	-2.59	-2.62	-2.54	-2.54	0.00	0.00	-4.60	0.00	-4.60	0.00	-2.55	-2.47
TCGA-06-5408-10A-01D-1696-08_GBM	-2.57	-2.75	-2.71	-2.96	-2.50	-2.59	-2.64	-2.61	-2.55	0.00	-2.99	-2.73	-4.58	-4.58	0.00	-2.50	-2.51
TCGA-06-5410-10A-01D-1696-08_GBM	-2.49	-2.77	-2.80	-3.01	-2.53	-2.61	-2.59	-2.64	-2.73	-3.18	-2.74	-2.85	-2.91	-2.69	0.00	-2.79	-2.57
TCGA-06-5411-10A-01D-1696-08_GBM	-2.37	-4.49	0.00	-2.70	-2.47	-2.53	-2.57	-2.55	-2.50	0.00	0.00	0.00	0.00	-4.19	-3.08	-2.70	-2.43
TCGA-06-5412-10A-01D-1696-08_GBM	-2.46	-2.76	-2.67	-2.79	-2.67	-2.68	-2.67	-2.68	-2.62	0.00	-2.82	0.00	-2.70	-2.59	-3.03	-4.46	-2.38
TCGA-06-5413-10A-01D-1696-08_GBM	-2.47	-4.19	-4.50	-2.60	-2.51	-2.53	-2.54	-2.41	-2.43	0.00	0.00	0.00	0.00	-4.19	-3.08	-2.74	-2.42
TCGA-06-5414-10A-01D-1486-08_GBM	-2.66	-2.82	-2.82	-2.94	-2.53	-2.68	-2.69	-2.73	-2.81	-3.38	-2.81	-2.80	-2.86	-2.74	0.00	-2.82	-2.62
TCGA-06-5415-10A-01D-1486-08_GBM	-2.63	-2.82	-2.81	-2.93	-2.54	-2.66	-2.68	-2.50	-2.57	0.00	-2.89	-2.75	0.00	-4.22	0.00	-2.49	-2.59
TCGA-06-5416-10A-01D-1486-08_GBM	-2.43	0.00	-4.28	-2.68	-2.60	-2.62	-2.59	-2.64	-2.47	0.00	-4.58	-4.58	0.00	-4.28	0.00	-2.58	-2.46
TCGA-06-5417-10A-01D-1486-08_GBM	-2.59	0.00	-4.63	-2.69	-2.61	-2.68	-2.63	-2.44	-2.53	0.00	-4.33	-4.63	0.00	-4.63	-3.06	-2.68	-2.55
TCGA-06-5418-10A-01D-1486-08_GBM	-2.64	-2.85	-2.84	-3.04	-2.55	-2.70	-2.73	-2.66	-2.79	-3.37	-2.77	-2.78	-2.86	-2.82	0.00	-2.81	-2.61
TCGA-06-5856-10A-01D-1696-08_GBM	-2.50	0.00	0.00	-2.69	-2.53	-2.47	-2.54	-2.45	-2.48	0.00	0.00	0.00	-4.48	-4.48	-2.94	-2.70	-2.41
TCGA-06-5858-10A-01D-1696-08_GBM	-2.48	0.00	-4.49	-2.61	-2.51	-2.56	-2.56	-2.50	-2.44	0.00	-4.19	-4.01	0.00	-4.01	-3.03	-2.74	-2.46
TCGA-06-5859-10A-01D-1696-08_GBM	-2.50	0.00	0.00	-2.67	-2.46	-2.51	-2.55	-2.50	-2.46	0.00	0.00	0.00	0.00	-4.49	0.00	-2.59	-2.47
TCGA-06-6388-10A-01D-1845-08_GBM	-2.61	-2.83	-2.78	-2.94	-2.54	-2.68	-2.64	-2.58	-2.76	-3.52	-2.72	-2.81	-2.85	-2.74	-3.15	0.00	-2.52
TCGA-06-6389-10A-01D-1696-08_GBM	-2.57	-2.72	-2.72	-2.98	-2.66	-2.68	-2.65	-2.58	-2.73	-3.33	-2.97	-4.54	-2.74	-2.64	0.00	-2.69	-2.48
TCGA-06-6390-10A-01D-1696-08_GBM	-2.40	-2.70	-2.68	-2.79	-2.64	-2.57	-2.57	-2.46	-2.43	0.00	0.00	0.00	0.00	-4.50	-3.14	-2.77	-2.42
TCGA-06-6391-10A-01D-1696-08_GBM	-2.57	-4.54	-4.54	-2.77	-2.53	-2.59	-2.65	-2.54	-2.71	-3.37	-2.90	-4.07	-2.86	-2.69	0.00	-2.68	-2.48
TCGA-06-6693-10A-01D-1845-08_GBM	-2.58	-2.80	-2.79	-2.98	-2.58	-2.63	-2.60	-2.61	-2.82	-3.44	-2.66	-2.79	-2.84	-2.73	0.00	-2.87	-2.51
TCGA-06-6694-10A-01D-1845-08_GBM	-2.50	-2.68	-2.61	-2.83	-2.66	-4.59	-2.61	-2.58	-4.59	-3.17	-2.67	-4.59	-2.60	-2.57	0.00	0.00	-2.61
TCGA-06-6695-10A-01D-1845-08_GBM	-2.46	0.00	-4.27	-2.56	-2.48	-2.57	-2.51	-2.40	-2.48	0.00	0.00	0.00	-4.27	0.00	0.00	-2.46	-2.46
TCGA-06-6697-10A-01D-1845-08_GBM	-2.46	0.00	0.00	-2.58	-2.52	-2.54	-2.62	-2.44	-2.49	0.00	0.00	-4.27	0.00	0.00	0.00	-2.46	-2.40
TCGA-06-6698-10A-01D-1845-08_GBM	-2.52	-2.72	-2.72	-2.81	-2.73	-2.69	-2.53	-2.42	-2.40	0.00	0.00	-4.53	0.00	0.00	-3.01	-2.72	-2.45
TCGA-06-6699-10A-01D-1845-08_GBM	-2.51	-2.68	-2.69	0.00	-2.69	-2.70	-2.58	-2.42	-2.45	0.00	-4.58	0.00	0.00	0.00	-3.07	-2.68	-2.49
TCGA-06-6700-10A-01D-1845-08_GBM	-2.45	-2.71	-2.72	-2.83	-2.70	-2.69	-2.70	-2.73	-2.69	0.00	-2.84	0.00	-2.71	-2.61	0.00	-2.70	-2.47
TCGA-06-6701-10A-01D-1845-08_GBM	-2.45	-2.66	-2.71	-2.83	-2.67	-2.64	-2.58	-2.53	-2.44	0.00	-4.55	0.00	0.00	0.00	0.00	-2.55	-2.43
TCGA-06-A5U0-10A-01D-A33W-08_GBM	-2.55	-2.66	-2.70	-2.82	-2.64	-2.52	-2.57	-2.61	-2.52	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.51

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-06-A5U1-10A-01D-A33W-08_GBM	-2.54	0.00	0.00	-2.62	-2.58	-2.53	-2.62	-2.52	-2.55	0.00	0.00	0.00	0.00	0.00	-3.17	-2.75	-2.54
TCGA-06-A6S0-10A-01D-A33W-08_GBM	-2.60	-2.62	-2.81	0.00	-2.58	-2.62	-2.66	-2.59	-2.75	-3.23	-2.67	-2.82	-2.76	-2.69	0.00	-2.81	-2.56
TCGA-06-A6S1-10A-01D-A33W-08_GBM	-2.56	0.00	-4.47	-2.75	-2.46	-2.60	-2.62	-2.61	-2.53	0.00	-2.93	-2.76	0.00	0.00	-2.94	0.00	-2.52
TCGA-09-2044-10A-01D-0704-01_OV	-2.53	-2.71	-2.75	-2.92	-2.75	-2.76	-2.67	-2.66	-2.73	-3.33	-2.90	0.00	-2.81	-2.71	0.00	-2.80	-2.52
TCGA-12-0615-10A-01D-1492-08_GBM	-2.65	0.00	-4.62	-2.92	-2.67	-2.66	-2.66	-2.51	-2.59	0.00	0.00	0.00	0.00	-4.32	0.00	-2.49	-2.59
TCGA-12-0616-10A-01D-1492-08_GBM	-2.59	-2.76	-2.79	-2.97	-2.69	-2.75	-2.71	-2.52	-2.54	0.00	-4.61	0.00	0.00	-3.91	-3.00	-2.71	-2.59
TCGA-12-0618-10A-01D-1492-08_GBM	-2.61	-4.57	-4.57	-2.69	-2.61	-2.63	-2.69	-2.52	-2.61	0.00	0.00	0.00	0.00	0.00	-3.03	-2.75	-2.61
TCGA-12-0619-10A-01D-1492-08_GBM	-2.58	-2.77	-2.75	-2.95	-2.71	-2.71	-2.62	-2.47	-2.56	-4.56	0.00	-4.56	0.00	0.00	0.00	-2.41	-2.56
TCGA-12-0688-10A-01D-1492-08_GBM	-2.55	-2.78	-2.71	-2.95	-2.70	-2.71	-2.63	-2.49	-2.50	0.00	-4.62	0.00	0.00	0.00	-3.01	-2.69	-2.53
TCGA-12-0692-10A-01D-1492-08_GBM	-2.40	-4.30	0.00	-2.60	-2.39	-2.47	-2.47	-2.45	-2.48	0.00	0.00	0.00	-4.30	0.00	0.00	-2.51	-2.45
TCGA-12-0821-10A-01D-1492-08_GBM	-2.47	-2.69	-2.64	-2.85	-2.57	-3.76	-2.69	-2.64	-2.59	0.00	-4.53	0.00	0.00	-2.60	-2.99	-3.93	-2.59
TCGA-12-1597-10A-01D-1495-08_GBM	-2.49	-2.77	-2.68	-2.95	-2.63	-2.71	-2.73	-2.75	-2.67	0.00	-2.90	0.00	-2.76	-2.69	0.00	-2.72	-2.54
TCGA-12-3649-10A-01D-1495-08_GBM	-2.58	-4.26	-3.96	-2.62	-2.57	-2.59	-2.57	-2.60	-2.50	-4.56	-4.56	-4.56	0.00	-3.96	0.00	-2.50	-2.51
TCGA-12-3650-10A-01D-1495-08_GBM	-2.67	-2.83	-2.76	-3.02	-2.56	-2.74	-2.69	-2.65	-2.73	-3.44	-2.79	-2.73	-2.87	-2.77	0.00	-2.85	-2.67
TCGA-12-3652-10A-01D-1495-08_GBM	-2.65	-2.73	-2.74	0.00	-2.68	-2.66	-2.77	-2.57	-2.78	-3.46	-2.75	-2.69	-2.84	-2.78	0.00	-2.81	-2.61
TCGA-12-3653-10A-01D-1495-08_GBM	-2.66	-2.85	-2.76	-3.02	-2.60	-2.66	-2.68	-2.57	-2.77	-3.39	-2.79	-2.81	-2.80	-2.75	0.00	-2.86	-2.65
TCGA-12-5295-10A-01D-1486-08_GBM	-2.56	0.00	0.00	-2.83	-2.58	-2.59	-2.63	-2.59	-2.56	0.00	-4.34	-4.64	-4.34	0.00	-3.01	-4.34	-2.55
TCGA-12-5299-10A-01D-1486-08_GBM	-2.45	-2.66	-2.63	-4.34	-4.34	-4.64	-2.62	-2.52	-2.64	-3.32	-2.78	-4.64	-2.75	-2.71	-3.14	0.00	-2.53
TCGA-12-5301-10A-01D-1486-08_GBM	-2.60	-4.34	-4.34	-2.82	-2.51	-2.61	-2.64	-2.57	-2.72	-3.47	-2.95	0.00	-2.81	-2.72	-3.13	-3.87	-2.56
TCGA-13-0751-10A-01D-0446-08_OV	-2.48	0.00	0.00	-2.81	-2.52	-2.52	-2.64	-2.67	-4.82	-3.29	-2.77	0.00	-2.66	-2.56	0.00	0.00	-2.44
TCGA-13-0757-10A-01D-0356-01_OV	-2.46	-2.81	-2.80	-3.04	-2.51	-2.72	-2.70	-2.56	-2.74	-3.32	-2.77	-2.72	-2.85	-2.75	-3.15	0.00	-2.57
TCGA-13-0758-10A-01D-0356-01_OV	-2.45	-2.67	-2.75	-3.04	-2.41	-2.58	-2.67	-2.65	-2.56	0.00	-2.82	-2.68	0.00	-4.20	-3.04	-4.50	-2.46
TCGA-13-0883-10A-01D-0399-01_OV	-2.59	-2.92	-2.89	-3.39	-2.59	-2.65	-2.86	-2.90	-2.90	-3.77	-2.88	-2.73	-5.21	-2.83	0.00	-2.90	-2.61
TCGA-13-0886-10A-01D-0399-01_OV	-2.46	0.00	-4.59	-2.95	-2.51	-2.56	-2.72	-2.58	-2.46	0.00	0.00	-4.59	0.00	-4.19	0.00	-2.43	-2.50
TCGA-13-0888-10A-01D-0399-01_OV	-2.44	-2.73	-2.77	-3.11	-2.69	-2.78	-2.65	-2.56	-2.67	0.00	0.00	0.00	0.00	-4.53	0.00	-2.47	-2.50
TCGA-13-0891-10A-01D-0399-01_OV	-2.46	-2.68	-2.70	-3.01	-2.69	-2.73	-2.61	-2.52	-2.64	0.00	0.00	0.00	0.00	-4.75	0.00	-2.37	-2.56
TCGA-13-0899-10A-01D-0399-01_OV	-2.34	-2.72	-2.74	-3.06	-2.71	-2.72	-2.67	-2.60	-2.71	-3.39	-2.86	0.00	-2.82	-2.70	-3.10	0.00	-2.47
TCGA-13-0904-10A-01D-0399-01_OV	-2.40	-2.64	-2.74	-3.07	-2.57	-2.63	-2.67	-2.66	-2.42	0.00	0.00	0.00	0.00	-4.53	0.00	-2.48	-2.40
TCGA-13-0911-10A-01D-0399-01_OV	-2.42	-4.76	0.00	-2.77	-2.49	-2.54	-2.66	-2.57	-2.42	0.00	0.00	0.00	0.00	-4.76	-2.92	0.00	-2.46
TCGA-13-0913-10A-01D-0399-01_OV	-2.43	-2.74	-2.73	-3.08	-2.64	-2.67	-2.60	-2.46	-2.49	0.00	0.00	0.00	0.00	-4.75	0.00	-2.31	-2.47
TCGA-13-0916-10A-01D-0399-01_OV	-2.29	0.00	-4.73	-2.90	-2.35	-2.56	-2.70	-2.55	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.38	-2.52
TCGA-13-0921-10A-01D-0399-01_OV	-2.39	-2.72	-2.76	-3.14	-2.69	-2.71	-2.55	-2.58	-2.54	0.00	0.00	0.00	0.00	-4.36	0.00	-2.65	-2.45
TCGA-13-0923-10A-01D-0399-01_OV	-2.40	0.00	0.00	-3.00	-2.51	-2.52	-2.66	-2.72	-2.66	-3.39	-2.87	0.00	-2.80	-2.78	0.00	-2.76	-2.53
TCGA-13-1477-10A-01D-0472-01_OV	-2.50	-2.67	-2.73	0.00	-2.60	-2.72	-2.72	-2.65	-2.76	-3.50	-2.66	-2.60	0.00	-2.78	0.00	-2.87	-2.64
TCGA-13-1485-10A-01D-0472-01_OV	-2.49	-2.79	-2.74	-3.11	-2.49	-2.56	-2.69	-2.70	-2.64	0.00	-2.82	-2.77	0.00	-4.79	0.00	-2.65	-2.58
TCGA-13-1495-10A-01D-0472-01_OV	-2.37	0.00	0.00	-2.87	-2.56	-2.58	-2.66	-2.46	-2.53	0.00	0.00	0.00	0.00	-4.87	0.00	-2.45	-2.43
TCGA-13-1500-10A-01D-0472-01_OV	-2.44	-4.74	-4.74	-2.90	-2.52	-2.58	-2.62	-2.62	-2.72	-3.31	-2.87	-4.44	-2.79	-2.64	0.00	-2.74	-2.44
TCGA-13-1505-10A-01D-0472-01_OV	-2.35	0.00	0.00	-2.90	-2.47	-2.53	-2.61	-2.48	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.32	-2.41
TCGA-13-2057-10A-01D-1526-09_OV	-2.56	-2.53	-2.55	0.00	0.00	-4.71	-2.68	-2.81	-2.77	0.00	-2.69	0.00	-2.71	-2.65	0.00	-2.62	-2.65
TCGA-13-2059-10A-01D-1526-09_OV	-2.75	0.00	0.00	-2.74	-2.61	-2.67	-2.65	-2.61	-2.85	-3.41	-2.88	0.00	-2.77	-2.70	0.00	-2.77	-2.73
TCGA-13-2061-10A-01D-1526-09_OV	-2.70	0.00	-4.77	-2.70	-2.56	-2.56	-2.59	-2.66	-2.64	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.57
TCGA-13-2065-10A-01D-1526-09_OV	-2.61	0.00	-4.81	-2.80	-2.49	-2.53	-2.55	-2.54	-2.62	0.00	0.00	0.00	0.00	0.00	-2.85	-2.62	-2.63
TCGA-13-2066-10A-01D-1526-09_OV	-2.64	0.00	0.00	-2.68	-2.52	-2.53	-2.60	-2.47	-2.64	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.66
TCGA-13-2071-10A-01D-1526-09_OV	-2.78	-2.82	-2.86	-3.17	-2.63	-2.68	-2.78	-2.68	0.00	-3.45	-2.53	-2.80	-2.71	-2.69	0.00	0.00	-2.82
TCGA-14-0736-10C-01D-2280-08_GBM	-2.51	-2.58	-2.62	0.00	-2.56	-2.64	-2.59	-2.61	-2.48	0.00	-2.96	0.00	-2.80	-4.51	-2.96	0.00	-2.46
TCGA-14-0740-10B-01D-1845-08_GBM	-2.44	0.00	-4.59	-2.66	-2.53	-2.52	-2.53	-2.53	-2.48	0.00	0.00	0.00	0.00	0.00	-2.96	-4.11	-2.45
TCGA-14-0781-10A-01D-1696-08_GBM	-2.58	-2.75	-2.75	-2.94	-2.55	-2.60	-2.62	-2.62	-2.52	0.00	-2.95	-2.74	0.00	-4.56	-3.00	-4.26	-2.51
TCGA-14-0786-10A-01D-1492-08_GBM	-2.49	-2.61	-2.59	-4.59	-4.59	-3.99	-2.59	-2.45	-2.47	0.00	0.00	-4.59	0.00	-4.59	0.00	-2.39	-2.48
TCGA-14-0787-10A-01D-1492-08_GBM	-2.60	-2.79	-2.76	-3.03	-2.74	-2.73	-2.70	-2.54	-2.70	-3.39	-2.86	0.00	-2.82	-2.79	-3.06	0.00	-2.60
TCGA-14-0789-10A-01D-1492-08_GBM	-2.52	0.00	-4.56	-2.65	-2.56	-2.59	-2.64	-2.53	-2.54	0.00	0.00	0.00	0.00	-4.08	-3.07	-2.71	-2.51
TCGA-14-0790-10A-01D-1494-08_GBM	-2.49	-4.65	-4.35	-2.72	-2.60	-2.64	-2.63	-2.57	-2.72	-3.35	-2.96	-4.35	-2.82	-2.71	0.00	-2.77	-2.51
TCGA-14-0813-10A-01D-1492-08_GBM	-2.57	-4.28	-4.59	-2.64	-2.55	-2.60	-2.66	-2.42	-2.53	0.00	0.00	0.00	0.00	0.00	-3.05	-2.79	-2.49
TCGA-14-0817-10A-01D-1492-08_GBM	-2.58	-4.28	-4.58	-2.79	-2.52	-2.60	-2.66	-2.57	-2.63	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.55
TCGA-14-0862-10C-01D-1845-08_GBM	-2.51	0.00	0.00	-2.60	-2.53	-2.56	-2.59	-2.47	-2.49	0.00	-4.55	0.00	0.00	0.00	-3.01	-2.75	-2.51
TCGA-14-0871-10A-01D-1492-08_GBM	-2.61	-2.71	-2.70	-4.39	-2.76	-2.77	-2.73	-2.71	-4.69	-3.18	-2.69	-2.64	-2.82	-2.68	0.00	-4.69	-2.59
TCGA-14-1034-10A-01D-1492-08_GBM	-2.58	0.00	-4.67	-2.72	-2.58	-2.58	-2.65	-2.55	-2.51	0.00	0.00	0.00	-4.37	-4.19	-3.13	-2.80	-2.56
TCGA-14-1043-10A-01D-1845-08_GBM	-2.45	-2.69	-2.69	-2.79	-2.65	-2.67	-2.55	-2.43	-2.43	0.00	0.00	-4.56	0.00	0.00	-3.00	-2.73	-2.42
TCGA-14-1395-10A-01D-1845-08_GBM	-2.52	0.00	0.00	-2.58	-2.54	-2.50	-2.55	-2.59	-2.42	0.00	0.00	0.00	-4.57	-4.57	0.00	-2.59	-2.44
TCGA-14-1450-10B-01D-1845-08_GBM	-2.63	-2.69	-2.65	0.00	-2.68	-2.55	-2.65	-2.60	-2.78	-3.60	-2.70	-2.70	-2.87	-2.82	-3.21	0.00	-2.61
TCGA-14-1456-10A-01D-1494-08_GBM	-2.57	0.00	-4.65	-2.68	-2.55	-2.56	-2.67	-2.52	-2.56	0.00	0.00	0.00	-4.65	0.00	-3.16	-2.80	-2.51
TCGA-14-1823-10A-01D-1494-08_GBM	-2.52	-4.10	-4.58	-2.85	-2.60	-2.58	-2.67	-2.58	-2.53	0.00	-4.58	-4.10	0.00	-4.28	-3.09	-2.73	-2.62
TCGA-14-1825-10A-01D-1494-08_GBM	-2.60	0.00	-4.36	-2.74	-2.61	-2.63	-2.70	-2.55	-2.72	-3.32	-2.90	-4.36	-2.77	-2.68	0.00	-2.76	-2.58
TCGA-14-1829-10A-01D-1494-08_GBM	-2.61	-2.83	-2.79	-3.03	-2.56	-2.64	-2.73	-2.65	-2.65	0.00	-2.91	-2.80	-4.41	-4.72	-2.88	0.00	-2.64
TCGA-14-2554-10A-01D-1494-08_GBM	-2.55	-2.72	-2.72	-2.90	-2.68	-2.65	-2.76	-2.68	-2.63	-4.64	-2.93	-2.68	-4.64	-2.67	0.00	-2.70	-2.53
TCGA-14-3476-10A-01D-1353-08_GBM	-2.63	-2.83	-2.81	-2.93	-2.54	-2.60	-2.52	-2.60	-2.80	-3.35	-2.85	-2.60	0.00	-2.74	0.00	-2.85	-2.58
TCGA-14-4157-10A-01D-1353-08_GBM	-2.51	-2.61	-2.61	-4.35	-2.65	-2.67	-2.63	-2.59	-2.58	0.00	-2.97	-2.70	0.00	0.00	0.00	-2.56	-2.47
TCGA-15-0742-10A-01D-1492-08_GBM	-2.53	-2.72	-2.70	-2.94	-2.70	-2.71	-2.61	-2.58	-2.66	0.00	0.00	-4.61	-4.61	0.00	0.00	-2.54	-2.54
TCGA-15-1444-10A-01D-1696-08_GBM	-2.53	-2.58	-2.60	-4.23	-2.74	-2.66	-2.61	-2.55	-2.49	0.00	-2.89	-2.71	-4.53	-4.53	0.00	-2.58	-2.47
TCGA-16-0846-10A-01D-1492-08_GBM	-2.66	-2.73	-2.74	-4.67	-2.75	-2.77	-2.66	-2.59	-2.69	-3.59	-2.92	-2.79	0.00	-4.67	0.00	-2.65	-2.68
TCGA-16-0848-10A-01D-1492-08_GBM	-2.61	-4.14	0.00	-2.71	-2.52	-2.55	-2.66	-2.59	-2.61	0.00	-4.32	0.00	0.00	-4.01	-3.06	-2.70	-2.62
TCGA-16-0861-10A-01D-1492-08_GBM	-2.69	-4.41	-4.41	-2.89	-2.66	-2.68	-2.82	-2.56	-2.76	-3.41	-2.88	-4.41	-2.88	-2.73	0.00	-2.76	-2.61
TCGA-16-1045-10B-01D-1492-08_GBM	-2.63	-4.69	-4.69	-2.88	-2.61	-2.62	-2.67	-2.62	-4.39	-3.20	-2.80	-2.78	-2.84	-2.62	0.00	0.00	-2.61
TCGA-16-1048-10A-01D-1353-08_GBM	-2.46	0.00	-4.68	-2.71	-2.53	-2.56	-2.59	-2.48	-2.61	0.00	0.00	-4.68	0.00	-4.68	0.00	-2.51	-2.45
TCGA-19-1390-10C-01D-1495-08_GBM	-2.61	-2.75	-4.64	-2.95	-2.51	-2.64	-2.68	-2.67	-2.73	-3.41	-2.89	-4.64	-2.81	-2.71	0.00	-2.74	-2.56
TCGA-19-1787-10A-01D-1495-08_GBM	-2.49	0.00	0.00	-2.69	-2.58	-2.59	-2.68	-2.54	-2.49	0.00	0.00	0.00	0.00	0.00	-3.00	-2.72	-2.52
TCGA-19-1790-10B-01D-1353-08_GBM	-2.55	0.00	-4.38	-2.68	-2.48	-2.53	-2.59	-2.48	-2.45	0.00	0.00	0.00	0.00	0.00	-3.07	-2.72	-2.48
TCGA-19-2619-10A-01D-1495-08_GBM	-2.68	-2.85	-2.81	-3.04	-2.57	-2.69	-2.68	-2.57	-2.80	-3.27	-2.81	-2.82	-2.92	-2.81	-3.21	-3.59	-2.64
TCGA-19-2620-10A-01D-1495-08_GBM	-2.54	-4.58	-3.98	-2.70	-2.59	-2.62	-2.60	-2.51	-2.57	0.00	0.00	0.00	0.00	-4.58	-3.10	-2.72	-2.53
TCGA-19-2623-10A-01D-1495-08_GBM	-2.53	-2.73	-2.71	-2.94	-2.63	-2.69	-2.64	-2.54	-2.48	0.00	-4.58	0.00	0.00	0.00	0.00	-2.44	-2.52
TCGA-19-2624-10A-01D-1495-08_GBM	-2.45	-4.48	-4.48	-2.56	-2.48	-2.57	-2.59	-2.56	-2.55	0.00	0.00	0.00	0.00	-2.60	-3.02	-4.48	-2.52
TCGA-19-2625-10A-01D-1495-08_GBM	-2.60	-4.72	-4.12	-2.78	-2.51	-2.67	-2.68	-2.71	-2.84	-3.27	-2.83	-2.84	-2.90	-2.82	0.00	-2.86	-2.68
TCGA-19-2629-10A-01D-1495-08_GBM	-2.67	-2.76	-2.78	-3.00	-2.49	-2.66	-2.68	-2.70	-2.65	0.00	-2.90	-2.75	-4.35	-4.35	-2.97	0.00	-2.64
TCGA-19-2631-10B-01D-1353-08_GBM	-2.49	-4.62	-4.62	-2.79	-2.51	-2.53	-2.57	-2.46	-2.43	0.00	-4.62	0.00	-4.62	-4.32	-3.08	-2.76	-2.45
TCGA-19-4065-10A-01D-2280-08_GBM	-2.33	-2.69	-2.68	-2.77	-2.53	-2.61	-2.54	-2.49	-2.47	0.00	0.00	0.00	0.00	-4.43	-3.04	-2.66	-2.44
TCGA-19-4068-10A-01D-1353-08_GBM	-2.58	-2.77	-2.73	-2.93	-2.51	-2.61	-2.70	-2.58	-2.56	0.00	-3.06	-2.79	-4.70	-4.40	-3.13	-2.83	-2.55
TCGA-19-5947-10A-01D-1696-08_GBM	-2.53	0.00	0.00	-2.78	-2.46	-2.52	-2.61	-2.47	-2.47	0.00	0.00	0.00	0.00	-4.06	-2.92	-2.73	-2.44
TCGA-19-5950-10A-01D-1696-08_GBM	-2.52	0.00	-4.50	-2.73	-2.47	-2.48	-2.54	-2.43	-2.44	-4.50	-4.50	0.00	0.00	-4.50	0.00	-2.46	-2.47
TCGA-19-5951-10A-01D-1696-08_GBM	-2.55	-4.57	-4.10	-2.78	-2.56	-2.67	-2.51	-2.44	-2.73	-3.14	-2.86	-4.57	-2.85	-2.72	0.00	-2.78	-2.47
TCGA-19-5952-10A-01D-1696-08_GBM	-2.54	-2.71	-2.77	-3.00	-2.48	-2.57	-2.60	-2.54	-2.57	0.00	-2.92	-2.76	-4.57	-4.57	-3.17	-2.73	-2.48
TCGA-19-5953-10A-01D-1845-08_GBM	-2.54	-2.61	-2.59	0.00	-2.71	-2.79	-2.64	-2.62	-2.51	0.00	-2.84	-2.67	-4.62	-4.62	0.00	-2.58	-2.41
TCGA-19-5954-10A-01D-1696-08_GBM	-2.56	-2.78	-2.76	-2.99	-2.55	-2.60	-2.63	-2.58	-2.78	-3.27	-2.76	-2.61	0.00	-2.69	0.00	-2.81	-2.48
TCGA-19-5955-10A-01D-1696-08_GBM	-2.50	0.00	-4.53	-2.66	-2.56	-2.57	-2.59	-2.53	-2.67	-3.49	-2.87	0.00	-2.79	-2.67	0.00	-2.75	-2.51
TCGA-19-5956-10A-01D-1696-08_GBM	-2.33	-2.68	-2.55	-2.80	-2.63	-2.65	-2.53	-2.50	-2.43	0.00	-4.50	0.00	-4.50	0.00	-2.93	-2.64	-2.40
TCGA-19-5958-10A-01D-1696-08_GBM	-2.47	-2.70	-2.69	-2.91	-2.68	-2.72	-2.60	-2.54	-2.70	-3.36	-2.93	-4.06	-2.77	-2.67	0.00	-2.72	-2.49
TCGA-19-5959-10A-01D-1696-08_GBM	-2.42	0.00	0.00	-2.70	-2.46	-2.53	-2.57	-2.61	-2.65	-3.34	-2.97	-2.66	0.00	-2.62	0.00	-2.87	-2.43
TCGA-19-5960-10A-01D-1696-08_GBM	-2.49	-2.68	-2.71	-2.87	-2.65	-2.70	-2.51	-2.50	-2.68	-3.38	-2.92	-3.89	-2.78	-2.63	0.00	-2.78	-2.46

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-19-A60I-10A-01D-A33W-08_GBM	-2.59	-2.73	-2.72	-2.85	-2.51	-2.62	-2.65	-2.60	-2.62	0.00	-2.89	-2.72	0.00	0.00	-3.05	-2.72	-2.58
TCGA-19-A6J4-10A-01D-A33W-08_GBM	-2.51	0.00	-4.42	-2.58	-2.51	-2.54	-2.59	-2.52	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.47
TCGA-19-A6J5-10A-01D-A33W-08_GBM	-2.57	-2.68	-2.71	-2.80	-2.55	-2.53	-2.61	-2.52	-2.51	0.00	-2.84	0.00	-2.77	0.00	-2.92	0.00	-2.61
TCGA-20-0991-10A-01D-0428-01_OV	-2.52	0.00	-4.24	-2.97	-2.49	-2.59	-2.63	-2.39	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.37	-2.50
TCGA-21-1081-10B-01D-1521-08_LUSC	-2.63	-2.83	-2.81	-2.95	-2.56	-2.69	-2.72	-2.58	-2.71	-4.73	-2.89	-2.73	0.00	-4.25	0.00	-2.49	-2.54
TCGA-21-1082-10B-01D-1521-08_LUSC	-2.56	0.00	-4.31	-2.82	-2.52	-2.58	-2.58	-2.60	-2.55	0.00	0.00	-4.61	-4.61	-4.61	0.00	-2.57	-2.50
TCGA-21-5782-10A-01D-1632-08_LUSC	-2.53	-2.56	-2.60	-4.25	-2.76	-2.75	-2.60	-2.62	-2.69	-3.35	-2.79	-2.52	-4.55	-2.73	0.00	-2.85	-2.46
TCGA-21-5783-10A-01D-2184-08_LUSC	-2.40	0.00	0.00	-2.70	-2.58	-2.50	-2.55	-2.55	-2.68	-3.35	-2.83	0.00	-2.78	-2.61	0.00	-2.68	-2.46
TCGA-21-5784-10A-01D-1632-08_LUSC	-2.55	-2.73	-2.69	-2.95	-2.69	-2.73	-2.52	-2.60	-4.50	-3.24	-2.74	-4.50	-2.61	-2.48	0.00	-4.20	-2.42
TCGA-21-5786-10A-01D-1632-08_LUSC	-2.44	0.00	-4.51	-2.65	-2.45	-2.48	-2.52	-2.57	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-3.15	-2.72	-2.45
TCGA-21-5787-10A-01D-1632-08_LUSC	-2.45	-2.72	-2.64	-2.89	-2.60	-2.72	-2.51	-2.55	-2.42	0.00	0.00	-4.16	0.00	0.00	-3.14	-2.69	-2.38
TCGA-21-A5DI-10A-01D-A26K-08_LUSC	-2.50	0.00	-4.50	-2.62	-2.53	-2.56	-2.52	-2.54	-2.66	-3.55	-2.88	-4.50	-2.75	-2.66	-3.02	-4.20	-2.46
TCGA-22-A5C4-10A-01D-A27N-08_LUSC	-2.50	0.00	-4.39	-2.59	-2.48	-2.50	-2.57	-2.51	-2.42	0.00	-4.39	0.00	0.00	0.00	0.00	-2.40	-2.48
TCGA-23-1110-10A-01D-0428-01_OV	-2.37	0.00	-4.27	-2.93	-2.56	-2.55	-2.59	-2.52	-2.46	0.00	0.00	0.00	0.00	-4.75	-3.03	-2.65	-2.40
TCGA-23-2641-10A-01D-1526-09_OV	-2.65	-2.64	-2.66	-2.93	-2.70	-2.69	-2.58	-2.58	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.65
TCGA-23-2643-10A-01D-1526-09_OV	-2.71	-2.69	-2.66	0.00	-2.78	-2.71	-2.71	-2.50	-2.55	0.00	-2.74	-2.75	0.00	0.00	-2.82	-2.63	-2.77
TCGA-23-2647-10A-01D-1526-09_OV	-2.61	-2.75	-2.83	-3.04	-2.55	-2.58	-2.70	-2.81	-2.81	0.00	-3.01	-2.89	0.00	0.00	-2.83	-2.78	-2.72
TCGA-23-2649-10A-01D-1526-09_OV	-2.74	-2.64	-2.66	0.00	-2.75	-2.77	-2.70	-2.61	-2.60	0.00	-2.78	-2.80	0.00	0.00	-2.90	-2.70	-2.77
TCGA-24-1430-10A-01D-0472-01_OV	-2.32	-2.48	-2.53	-4.51	-4.82	-4.51	-2.64	-2.68	-2.63	0.00	-2.81	0.00	-2.79	-2.70	0.00	-2.68	-2.39
TCGA-24-1431-10A-01D-0472-01_OV	-2.48	0.00	-4.86	-2.83	-2.58	-2.60	-2.77	-2.54	-2.78	-3.45	-2.85	0.00	-2.80	-2.73	0.00	-2.72	-2.51
TCGA-25-1319-10A-01D-0452-01_OV	-2.45	0.00	0.00	-2.71	-2.53	-2.58	-2.68	-2.45	-2.51	0.00	0.00	0.00	0.00	0.00	-2.98	-2.71	-2.59
TCGA-25-2397-10A-01D-0704-01_OV	-2.55	-2.80	-2.78	-3.01	-2.70	-2.80	-2.69	-2.61	-2.78	-3.39	-2.93	0.00	-2.78	-2.76	0.00	-2.77	-2.62
TCGA-25-2398-10A-01D-0704-01_OV	-2.48	0.00	-4.67	-2.64	-2.49	-2.59	-2.63	-2.45	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.41
TCGA-26-1439-10A-01D-1353-08_GBM	-2.47	-2.74	-2.62	-2.81	-2.57	-2.63	-2.55	-2.53	-2.53	0.00	-4.23	-4.53	0.00	0.00	-3.13	-2.70	-2.40
TCGA-26-1442-10A-01D-1696-08_GBM	-2.58	-2.65	-2.63	0.00	-2.72	-2.77	-2.50	-2.45	-2.57	-3.39	-2.92	-2.75	-4.54	-4.54	-3.06	-2.74	-2.50
TCGA-26-5132-10A-01D-1486-08_GBM	-2.51	-2.79	-2.81	-3.03	-2.51	-2.65	-2.66	-2.70	-2.62	0.00	-2.86	-2.75	-4.66	-4.66	-3.01	-3.66	-2.59
TCGA-26-5133-10A-01D-1486-08_GBM	-2.41	-2.68	-2.69	-2.89	-2.67	-2.67	-2.65	-2.59	-2.49	0.00	0.00	0.00	-4.59	-4.29	0.00	-2.59	-2.51
TCGA-26-5134-10A-01D-1486-08_GBM	-2.58	-4.11	-4.28	-2.79	-2.51	-2.54	-2.66	-2.47	-2.57	0.00	0.00	-4.58	-4.11	-4.28	0.00	-2.38	-2.51
TCGA-26-5135-10A-01D-1486-08_GBM	-2.50	-4.28	-4.28	-2.80	-2.53	-2.53	-2.58	-2.57	-2.62	0.00	-4.58	0.00	0.00	0.00	0.00	-2.56	-2.50
TCGA-26-5136-10A-01D-1486-08_GBM	-2.55	-2.76	-2.69	-2.89	-2.67	-2.67	-2.62	-2.56	-2.58	0.00	0.00	0.00	0.00	-4.57	0.00	-2.54	-2.52
TCGA-26-5139-10A-01D-1486-08_GBM	-2.60	-4.71	0.00	-2.89	-2.66	-2.70	-2.67	-2.56	-2.75	-3.48	-2.92	0.00	-2.83	-2.76	-3.08	0.00	-2.57
TCGA-26-6173-10A-01D-1845-08_GBM	-2.55	-4.63	-4.33	-2.58	-2.58	-2.60	-2.60	-2.64	-2.74	-3.42	-2.88	-4.63	-2.82	-2.69	0.00	-2.77	-2.52
TCGA-26-6174-10A-01D-1845-08_GBM	-2.60	-2.65	-2.62	-4.39	-2.71	-2.77	-2.67	-2.59	-2.69	-3.54	-2.76	-2.67	0.00	-2.74	0.00	-2.77	-2.54
TCGA-27-1830-10A-01D-1494-08_GBM	-2.54	0.00	0.00	-2.71	-2.56	-2.57	-2.67	-2.58	-2.52	0.00	-4.65	-4.65	0.00	0.00	0.00	-2.52	-2.56
TCGA-27-1831-10A-01D-1494-08_GBM	-2.53	-2.71	-2.69	-2.90	-2.62	-2.65	-2.73	-2.74	-3.92	-3.37	-2.71	0.00	-2.65	-2.51	0.00	0.00	-2.51
TCGA-27-1832-10A-01D-1494-08_GBM	-2.43	-4.51	-4.51	-2.62	-2.42	-2.50	-2.60	-2.61	-2.64	0.00	0.00	0.00	0.00	-4.21	0.00	-2.64	-2.60
TCGA-27-1833-10A-01D-1494-08_GBM	-2.54	-2.77	-2.74	-2.91	-2.68	-2.67	-2.65	-2.43	-2.52	0.00	-4.64	0.00	-4.64	-4.34	-3.03	-2.69	-2.53
TCGA-27-1834-10A-01D-1494-08_GBM	-2.57	0.00	-4.63	-2.90	-2.58	-2.55	-2.68	-2.45	-2.55	0.00	0.00	0.00	0.00	-4.63	0.00	-2.49	-2.56
TCGA-27-1835-10A-01D-1494-08_GBM	-2.63	-2.84	-2.80	-3.00	-2.53	-2.65	-2.72	-2.53	-2.59	-4.72	-2.99	-2.75	0.00	0.00	0.00	-2.51	-2.63
TCGA-27-1836-10A-01D-1494-08_GBM	-2.53	0.00	0.00	-2.62	-2.49	-2.56	-2.64	-2.59	-2.58	0.00	0.00	0.00	-4.61	-4.61	-2.94	0.00	-2.50
TCGA-27-1837-10A-01D-1494-08_GBM	-2.57	-2.74	-2.72	-2.92	-2.65	-2.69	-2.59	-2.60	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.49
TCGA-27-1838-10A-01D-1494-08_GBM	-2.52	-2.77	-2.70	-2.95	-2.63	-2.75	-2.67	-2.57	-2.57	0.00	0.00	0.00	0.00	-4.35	0.00	-2.58	-2.52
TCGA-27-2518-10A-01D-1494-08_GBM	-2.55	-2.74	-2.69	-2.90	-2.64	-2.69	-2.65	-2.52	-2.57	0.00	0.00	-4.63	-4.63	0.00	-3.03	-2.74	-2.54
TCGA-27-2519-10A-01D-1494-08_GBM	-2.55	-2.69	-2.73	-2.88	-2.64	-2.72	-2.75	-2.69	-4.01	-3.34	-2.77	0.00	-2.64	-2.55	0.00	-4.31	-2.54
TCGA-27-2521-10A-01D-1494-08_GBM	-2.53	0.00	-4.06	-2.71	-2.56	-2.62	-2.62	-2.59	-2.58	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.53
TCGA-27-2523-10A-01D-1494-08_GBM	-2.58	-4.62	-4.62	-2.77	-2.57	-2.58	-2.58	-2.54	-2.55	-4.62	-4.62	-4.62	0.00	0.00	0.00	-2.43	-2.55
TCGA-27-2524-10A-01D-1494-08_GBM	-2.56	-4.62	-3.93	-2.85	-2.52	-2.60	-2.59	-2.51	-2.56	0.00	-4.32	0.00	-4.15	-4.02	-3.07	-2.72	-2.53
TCGA-27-2526-10A-01D-1494-08_GBM	-2.55	-4.60	-4.30	-2.63	-2.53	-2.58	-2.64	-2.57	-2.51	0.00	0.00	0.00	-4.30	0.00	0.00	-2.63	-2.49
TCGA-27-2527-10A-01D-1494-08_GBM	-2.56	-2.73	-2.76	-2.97	-2.50	-2.63	-2.76	-2.74	-4.37	-3.29	-2.72	-2.71	-2.77	-2.70	0.00	-4.67	-2.59
TCGA-27-2528-10A-01D-1494-08_GBM	-2.62	0.00	-4.68	-2.90	-2.51	-2.63	-2.64	-2.60	-2.72	-3.30	-2.90	-4.68	-2.77	-2.76	-3.14	0.00	-2.54
TCGA-28-1747-10B-01D-1494-08_GBM	-2.50	-4.62	0.00	-2.78	-2.56	-2.57	-2.64	-2.51	-2.48	0.00	0.00	0.00	0.00	-4.62	-3.16	-2.74	-2.52
TCGA-28-1753-10B-01D-1494-08_GBM	-2.54	-4.33	-4.63	-2.63	-2.51	-2.52	-2.60	-2.49	-2.65	0.00	-4.63	0.00	0.00	-4.63	-3.06	-2.74	-2.58
TCGA-28-2499-10A-01D-1494-08_GBM	-2.60	-4.32	0.00	-2.85	-2.54	-2.58	-2.66	-2.44	-2.50	0.00	-4.62	0.00	0.00	-4.62	0.00	-2.48	-2.54
TCGA-28-2501-10A-01D-1696-08_GBM	-2.55	-4.50	-4.50	-2.77	-2.50	-2.56	-2.58	-2.63	-4.50	-3.22	-2.73	0.00	-2.61	-2.49	0.00	0.00	-2.47
TCGA-28-2502-10A-01D-1494-08_GBM	-2.61	-2.83	-2.84	-3.03	-2.50	-2.65	-2.69	-2.56	-2.66	0.00	-2.93	-2.77	-4.74	0.00	0.00	-2.53	-2.62
TCGA-28-2509-10A-01D-1494-08_GBM	-2.51	-2.67	-2.69	-4.38	-2.78	-2.74	-2.73	-2.64	-2.75	-3.34	-2.82	-2.69	-4.08	-2.72	-3.13	0.00	-2.60
TCGA-28-2510-10A-01D-1696-08_GBM	-2.48	-2.74	-2.71	-2.92	-2.45	-2.55	-2.55	-2.62	-2.52	0.00	-3.09	-2.72	0.00	-4.53	-2.94	-4.53	-2.47
TCGA-28-2513-10A-01D-1494-08_GBM	-2.59	-4.64	-4.34	-2.78	-2.48	-2.55	-2.59	-2.50	-2.54	0.00	0.00	0.00	0.00	0.00	-3.03	-2.74	-2.48
TCGA-28-2514-10A-01D-1494-08_GBM	-2.50	0.00	-4.30	-2.80	-2.54	-2.55	-2.64	-2.57	-2.50	0.00	0.00	-4.60	-4.60	-4.30	0.00	-2.60	-2.50
TCGA-28-5204-10A-01D-1486-08_GBM	-2.66	-2.69	-2.65	-4.38	-2.75	-2.74	-2.68	-2.57	-2.75	-3.45	-2.76	-2.79	-2.82	-2.75	0.00	-2.79	-2.57
TCGA-28-5207-10A-01D-1486-08_GBM	-2.50	-3.75	-3.69	-2.79	-2.51	-2.60	-2.55	-2.59	-2.54	0.00	-4.29	-3.75	-4.59	-3.69	0.00	-2.56	-2.42
TCGA-28-5208-10A-01D-1486-08_GBM	-2.53	-2.66	-2.67	-2.93	-2.64	-2.66	-2.43	-2.50	-2.48	0.00	0.00	-4.30	-4.60	-4.60	0.00	-2.41	-2.45
TCGA-28-5209-10A-01D-1486-08_GBM	-2.66	0.00	-4.78	-2.81	-2.47	-2.63	-2.64	-2.54	-2.83	-3.37	-2.81	-2.85	-2.87	-2.83	0.00	-2.84	-2.56
TCGA-28-5211-10B-01D-1845-08_GBM	-2.47	0.00	-4.54	-2.65	-2.52	-2.53	-2.55	-2.56	-2.51	0.00	0.00	-4.54	0.00	0.00	-2.87	0.00	-2.40
TCGA-28-5213-10A-01D-1486-08_GBM	-2.66	-2.80	-2.79	-2.97	-2.59	-2.68	-2.70	-2.59	-2.64	0.00	-2.96	-2.79	0.00	-4.43	0.00	-2.52	-2.61
TCGA-28-5214-10A-01D-1486-08_GBM	-2.54	-2.71	-2.72	-2.92	-2.61	-2.71	-2.64	-2.58	-2.60	0.00	0.00	-4.34	-4.64	-4.34	-2.95	-4.64	-2.47
TCGA-28-5215-10A-01D-1486-08_GBM	-2.52	-2.73	-2.68	-2.96	-2.66	-2.68	-2.61	-2.59	-2.57	0.00	0.00	0.00	0.00	-4.30	-2.89	0.00	-2.50
TCGA-28-5216-10A-01D-1486-08_GBM	-2.61	-2.75	-2.72	-2.92	-2.72	-2.71	-2.67	-2.61	-2.56	0.00	-4.66	0.00	0.00	-4.66	0.00	-2.59	-2.58
TCGA-28-5218-10A-01D-1486-08_GBM	-2.56	-2.77	-2.81	-2.92	-2.73	-2.75	-2.65	-2.61	-4.20	-3.23	-2.75	0.00	-2.68	-2.61	0.00	-4.68	-2.56
TCGA-28-5219-10A-01D-1486-08_GBM	-2.50	-4.28	0.00	-2.76	-2.50	-2.52	-2.57	-2.45	-2.47	-4.58	-4.58	-4.58	-4.58	-4.10	-3.01	-2.71	-2.50
TCGA-28-5220-10A-01D-1486-08_GBM	-2.51	-4.59	0.00	-2.70	-2.56	-2.55	-2.55	-2.47	-2.51	0.00	0.00	0.00	-4.59	-4.29	-3.00	-2.74	-2.48
TCGA-28-6450-10A-01D-1696-08_GBM	-2.63	-2.63	-2.62	-4.11	-2.57	-2.58	-2.60	-2.65	-2.71	-3.33	-2.69	-2.52	-4.11	-2.75	0.00	-2.80	-2.53
TCGA-29-2429-10A-01D-1526-09_OV	-2.65	-2.66	-2.72	-3.03	-2.70	-2.70	-2.60	-2.56	-2.51	0.00	0.00	0.00	0.00	0.00	-2.88	-2.69	-2.68
TCGA-29-2431-10A-01D-1526-09_OV	-2.64	-2.66	-2.77	-2.95	-2.71	-2.72	-2.58	-2.60	-2.61	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.65
TCGA-29-2432-10A-01D-1526-09_OV	-2.66	0.00	-4.70	-2.66	-2.56	-2.56	-2.58	-2.59	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.40	-2.68
TCGA-29-2434-10A-01D-1526-09_OV	-2.60	0.00	0.00	-2.70	-2.53	-2.52	-2.62	-2.55	-2.67	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.70
TCGA-29-2436-10A-01D-1526-09_OV	-2.63	0.00	0.00	-2.82	-2.52	-2.53	-2.64	-2.46	-2.65	0.00	0.00	0.00	0.00	0.00	0.00	-2.30	-2.69
TCGA-32-1970-10A-01D-1494-08_GBM	-2.59	-2.83	-2.79	-3.01	-2.56	-2.61	-2.70	-2.53	-2.63	0.00	-2.95	-2.73	-4.70	-4.40	0.00	-2.54	-2.60
TCGA-32-1977-10C-01D-1353-08_GBM	-2.56	-2.80	-2.80	-2.99	-2.49	-2.58	-2.67	-2.70	-2.73	-3.27	-2.86	-2.72	-2.82	-2.69	0.00	-2.85	-2.57
TCGA-32-1979-10A-01D-1696-08_GBM	-2.42	0.00	-4.47	-2.54	-2.52	-2.51	-2.52	-2.48	-2.55	0.00	0.00	0.00	0.00	-4.47	0.00	-2.41	-2.42
TCGA-32-1980-10A-01D-1696-08_GBM	-2.47	-2.59	-2.64	-2.82	-2.65	-2.63	-2.50	-2.56	-2.45	0.00	0.00	-4.45	0.00	-3.67	-2.91	0.00	-2.45
TCGA-32-1982-10A-01D-1494-08_GBM	-2.54	-2.72	-2.66	0.00	-2.73	-2.72	-2.67	-2.54	-2.63	-4.69	-2.88	0.00	0.00	0.00	0.00	-2.50	-2.57
TCGA-32-1986-10A-01D-1494-08_GBM	-2.54	0.00	-4.61	-2.89	-2.55	-2.60	-2.62	-2.51	-2.48	0.00	0.00	-4.61	-4.61	0.00	0.00	-2.48	-2.51
TCGA-32-1991-10C-01D-1353-08_GBM	-2.50	-4.63	0.00	-2.65	-2.53	-2.53	-2.59	-2.51	-2.62	0.00	0.00	0.00	-4.63	0.00	0.00	-2.44	-2.47
TCGA-32-2491-10A-01D-1353-08_GBM	-2.62	-2.80	-2.77	-3.01	-2.51	-2.63	-2.59	-2.63	-2.73	-3.37	-2.80	-2.55	0.00	-2.78	0.00	-2.84	-2.54
TCGA-32-2494-10A-01D-1353-08_GBM	-2.51	-2.78	-2.78	-2.94	-2.68	-2.76	-2.62	-2.52	-2.65	-3.24	-2.98	0.00	-2.81	-2.65	-3.16	-4.64	-2.49
TCGA-32-2495-10B-01D-1353-08_GBM	-2.49	-2.74	-2.70	-2.89	-2.62	-2.65	-2.60	-2.53	-2.45	0.00	0.00	0.00	0.00	-4.31	0.00	-2.60	-2.49
TCGA-32-2498-10B-01D-1353-08_GBM	-2.61	-2.78	-2.79	-2.98	-2.50	-2.66	-2.67	-2.66	-2.76	-3.38	-2.86	-2.61	0.00	-2.69	-3.18	0.00	-2.60
TCGA-32-2615-10A-01D-1495-08_GBM	-2.57	0.00	-4.26	-2.81	-2.60	-2.60	-2.59	-2.51	-2.57	0.00	-4.56	0.00	0.00	0.00	0.00	-2.60	-2.46
TCGA-32-2616-10A-01D-1495-08_GBM	-2.62	-4.62	-3.92	-2.90	-2.60	-2.63	-2.69	-2.58	-2.69	-3.42	-2.87	-2.77	-3.67	-2.72	-3.09	-3.92	-2.60
TCGA-32-2632-10A-01D-1495-08_GBM	-2.48	-2.76	-2.80	-2.92	-2.72	-2.68	-2.62	-2.64	-4.63	-3.19	-2.73	-4.63	-2.70	-2.57	0.00	-4.63	-2.54
TCGA-32-2634-10A-01D-1495-08_GBM	-2.63	-2.66	-2.65	0.00	-2.73	-2.79	-2.68	-2.68	-2.70	-3.37	-2.76	-2.72	-2.80	-2.73	0.00	-2.77	-2.58
TCGA-32-2638-10A-01D-1495-08_GBM	-2.63	-2.80	-2.78	-3.09	-2.53	-2.72	-2.68	-2.60	-2.74	-3.37	-2.80	-2.68	0.00	-2.75	-3.12	0.00	-2.60
TCGA-32-4208-10A-01D-1353-08_GBM	-2.47	0.00	0.00	-2.78	-2.53	-2.51	-2.58	-2.57	-2.44	0.00	-4.63	-4.63	0.00	-4.15	0.00	-2.58	-2.46
TCGA-32-4209-10A-01D-1353-08_GBM	-2.47	-2.70	-2.68	-2.87	-2.66	-2.65	-2.58	-2.54	-2.50	0.00	-4.61	0.00	0.00	-4.30	-2.91	0.00	-2.44
TCGA-32-4210-10A-01D-1353-08_GBM	-2.62	-2.84	-2.78	-3.02	-2.57	-2.66	-2.59	-2.47	-2.54	-3.41	-3.00	-2.76	-4.72	-4.41	-3.14	-2.85	-2.58

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-32-4211-10A-01D-1353-08_GBM	-2.49	0.00	0.00	-2.69	-2.53	-2.57	-2.60	-2.65	-2.67	-3.32	-3.01	0.00	-2.78	-2.69	0.00	-2.78	-2.48
TCGA-32-4213-10A-01D-1353-08_GBM	-2.60	-2.67	-2.64	-4.37	-2.75	-2.74	-2.69	-2.58	-2.74	-3.31	-2.82	-2.73	-2.82	-2.70	-3.22	-4.67	-2.55
TCGA-32-4719-10A-01D-1353-08_GBM	-2.45	-4.31	-4.31	-2.77	-2.47	-2.58	-2.58	-2.54	-2.48	0.00	-4.61	0.00	0.00	-4.14	-2.94	0.00	-2.44
TCGA-32-5222-10A-01D-1486-08_GBM	-2.66	-2.84	-2.81	-3.01	-2.57	-2.72	-2.73	-2.60	-2.81	-3.43	-2.85	-2.63	0.00	-2.80	-3.18	-4.15	-2.64
TCGA-33-A4WN-10A-01D-A25L-08_LUSC	-2.65	-2.79	-2.80	-3.00	-2.50	-2.67	-2.69	-2.63	-2.79	-3.32	-2.79	-2.80	-2.81	-2.79	0.00	-2.81	-2.58
TCGA-33-A5GW-10A-01D-A27N-08_LUSC	-2.54	-4.45	-4.15	-2.79	-2.51	-2.56	-2.54	-2.62	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.51
TCGA-34-5231-10A-01D-1817-08_LUSC	-2.56	0.00	0.00	-2.67	-2.54	-2.53	-2.62	-2.47	-2.47	0.00	0.00	0.00	-4.55	0.00	-3.09	-2.73	-2.53
TCGA-34-5232-10A-01D-1817-08_LUSC	-2.57	0.00	-4.27	-2.71	-2.46	-2.57	-2.55	-2.49	-2.61	-3.27	0.00	0.00	0.00	0.00	-3.01	0.00	-2.52
TCGA-34-5234-10A-01D-1632-08_LUSC	-2.51	-2.57	-2.59	-4.59	-2.60	-2.55	-2.60	-2.68	-2.49	0.00	-2.84	-2.59	0.00	-4.29	0.00	-2.66	-2.46
TCGA-34-5236-10A-01D-1817-08_LUSC	-2.48	-4.50	-3.90	-2.71	-2.54	-2.57	-2.57	-2.56	-2.52	0.00	-4.50	0.00	0.00	-4.20	-2.99	-2.70	-2.48
TCGA-34-5239-10A-01D-1817-08_LUSC	-2.54	-2.55	-2.58	-4.53	0.00	-3.92	-2.57	-2.59	-2.66	-3.25	-2.83	0.00	-2.73	-2.67	0.00	-2.69	-2.47
TCGA-34-5240-10A-01D-1441-08_LUSC	-2.58	0.00	-4.61	-2.85	-2.62	-2.65	-2.65	-2.53	-2.75	-3.29	-2.88	0.00	-2.85	-2.75	-3.05	-4.31	-2.62
TCGA-34-5241-10A-01D-1441-08_LUSC	-2.48	-4.05	-4.53	-2.83	-2.53	-2.58	-2.57	-2.48	-2.45	0.00	0.00	0.00	0.00	-4.23	-3.02	-2.61	-2.54
TCGA-34-5927-10A-01D-1817-08_LUSC	-2.50	-4.52	0.00	-2.57	-2.57	-2.53	-2.60	-2.58	-2.52	0.00	0.00	-4.52	0.00	-4.22	0.00	-2.59	-2.44
TCGA-34-5928-10A-01D-1817-08_LUSC	-2.41	-2.63	-2.72	-2.81	-2.68	-2.66	-2.65	-2.71	-2.66	0.00	-2.85	-2.70	0.00	-2.64	0.00	-2.79	-2.55
TCGA-34-7107-10A-01D-1945-08_LUSC	-2.52	-2.77	-2.72	-2.86	-2.67	-2.69	-2.54	-2.62	-2.74	-3.32	-2.80	-2.74	0.00	-2.63	0.00	-2.74	-2.50
TCGA-34-8454-10A-01D-2323-08_LUSC	-2.60	-2.75	-2.76	-2.96	-2.50	-2.65	-2.68	-2.60	-2.67	-3.38	-2.78	-2.74	-2.85	-2.71	-3.13	0.00	-2.54
TCGA-34-8455-10A-01D-2323-08_LUSC	-2.54	-2.60	-2.61	-4.33	-2.73	-2.75	-2.56	-2.63	-2.70	-3.33	-2.77	-2.59	0.00	-2.68	0.00	-2.76	-2.51
TCGA-34-8456-10A-01D-2323-08_LUSC	-2.59	0.00	-4.17	-2.62	-2.55	-2.53	-2.57	-2.55	-2.56	0.00	0.00	-4.47	0.00	0.00	-3.09	-2.78	-2.49
TCGA-34-A5IX-10A-01D-A27N-08_LUSC	-2.54	0.00	-4.47	-2.73	-2.53	-2.52	-2.55	-2.56	-2.52	0.00	0.00	0.00	0.00	-4.47	-2.98	0.00	-2.46
TCGA-35-3615-10A-01D-1489-08_LUAD	-2.50	-3.39	-4.04	-2.69	-2.59	-2.54	-2.58	-2.54	-2.53	-4.64	-4.16	-3.86	-4.64	-3.74	-3.00	-2.72	-2.55
TCGA-35-4122-10A-01D-1105-08_LUAD	-2.58	0.00	-4.64	-2.68	-2.54	-2.53	-2.65	-2.66	-4.64	-3.21	-2.72	-2.71	-2.73	-2.59	0.00	-4.64	-2.54
TCGA-35-4123-10A-01D-1105-08_LUAD	-2.52	-2.72	-2.72	-2.88	-2.63	-2.64	-2.60	-2.54	-2.55	0.00	-4.29	-4.59	0.00	0.00	0.00	-2.57	-2.50
TCGA-35-5375-10A-01D-1625-08_LUAD	-2.60	-2.83	-2.78	-2.93	-2.54	-2.54	-2.60	-2.61	-2.79	-3.53	-2.84	-2.66	0.00	-2.74	0.00	-2.81	-2.52
TCGA-36-2530-10A-01D-1526-09_OV	-2.61	-4.24	0.00	-2.87	-2.58	-2.60	-2.68	-2.77	-2.89	-3.51	-2.94	0.00	-2.83	-2.70	0.00	-2.69	-2.68
TCGA-36-2532-10A-01D-1526-09_OV	-2.77	-4.78	0.00	-2.78	-2.63	-2.66	-2.69	-2.64	-2.89	-3.48	-2.74	-4.78	-2.79	-2.76	-2.83	0.00	-2.77
TCGA-36-2533-10A-01D-1526-09_OV	-2.54	0.00	0.00	-2.74	-2.57	-2.46	-2.79	-3.30	-3.25	-3.45	-3.39	0.00	-2.89	-2.71	0.00	-2.69	-2.58
TCGA-36-2534-10A-01D-1526-09_OV	-2.66	0.00	0.00	-2.82	-2.56	-2.56	-2.59	-2.60	-2.55	0.00	0.00	0.00	0.00	0.00	-2.66	0.00	-2.62
TCGA-36-2537-10A-01D-1526-09_OV	-2.57	0.00	-4.70	-2.95	-2.51	-2.51	-2.57	-2.62	-2.60	0.00	0.00	0.00	0.00	0.00	-2.63	0.00	-2.66
TCGA-36-2538-10A-01D-1526-09_OV	-2.70	0.00	0.00	-2.86	-2.60	-2.56	-2.53	-2.52	-2.88	-3.19	-2.80	0.00	-2.76	-2.73	0.00	-2.71	-2.66
TCGA-36-2539-10A-01D-1526-09_OV	-2.64	0.00	0.00	-2.67	-2.52	-2.54	-2.61	-2.57	-2.58	0.00	0.00	0.00	0.00	0.00	-2.90	-2.69	-2.61
TCGA-36-2540-10A-01D-1526-09_OV	-2.65	-2.70	-2.72	-2.98	-2.67	-2.74	-2.61	-2.43	-2.56	0.00	0.00	0.00	0.00	0.00	-2.81	-2.65	-2.70
TCGA-36-2542-10A-01D-1526-09_OV	-2.70	-2.59	-2.64	0.00	-2.82	-2.80	-2.71	-2.79	-2.95	-3.50	-2.73	-2.64	0.00	-2.75	0.00	-2.67	-2.75
TCGA-36-2543-10A-01D-1526-09_OV	-2.59	-2.63	-2.63	-2.94	-2.67	-2.67	-2.61	-2.67	-2.64	0.00	0.00	0.00	0.00	0.00	-2.71	-2.64	-2.60
TCGA-36-2544-10A-01D-1526-09_OV	-2.57	-2.46	-2.50	0.00	-2.70	-2.72	-2.56	-2.57	-2.60	0.00	-2.79	-2.67	0.00	0.00	0.00	-2.52	-2.63
TCGA-36-2545-10A-01D-1526-09_OV	-2.66	0.00	0.00	-2.84	-2.57	-2.57	-2.60	-2.56	-2.58	0.00	0.00	0.00	0.00	0.00	-2.91	-2.65	-2.69
TCGA-36-2547-10A-01D-1526-09_OV	-2.68	-2.72	-2.80	-3.03	-2.75	-2.74	-2.66	-2.55	-2.84	-3.36	-2.80	0.00	-2.77	-2.76	-2.76	0.00	-2.73
TCGA-36-2548-10A-01D-1526-09_OV	-2.61	0.00	0.00	-2.64	-2.52	-2.50	-2.59	-2.53	-2.58	0.00	0.00	0.00	0.00	0.00	-2.87	-2.73	-2.61
TCGA-36-2551-10A-01D-1526-09_OV	-2.69	-2.76	-2.75	-3.02	-2.77	-2.84	-2.65	-2.57	-2.78	-3.50	-2.73	0.00	-2.78	-2.75	0.00	-2.64	-2.74
TCGA-36-2552-10A-01D-1526-09_OV	-2.64	-2.75	-2.75	-3.01	-2.51	-2.62	-2.63	-2.64	-2.69	0.00	-2.89	-2.78	0.00	0.00	-2.87	-2.74	-2.72
TCGA-37-3783-10A-01D-1267-08_LUSC	-2.42	0.00	0.00	-2.63	-2.40	-2.62	-2.71	-2.75	-2.70	0.00	0.00	0.00	0.00	-2.59	0.00	-2.67	-2.59
TCGA-37-3789-10A-01D-0983-08_LUSC	-2.57	-2.80	-2.82	-2.92	-2.44	-2.60	-2.56	-2.72	-2.61	0.00	-2.89	-2.86	-4.70	-4.70	0.00	-2.62	-2.51
TCGA-37-3792-10A-01D-0983-08_LUSC	-2.50	-2.68	-2.75	-2.93	-2.62	-2.70	-2.77	-2.85	-2.67	0.00	-2.98	0.00	-2.74	-2.74	-3.18	0.00	-2.47
TCGA-37-4129-10A-01D-1352-08_LUSC	-2.74	0.00	-4.98	-3.02	-2.64	-2.70	-2.76	-2.90	-2.70	0.00	0.00	0.00	0.00	0.00	0.00	-2.92	-2.61
TCGA-37-4130-10A-01D-1352-08_LUSC	-2.48	-2.84	-2.79	-3.01	-2.63	-2.67	-2.57	-2.62	-2.60	0.00	0.00	-4.56	0.00	0.00	0.00	-2.56	-2.45
TCGA-37-4132-10A-01D-1352-08_LUSC	-2.50	0.00	-4.82	-2.67	-2.51	-2.59	-2.56	-2.57	-2.61	0.00	-4.82	-4.82	0.00	-4.52	-3.25	-2.80	-2.55
TCGA-37-4133-10A-01D-1352-08_LUSC	-2.51	-2.79	-2.78	-2.86	-2.75	-2.73	-2.57	-2.64	-2.53	0.00	0.00	0.00	-4.87	0.00	0.00	-2.63	-2.39
TCGA-37-4135-10A-01D-1352-08_LUSC	-2.57	-4.83	0.00	-2.76	-2.55	-2.54	-2.60	-2.58	-2.56	0.00	0.00	0.00	0.00	-4.83	0.00	-2.65	-2.52
TCGA-37-4141-10A-01D-1352-08_LUSC	-2.48	0.00	-4.81	-2.70	-2.48	-2.56	-2.61	-2.65	-2.58	0.00	0.00	-4.81	0.00	-4.51	0.00	-2.60	-2.47
TCGA-37-5819-10A-01D-1632-08_LUSC	-2.37	-2.70	-2.66	-2.83	-2.65	-2.67	-2.51	-2.50	-2.44	0.00	0.00	0.00	0.00	-4.20	0.00	-2.49	-2.37
TCGA-37-A5EL-10A-01D-A26K-08_LUSC	-2.67	-2.75	-2.73	-3.03	-2.57	-2.64	-2.64	-2.64	-2.80	-3.46	-2.70	-2.59	-4.10	-2.77	0.00	-2.81	-2.56
TCGA-37-A5EM-10A-01D-A27N-08_LUSC	-2.63	-2.80	-2.75	-3.02	-2.52	-2.68	-2.71	-2.60	-2.76	-3.35	-2.68	-2.77	-2.76	-2.70	-3.19	-4.55	-2.60
TCGA-37-A5EN-10A-01D-A26K-08_LUSC	-2.53	-2.78	-2.72	-2.82	-2.48	-2.57	-2.59	-2.60	-2.54	0.00	-2.98	-2.68	0.00	-4.60	0.00	-2.67	-2.49
TCGA-38-6178-10A-01D-1753-08_LUAD	-2.46	0.00	0.00	-2.56	-2.48	-2.42	-2.52	-2.55	-2.44	0.00	0.00	0.00	0.00	0.00	-3.00	-2.81	-2.39
TCGA-38-A44F-10A-01D-A24F-08_LUAD	-2.52	-2.66	-2.63	-2.86	-2.61	-2.68	-2.75	-2.73	-3.66	-3.33	-2.67	0.00	-2.60	-2.56	0.00	-4.50	-2.52
TCGA-41-2571-10A-01D-1495-08_GBM	-2.68	-2.83	-2.82	-2.97	-2.55	-2.67	-2.72	-2.62	-2.83	-3.41	-2.73	-2.81	-2.83	-2.75	0.00	-2.91	-2.65
TCGA-41-2572-10A-01D-1353-08_GBM	-2.43	-2.70	-2.64	-2.84	-2.64	-2.67	-2.57	-2.49	-2.46	0.00	0.00	-4.61	0.00	0.00	-3.05	-2.76	-2.46
TCGA-41-2573-10A-01D-1495-08_GBM	-2.70	-2.82	-2.81	-3.02	-2.59	-2.71	-2.73	-2.73	-2.74	-3.38	-2.83	-2.80	-2.86	-2.80	0.00	-2.94	-2.67
TCGA-41-2575-10A-01D-1495-08_GBM	-2.55	-2.67	-2.69	-2.89	-2.64	-2.68	-2.60	-2.59	-2.52	0.00	0.00	0.00	0.00	0.00	-2.96	-4.07	-2.50
TCGA-41-3392-10A-01D-1495-08_GBM	-2.48	-2.77	-2.74	-2.94	-2.70	-2.65	-2.63	-2.42	-2.53	0.00	0.00	0.00	0.00	-4.57	-3.07	-2.80	-2.55
TCGA-41-3393-10A-01D-1353-08_GBM	-2.47	-4.30	-4.30	-2.61	-2.52	-2.58	-2.56	-2.53	-2.42	0.00	-4.30	0.00	-4.60	-4.12	0.00	-2.54	-2.44
TCGA-41-3915-10A-01D-1353-08_GBM	-2.55	0.00	-4.69	-2.81	-2.56	-2.58	-2.76	-2.55	-2.66	-3.22	-2.95	0.00	-2.80	-2.73	0.00	-2.83	-2.53
TCGA-41-4097-10A-01D-1353-08_GBM	-2.54	0.00	-4.65	-2.67	-2.53	-2.59	-2.59	-2.55	-2.66	-3.27	-3.06	0.00	-2.81	-2.72	0.00	-2.71	-2.47
TCGA-41-5651-10A-01D-1696-08_GBM	-2.46	-2.70	-2.64	-2.90	-2.62	-2.63	-2.56	-2.42	-2.45	0.00	0.00	0.00	0.00	0.00	-2.99	-2.70	-2.48
TCGA-41-6646-10A-01D-1845-08_GBM	-2.50	-4.33	0.00	-2.85	-2.59	-2.65	-2.62	-2.53	-2.75	-3.35	-2.86	-4.63	-2.72	-2.71	0.00	-2.73	-2.47
TCGA-42-2582-10A-01D-1526-09_OV	-2.62	0.00	0.00	-2.63	-2.54	-2.57	-2.61	-2.58	-2.66	0.00	0.00	0.00	-4.79	0.00	0.00	-2.35	-2.65
TCGA-42-2587-10A-01D-1526-09_OV	-2.58	-2.69	-2.69	-3.01	-2.65	-2.71	-2.63	-2.55	-2.63	0.00	0.00	0.00	0.00	0.00	-2.80	-2.59	-2.72
TCGA-42-2588-10A-01D-1526-09_OV	-2.55	-2.46	-2.51	0.00	0.00	0.00	-2.58	-2.60	-2.61	0.00	0.00	0.00	0.00	0.00	-2.82	-2.57	-2.56
TCGA-42-2589-10A-01D-1526-09_OV	-2.70	-2.69	-2.66	-3.05	-2.68	-2.64	-2.62	-2.48	-2.59	0.00	0.00	-4.75	0.00	0.00	-2.79	-2.64	-2.66
TCGA-42-2590-10A-01D-1526-09_OV	-2.54	0.00	0.00	-2.87	-2.56	-2.55	-2.60	-2.58	-2.63	0.00	0.00	0.00	0.00	0.00	-2.85	-2.62	-2.66
TCGA-42-2591-10A-01D-1526-09_OV	-2.72	-2.64	-2.59	0.00	-4.74	-4.74	-2.65	-2.59	-2.74	-3.26	-2.78	-2.69	0.00	-2.74	0.00	-2.60	-2.67
TCGA-42-2593-10A-01D-1764-09_OV	-2.70	0.00	0.00	-2.79	-2.67	-2.69	-2.73	-2.58	-2.84	-3.54	-2.78	0.00	-2.87	-2.82	-2.92	0.00	-2.78
TCGA-43-3394-10A-01D-0983-08_LUSC	-2.57	-2.77	-4.67	-2.88	-2.65	-2.74	-2.78	-2.91	-2.69	0.00	-2.70	-2.76	-2.77	-2.71	-3.18	-4.67	-2.42
TCGA-43-3920-10A-01D-0983-08_LUSC	-2.55	-2.84	-2.82	-2.98	-2.51	-2.57	-2.58	-2.74	-2.66	0.00	-2.97	-2.83	0.00	0.00	0.00	-2.64	-2.48
TCGA-43-5668-10A-01D-1632-08_LUSC	-2.49	-2.74	-2.70	-3.05	-2.69	-2.74	-2.55	-2.58	-2.68	-3.45	-2.95	0.00	-2.73	-2.65	-3.13	0.00	-2.39
TCGA-43-5670-10A-01D-2122-08_LUSC	-2.60	-2.74	-2.75	-2.92	-2.60	-2.65	-2.67	-2.70	-2.76	-3.31	-2.75	-2.65	0.00	-2.78	0.00	-2.79	-2.58
TCGA-43-6143-10A-01D-1817-08_LUSC	-2.57	0.00	-4.54	-2.60	-2.53	-2.61	-2.63	-2.51	-2.46	0.00	0.00	0.00	0.00	-4.54	-3.08	-2.72	-2.52
TCGA-43-6647-10A-01D-1817-08_LUSC	-2.56	-4.26	-4.56	-2.70	-2.59	-2.58	-2.64	-2.59	-2.63	-3.29	-2.82	-4.26	-2.80	-2.67	0.00	-2.74	-2.56
TCGA-43-6770-10A-01D-1817-08_LUSC	-2.60	-2.82	-2.73	-2.93	-2.56	-2.55	-2.71	-2.57	-2.64	-4.61	-2.94	-2.75	0.00	-4.00	-3.19	-2.92	-2.64
TCGA-43-6771-10A-01D-1817-08_LUSC	-2.50	0.00	-4.55	-2.55	-2.53	-2.58	-2.59	-2.39	-2.57	-4.55	0.00	0.00	0.00	-4.25	-3.05	-2.66	-2.51
TCGA-43-6773-10A-01D-1945-08_LUSC	-2.50	0.00	0.00	-2.68	-2.53	-2.54	-2.57	-2.51	-2.43	0.00	0.00	0.00	0.00	-4.53	0.00	-2.42	-2.49
TCGA-43-7656-10A-01D-2122-08_LUSC	-2.55	-4.18	-3.63	-2.71	-2.51	-2.54	-2.55	-2.53	-2.58	-4.18	0.00	-3.78	-4.48	-4.48	0.00	-2.57	-2.46
TCGA-43-7657-10A-01D-2122-08_LUSC	-2.51	0.00	-4.15	-2.76	-2.51	-2.52	-2.58	-2.59	-2.52	0.00	-4.45	-4.45	-4.45	-4.15	0.00	-2.56	-2.45
TCGA-43-7658-10A-01D-2122-08_LUSC	-2.59	-2.71	-2.70	-2.76	-2.68	-2.70	-2.60	-2.54	-2.66	-3.27	-2.89	0.00	-2.69	-2.65	-3.16	-4.50	-2.60
TCGA-43-8115-10A-01D-2244-08_LUSC	-2.41	0.00	0.00	-2.61	-2.45	-2.47	-2.43	-2.49	-2.36	0.00	0.00	0.00	0.00	-4.35	0.00	-2.42	-2.34
TCGA-43-8116-10A-01D-2244-08_LUSC	-2.44	-2.63	-2.67	-2.73	-2.56	-2.58	-2.51	-2.60	-2.41	0.00	0.00	0.00	-4.41	-4.41	0.00	-2.55	-2.43
TCGA-43-8118-10A-01D-2395-08_LUSC	-2.66	-2.78	-2.83	-3.00	-2.59	-2.72	-2.72	-2.63	-2.77	-3.37	-2.76	-2.73	0.00	-2.78	-3.11	0.00	-2.70
TCGA-43-A474-10A-01D-A24F-08_LUSC	-2.61	-3.77	-3.77	-2.71	-2.57	-2.59	-2.60	-2.63	-2.49	0.00	-4.47	0.00	0.00	0.00	0.00	-2.61	-2.50
TCGA-43-A475-10A-01D-A24F-08_LUSC	-2.47	-4.37	0.00	-2.68	-2.48	-2.53	-2.49	-2.54	-2.44	0.00	0.00	-4.37	0.00	0.00	0.00	-2.56	-2.46
TCGA-43-A56U-10A-01D-A26K-08_LUSC	-2.53	-2.54	-2.57	0.00	-2.63	-2.72	-2.59	-2.42	-2.49	0.00	-2.89	-2.67	-4.53	-3.75	0.00	-2.41	-2.49
TCGA-43-A56V-10A-01D-A26K-08_LUSC	-2.46	-2.70	0.00	-2.81	-2.72	-2.71	-2.71	-2.74	-2.65	-4.39	-2.86	0.00	-2.66	-2.64	0.00	-2.69	-2.43
TCGA-44-2656-10A-01D-0969-08_LUAD	-2.58	0.00	-4.63	-2.64	-2.60	-2.62	-2.66	-2.50	-2.56	0.00	0.00	0.00	0.00	-4.63	0.00	-2.61	-2.58
TCGA-44-2657-10A-01D-1105-08_LUAD	-2.53	-2.75	-2.68	-2.98	-2.65	-2.72	-2.61	-2.54	-2.54	0.00	0.00	0.00	0.00	-4.17	-3.20	-2.76	-2.49
TCGA-44-2659-10A-01D-0969-08_LUAD	-2.58	-2.77	-2.72	-2.94	-2.73	-2.74	-2.63	-2.66	-2.73	-3.33	-2.86	-2.72	0.00	-2.77	0.00	-2.76	-2.61
TCGA-44-2661-10A-01D-1105-08_LUAD	-2.46	-2.63	-2.55	0.00	-4.27	-4.57	-2.57	-2.62	-2.44	0.00	0.00	0.00	0.00	-4.57	0.00	-2.55	-2.47
TCGA-44-2662-10A-01D-0969-08_LUAD	-2.55	-2.74	-2.69	-2.91	-2.71	-2.66	-2.63	-2.47	-2.49	0.00	-4.64	0.00	-4.64	0.00	-3.08	-2.69	-2.46

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-44-2665-10A-01D-1040-01_LUAD	-2.64	-2.72	-2.67	0.00	-2.74	-2.76	-2.69	-2.56	-2.77	-3.46	-2.79	-2.63	-4.69	-2.71	0.00	-2.82	-2.55
TCGA-44-2666-10A-01D-A271-08_LUAD	-2.48	0.00	0.00	-2.57	-2.50	-2.50	-2.51	-2.54	-2.49	0.00	0.00	0.00	0.00	-4.49	0.00	-2.56	-2.42
TCGA-44-2668-10A-01D-1489-08_LUAD	-2.56	0.00	0.00	-2.87	-2.60	-2.66	-2.69	-2.62	-2.69	-3.24	-2.89	0.00	-2.75	-2.72	0.00	-2.75	-2.59
TCGA-44-3396-10A-01D-1265-08_LUAD	-2.46	0.00	-4.60	-2.85	-2.44	-2.47	-2.58	-2.60	-2.51	0.00	-4.60	0.00	0.00	-4.30	-2.90	-4.60	-2.49
TCGA-44-3398-10A-01D-1105-08_LUAD	-2.42	0.00	-4.62	-2.85	-2.50	-2.55	-2.59	-2.53	-2.47	0.00	0.00	-4.62	-4.62	-4.32	0.00	-2.51	-2.51
TCGA-44-3917-10A-01D-A271-08_LUAD	-2.49	-4.46	0.00	-2.54	-2.47	-2.46	-2.49	-2.49	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.46
TCGA-44-3918-10A-01D-A271-08_LUAD	-2.49	-4.49	-4.49	-2.74	-2.49	-2.50	-2.51	-2.47	-2.40	0.00	-4.49	0.00	0.00	0.00	0.00	-2.51	-2.44
TCGA-44-3919-10A-01D-1458-08_LUAD	-2.58	-2.80	-2.74	-2.97	-2.69	-2.70	-2.64	-2.51	-2.60	0.00	0.00	0.00	0.00	0.00	-3.04	-2.76	-2.53
TCGA-44-4112-10A-01D-1458-08_LUAD	-2.59	-2.78	-2.81	-3.04	-2.52	-2.69	-2.72	-2.63	-2.78	-3.45	-2.78	-2.79	-2.84	-2.78	-3.17	0.00	-2.64
TCGA-44-5643-10A-01D-1625-08_LUAD	-2.52	0.00	-4.24	-2.66	-2.52	-2.56	-2.59	-2.55	-2.59	-3.43	-3.00	0.00	-2.71	-2.67	-3.09	0.00	-2.39
TCGA-44-5644-10A-01D-2036-08_LUAD	-2.52	0.00	-4.54	-2.61	-2.52	-2.54	-2.55	-2.43	-2.44	0.00	-4.54	0.00	-4.24	-4.54	0.00	-2.42	-2.46
TCGA-44-5645-10A-01D-1625-08_LUAD	-2.38	-4.47	-4.47	-2.69	-2.52	-2.50	-2.53	-2.50	-2.36	0.00	0.00	0.00	0.00	-4.47	-3.19	-2.80	-2.32
TCGA-44-6144-10A-01D-1753-08_LUAD	-2.43	0.00	-4.47	-2.59	-2.50	-2.55	-2.46	-2.56	-2.44	-4.47	0.00	-4.47	0.00	-4.47	0.00	-2.63	-2.38
TCGA-44-6145-10A-01D-1753-08_LUAD	-2.55	-2.75	-2.76	-2.92	-2.46	-2.53	-2.62	-2.65	-2.69	-3.26	-2.78	-2.60	0.00	-2.68	0.00	-2.82	-2.44
TCGA-44-6146-10A-01D-1753-08_LUAD	-2.54	-2.72	-2.70	-2.96	-2.47	-2.57	-2.58	-2.64	-4.54	-3.13	-2.69	-2.59	-2.80	-2.51	0.00	0.00	-2.57
TCGA-44-6147-10A-01D-1753-08_LUAD	-2.49	-4.46	0.00	-2.69	-2.43	-2.46	-2.56	-2.62	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.35
TCGA-44-6148-10A-01D-1753-08_LUAD	-2.45	-4.15	-4.45	-2.58	-2.41	-2.49	-2.52	-2.54	-2.42	0.00	0.00	0.00	-4.45	0.00	0.00	-2.59	-2.37
TCGA-44-6774-10A-01D-1855-08_LUAD	-2.49	-2.57	-2.56	-4.56	0.00	-4.26	-2.59	-2.49	-2.65	-3.36	-2.78	0.00	-2.70	-2.65	-3.06	-3.72	-2.47
TCGA-44-6775-10A-01D-1855-08_LUAD	-2.59	-2.78	-2.76	-2.92	-2.51	-2.68	-2.70	-2.54	-2.59	0.00	-2.96	-2.74	0.00	-4.65	0.00	-2.54	-2.58
TCGA-44-6776-10A-01D-1855-08_LUAD	-2.55	-2.61	-2.58	0.00	-2.73	-2.68	-2.65	-2.43	-2.50	0.00	-2.89	-2.67	0.00	0.00	-3.14	-2.74	-2.51
TCGA-44-6777-10A-01D-1855-08_LUAD	-2.42	0.00	0.00	-2.60	-2.55	-2.60	-2.62	-2.47	-2.46	0.00	-4.56	0.00	0.00	0.00	0.00	-2.49	-2.49
TCGA-44-6778-10A-01D-1855-08_LUAD	-2.60	0.00	0.00	-2.84	-2.49	-2.64	-2.61	-2.56	-2.53	0.00	-2.89	0.00	-2.78	0.00	-3.24	-2.75	-2.58
TCGA-44-7659-10A-01D-2063-08_LUAD	-2.53	-2.71	-2.69	-2.84	-2.65	-2.66	-2.58	-2.57	-2.55	0.00	0.00	0.00	-4.51	0.00	0.00	-2.58	-2.51
TCGA-44-7660-10A-01D-2063-08_LUAD	-2.56	-2.50	-2.54	-4.20	-4.20	-3.89	-2.56	-2.43	-2.52	0.00	0.00	-4.20	0.00	-4.50	-3.02	-2.66	-2.48
TCGA-44-7661-10A-01D-2063-08_LUAD	-2.48	-2.73	-2.76	-2.92	-2.72	-2.71	-2.58	-2.60	-3.96	-3.20	-2.68	0.00	-2.63	-2.52	0.00	-4.56	-2.46
TCGA-44-7662-10A-01D-2063-08_LUAD	-2.61	-2.64	-2.65	0.00	-2.74	-2.74	-2.58	-2.48	-2.53	0.00	-2.88	-2.69	0.00	0.00	-3.05	-2.69	-2.53
TCGA-44-7667-10A-01D-2063-08_LUAD	-2.47	-4.25	-3.95	-2.61	-2.56	-2.62	-2.57	-2.53	-2.48	0.00	0.00	-4.07	0.00	0.00	-3.07	-2.72	-2.49
TCGA-44-7669-10A-01D-2063-08_LUAD	-2.58	-2.60	-2.56	0.00	-2.65	-2.74	-2.54	-2.51	-2.47	0.00	-2.85	-2.66	-4.52	-4.21	0.00	-2.56	-2.49
TCGA-44-7670-10A-01D-2063-08_LUAD	-2.54	-4.03	-3.91	-2.73	-2.52	-2.56	-2.59	-2.59	-2.46	0.00	0.00	-4.21	0.00	-4.51	0.00	-2.58	-2.47
TCGA-44-7671-10A-01D-2063-08_LUAD	-2.53	-4.51	-4.04	-2.74	-2.40	-2.56	-2.60	-2.61	-2.55	0.00	0.00	-4.04	-4.51	-4.04	-3.01	-2.61	-2.47
TCGA-44-7672-10A-01D-2063-08_LUAD	-2.54	0.00	-4.51	-2.71	-2.53	-2.56	-2.59	-2.44	-2.45	0.00	0.00	-4.51	0.00	-4.51	-2.97	-2.74	-2.47
TCGA-44-8117-10A-01D-2238-08_LUAD	-2.48	0.00	0.00	-2.72	-2.49	-2.53	-2.49	-2.50	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.36	-2.45
TCGA-44-8119-10A-01D-2238-08_LUAD	-2.52	-2.67	-2.66	-2.80	-2.62	-2.56	-2.65	-2.71	-2.59	0.00	-2.80	0.00	-2.79	-2.56	-3.12	-4.12	-2.41
TCGA-44-8120-10A-01D-2238-08_LUAD	-2.58	-2.66	-2.69	-4.04	-2.76	-2.75	-2.58	-2.61	-2.69	-3.62	-2.81	-2.70	-2.92	-2.65	0.00	-2.79	-2.50
TCGA-44-A479-10A-01D-A24F-08_LUAD	-2.60	-2.72	-2.73	-2.90	-2.62	-2.65	-2.65	-2.65	-2.57	0.00	-2.88	-4.54	-2.67	-3.76	-3.02	-4.54	-2.59
TCGA-44-A47A-10A-01D-A24F-08_LUAD	-2.37	-4.43	-3.82	-2.77	-2.52	-2.56	-2.51	-2.51	-2.49	0.00	-3.82	0.00	-4.13	-3.73	-3.00	-2.69	-2.48
TCGA-44-A47B-10A-01D-A24F-08_LUAD	-2.57	-2.77	-2.72	-2.88	-2.72	-2.70	-2.62	-2.52	-2.63	-3.29	-2.81	-2.76	0.00	-2.66	-3.03	0.00	-2.57
TCGA-44-A47F-10A-01D-A24F-08_LUAD	-2.69	-2.73	-2.73	-2.94	-2.51	-2.62	-2.66	-2.76	-2.76	-3.42	-2.69	-2.71	-2.82	-2.71	0.00	-2.78	-2.58
TCGA-44-A47G-10A-01D-A24F-08_LUAD	-2.58	-4.48	-4.01	-2.78	-2.60	-2.63	-2.66	-2.58	-2.73	-3.25	-2.87	-2.71	-4.18	-2.67	0.00	-2.68	-2.52
TCGA-44-A4SS-10A-01D-A24P-08_LUAD	-2.53	0.00	-4.46	-2.78	-2.57	-2.56	-2.63	-2.45	-2.56	0.00	0.00	0.00	-3.86	-4.46	0.00	-2.40	-2.51
TCGA-44-A4SU-10A-01D-A24P-08_LUAD	-2.60	-4.03	-3.81	-2.74	-2.59	-2.61	-2.61	-2.53	-2.51	0.00	-4.03	0.00	-4.03	-3.66	-2.97	-2.65	-2.58
TCGA-46-3765-10A-01D-0983-08_LUSC	-2.52	-2.60	-2.55	0.00	-2.68	-2.80	-2.58	-2.59	-2.57	0.00	-2.89	-2.83	0.00	0.00	-3.21	-2.89	-2.51
TCGA-46-3766-10A-01D-0983-08_LUSC	-2.52	-2.75	-2.72	-2.87	-2.70	-2.73	-2.54	-2.63	-2.49	0.00	0.00	0.00	0.00	0.00	-3.23	-2.80	-2.43
TCGA-46-3767-10A-01D-0983-08_LUSC	-2.60	-4.67	0.00	-2.59	-2.51	-2.52	-2.56	-2.63	-2.86	-3.49	-2.97	0.00	-2.85	-2.77	0.00	-2.81	-2.50
TCGA-46-3768-10A-01D-0983-08_LUSC	-2.48	-2.73	-2.67	-2.78	-2.68	-2.78	-2.50	-2.65	-2.46	0.00	0.00	0.00	0.00	-4.59	-3.21	-2.86	-2.35
TCGA-46-3769-10A-01D-0983-08_LUSC	-2.49	-2.78	-2.77	-2.84	-2.68	-2.72	-2.50	-2.61	-2.44	0.00	0.00	-4.60	0.00	-4.60	0.00	-2.48	-2.43
TCGA-46-6025-10A-01D-1817-08_LUSC	-2.62	-2.84	-2.80	-2.94	-2.54	-2.67	-2.67	-2.67	-2.80	-3.16	-2.73	-2.79	-2.84	-2.77	0.00	-2.85	-2.61
TCGA-46-6026-10A-01D-1817-08_LUSC	-2.48	-2.65	-2.67	-2.82	-2.66	-2.63	-2.57	-2.45	-2.47	0.00	0.00	-4.51	-4.51	-4.21	-2.99	-2.73	-2.47
TCGA-50-5044-10A-01D-1855-08_LUAD	-2.57	-2.77	-2.79	-2.89	-2.59	-2.68	-2.69	-2.61	-2.76	-3.45	-2.79	-2.76	-2.84	-2.78	0.00	-2.84	-2.56
TCGA-50-5045-10A-01D-1625-08_LUAD	-2.42	0.00	0.00	-2.61	-2.49	-2.53	-2.49	-2.53	-2.44	0.00	0.00	-4.48	0.00	-4.48	0.00	-2.50	-2.37
TCGA-50-5049-10A-01D-1625-08_LUAD	-2.53	-2.74	-2.61	-2.94	-2.61	-2.61	-2.51	-2.54	-2.38	0.00	0.00	-4.48	0.00	-4.48	0.00	-2.49	-2.43
TCGA-50-5051-10A-01D-1855-08_LUAD	-2.52	-2.78	-2.75	-2.89	-2.49	-2.62	-2.63	-2.66	-2.52	0.00	-2.88	-2.78	0.00	-4.16	0.00	-2.67	-2.52
TCGA-50-5055-10A-01D-1625-08_LUAD	-2.62	-2.84	-2.74	-2.92	-2.55	-2.72	-2.73	-2.66	-2.73	-3.40	-2.75	-2.81	-2.94	-2.76	0.00	-2.77	-2.63
TCGA-50-5066-10A-01D-1625-08_LUAD	-2.46	-2.72	-2.67	-2.86	-2.67	-2.66	-2.52	-2.43	-2.38	0.00	0.00	0.00	0.00	0.00	-3.10	-2.74	-2.36
TCGA-50-5068-10A-01D-1625-08_LUAD	-2.49	0.00	-4.19	-2.69	-2.47	-2.49	-2.50	-2.50	-2.42	0.00	0.00	0.00	-4.49	0.00	0.00	-2.50	-2.40
TCGA-50-5072-10A-01D-1855-08_LUAD	-2.48	0.00	-4.56	-2.67	-2.49	-2.58	-2.55	-2.59	-2.52	0.00	-4.56	0.00	0.00	0.00	-2.96	0.00	-2.42
TCGA-50-5941-10A-01D-1753-08_LUAD	-2.38	0.00	-4.44	-2.56	-2.48	-2.48	-2.50	-2.54	-2.38	0.00	-4.44	0.00	0.00	0.00	-3.18	-2.67	-2.39
TCGA-50-5942-10A-01D-1753-08_LUAD	-2.47	0.00	0.00	-2.69	-2.43	-2.43	-2.51	-2.52	-2.43	0.00	0.00	0.00	0.00	-4.46	-3.02	-2.71	-2.40
TCGA-50-5944-10A-01D-1753-08_LUAD	-2.53	-2.70	-2.65	-2.79	-2.57	-2.66	-2.60	-2.58	-2.72	-3.21	-2.89	-2.61	0.00	-2.64	0.00	-2.76	-2.45
TCGA-50-5946-10A-01D-1753-08_LUAD	-2.58	-2.74	-2.78	-2.91	-2.49	-2.62	-2.60	-2.60	-2.74	-3.33	-2.79	-2.58	0.00	-2.68	-3.14	0.00	-2.49
TCGA-50-6597-10A-01D-1855-08_LUAD	-2.53	-2.70	-2.67	-2.85	-2.68	-2.65	-2.79	-2.67	-2.61	0.00	-2.78	-2.67	-4.57	-2.67	-3.11	0.00	-2.51
TCGA-50-8457-10A-01D-2323-08_LUAD	-2.44	0.00	0.00	-2.71	-2.46	-2.48	-2.51	-2.48	-2.43	0.00	0.00	0.00	-4.53	0.00	-3.04	-2.68	-2.46
TCGA-50-8459-10A-01D-2323-08_LUAD	-2.47	-2.45	-2.48	0.00	-4.18	0.00	-2.49	-2.48	-2.43	0.00	0.00	0.00	0.00	0.00	-2.99	-2.63	-2.29
TCGA-50-8460-10A-01D-2323-08_LUAD	-2.51	-2.57	-2.59	0.00	-2.53	-2.58	-2.57	-2.63	-2.71	-3.39	-2.69	-2.50	0.00	-2.71	0.00	-2.88	-2.50
TCGA-52-7622-10A-01D-2122-08_LUSC	-2.41	-4.46	0.00	-2.77	-2.52	-2.53	-2.56	-2.48	-2.52	0.00	0.00	0.00	0.00	-4.16	-3.00	-2.71	-2.50
TCGA-52-7809-10A-01D-2122-08_LUSC	-2.51	-2.65	-2.64	-2.83	-2.64	-2.63	-2.59	-2.49	-2.52	0.00	-4.16	0.00	-4.46	-3.68	0.00	-2.42	-2.45
TCGA-52-7810-10A-01D-2122-08_LUSC	-2.59	-4.51	-3.90	-2.77	-2.54	-2.56	-2.60	-2.64	-3.90	-3.16	-2.69	0.00	-2.65	-2.57	0.00	-4.03	-2.51
TCGA-52-7811-10A-01D-2122-08_LUSC	-2.59	0.00	-4.51	-2.56	-2.51	-2.53	-2.59	-2.47	-2.45	0.00	0.00	0.00	0.00	-4.21	0.00	-2.40	-2.50
TCGA-52-7812-10A-01D-2122-08_LUSC	-2.53	-3.91	-3.91	-2.85	-2.45	-2.44	-2.59	-2.62	-2.75	-3.21	-2.77	-2.74	-2.79	-2.77	0.00	-2.74	-2.58
TCGA-53-7624-10A-01D-2063-08_LUAD	-2.45	-2.65	-2.70	-2.76	-2.60	-2.69	-2.48	-2.59	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.32
TCGA-53-7626-10A-01D-2063-08_LUAD	-2.50	0.00	-4.48	-2.60	-2.48	-2.57	-2.56	-2.54	-2.45	0.00	0.00	0.00	0.00	0.00	-3.08	-2.74	-2.47
TCGA-53-7813-10A-01D-2167-08_LUAD	-2.43	-2.71	-2.70	-2.79	-2.62	-2.68	-2.67	-2.90	-2.65	0.00	-2.94	-4.46	-2.85	-2.60	0.00	-2.68	-2.36
TCGA-53-A4EZ-10A-01D-A24P-08_LUAD	-2.61	-2.67	-2.66	-2.85	-2.71	-2.68	-2.65	-2.52	-2.60	0.00	-4.51	0.00	-3.67	-3.81	-3.04	-2.68	-2.56
TCGA-55-5899-10A-01D-1625-08_LUAD	-2.50	0.00	0.00	-2.65	-2.52	-2.52	-2.57	-2.55	-2.75	-3.46	-3.01	-2.64	0.00	-2.70	0.00	-2.82	-2.46
TCGA-55-6543-10A-01D-1753-08_LUAD	-2.44	-2.67	-2.59	-2.82	-2.57	-2.55	-2.47	-2.64	-2.49	0.00	0.00	-4.40	0.00	0.00	0.00	-2.52	-2.40
TCGA-55-6712-10A-01D-1855-08_LUAD	-2.60	-2.79	-2.78	-2.92	-2.55	-2.70	-2.71	-2.58	-2.88	-3.45	-2.80	-2.69	-4.68	-2.76	0.00	-2.85	-2.63
TCGA-55-7227-10A-01D-2036-08_LUAD	-2.49	-2.68	-2.62	-2.85	-2.62	-2.66	-2.52	-2.57	-2.46	0.00	0.00	0.00	0.00	0.00	-2.93	-4.46	-2.43
TCGA-55-7281-10A-01D-2036-08_LUAD	-2.53	-4.01	-4.19	-2.56	-2.41	-2.53	-2.48	-2.49	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.45
TCGA-55-7283-10A-01D-2036-08_LUAD	-2.55	-2.82	-2.72	-2.88	-2.51	-2.63	-2.63	-2.59	-2.53	0.00	-2.91	-2.69	0.00	0.00	-3.15	-2.86	-2.52
TCGA-55-7284-10A-01D-2238-08_LUAD	-2.57	0.00	-4.52	-2.74	-2.42	-2.55	-2.59	-2.57	-2.59	-3.29	-2.83	-4.05	-2.78	-2.69	-3.02	0.00	-2.44
TCGA-55-7570-10A-01D-2036-08_LUAD	-2.55	-4.04	-4.21	-2.77	-2.57	-2.60	-2.59	-2.46	-2.50	0.00	-4.51	-4.51	-4.51	-3.91	-3.02	-2.76	-2.50
TCGA-55-7574-10A-01D-2036-08_LUAD	-2.51	0.00	0.00	-2.73	-2.53	-2.57	-2.61	-2.41	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.45
TCGA-55-7576-10A-01D-2063-08_LUAD	-2.41	0.00	0.00	-2.62	-2.36	-2.53	-2.50	-2.62	-2.44	0.00	-4.19	0.00	-4.49	-3.71	-3.19	-2.87	-2.33
TCGA-55-7724-10A-01D-2167-08_LUAD	-2.43	0.00	0.00	-2.62	-2.46	-2.51	-2.48	-2.54	-2.56	0.00	0.00	0.00	-4.51	-4.21	0.00	-2.53	-2.37
TCGA-55-7725-10A-01D-2167-08_LUAD	-2.47	0.00	0.00	-2.52	-2.44	-2.51	-2.50	-2.57	-2.50	0.00	0.00	-4.50	-4.50	0.00	-2.99	-2.65	-2.39
TCGA-55-7726-10A-01D-2167-08_LUAD	-2.49	0.00	0.00	-2.67	-2.44	-2.47	-2.48	-2.60	-2.38	0.00	0.00	-4.12	0.00	0.00	-3.03	-2.73	-2.40
TCGA-55-7727-10A-01D-2167-08_LUAD	-2.56	0.00	0.00	-2.55	-2.54	-2.52	-2.56	-2.69	-4.07	-3.13	-2.75	-2.67	-2.79	-2.55	0.00	0.00	-2.46
TCGA-55-7728-10A-01D-2184-08_LUAD	-2.46	-4.45	0.00	-2.71	-2.49	-2.48	-2.57	-2.59	-2.41	-4.45	-4.15	0.00	0.00	0.00	0.00	-2.53	-2.46
TCGA-55-7815-10A-01D-2167-08_LUAD	-2.48	0.00	0.00	-2.58	-2.42	-2.48	-2.53	-2.63	-2.42	-4.51	0.00	0.00	-4.51	-4.03	0.00	-2.56	-2.38
TCGA-55-7816-10A-01D-2167-08_LUAD	-2.58	-2.86	-2.80	-2.89	-2.48	-2.53	-2.54	-2.68	-2.54	0.00	-3.04	-2.78	0.00	0.00	-3.11	-2.75	-2.44
TCGA-55-7903-10A-01D-2167-08_LUAD	-2.69	-2.88	-2.92	-2.91	-2.49	-2.55	-2.62	-2.72	-2.76	-3.27	-2.77	-2.64	-2.99	-2.78	0.00	-2.90	-2.49
TCGA-55-7907-10A-01D-2167-08_LUAD	-2.46	0.00	-4.46	-2.49	-2.44	-2.49	-2.48	-2.57	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.39
TCGA-55-7911-10A-01D-2167-08_LUAD	-2.53	-2.78	-2.76	-2.82	-2.65	-2.58	-2.56	-2.58	-2.51	0.00	0.00	0.00	0.00	-4.49	-3.13	-2.79	-2.39
TCGA-55-7913-10A-01D-2238-08_LUAD	-2.55	-2.63	-2.65	-4.53	-2.67	-2.75	-2.63	-2.61	-2.47	0.00	-2.80	0.00	-2.78	-4.53	0.00	-2.56	-2.48
TCGA-55-7914-10A-01D-2167-08_LUAD	-2.45	-2.73	-2.68	-2.73	-2.58	-2.61	-2.52	-2.65	-2.46	0.00	0.00	-4.12	0.00	0.00	-3.19	-2.75	-2.36
TCGA-55-7994-10A-01D-2184-08_LUAD	-2.53	-2.55	-2.57	-4.47	-2.61	-2.67	-2.56	-2.53	-2.49	0.00	-2.85	-2.64	0.00	0.00	0.00	-2.45	-2.46

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-55-7995-10A-01D-2184-08_LUAD	-2.45	-4.43	-4.13	-2.52	-2.50	-2.46	-2.47	-2.62	-2.56	0.00	0.00	0.00	0.00	-4.13	0.00	-2.52	-2.36
TCGA-55-8085-10A-01D-2238-08_LUAD	-2.58	0.00	-4.51	-2.72	-2.55	-2.53	-2.56	-2.55	-2.70	-3.36	-2.85	0.00	-2.75	-2.66	0.00	-2.68	-2.48
TCGA-55-8087-10A-01D-2238-08_LUAD	-2.56	-2.68	-2.71	-2.80	-2.63	-2.63	-2.61	-2.60	-2.63	-3.29	-2.84	0.00	-2.83	-2.61	-3.06	0.00	-2.51
TCGA-55-8089-10A-01D-2238-08_LUAD	-2.50	-2.66	-2.62	-2.80	-2.57	-2.59	-2.52	-2.53	-2.47	0.00	0.00	0.00	0.00	-4.46	-2.84	-4.46	-2.43
TCGA-55-8090-10A-01D-2238-08_LUAD	-2.57	-4.52	-3.91	-2.76	-2.55	-2.51	-2.57	-2.55	-2.62	-3.34	-2.83	-4.52	-2.78	-2.58	-3.07	-4.52	-2.47
TCGA-55-8091-10A-01D-2238-08_LUAD	-2.59	0.00	-4.47	-2.67	-2.49	-2.54	-2.53	-2.59	-2.44	0.00	-4.17	0.00	0.00	-3.99	0.00	-2.56	-2.46
TCGA-55-8092-10A-01D-2238-08_LUAD	-2.47	0.00	0.00	-2.73	-2.52	-2.55	-2.54	-2.49	-2.58	0.00	0.00	0.00	0.00	-4.46	0.00	-2.33	-2.35
TCGA-55-8094-10A-01D-2238-08_LUAD	-2.52	0.00	-4.52	-2.58	-2.52	-2.55	-2.62	-2.47	-2.44	0.00	0.00	0.00	0.00	-4.52	0.00	-2.38	-2.49
TCGA-55-8096-10A-01D-2238-08_LUAD	-2.47	-2.75	-2.64	-2.77	-2.62	-2.68	-2.55	-2.50	-2.49	0.00	0.00	0.00	0.00	0.00	-2.96	-2.73	-2.44
TCGA-55-8097-10A-01D-2238-08_LUAD	-2.52	0.00	0.00	-2.68	-2.54	-2.55	-2.58	-2.60	-3.90	-3.14	-2.63	-4.50	-2.64	-2.52	0.00	-4.50	-2.47
TCGA-55-8203-10A-01D-2238-08_LUAD	-2.46	0.00	-4.46	-2.66	-2.46	-2.52	-2.49	-2.47	-2.54	0.00	0.00	-4.46	-4.46	0.00	0.00	-2.35	-2.43
TCGA-55-8204-10A-01D-2238-08_LUAD	-2.54	0.00	0.00	-2.70	-2.52	-2.51	-2.55	-2.46	-2.42	0.00	-4.51	0.00	-4.51	-4.21	0.00	-2.35	-2.45
TCGA-55-8205-10A-01D-2238-08_LUAD	-2.58	-2.72	-2.77	-2.88	-2.68	-2.69	-2.64	-2.62	-2.64	-3.17	-2.83	-4.05	-2.72	-2.69	0.00	-2.69	-2.49
TCGA-55-8206-10A-01D-2238-08_LUAD	-2.50	0.00	-4.50	-2.70	-2.53	-2.53	-2.51	-2.51	-2.61	0.00	-4.50	0.00	-4.50	-4.50	0.00	-2.40	-2.39
TCGA-55-8207-10A-01D-2238-08_LUAD	-2.48	-2.65	-2.68	-2.77	-2.56	-2.60	-2.45	-2.62	-2.49	0.00	0.00	0.00	0.00	-4.17	0.00	-2.48	-2.40
TCGA-55-8208-10A-01D-2238-08_LUAD	-2.54	-2.65	-2.69	-2.77	-2.63	-2.59	-2.50	-2.53	-2.43	0.00	0.00	0.00	0.00	-4.49	-2.97	-2.65	-2.43
TCGA-55-8299-10B-01D-2323-08_LUAD	-2.42	-2.48	-2.45	-4.52	0.00	0.00	-2.45	-2.44	-2.43	0.00	-4.52	0.00	0.00	-4.52	-2.95	-2.66	-2.42
TCGA-55-8301-10A-01D-2284-08_LUAD	-2.52	0.00	0.00	-2.67	-2.47	-2.57	-2.59	-2.65	-2.71	-3.30	-2.80	-2.79	-2.89	-2.72	0.00	-2.84	-2.55
TCGA-55-8302-10A-01D-2323-08_LUAD	-2.52	-2.69	-2.65	-2.79	-2.64	-2.56	-2.55	-2.45	-2.41	0.00	0.00	0.00	0.00	0.00	-3.04	-2.75	-2.41
TCGA-55-8505-10A-01D-2393-08_LUAD	-2.68	-2.81	-2.79	-2.97	-2.54	-2.66	-2.73	-2.57	-2.74	-3.32	-2.79	-2.76	-2.85	-2.79	0.00	-2.78	-2.65
TCGA-55-8506-10A-01D-2393-08_LUAD	-2.47	-2.69	-2.66	-2.85	-2.72	-2.67	-2.60	-2.43	-2.52	0.00	0.00	0.00	0.00	-4.57	-3.00	-2.66	-2.56
TCGA-55-8507-10A-01D-2393-08_LUAD	-2.45	-2.46	-2.46	-4.21	0.00	0.00	-2.47	-2.41	-2.37	0.00	0.00	0.00	0.00	-4.51	0.00	-2.34	-2.37
TCGA-55-8508-10A-01D-2393-08_LUAD	-2.66	-2.77	-2.77	-3.04	-2.58	-2.66	-2.72	-2.59	-2.68	0.00	-2.87	-2.75	0.00	-4.67	-3.12	-2.78	-2.60
TCGA-55-8510-10A-01D-2393-08_LUAD	-2.55	-2.57	-2.56	0.00	-2.68	-2.63	-2.52	-2.65	-2.51	0.00	-2.98	-2.62	-4.58	0.00	-2.91	-4.58	-2.46
TCGA-55-8511-10A-01D-2393-08_LUAD	-2.53	0.00	0.00	-2.70	-2.50	-2.54	-2.50	-2.58	-2.70	-3.38	-2.95	0.00	-2.75	-2.61	0.00	-2.78	-2.44
TCGA-55-8512-10A-01D-2393-08_LUAD	-2.68	-2.79	-2.77	-2.95	-2.57	-2.69	-2.77	-2.68	-2.77	-3.46	-2.78	-2.69	-4.69	-2.82	-3.24	-3.99	-2.68
TCGA-55-8513-10A-01D-2393-08_LUAD	-2.52	0.00	-4.43	-2.79	-2.53	-2.54	-2.58	-2.63	-2.42	-4.43	0.00	0.00	0.00	0.00	0.00	-2.58	-2.52
TCGA-55-8514-10A-01D-2393-08_LUAD	-2.52	-2.67	-2.70	-2.85	-2.60	-2.62	-2.47	-2.49	-2.41	0.00	0.00	0.00	0.00	-4.53	0.00	-2.42	-2.45
TCGA-55-8614-10A-01D-2393-08_LUAD	-2.55	0.00	-4.59	-2.61	-2.54	-2.58	-2.58	-2.52	-2.70	-3.31	-2.93	0.00	-2.74	-2.67	0.00	-2.76	-2.46
TCGA-55-8615-10A-01D-2393-08_LUAD	-2.66	-4.13	-3.83	-2.81	-2.46	-2.67	-2.67	-2.67	-2.71	-3.31	-2.77	0.00	-2.75	-2.73	0.00	-2.80	-2.58
TCGA-55-8616-10A-01D-2393-08_LUAD	-2.59	-2.80	-2.75	-2.90	-2.49	-2.44	-2.63	-2.69	-2.79	-3.36	-2.75	-2.80	-2.77	-2.69	0.00	-2.83	-2.57
TCGA-55-8619-10A-01D-2393-08_LUAD	-2.65	-2.65	-2.65	-4.29	-2.79	-2.70	-2.66	-2.60	-2.76	-3.36	-2.78	-2.60	0.00	-2.71	0.00	-2.73	-2.60
TCGA-55-8620-10A-01D-2393-08_LUAD	-2.57	0.00	0.00	-2.80	-2.52	-2.55	-2.62	-2.63	-2.65	-3.36	-2.99	0.00	-2.77	-2.63	0.00	-2.80	-2.40
TCGA-55-8621-10A-01D-2393-08_LUAD	-2.55	0.00	-4.60	-2.76	-2.47	-2.58	-2.56	-2.62	-2.73	-3.32	-2.92	0.00	-2.76	-2.65	0.00	-2.79	-2.48
TCGA-55-A48X-10A-01D-A24F-08_LUAD	-2.47	-4.49	-4.49	-2.78	-2.58	-2.63	-2.60	-2.62	-2.69	-3.29	-2.81	0.00	-2.74	-2.63	0.00	-2.72	-2.54
TCGA-55-A48Y-10A-01D-A24F-08_LUAD	-2.44	-4.46	-3.77	-2.61	-2.54	-2.57	-2.58	-2.53	-2.61	0.00	-3.56	-3.51	0.00	-4.16	0.00	-2.42	-2.58
TCGA-55-A48Z-10A-01D-A24P-08_LUAD	-2.55	-2.67	-2.66	-2.84	-2.63	-2.70	-2.63	-2.64	-2.58	0.00	0.00	0.00	-4.50	0.00	0.00	-2.58	-2.57
TCGA-55-A490-10A-01D-A24F-08_LUAD	-2.54	-4.11	-3.89	-2.96	-2.52	-2.65	-2.72	-2.65	-2.83	-3.27	-2.73	-2.75	-2.77	-2.75	0.00	-2.80	-2.64
TCGA-55-A491-10A-01D-A24F-08_LUAD	-2.55	-2.69	-2.65	-2.85	-2.64	-2.63	-2.62	-2.56	-2.59	0.00	-4.47	-4.47	0.00	0.00	0.00	-2.55	-2.52
TCGA-55-A492-10A-01D-A24F-08_LUAD	-2.61	-3.89	-4.02	-2.80	-2.60	-2.58	-2.57	-2.59	-2.53	0.00	-4.49	-3.72	0.00	-3.89	0.00	-2.64	-2.58
TCGA-55-A493-10A-01D-A24F-08_LUAD	-2.57	-2.61	-2.60	-4.51	-2.66	-2.69	-2.61	-2.61	-2.60	0.00	-2.87	-2.70	0.00	-4.51	-2.92	0.00	-2.56
TCGA-55-A494-10A-01D-A24P-08_LUAD	-2.62	-3.68	-3.93	-2.82	-2.57	-2.64	-2.64	-2.61	-2.68	-3.42	-2.86	-4.05	-2.74	-2.68	0.00	-2.77	-2.54
TCGA-55-A4DF-10A-01D-A24F-08_LUAD	-2.60	-2.64	-2.63	-4.63	-2.60	-2.62	-2.60	-2.52	-2.71	-3.45	-2.69	-2.51	0.00	-2.77	-3.15	-4.63	-2.54
TCGA-55-A4DG-10A-01D-A24F-08_LUAD	-2.63	-2.79	-2.71	-2.94	-2.50	-2.58	-2.63	-2.67	0.00	-3.31	-2.66	-2.63	-2.81	-2.58	0.00	0.00	-2.53
TCGA-56-5897-10A-01D-1632-08_LUSC	-2.49	0.00	-4.03	-2.83	-2.46	-2.46	-2.53	-2.57	-2.46	0.00	-4.51	0.00	0.00	-4.51	-3.09	-2.73	-2.38
TCGA-56-5898-10A-01D-1632-08_LUSC	-2.53	0.00	-4.52	-2.62	-2.53	-2.52	-2.58	-2.57	-2.76	-3.62	-2.95	0.00	-2.79	-2.72	0.00	-2.79	-2.49
TCGA-56-6545-10A-01D-1817-08_LUSC	-2.53	-2.63	-2.68	-2.88	-2.66	-2.70	-2.53	-2.51	-2.53	0.00	0.00	0.00	0.00	-4.51	-2.96	-2.77	-2.47
TCGA-56-6546-10A-01D-1817-08_LUSC	-2.55	-4.55	-4.55	-2.77	-2.57	-2.59	-2.59	-2.60	-2.65	-3.32	-2.83	0.00	-2.75	-2.69	0.00	-2.74	-2.56
TCGA-56-7221-10A-01D-2042-08_LUSC	-2.58	-2.73	-2.79	-2.90	-2.52	-2.63	-2.64	-2.62	-2.62	0.00	-2.88	-2.71	0.00	0.00	0.00	-2.63	-2.54
TCGA-56-7222-10A-01D-2042-08_LUSC	-2.47	0.00	0.00	-2.75	-2.54	-2.49	-2.55	-2.45	-2.52	0.00	-4.48	-4.48	0.00	-4.48	0.00	-2.36	-2.46
TCGA-56-7223-10A-01D-2042-08_LUSC	-2.56	-2.74	-2.77	-2.93	-2.49	-2.64	-2.64	-2.56	-2.53	0.00	-2.89	-2.67	0.00	0.00	-3.09	-2.79	-2.50
TCGA-56-7579-10A-01D-2042-08_LUSC	-2.57	-2.78	-2.76	-3.00	-2.54	-2.63	-2.58	-2.51	-2.65	-3.52	-2.91	-2.76	0.00	0.00	-3.13	-2.82	-2.53
TCGA-56-7580-10A-01D-2042-08_LUSC	-2.55	-2.68	-2.68	-2.91	-2.68	-2.72	-2.61	-2.66	-2.70	-3.29	-2.84	0.00	-2.75	-2.68	0.00	-2.70	-2.45
TCGA-56-7582-10A-01D-2042-08_LUSC	-2.46	0.00	0.00	-2.73	-2.52	-2.54	-2.52	-2.45	-2.44	0.00	0.00	-4.52	0.00	0.00	-3.10	-2.76	-2.43
TCGA-56-7731-10A-01D-2122-08_LUSC	-2.49	0.00	0.00	-2.58	-2.48	-2.55	-2.53	-2.41	-2.50	0.00	0.00	0.00	-4.41	-3.81	0.00	-2.45	-2.45
TCGA-56-7822-10A-01D-2122-08_LUSC	-2.64	-2.75	-2.68	-2.97	-2.51	-2.68	-2.65	-2.67	-2.63	-4.56	-2.86	-2.74	-4.08	-3.71	0.00	-2.50	-2.53
TCGA-56-7823-10A-01D-2244-08_LUSC	-2.72	-2.83	-2.84	-2.99	-2.66	-2.73	-2.79	-2.81	-2.82	-3.42	-2.82	-2.86	-2.88	-2.86	0.00	-2.84	-2.66
TCGA-56-8082-10A-01D-2244-08_LUSC	-2.43	-4.36	0.00	-2.62	-2.41	-2.42	-2.47	-2.50	-2.36	-4.36	0.00	0.00	0.00	-4.36	0.00	-2.51	-2.40
TCGA-56-8083-10A-01D-2244-08_LUSC	-2.40	-4.16	0.00	-2.56	-2.56	-2.55	-2.58	-2.53	-2.64	-3.16	-2.93	0.00	-2.78	-2.64	-3.10	0.00	-2.49
TCGA-56-8201-10A-01D-2244-08_LUSC	-2.59	-2.79	-2.80	-2.90	-2.46	-2.63	-2.64	-2.64	-2.73	-3.45	-2.76	-2.69	-2.85	-2.68	0.00	-2.79	-2.51
TCGA-56-8304-10A-01D-2323-08_LUSC	-2.69	-2.68	-2.71	0.00	-2.74	-2.79	-2.68	-2.60	-2.56	0.00	-2.85	-2.79	0.00	-4.62	0.00	-2.54	-2.63
TCGA-56-8307-10A-01D-2293-08_LUSC	-2.47	-4.19	0.00	-2.71	-2.56	-2.55	-2.55	-2.59	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.46
TCGA-56-8308-10A-01D-2293-08_LUSC	-2.56	0.00	-4.51	-2.71	-2.54	-2.57	-2.57	-2.54	-2.66	-3.28	-2.81	0.00	-2.79	-2.66	0.00	-2.71	-2.44
TCGA-56-8309-10A-01D-2293-08_LUSC	-2.48	0.00	0.00	-2.53	-2.52	-2.50	-2.44	-2.58	-2.44	0.00	0.00	0.00	0.00	-4.43	0.00	-2.51	-2.40
TCGA-56-8503-10A-01D-2395-08_LUSC	-2.57	-2.57	-2.58	-3.80	-3.60	-3.80	-2.60	-2.61	-3.72	-3.12	-2.71	-4.50	-2.63	-2.57	0.00	-4.02	-2.52
TCGA-56-8504-10A-01D-2395-08_LUSC	-2.66	-2.75	-2.75	-2.96	-2.52	-2.64	-2.65	-2.58	-2.59	-4.58	-2.86	-2.82	-4.58	-3.98	-3.13	-2.70	-2.63
TCGA-56-8622-10A-01D-2395-08_LUSC	-2.54	-2.68	-2.65	-2.86	-2.69	-2.65	-2.59	-2.51	-2.48	0.00	-4.20	-4.50	0.00	-4.20	0.00	-2.43	-2.53
TCGA-56-8623-10A-01D-2395-08_LUSC	-2.45	-3.83	-4.05	-2.63	-2.60	-2.55	-2.60	-2.46	-2.52	0.00	0.00	-3.93	0.00	0.00	-3.05	-2.73	-2.51
TCGA-56-8624-10A-01D-2395-08_LUSC	-2.62	-2.68	-2.61	-4.27	-2.70	-2.68	-2.61	-2.54	-2.62	-3.25	-2.84	-2.76	0.00	-4.57	-3.09	-2.74	-2.55
TCGA-56-8625-10A-01D-2395-08_LUSC	-2.56	-3.89	-4.50	-2.72	-2.56	-2.56	-2.55	-2.50	-2.61	0.00	-4.50	-4.19	-3.89	0.00	0.00	-2.44	-2.53
TCGA-56-8626-10A-01D-2395-08_LUSC	-2.51	-2.62	-2.60	-2.85	-2.56	-2.63	-2.51	-2.50	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.40
TCGA-56-8628-10A-01D-2395-08_LUSC	-2.63	-2.76	-2.72	-2.93	-2.54	-2.68	-2.68	-2.72	-3.69	-3.25	-2.68	-2.81	-2.72	-2.70	0.00	-3.99	-2.61
TCGA-56-8629-10A-01D-2395-08_LUSC	-2.46	-4.02	-3.90	-2.77	-2.55	-2.53	-2.58	-2.49	-2.51	-4.50	-4.20	-3.90	-4.02	-3.90	0.00	-2.43	-2.49
TCGA-56-A49D-10A-01D-A24F-08_LUSC	-2.48	-4.37	0.00	-2.58	-2.45	-2.48	-2.54	-2.55	-2.47	0.00	-4.37	0.00	0.00	-4.37	0.00	-2.55	-2.45
TCGA-56-A4BW-10A-01D-A24F-08_LUSC	-2.54	-2.66	-2.69	-2.86	-2.70	-2.69	-2.58	-2.57	-2.59	-3.42	-2.87	0.00	-2.77	-2.65	-3.08	-4.46	-2.51
TCGA-56-A4BX-10A-01D-A24F-08_LUSC	-2.57	-2.76	-2.73	-2.93	-2.50	-2.63	-2.60	-2.69	-2.74	-3.31	-2.76	-2.75	-2.81	-2.71	0.00	-2.76	-2.48
TCGA-56-A4BY-10A-01D-A24F-08_LUSC	-2.47	-2.47	-2.50	-4.38	-3.90	-4.38	-2.49	-2.39	-2.42	-4.08	-4.38	-4.38	-4.08	-3.90	-2.92	-2.66	-2.46
TCGA-56-A4ZJ-10A-01D-A25L-08_LUSC	-2.63	-2.60	-2.58	-4.08	-3.66	-3.78	-2.58	-2.47	-2.57	-3.38	-2.85	-3.60	-2.83	-3.96	-3.05	-2.71	-2.54
TCGA-56-A4ZK-10A-01D-A25L-08_LUSC	-2.56	-4.28	0.00	-2.76	-2.62	-2.64	-2.74	-2.51	-2.69	-3.44	-2.89	0.00	-2.78	-2.67	-3.11	-3.68	-2.53
TCGA-56-A5DR-10A-01D-A27N-08_LUSC	-2.56	-2.67	-2.71	-2.85	-2.67	-2.64	-2.63	-2.65	0.00	-3.20	-2.72	0.00	-2.61	-2.59	0.00	-4.51	-2.56
TCGA-56-A5DS-10A-01D-A27N-08_LUSC	-2.56	0.00	0.00	-2.77	-2.53	-2.55	-2.57	-2.47	-2.57	0.00	0.00	0.00	0.00	0.00	0.00	-2.40	-2.51
TCGA-58-8386-10A-01D-2293-08_LUSC	-2.51	-2.73	-2.69	-2.87	-2.65	-2.65	-2.62	-2.60	-2.68	-3.21	-2.86	-4.53	-2.79	-2.61	0.00	-2.68	-2.45
TCGA-58-8387-10A-01D-2293-08_LUSC	-2.60	-2.79	-2.76	-2.88	-2.43	-2.58	-2.60	-2.55	-2.48	0.00	-2.96	-2.72	0.00	-4.50	0.00	-2.47	-2.46
TCGA-58-8388-10A-01D-2323-08_LUSC	-2.55	-2.65	-4.28	-2.95	-2.44	-2.53	-2.61	-2.55	-2.75	-3.35	-2.87	0.00	-2.75	-2.66	0.00	-2.74	-2.47
TCGA-58-8390-10A-01D-2323-08_LUSC	-2.45	0.00	0.00	-2.69	-2.51	-2.55	-2.52	-2.51	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.44	-2.47
TCGA-58-8391-10A-01D-2323-08_LUSC	-2.50	0.00	-4.57	-2.58	-2.54	-2.54	-2.54	-2.58	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.43
TCGA-58-8392-10A-01D-2323-08_LUSC	-2.49	-4.64	0.00	-2.77	-2.53	-2.54	-2.53	-2.63	-2.54	-3.34	-2.90	-2.78	0.00	-2.67	0.00	-2.87	-2.56
TCGA-58-8393-10A-01D-2323-08_LUSC	-2.52	-2.75	-2.71	-2.91	-2.51	-2.58	-2.58	-2.56	-2.50	0.00	-2.92	-2.71	0.00	-4.61	0.00	-2.67	-2.49
TCGA-58-A46J-10A-01D-A24F-08_LUSC	-2.65	-2.66	-2.64	0.00	-2.70	-2.74	-2.69	-2.66	-2.69	-3.40	-2.69	-2.74	-2.78	-2.71	0.00	-2.78	-2.56
TCGA-58-A46K-10A-01D-A24F-08_LUSC	-2.62	-2.78	-2.78	-2.90	-2.51	-2.61	-2.65	-2.57	-2.54	0.00	-2.88	-2.68	0.00	-3.85	-3.07	-2.78	-2.58
TCGA-58-A46L-10A-01D-A24F-08_LUSC	-2.60	-2.76	-2.73	-2.98	-2.66	-2.72	-2.62	-2.48	-2.72	-3.59	-2.82	-4.07	-2.70	-2.69	0.00	-2.71	-2.60
TCGA-58-A46M-10A-01D-A24F-08_LUSC	-2.59	0.00	-4.48	-2.83	-2.54	-2.59	-2.62	-2.48	-2.46	-4.48	-3.79	0.00	-3.88	-3.88	0.00	-2.49	-2.51
TCGA-58-A46N-10A-01D-A24F-08_LUSC	-2.67	-2.74	-2.81	-2.99	-2.54	-2.69	-2.67	-2.58	-2.74	-3.39	-2.75	-2.65	0.00	-2.72	0.00	-2.85	-2.64
TCGA-59-2372-10A-01D-1526-09_OV	-2.81	-2.68	-2.73	0.00	-2.65	-2.69	-2.76	-2.72	-2.65	0.00	-2.62	-2.67	0.00	0.00	0.00	-2.52	-2.75
TCGA-62-8394-10A-01D-2323-08_LUAD	-2.36	-4.62	0.00	-2.56	-2.46	-2.47	-2.45	-2.48	-2.41	0.00	0.00	0.00	-4.62	-4.62	-3.08	-2.64	-2.41
TCGA-62-8395-10A-01D-2323-08_LUAD	-2.46	0.00	-4.34	-2.58	-2.49	-2.50	-2.53	-2.58	-2.67	-3.44	-2.91	0.00	-2.72	-2.66	0.00	-2.68	-2.41

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-62-8397-10A-01D-2323-08_LUAD	-2.54	0.00	0.00	-2.68	-2.52	-2.55	-2.60	-2.55	-2.67	-3.43	-2.91	0.00	-2.72	-2.63	-3.14	0.00	-2.51
TCGA-62-8398-10A-01D-2323-08_LUAD	-2.42	-2.69	-2.66	-2.77	-2.66	-2.59	-2.64	-2.69	-2.65	0.00	-2.85	0.00	-2.69	-2.51	0.00	-2.66	-2.40
TCGA-62-8399-10A-01D-2323-08_LUAD	-2.49	-2.60	-2.57	-2.83	-2.63	-2.65	-2.49	-2.54	-2.41	0.00	0.00	0.00	0.00	-4.52	0.00	-2.54	-2.37
TCGA-62-8402-10A-01D-2323-08_LUAD	-2.60	-2.80	-2.73	-2.93	-2.53	-2.59	-2.65	-2.56	-2.81	-3.38	-2.71	-2.59	0.00	-2.71	0.00	-2.82	-2.51
TCGA-62-A46O-10A-01D-A24F-08_LUAD	-2.55	-2.77	-2.67	-2.81	-2.66	-2.65	-2.59	-2.62	-2.64	-3.27	-2.84	-4.48	-2.73	-2.66	0.00	-2.77	-2.53
TCGA-62-A46P-10A-01D-A24F-08_LUAD	-2.50	-2.68	-2.63	-2.87	-2.60	-2.66	-2.49	-2.50	-2.57	0.00	0.00	0.00	-4.56	0.00	0.00	-2.46	-2.41
TCGA-62-A46R-10A-01D-A24F-08_LUAD	-2.60	-2.73	-2.73	-2.95	-2.67	-2.66	-2.67	-2.66	-3.82	-3.18	-2.68	-2.67	-2.73	-2.62	0.00	-4.52	-2.62
TCGA-62-A46S-10A-01D-A24F-08_LUAD	-2.58	-4.50	-4.20	-2.69	-2.61	-2.61	-2.64	-2.65	-2.65	-3.30	-2.92	0.00	-2.80	-2.70	0.00	-2.80	-2.59
TCGA-62-A46U-10A-01D-A24F-08_LUAD	-2.67	-2.60	-2.61	-4.51	-2.70	-2.74	-2.64	-2.67	-2.71	-3.34	-2.66	-2.65	0.00	-2.69	0.00	-2.75	-2.59
TCGA-62-A46V-10A-01D-A24F-08_LUAD	-2.49	-3.90	-4.03	-2.84	-2.61	-2.65	-2.64	-2.55	-2.68	-3.30	-2.86	-4.51	-2.72	-2.65	0.00	-2.75	-2.59
TCGA-62-A46Y-10A-01D-A24F-08_LUAD	-2.32	-2.56	-2.60	-3.87	-3.87	-4.35	-2.55	-2.57	-2.52	0.00	0.00	0.00	0.00	-2.54	0.00	-2.60	-2.36
TCGA-62-A470-10A-01D-A24F-08_LUAD	-2.69	-2.78	-2.80	-2.99	-2.54	-2.72	-2.71	-2.63	-2.75	-3.43	-2.74	-2.81	-2.81	-2.76	-3.10	-4.61	-2.67
TCGA-62-A471-10A-01D-A24F-08_LUAD	-2.66	-2.79	-2.72	-2.94	-2.53	-2.65	-2.71	-2.61	-2.73	-3.42	-2.66	-2.74	-2.83	-2.76	-3.03	-4.09	-2.63
TCGA-62-A472-10A-01D-A24F-08_LUAD	-2.60	0.00	0.00	-2.77	-2.60	-2.64	-2.63	-2.50	-2.78	-3.42	-2.83	-2.76	0.00	-2.74	0.00	-2.77	-2.61
TCGA-63-5128-10A-01D-1441-08_LUSC	-2.51	-4.51	0.00	-2.80	-2.54	-2.61	-2.60	-2.50	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.43
TCGA-63-5131-10A-01D-1441-08_LUSC	-2.46	-2.73	0.00	-3.01	-2.52	-2.65	-2.68	-2.67	-2.67	-3.32	-2.91	0.00	-2.82	-2.71	0.00	-2.76	-2.52
TCGA-63-6202-10A-01D-1817-08_LUSC	-2.43	-4.54	-4.54	-2.65	-2.57	-2.59	-2.60	-2.52	-2.52	-4.54	0.00	0.00	0.00	-4.23	0.00	-2.63	-2.55
TCGA-63-7020-10A-01D-1945-08_LUSC	-2.54	-2.61	-2.61	0.00	-2.54	-2.65	-2.62	-2.52	-2.55	0.00	-2.68	-2.59	0.00	0.00	0.00	-2.47	-2.49
TCGA-63-7021-10A-01D-1945-08_LUSC	-2.53	-4.57	0.00	-2.70	-2.57	-2.59	-2.53	-2.52	-2.60	0.00	-4.57	0.00	0.00	0.00	0.00	-2.43	-2.47
TCGA-63-7022-10A-01D-1945-08_LUSC	-2.55	0.00	-4.33	-2.60	-2.50	-2.60	-2.59	-2.57	-2.50	0.00	0.00	0.00	0.00	-4.63	-2.99	-4.15	-2.47
TCGA-63-7023-10A-01D-1945-08_LUSC	-2.50	0.00	0.00	-2.54	-2.50	-2.51	-2.56	-2.54	-2.40	-4.51	0.00	-4.51	0.00	0.00	0.00	-2.43	-2.47
TCGA-63-A5M9-10A-01D-A26K-08_LUSC	-2.50	-4.00	-4.47	-2.54	-2.51	-2.52	-2.51	-2.52	-2.45	0.00	-4.47	0.00	-3.77	-4.47	0.00	-2.52	-2.43
TCGA-63-A5MB-10A-01D-A26K-08_LUSC	-2.46	-2.71	-2.71	-2.79	-2.63	-2.56	-2.47	-2.52	-2.49	0.00	0.00	0.00	0.00	-3.84	0.00	-2.46	-2.46
TCGA-63-A5MG-10A-01D-A27N-08_LUSC	-2.52	-2.63	-2.67	-2.85	-2.61	-2.67	-2.60	-2.49	-2.53	0.00	-4.17	0.00	0.00	0.00	-2.99	-2.69	-2.47
TCGA-63-A5MH-10A-01D-A27N-08_LUSC	-2.42	-4.47	-4.47	-2.61	-2.53	-2.58	-2.60	-2.49	-2.44	0.00	0.00	0.00	0.00	-4.47	-3.09	-2.73	-2.50
TCGA-63-A5MI-10A-01D-A27N-08_LUSC	-2.59	-2.66	-2.62	-2.82	-2.58	-2.66	-2.60	-2.40	-2.44	0.00	0.00	0.00	0.00	0.00	-2.96	-2.71	-2.48
TCGA-63-A5MJ-10A-01D-A27N-08_LUSC	-2.43	0.00	0.00	-2.81	-2.59	-2.58	-2.59	-2.64	-4.51	-3.15	-2.72	0.00	-2.64	-2.58	0.00	0.00	-2.51
TCGA-63-A5ML-10A-01D-A27N-08_LUSC	-2.62	-2.75	-2.74	-2.93	-2.49	-2.66	-2.64	-2.58	-2.58	0.00	-2.91	-2.73	0.00	0.00	-3.16	-2.77	-2.62
TCGA-63-A5MM-10A-01D-A26K-08_LUSC	-2.48	0.00	-4.49	-2.77	-2.51	-2.35	-2.54	-2.46	-2.45	0.00	-4.49	0.00	0.00	0.00	0.00	-2.54	-2.47
TCGA-63-A5MN-10A-01D-A27N-08_LUSC	-2.38	0.00	0.00	-2.74	-2.54	-2.55	-2.57	-2.50	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.50
TCGA-63-A5MP-10A-01D-A26K-08_LUSC	-2.46	0.00	0.00	-2.69	-2.54	-2.46	-2.49	-2.51	-2.50	0.00	0.00	0.00	-4.12	-3.95	-2.83	-4.42	-2.39
TCGA-63-A5MR-10A-01D-A27N-08_LUSC	-2.45	-2.63	-2.63	-2.81	-2.58	-2.59	-2.52	-2.58	-2.48	0.00	0.00	0.00	0.00	0.00	-2.89	-4.42	-2.48
TCGA-63-A5MS-10A-01D-A26K-08_LUSC	-2.57	0.00	0.00	-2.68	-2.59	-2.57	-2.62	-2.50	-2.71	-3.40	-2.83	0.00	-2.78	-2.63	-3.05	-3.74	-2.54
TCGA-63-A5MT-10A-01D-A26K-08_LUSC	-2.53	-2.78	-2.75	-2.84	-2.66	-2.69	-2.58	-2.53	-2.67	-3.44	-2.80	0.00	-2.70	-2.69	-3.03	-3.74	-2.47
TCGA-63-A5MU-10A-01D-A26K-08_LUSC	-2.54	-4.19	-3.79	-2.57	-2.52	-2.55	-2.60	-2.56	-2.48	-4.49	-4.19	-4.01	0.00	-3.71	0.00	-2.53	-2.46
TCGA-63-A5MV-10A-01D-A26K-08_LUSC	-2.58	-2.58	-2.57	-4.54	-2.67	-2.74	-2.57	-2.59	-3.76	-3.23	-2.61	-2.61	-2.80	-2.54	0.00	-3.84	-2.49
TCGA-63-A5MW-10A-01D-A26K-08_LUSC	-2.51	-2.68	-2.62	-2.87	-2.61	-2.60	-2.53	-2.48	-2.37	0.00	0.00	0.00	-4.44	-4.44	-2.94	-2.67	-2.41
TCGA-63-A5MY-10A-01D-A26K-08_LUSC	-2.42	-4.13	0.00	-2.53	-2.50	-2.51	-2.50	-2.49	-2.49	0.00	0.00	0.00	-4.43	-3.95	0.00	-2.47	-2.41
TCGA-64-1676-10A-01D-0969-08_LUAD	-2.52	-4.66	0.00	-2.72	-2.60	-2.55	-2.71	-2.60	-2.72	-3.41	-2.94	0.00	-2.78	-2.79	0.00	-2.72	-2.61
TCGA-64-1678-10A-01D-1489-08_LUAD	-2.53	0.00	0.00	-2.87	-2.63	-2.59	-2.64	-2.52	-2.65	-3.36	-2.86	-4.64	-2.83	-2.66	0.00	-2.75	-2.48
TCGA-64-1679-10A-01D-2063-08_LUAD	-2.52	-2.67	-2.65	-2.84	-2.67	-2.65	-2.56	-2.51	-2.51	0.00	0.00	0.00	0.00	-4.48	0.00	-2.60	-2.47
TCGA-64-1680-10A-01D-1040-01_LUAD	-2.54	-2.57	-2.52	0.00	-2.66	-2.72	-2.60	-2.52	-2.48	0.00	-3.00	-2.71	0.00	0.00	-3.03	-2.72	-2.44
TCGA-64-1681-10A-01D-2063-08_LUAD	-2.54	0.00	-4.50	-2.73	-2.52	-2.50	-2.53	-2.51	-2.41	0.00	0.00	0.00	-4.50	0.00	-3.09	-2.74	-2.42
TCGA-64-5774-10A-01D-1625-08_LUAD	-2.43	-4.51	-4.51	-2.59	-2.53	-2.48	-2.51	-2.46	-2.42	0.00	0.00	0.00	0.00	-4.51	-3.14	-2.71	-2.39
TCGA-64-5775-10A-01D-1625-08_LUAD	-2.49	-4.07	0.00	-2.71	-2.51	-2.52	-2.52	-2.53	-2.66	-3.24	-2.91	-4.24	-2.79	-2.65	-3.14	0.00	-2.43
TCGA-64-5778-10A-01D-1625-08_LUAD	-2.55	-2.75	-2.78	-3.01	-2.49	-2.57	-2.69	-2.65	-4.02	-3.42	-2.66	-2.63	-2.77	-2.57	0.00	0.00	-2.50
TCGA-64-5779-10A-01D-1625-08_LUAD	-2.48	-2.60	-2.57	-4.56	-2.69	-2.58	-2.60	-2.53	-2.50	0.00	-3.08	-2.70	0.00	0.00	-3.20	-2.78	-2.45
TCGA-64-5781-10A-01D-1625-08_LUAD	-2.50	-4.49	-4.49	-2.71	-2.52	-2.53	-2.52	-2.63	-2.69	-3.45	-2.83	0.00	-2.74	-2.74	0.00	-2.73	-2.42
TCGA-64-5815-10A-01D-1625-08_LUAD	-2.39	-2.75	-2.66	-2.83	-2.38	-2.65	-2.69	-2.79	0.00	-3.31	-2.69	-2.62	-2.70	-2.48	0.00	-4.51	-2.49
TCGA-67-3770-10A-01D-0969-08_LUAD	-2.54	0.00	-4.30	-2.87	-2.51	-2.59	-2.59	-2.60	-2.56	0.00	-4.30	0.00	0.00	0.00	-2.93	-4.13	-2.49
TCGA-67-3771-10A-01D-1040-01_LUAD	-2.50	-2.63	-2.55	0.00	-4.32	-4.14	-2.61	-2.40	-2.46	0.00	-4.62	0.00	-4.62	-4.62	-2.97	-2.71	-2.46
TCGA-67-3773-10A-01D-1489-08_LUAD	-2.54	-4.64	-4.33	-2.69	-2.59	-2.63	-2.67	-2.57	-2.49	0.00	0.00	0.00	-4.64	0.00	0.00	-2.60	-2.54
TCGA-67-3774-10A-01D-1489-08_LUAD	-2.44	-4.65	-4.65	-2.68	-2.58	-2.60	-2.65	-2.54	-2.62	0.00	0.00	-4.65	-4.35	-4.65	-3.09	-2.68	-2.49
TCGA-67-4679-10A-01D-1753-08_LUAD	-2.56	-2.78	-2.71	-2.97	-2.45	-2.57	-2.59	-2.60	-2.48	-4.53	-2.97	-2.69	0.00	-4.22	0.00	-2.51	-2.44
TCGA-67-6215-10A-01D-1753-08_LUAD	-2.56	-2.74	-2.74	-2.95	-2.47	-2.57	-2.56	-2.65	-2.65	-3.46	-2.73	-2.77	-2.81	-2.70	0.00	-2.85	-2.46
TCGA-67-6216-10A-01D-1753-08_LUAD	-2.49	-2.70	-2.62	0.00	-2.68	-2.57	-2.56	-2.55	-2.62	-3.52	-3.09	0.00	-2.76	-2.59	0.00	-2.85	-2.38
TCGA-67-6217-10A-01D-1753-08_LUAD	-2.36	0.00	-4.16	-2.63	-2.42	-2.47	-2.51	-2.50	-2.42	0.00	0.00	0.00	0.00	-4.46	-3.08	-2.82	-2.34
TCGA-68-7755-10A-01D-2122-08_LUSC	-2.43	0.00	-4.01	-2.81	-2.52	-2.62	-2.64	-2.54	-2.62	-3.31	-2.90	-4.48	-2.71	-2.71	-3.10	-4.18	-2.54
TCGA-68-7756-10A-01D-2122-08_LUSC	-2.46	-4.25	-4.55	-2.59	-2.58	-2.59	-2.48	-2.60	-4.25	-3.21	-2.71	0.00	-2.65	-2.54	0.00	0.00	-2.54
TCGA-68-7757-10A-01D-2293-08_LUSC	-2.57	-2.71	-2.73	-2.86	-2.65	-2.69	-2.62	-2.54	-2.66	-3.24	-2.88	-2.64	0.00	-2.65	0.00	-2.74	-2.47
TCGA-68-8250-10A-01D-2293-08_LUSC	-2.53	-4.50	-4.50	-2.56	-2.49	-2.55	-2.56	-2.51	-2.53	0.00	-4.50	-4.50	0.00	0.00	-2.94	-2.61	-2.46
TCGA-68-8251-10A-01D-2293-08_LUSC	-2.43	-2.50	-2.51	-4.40	0.00	-3.70	-2.44	-2.35	-2.33	0.00	0.00	0.00	0.00	0.00	-2.92	-2.60	-2.39
TCGA-68-A59J-10A-01D-A26K-08_LUSC	-2.59	0.00	0.00	-2.62	-2.59	-2.63	-2.59	-2.64	-2.68	-3.40	-2.88	0.00	-2.83	-2.73	0.00	-2.74	-2.51
TCGA-69-7760-10A-01D-2167-08_LUAD	-2.60	-2.80	-2.88	-2.85	-2.47	-2.63	-2.58	-2.73	-2.78	-3.40	-2.78	-2.63	0.00	-2.74	0.00	-2.73	-2.48
TCGA-69-7761-10A-01D-2167-08_LUAD	-2.45	0.00	-4.45	-2.54	-2.43	-2.44	-2.53	-2.61	-2.47	0.00	0.00	0.00	0.00	0.00	-2.97	-2.69	-2.32
TCGA-69-7763-10A-01D-2167-08_LUAD	-2.57	-2.81	-2.85	-2.83	-2.46	-2.54	-2.52	-2.69	-2.74	-3.33	-2.79	-2.78	-2.85	-2.64	0.00	-2.86	-2.46
TCGA-69-7764-10A-01D-2167-08_LUAD	-2.54	-2.57	-2.63	0.00	-2.64	-2.74	-2.49	-2.60	-2.48	0.00	-2.92	-2.71	-4.57	-4.27	-3.06	-2.72	-2.42
TCGA-69-7765-10A-01D-2167-08_LUAD	-2.48	-2.78	-2.81	-2.80	-2.35	-2.51	-2.55	-2.57	-2.49	0.00	-3.03	0.00	-2.83	0.00	-3.05	-4.48	-2.52
TCGA-69-7973-10A-01D-2184-08_LUAD	-2.63	-2.80	-2.72	-2.88	-2.53	-2.59	-2.64	-2.66	-4.54	-3.15	-2.61	-2.74	-2.73	-2.61	0.00	-4.24	-2.52
TCGA-69-7974-10A-01D-2184-08_LUAD	-2.55	0.00	-4.02	-2.55	-2.54	-2.58	-2.60	-2.58	-2.62	-3.35	-2.90	0.00	-2.78	-2.66	-3.02	-4.49	-2.54
TCGA-69-7978-10A-01D-2184-08_LUAD	-2.58	-2.62	-2.64	-4.55	-2.56	-2.58	-2.60	-2.50	-2.53	0.00	-2.78	-2.68	0.00	0.00	0.00	-2.45	-2.50
TCGA-69-7979-10A-01D-2184-08_LUAD	-2.58	-2.66	-2.62	0.00	-2.67	-2.69	-2.51	-2.48	-2.59	-3.34	-2.98	-2.67	0.00	-4.51	-2.95	-4.51	-2.51
TCGA-69-7980-10A-01D-2184-08_LUAD	-2.46	-2.72	-2.77	-2.84	-2.48	-2.61	-2.67	-2.61	-2.73	-3.34	-2.76	-2.61	0.00	-2.70	0.00	-2.80	-2.53
TCGA-69-8253-10A-01D-2284-08_LUAD	-2.55	-2.67	-2.71	-2.94	-2.65	-2.66	-2.58	-2.49	-2.56	-4.45	-3.68	0.00	-4.15	-3.68	-3.01	-2.74	-2.48
TCGA-69-8254-10A-01D-2284-08_LUAD	-2.57	-2.79	-2.73	-3.03	-2.49	-2.68	-2.53	-2.52	-2.57	-3.49	-3.01	-2.73	0.00	0.00	-2.96	0.00	-2.51
TCGA-69-8255-10A-01D-2284-08_LUAD	-2.51	0.00	-4.49	-2.72	-2.46	-2.41	-2.48	-2.54	-2.42	0.00	0.00	0.00	0.00	0.00	-2.85	0.00	-2.39
TCGA-69-A59K-10A-01D-A25L-08_LUAD	-2.58	0.00	0.00	-2.61	-2.42	-2.58	-2.60	-2.60	-2.55	0.00	0.00	-4.52	0.00	-4.52	-2.95	-3.92	-2.50
TCGA-70-6722-10A-01D-1817-08_LUSC	-2.45	0.00	0.00	-2.68	-2.60	-2.65	-2.65	-2.65	-2.73	-3.29	-2.84	0.00	-2.80	-2.63	0.00	-2.82	-2.55
TCGA-70-6723-10A-01D-1817-08_LUSC	-2.40	-2.68	-2.66	-2.83	-2.62	-2.68	-2.51	-2.58	-2.46	0.00	0.00	0.00	0.00	-4.52	-2.89	-4.22	-2.41
TCGA-71-6725-10A-01D-1855-08_LUAD	-2.55	0.00	-4.26	-2.72	-2.51	-2.56	-2.58	-2.48	-2.51	0.00	0.00	0.00	-4.56	-4.26	-3.01	-2.72	-2.51
TCGA-71-8520-10A-01D-2393-08_LUAD	-2.46	-2.76	-2.78	-2.98	-2.50	-2.55	-2.66	-2.65	-2.76	-3.42	-2.80	-2.73	-2.80	-2.67	0.00	-2.84	-2.50
TCGA-73-7498-10A-01D-2184-08_LUAD	-2.50	-4.45	0.00	-2.72	-2.49	-2.52	-2.54	-2.50	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.36	-2.48
TCGA-73-7499-10A-01D-2184-08_LUAD	-2.50	-4.41	0.00	-2.53	-2.46	-2.53	-2.52	-2.64	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.42
TCGA-74-6575-10A-01D-1845-08_GBM	-2.54	-2.63	-2.59	0.00	-2.70	-2.72	-2.63	-2.62	-2.56	0.00	-2.83	-2.68	0.00	-4.02	-2.93	-4.62	-2.54
TCGA-74-6577-10A-01D-1845-08_GBM	-2.50	-2.65	-2.74	-2.84	-2.61	-2.68	-2.55	-2.48	-2.45	0.00	0.00	0.00	0.00	0.00	-3.07	-2.77	-2.42
TCGA-74-6578-10A-01D-1845-08_GBM	-2.56	-2.80	-2.84	-2.85	-2.54	-2.55	-2.67	-2.49	-2.54	0.00	-2.88	-2.76	-4.69	-4.69	-3.12	-2.85	-2.53
TCGA-74-6581-10A-01D-1845-08_GBM	-2.42	-4.62	0.00	-2.58	-2.58	-2.58	-2.53	-2.50	-2.46	0.00	0.00	0.00	0.00	-4.62	-3.01	-2.71	-2.49
TCGA-74-6584-10A-01D-1845-08_GBM	-2.48	-4.72	-4.72	-2.61	-2.51	-2.63	-2.52	-2.60	-2.48	0.00	0.00	-4.72	0.00	0.00	0.00	-2.70	-2.51
TCGA-75-5122-10A-01D-1753-08_LUAD	-2.38	0.00	-4.41	-2.71	-2.48	-2.48	-2.51	-2.47	-2.44	0.00	0.00	0.00	0.00	0.00	-3.11	-2.81	-2.37
TCGA-75-5125-10A-01D-1753-08_LUAD	-2.42	-4.44	0.00	-2.56	-2.41	-2.44	-2.50	-2.55	-2.46	0.00	0.00	-4.44	0.00	0.00	0.00	-2.59	-2.34
TCGA-75-5126-10A-01D-1753-08_LUAD	-2.59	-2.82	-2.78	-2.90	-2.52	-2.60	-2.53	-2.53	-2.53	-3.37	-3.03	-2.73	0.00	-4.60	0.00	-2.57	-2.48
TCGA-75-5146-10A-01D-1625-08_LUAD	-2.52	0.00	-4.55	-2.63	-2.48	-2.51	-2.50	-2.60	-2.58	-3.43	-3.07	-4.55	-2.73	-2.74	0.00	-2.78	-2.41
TCGA-75-5147-10A-01D-1625-08_LUAD	-2.46	-2.64	-2.57	0.00	-2.71	-2.54	-2.57	-2.54	-2.75	-3.44	-2.68	-2.73	-2.77	0.00	-3.35	0.00	-2.49
TCGA-75-6203-10A-01D-1753-08_LUAD	-2.45	-2.65	-2.65	-2.85	-2.56	-2.61	-2.48	-2.54	-2.39	0.00	-4.42	0.00	-4.42	-4.42	0.00	-2.56	-2.36
TCGA-75-6205-10A-01D-1753-08_LUAD	-2.48	0.00	0.00	-2.66	-2.47	-2.44	-2.51	-2.54	-2.44	0.00	0.00	-4.46	0.00	0.00	-3.01	-2.75	-2.37
TCGA-75-6206-10A-01D-1753-08_LUAD	-2.53	-2.68	0.00	-2.90	-2.39	-2.54	-2.62	-2.65	-2.65	-3.19	-2.91	-4.51	-2.77	-2.63	0.00	-2.81	-2.49

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-75-6207-10A-01D-1753-08_LUAD	-2.41	-4.44	0.00	-2.68	-2.44	-2.47	-2.51	-2.46	-2.37	0.00	0.00	0.00	0.00	0.00	-2.98	-2.71	-2.43
TCGA-75-6211-10A-01D-1753-08_LUAD	-2.51	-2.73	-2.64	-2.95	-2.49	-2.58	-2.57	-2.56	-2.75	-3.41	-2.78	-2.54	0.00	-2.65	0.00	-2.86	-2.54
TCGA-75-6212-10A-01D-1753-08_LUAD	-2.48	0.00	-4.46	-2.55	-2.48	-2.50	-2.50	-2.50	-2.41	-4.46	-4.16	-3.99	0.00	-4.46	0.00	-2.40	-2.42
TCGA-75-6214-10A-01D-1946-08_LUAD	-2.53	0.00	-4.51	-2.74	-2.53	-2.55	-2.60	-2.47	-2.64	-3.26	-2.86	0.00	-2.69	-2.62	-3.08	0.00	-2.47
TCGA-75-7025-10A-01D-1946-08_LUAD	-2.60	0.00	-3.85	-2.63	-2.55	-2.62	-2.59	-2.64	-2.47	0.00	0.00	0.00	-4.55	-4.55	0.00	-2.59	-2.53
TCGA-75-7027-10A-01D-1946-08_LUAD	-2.47	-4.66	-4.66	-2.63	-2.52	-2.53	-2.55	-2.62	-2.45	0.00	-4.66	0.00	0.00	-4.36	0.00	-2.63	-2.43
TCGA-75-7030-10A-01D-1946-08_LUAD	-2.33	-4.39	0.00	-2.59	-2.39	-2.57	-2.58	-2.62	-2.55	0.00	0.00	-4.39	0.00	-2.55	-3.03	0.00	-2.47
TCGA-75-7031-10A-01D-1946-08_LUAD	-2.44	-2.72	-2.71	-2.88	-2.72	-2.69	-2.56	-2.63	-2.69	-3.54	-2.91	-4.65	-2.79	-2.70	0.00	-2.73	-2.46
TCGA-76-4925-10A-01D-1486-08_GBM	-2.50	-4.13	-4.60	-2.80	-2.54	-2.58	-2.57	-2.51	-2.57	0.00	0.00	-4.60	0.00	-4.60	0.00	-2.57	-2.53
TCGA-76-4926-10A-01D-1486-08_GBM	-2.56	-4.67	-4.67	-2.72	-2.62	-2.55	-2.65	-2.71	-2.75	-3.27	-2.95	-2.73	0.00	-2.73	0.00	-2.73	-2.56
TCGA-76-4927-10A-01D-1486-08_GBM	-2.53	0.00	-4.32	-2.66	-2.57	-2.60	-2.66	-2.52	-2.60	0.00	0.00	0.00	0.00	-4.32	0.00	-2.43	-2.53
TCGA-76-4928-10A-01D-1486-08_GBM	-2.54	0.00	-4.61	-2.81	-2.52	-2.59	-2.56	-2.43	-2.50	0.00	-4.61	0.00	0.00	0.00	0.00	-2.39	-2.51
TCGA-76-4929-10A-01D-1486-08_GBM	-2.62	-4.71	-4.71	-2.73	-2.60	-2.61	-2.72	-2.62	-2.78	-3.33	-2.93	-2.79	0.00	-2.79	0.00	-2.79	-2.59
TCGA-76-4931-10A-01D-1486-08_GBM	-2.55	-2.61	-2.64	-4.66	-4.66	-4.18	-2.67	-2.59	-2.71	-3.38	-2.87	-4.66	-2.74	-2.72	0.00	-2.77	-2.52
TCGA-76-4932-10A-01D-1486-08_GBM	-2.47	-2.59	-2.51	-4.29	-4.59	-4.29	-2.58	-2.46	-2.50	0.00	-4.59	0.00	-4.59	0.00	-3.01	-2.68	-2.43
TCGA-76-4934-10A-01D-1486-08_GBM	-2.63	-2.78	-2.82	-2.98	-2.53	-2.64	-2.71	-2.71	-4.38	-3.25	-2.68	-2.67	-2.88	-2.64	0.00	-4.68	-2.59
TCGA-76-4935-10A-01D-1486-08_GBM	-2.60	-4.20	-4.38	-2.90	-2.58	-2.64	-2.69	-2.62	-2.73	-3.40	-2.90	0.00	-2.80	-2.73	0.00	-2.79	-2.54
TCGA-76-6191-10A-01D-1696-08_GBM	-2.49	-4.46	-3.98	-2.70	-2.44	-2.46	-2.48	-2.49	-2.52	-4.46	-4.46	0.00	0.00	-4.46	0.00	-2.43	-2.39
TCGA-76-6192-10A-01D-1696-08_GBM	-2.56	0.00	0.00	-2.81	-2.42	-2.55	-2.53	-2.48	-2.58	-3.35	-3.02	-2.76	0.00	-4.58	-3.15	-2.80	-2.52
TCGA-76-6193-10A-01D-1696-08_GBM	-2.35	0.00	0.00	-2.73	-2.45	-2.56	-2.52	-2.47	-2.51	0.00	0.00	0.00	0.00	-4.17	0.00	-2.42	-2.41
TCGA-76-6280-10A-01D-1845-08_GBM	-2.42	-2.66	-2.60	-2.77	-2.59	-4.24	-2.63	-2.61	-2.55	0.00	0.00	0.00	0.00	-2.57	0.00	-2.64	-2.51
TCGA-76-6282-10A-01D-1696-08_GBM	-2.53	0.00	-4.53	-2.62	-2.50	-2.57	-2.57	-2.59	-2.62	-3.35	-2.90	-2.63	0.00	-2.71	0.00	-2.73	-2.46
TCGA-76-6283-10A-01D-1845-08_GBM	-2.49	0.00	0.00	-2.67	-2.54	-2.59	-2.59	-2.52	-2.57	0.00	0.00	0.00	0.00	-4.59	-3.06	-2.72	-2.43
TCGA-76-6285-10A-01D-1696-08_GBM	-2.48	-2.67	-2.70	-2.96	-2.61	-2.71	-2.56	-2.56	-2.65	-3.32	-2.90	-3.90	-2.74	-2.63	-3.10	0.00	-2.45
TCGA-76-6286-10A-01D-1845-08_GBM	-2.46	-2.68	-2.69	-2.77	-2.63	-2.69	-2.59	-2.48	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.40	-2.51
TCGA-76-6656-10A-01D-1845-08_GBM	-2.53	0.00	0.00	-2.80	-2.55	-2.60	-2.65	-2.56	-2.74	-3.35	-2.95	0.00	-2.73	-2.71	0.00	-2.78	-2.46
TCGA-76-6657-10A-01D-1845-08_GBM	-2.58	-2.66	-2.65	-4.68	-2.56	-2.58	-2.62	-2.53	-2.58	0.00	-2.77	-2.63	0.00	0.00	-3.16	-2.85	-2.53
TCGA-76-6660-10A-01D-1845-08_GBM	-2.49	-2.74	-2.66	-2.85	-2.65	-2.66	-2.54	-2.54	-2.47	0.00	0.00	0.00	-4.57	-4.27	0.00	-2.58	-2.48
TCGA-76-6661-10A-01D-1845-08_GBM	-2.57	-2.84	-2.77	-2.84	-2.54	-2.59	-2.66	-2.56	-2.65	0.00	-2.94	-2.72	0.00	-4.66	0.00	-2.51	-2.50
TCGA-76-6662-10A-01D-1845-08_GBM	-2.48	-2.74	-2.69	-2.82	-2.68	-2.68	-2.58	-2.43	-2.46	0.00	-4.61	0.00	0.00	0.00	-3.02	-2.72	-2.43
TCGA-76-6663-10A-01D-1845-08_GBM	-2.47	-2.72	-2.49	-2.86	-2.63	-2.66	-2.59	-2.48	-2.57	0.00	0.00	0.00	-4.57	0.00	0.00	-2.59	-2.45
TCGA-76-6664-10A-01D-1845-08_GBM	-2.42	-2.71	-2.68	-2.81	-2.64	-2.59	-2.50	-2.50	-2.51	0.00	0.00	0.00	0.00	0.00	-2.95	-4.25	-2.40
TCGA-77-6842-10A-01D-1945-08_LUSC	-2.55	-2.79	-2.71	-2.95	-2.44	-2.53	-2.65	-2.51	-2.51	0.00	-3.04	-2.73	0.00	-4.57	-3.09	-2.84	-2.59
TCGA-77-6843-10A-01D-1945-08_LUSC	-2.58	-2.72	-2.76	-2.89	-2.51	-2.57	-2.62	-2.53	-2.52	0.00	-3.03	-2.76	0.00	0.00	-3.03	-2.79	-2.54
TCGA-77-6844-10A-01D-1945-08_LUSC	-2.63	-2.74	-2.76	-3.02	-2.55	-2.63	-2.65	-2.67	-2.54	0.00	-2.91	-2.75	0.00	-4.14	0.00	-2.69	-2.59
TCGA-77-6845-10A-01D-1945-08_LUSC	-2.49	0.00	-4.41	-2.53	-2.51	-2.58	-2.59	-2.50	-2.52	0.00	0.00	0.00	0.00	-4.41	-2.99	-2.69	-2.46
TCGA-77-7138-10A-01D-2042-08_LUSC	-2.56	0.00	0.00	-2.81	-2.55	-2.58	-2.57	-2.52	-2.66	-3.52	-2.87	-4.52	-2.70	-2.69	-2.98	0.00	-2.44
TCGA-77-7139-10A-01D-2042-08_LUSC	-2.53	-4.50	-4.20	-2.59	-2.55	-2.51	-2.53	-2.48	-2.45	0.00	0.00	0.00	0.00	0.00	-3.05	-2.66	-2.50
TCGA-77-7140-10A-01D-2042-08_LUSC	-2.48	-2.69	-2.64	-2.76	-2.56	-2.70	-2.57	-2.49	-2.49	0.00	0.00	0.00	0.00	-4.45	-2.99	-2.64	-2.45
TCGA-77-7463-10A-01D-2042-08_LUSC	-2.46	-2.69	-2.68	-2.80	-2.60	-2.66	-2.55	-2.41	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.34	-2.41
TCGA-77-7465-10A-01D-2042-08_LUSC	-2.58	0.00	0.00	-2.74	-2.59	-2.62	-2.58	-2.50	-2.68	-3.36	-2.84	0.00	-2.83	-2.68	0.00	-2.73	-2.51
TCGA-77-8128-10A-01D-2244-08_LUSC	-2.39	-2.71	0.00	-2.78	-2.42	-2.55	-2.56	-2.60	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.42
TCGA-77-8130-10A-01D-2244-08_LUSC	-2.46	0.00	0.00	-2.51	-2.44	-2.56	-2.47	-2.55	-2.47	0.00	0.00	0.00	-4.39	0.00	0.00	-2.53	-2.39
TCGA-77-8131-10A-01D-2244-08_LUSC	-2.54	-2.72	-2.77	-2.83	-2.48	-2.53	-2.57	-2.56	-2.45	0.00	-2.96	-2.70	-4.48	-4.00	-3.08	-2.75	-2.50
TCGA-77-8133-10A-01D-2244-08_LUSC	-2.29	-2.63	-2.57	-2.72	-2.51	-2.53	-2.48	-2.56	-2.42	0.00	0.00	0.00	-4.34	0.00	-2.82	0.00	-2.40
TCGA-77-8136-10A-01D-2244-08_LUSC	-2.61	-3.88	-4.02	-2.66	-2.59	-2.71	-2.62	-2.62	-2.54	-4.42	-4.12	-4.25	-4.25	-3.58	-3.11	-2.80	-2.49
TCGA-77-8138-10A-01D-2244-08_LUSC	-2.58	-2.62	-2.62	-4.52	-2.57	-2.61	-2.57	-2.54	-2.70	-3.12	-2.69	-2.58	0.00	-2.65	0.00	-2.68	-2.49
TCGA-77-8139-10A-01D-2244-08_LUSC	-2.53	0.00	0.00	-2.71	-2.47	-2.55	-2.50	-2.54	-2.47	0.00	-4.41	0.00	0.00	0.00	-3.05	-2.61	-2.47
TCGA-77-8140-10A-01D-2244-08_LUSC	-2.44	-2.67	-2.54	-2.74	-2.58	-2.58	-2.46	-2.54	-2.50	0.00	0.00	-4.38	0.00	0.00	0.00	-2.54	-2.42
TCGA-77-8143-10A-01D-2244-08_LUSC	-2.43	-4.05	-4.35	-2.58	-2.38	-2.48	-2.45	-2.59	-2.48	0.00	0.00	0.00	0.00	-4.05	0.00	-2.48	-2.36
TCGA-77-8144-10A-01D-2244-08_LUSC	-2.47	-2.72	-2.71	-2.92	-2.57	-2.62	-2.59	-2.47	-2.61	-3.31	-2.82	0.00	-2.77	-2.66	-3.00	0.00	-2.53
TCGA-77-8145-10A-01D-2244-08_LUSC	-2.44	-4.37	0.00	-2.54	-2.49	-2.48	-2.48	-2.51	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.36	-2.41
TCGA-77-8146-10A-01D-2244-08_LUSC	-2.56	-2.75	-2.74	-2.85	-2.41	-2.57	-2.59	-2.72	0.00	-3.19	-2.68	-2.65	-2.69	-2.51	0.00	0.00	-2.49
TCGA-77-8148-10A-01D-2244-08_LUSC	-2.48	-2.65	-2.66	-2.77	-2.37	-2.61	-2.66	-2.81	-2.54	-4.43	-2.83	-2.61	0.00	-2.55	-3.00	0.00	-2.42
TCGA-77-8150-10A-01D-2244-08_LUSC	-2.35	-4.38	0.00	-2.69	-2.45	-2.54	-2.48	-2.47	-2.39	-3.27	0.00	0.00	0.00	-4.08	-2.98	-2.76	-2.42
TCGA-77-8154-10A-01D-2244-08_LUSC	-2.38	-2.74	-2.73	-2.82	-2.59	-2.64	-2.57	-2.52	-2.65	-3.20	-2.90	0.00	-2.76	-2.63	-3.06	0.00	-2.47
TCGA-77-8156-10A-01D-2244-08_LUSC	-2.52	-2.72	-2.74	-2.83	-2.43	-2.52	-2.52	-2.65	-2.52	0.00	-2.85	-2.65	0.00	-4.16	0.00	-2.59	-2.47
TCGA-77-A5FZ-10A-01D-A27N-08_LUSC	-2.51	-2.67	-2.60	-2.91	-2.57	-2.61	-2.56	-2.57	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.48
TCGA-77-A5G1-10A-01D-A27N-08_LUSC	-2.51	0.00	-4.43	-2.71	-2.48	-2.51	-2.57	-2.55	-2.45	0.00	0.00	0.00	0.00	-4.43	0.00	-2.52	-2.45
TCGA-77-A5G3-10A-01D-A27N-08_LUSC	-2.52	-2.61	-2.64	-2.84	-2.60	-2.63	-2.54	-2.59	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.46
TCGA-77-A5G6-10A-01D-A27N-08_LUSC	-2.52	-4.41	0.00	-2.77	-2.51	-2.54	-2.56	-2.40	-2.42	0.00	0.00	0.00	0.00	0.00	-2.89	-2.66	-2.47
TCGA-77-A5G7-10A-01D-A27N-08_LUSC	-2.39	-2.64	-2.59	-2.82	-2.59	-2.59	-2.53	-2.41	-2.41	0.00	0.00	0.00	0.00	0.00	-2.97	-2.66	-2.46
TCGA-77-A5G8-10A-01D-A27N-08_LUSC	-2.65	-2.79	-2.73	-2.93	-2.50	-2.64	-2.64	-2.59	-2.65	0.00	-2.85	-2.71	-4.57	0.00	0.00	-2.46	-2.62
TCGA-77-A5GA-10A-01D-A27N-08_LUSC	-2.58	0.00	-4.21	-2.60	-2.59	-2.58	-2.62	-2.48	-2.48	0.00	0.00	0.00	0.00	-4.51	0.00	-2.60	-2.50
TCGA-77-A5GB-10A-01D-A27N-08_LUSC	-2.53	-2.68	-2.62	-2.78	-2.63	-2.60	-2.54	-2.51	-2.45	0.00	0.00	0.00	-4.44	-4.13	0.00	-2.41	-2.47
TCGA-77-A5GF-10A-01D-A27N-08_LUSC	-2.63	-2.66	-2.61	0.00	-2.65	-2.69	-2.65	-2.55	-2.76	-3.32	-2.74	-2.76	-2.78	-2.68	0.00	-2.81	-2.59
TCGA-77-A5GH-10A-01D-A27N-08_LUSC	-2.59	0.00	0.00	-2.63	-2.48	-2.66	-2.64	-2.59	-2.77	-3.35	-2.90	0.00	-2.79	-2.71	0.00	-2.84	-2.63
TCGA-78-7143-10A-01D-2036-08_LUAD	-2.52	0.00	0.00	-2.59	-2.52	-2.53	-2.57	-2.50	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.41
TCGA-78-7145-10A-01D-2036-08_LUAD	-2.49	0.00	-4.56	-2.75	-2.57	-2.60	-2.57	-2.60	-2.67	-3.35	-2.85	0.00	-2.70	-2.65	0.00	-2.77	-2.48
TCGA-78-7146-10A-01D-2036-08_LUAD	-2.52	-2.64	-2.62	-2.86	-2.61	-2.69	-2.52	-2.54	-2.57	0.00	-4.47	0.00	0.00	0.00	0.00	-2.55	-2.50
TCGA-78-7147-10A-01D-2036-08_LUAD	-2.60	-2.75	-2.76	-2.90	-2.48	-2.61	-2.63	-2.69	-2.67	0.00	-2.93	-2.72	0.00	0.00	0.00	-2.66	-2.60
TCGA-78-7148-10A-01D-2036-08_LUAD	-2.53	-2.69	-2.67	-2.81	-2.62	-2.66	-2.57	-2.43	-2.46	0.00	0.00	0.00	0.00	-4.53	-3.03	-2.73	-2.48
TCGA-78-7149-10A-01D-2036-08_LUAD	-2.52	0.00	-4.47	-2.73	-2.51	-2.54	-2.58	-2.56	-2.43	0.00	0.00	0.00	0.00	-4.47	0.00	-2.56	-2.47
TCGA-78-7150-10A-01D-2036-08_LUAD	-2.50	-2.80	-2.73	-2.91	-2.57	-2.65	-2.67	-2.70	-2.56	0.00	-2.91	-2.78	0.00	-4.29	0.00	-2.71	-2.61
TCGA-78-7152-10A-01D-2036-08_LUAD	-2.51	-2.77	-2.71	-2.96	-2.55	-2.71	-2.69	-2.61	-2.59	0.00	-2.91	-2.77	0.00	-4.63	-3.11	-2.79	-2.56
TCGA-78-7153-10A-01D-2036-08_LUAD	-2.57	-2.84	-2.79	-2.97	-2.54	-2.63	-2.73	-2.74	-2.81	-3.34	-2.77	-2.79	-2.87	-2.78	0.00	-2.83	-2.67
TCGA-78-7154-10A-01D-2036-08_LUAD	-2.53	-4.52	0.00	-2.60	-2.57	-2.59	-2.59	-2.60	-2.47	0.00	-4.52	-4.04	0.00	-3.92	0.00	-2.60	-2.53
TCGA-78-7155-10A-01D-2036-08_LUAD	-2.55	0.00	0.00	-2.63	-2.50	-2.56	-2.62	-2.63	-2.74	-3.42	-2.98	0.00	-2.85	-2.70	0.00	-2.74	-2.50
TCGA-78-7156-10A-01D-2036-08_LUAD	-2.66	0.00	0.00	-2.83	-2.70	-2.68	-2.72	-2.71	-2.78	-3.29	-2.84	-2.81	-4.08	-2.75	0.00	-2.83	-2.60
TCGA-78-7158-10A-01D-2036-08_LUAD	-2.40	-2.55	-2.50	-3.96	-3.73	-3.83	-2.54	-2.40	-2.43	0.00	0.00	0.00	-4.43	-4.13	0.00	-2.37	-2.44
TCGA-78-7159-10A-01D-2036-08_LUAD	-2.56	-4.53	-3.83	-2.78	-2.56	-2.65	-2.59	-2.65	-2.69	-3.36	-2.89	0.00	-2.73	-2.66	0.00	-2.83	-2.53
TCGA-78-7160-10A-01D-2036-08_LUAD	-2.65	-2.78	-2.74	-2.92	-2.53	-2.67	-2.64	-2.63	-2.82	-3.40	-2.70	-2.66	0.00	-2.75	0.00	-2.73	-2.59
TCGA-78-7161-10A-01D-2036-08_LUAD	-2.44	-3.97	-4.45	-2.87	-2.43	-2.46	-2.49	-2.63	-2.52	0.00	-4.45	0.00	0.00	-4.15	0.00	-2.47	-2.43
TCGA-78-7220-10A-01D-2036-08_LUAD	-2.51	0.00	0.00	-2.71	-2.49	-2.55	-2.54	-2.48	-2.52	0.00	0.00	0.00	0.00	-4.50	0.00	-2.42	-2.45
TCGA-78-7535-10A-01D-2063-08_LUAD	-2.60	-2.76	-2.69	-2.85	-2.70	-2.75	-2.61	-2.65	-2.74	-3.31	-2.85	-4.26	-2.78	-2.68	0.00	-2.74	-2.59
TCGA-78-7536-10A-01D-2063-08_LUAD	-2.62	-2.62	-2.64	-4.58	-2.70	-2.71	-2.67	-2.58	-2.63	-3.30	-2.71	-2.62	0.00	-2.70	-3.17	-4.28	-2.57
TCGA-78-7537-10A-01D-2063-08_LUAD	-2.60	0.00	-4.25	-2.73	-2.51	-2.58	-2.60	-2.62	-2.75	-3.25	-2.98	-4.55	-2.75	-2.71	0.00	-2.73	-2.47
TCGA-78-7539-10A-01D-2063-08_LUAD	-2.56	-2.68	-2.71	-2.82	-2.63	-2.62	-2.54	-2.55	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.42
TCGA-78-7633-10A-01D-2063-08_LUAD	-2.50	0.00	0.00	-2.65	-2.53	-2.65	-2.62	-2.53	-2.76	-3.37	-2.90	0.00	-2.76	-2.63	0.00	-2.74	-2.49
TCGA-78-8648-10A-01D-2393-08_LUAD	-2.48	0.00	0.00	-2.73	-2.50	-2.57	-2.55	-2.53	-2.65	-3.36	-2.85	0.00	-2.78	-2.59	-3.06	0.00	-2.48
TCGA-78-8655-10A-01D-2393-08_LUAD	-2.64	-2.74	-2.66	-4.36	-2.75	-2.80	-2.69	-2.69	-2.77	-3.46	-2.73	-2.77	-2.82	-2.75	0.00	-2.80	-2.61
TCGA-78-8660-10A-01D-2393-08_LUAD	-2.48	0.00	0.00	-2.87	-2.50	-2.51	-2.53	-2.49	-2.52	0.00	0.00	0.00	0.00	-4.53	0.00	-2.40	-2.41
TCGA-78-8662-10A-01D-2393-08_LUAD	-2.76	-2.82	-2.83	-3.02	-2.57	-2.73	-2.71	-2.66	-2.81	-3.54	-2.77	-2.73	0.00	-2.81	-3.26	-4.72	-2.71
TCGA-79-5596-10A-01D-1945-08_LUSC	-2.55	-2.75	-2.72	-2.89	-2.50	-2.61	-2.65	-2.68	-2.69	-3.50	-2.77	-2.59	0.00	-2.70	0.00	-2.76	-2.51
TCGA-80-5607-10A-01D-1946-08_LUAD	-2.44	0.00	0.00	-2.58	-2.45	-2.50	-2.49	-2.60	-2.48	0.00	0.00	0.00	0.00	-4.54	0.00	-2.51	-2.39
TCGA-80-5608-10A-01D-1946-08_LUAD	-2.51	-4.64	-4.16	-2.63	-2.54	-2.61	-2.59	-2.61	-2.72	-3.36	-3.00	0.00	-2.77	-2.67	0.00	-2.73	-2.45

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-80-5611-10A-01D-1625-08_LUAD	-2.44	-2.70	-2.70	-2.90	-2.66	-2.62	-2.49	-2.48	-2.35	-4.46	-4.46	0.00	0.00	0.00	-3.38	-2.84	-2.43
TCGA-81-5910-10A-01D-1696-08_GBM	-2.55	-2.74	-2.69	-2.95	-2.45	-2.56	-2.58	-2.54	-2.45	0.00	-3.07	-2.75	-4.54	0.00	-3.16	-2.80	-2.48
TCGA-81-5911-10A-01D-1845-08_GBM	-2.59	0.00	-4.61	-2.60	-2.53	-2.55	-2.59	-2.57	-2.70	-3.41	-2.97	0.00	-2.84	-2.73	0.00	-2.79	-2.51
TCGA-83-5908-10A-01D-2284-08_LUAD	-2.63	-2.72	-2.76	-2.86	-2.66	-2.72	-2.62	-2.61	-2.70	-3.25	-2.88	0.00	-2.80	-2.67	0.00	-2.74	-2.56
TCGA-85-6175-10A-01D-1817-08_LUSC	-2.47	-2.74	0.00	-2.90	-2.44	-2.60	-2.58	-2.61	-2.70	-3.25	-2.88	0.00	-2.83	-2.67	-3.25	0.00	-2.53
TCGA-85-6560-10A-01D-1817-08_LUSC	-2.59	-2.64	-2.66	-4.30	-2.74	-2.74	-2.67	-2.64	-2.64	-3.28	-2.71	-2.71	-2.80	-2.70	0.00	-2.75	-2.58
TCGA-85-6561-10A-01D-1817-08_LUSC	-2.51	-2.70	-2.69	-2.80	-2.63	-2.68	-2.60	-2.51	-2.54	0.00	0.00	0.00	0.00	-4.53	-3.10	-2.73	-2.54
TCGA-85-6798-10A-01D-1945-08_LUSC	-2.37	-2.55	-2.57	0.00	-4.10	0.00	-2.50	-2.49	-2.40	0.00	0.00	-4.58	0.00	-4.27	0.00	-2.54	-2.40
TCGA-85-7696-10A-01D-2122-08_LUSC	-2.59	-2.75	-2.69	-3.00	-2.71	-2.70	-2.58	-2.51	-2.68	-3.28	-2.76	-4.12	-2.65	-2.69	-3.28	-4.12	-2.58
TCGA-85-7697-10A-01D-2122-08_LUSC	-2.49	-2.77	-2.77	-2.91	-2.51	-2.70	-2.66	-2.60	-2.77	-3.33	-2.76	-2.62	0.00	-2.73	0.00	-2.77	-2.58
TCGA-85-7698-10A-01D-2122-08_LUSC	-2.56	-3.74	-3.74	-2.57	-2.53	-2.55	-2.62	-2.55	-2.54	0.00	-4.04	-4.52	-3.82	-3.62	0.00	-2.41	-2.47
TCGA-85-7699-10A-01D-2122-08_LUSC	-2.67	-2.89	-2.86	-3.01	-2.60	-2.68	-2.68	-2.75	-2.85	-3.36	-2.81	-2.69	-4.81	-2.75	0.00	-2.81	-2.59
TCGA-85-7710-10A-01D-2122-08_LUSC	-2.61	-2.63	-2.57	0.00	-2.65	-2.84	-2.54	-2.62	-4.09	-3.14	-2.67	-2.60	-2.85	-2.49	0.00	0.00	-2.47
TCGA-85-7843-10A-01D-2122-08_LUSC	-2.65	-2.72	-2.74	-2.88	-2.45	-2.63	-2.65	-2.56	-2.63	0.00	-2.90	-2.72	0.00	-4.54	0.00	-2.49	-2.57
TCGA-85-7844-10A-01D-2122-08_LUSC	-2.56	-2.67	-2.66	-2.85	-2.57	-2.61	-2.56	-2.61	-2.52	-4.46	-4.46	0.00	-4.46	-4.16	0.00	-2.58	-2.47
TCGA-85-7950-10A-01D-2184-08_LUSC	-2.63	-2.71	-2.73	-2.85	-2.48	-2.62	-2.65	-2.64	-2.71	-3.38	-2.68	-2.71	-2.82	-2.65	0.00	-2.83	-2.51
TCGA-85-8048-10A-01D-2244-08_LUSC	-2.47	-2.61	-2.66	-2.80	-2.55	-2.60	-2.61	-2.84	-2.59	0.00	-2.91	0.00	-2.68	-2.57	0.00	-2.66	-2.37
TCGA-85-8049-10A-01D-2244-08_LUSC	-2.57	-2.74	-2.79	-2.85	-2.48	-2.57	-2.62	-2.44	-2.57	0.00	-2.73	-2.73	0.00	0.00	-3.00	-2.68	-2.56
TCGA-85-8052-10A-01D-2244-08_LUSC	-2.49	-2.72	-2.64	-2.77	-2.37	-2.66	-2.60	-2.67	-2.58	0.00	-2.85	-2.60	-4.41	-2.58	-2.95	0.00	-2.50
TCGA-85-8070-10A-01D-2244-08_LUSC	-2.32	0.00	0.00	-2.54	-2.45	-2.46	-2.47	-2.58	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.39
TCGA-85-8071-10A-01D-2244-08_LUSC	-2.48	0.00	0.00	-2.70	-2.48	-2.50	-2.55	-2.64	-2.65	-3.21	-2.88	0.00	-2.73	-2.63	0.00	-2.63	-2.45
TCGA-85-8072-10A-01D-2244-08_LUSC	-2.48	0.00	0.00	-2.65	-2.48	-2.48	-2.50	-2.47	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.35	-2.39
TCGA-85-8276-10A-01D-2293-08_LUSC	-2.59	0.00	-4.53	-2.89	-2.55	-2.52	-2.64	-2.59	-2.65	-3.38	-2.81	0.00	-2.72	-2.66	0.00	-2.70	-2.55
TCGA-85-8277-10A-01D-2293-08_LUSC	-2.40	-2.66	-2.62	-2.80	-2.63	-2.59	-2.58	-2.55	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.37	-2.46
TCGA-85-8287-10A-01D-2293-08_LUSC	-2.47	-2.75	-2.78	-2.90	-2.50	-2.55	-2.59	-2.66	-4.25	-3.07	-2.62	-2.61	-2.79	-2.59	0.00	0.00	-2.53
TCGA-85-8288-10A-01D-2293-08_LUSC	-2.50	-2.59	-2.67	-2.81	-2.60	-2.60	-2.57	-2.50	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.38	-2.48
TCGA-85-8350-10A-01D-2293-08_LUSC	-2.50	0.00	-4.46	-2.66	-2.49	-2.54	-2.50	-2.44	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.38
TCGA-85-8351-10A-01D-2293-08_LUSC	-2.63	-4.30	-4.30	-2.59	-2.55	-2.58	-2.59	-2.49	-2.50	-3.32	-4.60	-4.60	-4.60	-4.60	-3.10	-2.78	-2.56
TCGA-85-8352-10A-01D-2323-08_LUSC	-2.53	-2.69	-2.67	-2.89	-2.64	-2.63	-2.56	-2.61	-2.63	-3.58	-2.92	0.00	-2.68	-2.66	0.00	-2.74	-2.43
TCGA-85-8353-10A-01D-2293-08_LUSC	-2.54	0.00	0.00	-2.53	-2.55	-2.58	-2.59	-2.49	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.45
TCGA-85-8354-10A-01D-2323-08_LUSC	-2.57	0.00	0.00	-2.65	-2.40	-2.53	-2.58	-2.46	-2.53	-3.49	-3.01	-2.73	-4.64	0.00	0.00	-2.57	-2.56
TCGA-85-8355-10A-01D-2293-08_LUSC	-2.55	-4.51	-4.51	-2.60	-2.53	-2.56	-2.62	-2.45	-2.45	0.00	-4.51	0.00	0.00	-4.51	0.00	-2.41	-2.46
TCGA-85-8479-10A-01D-2323-08_LUSC	-2.53	-2.60	-2.54	0.00	-2.54	-2.55	-2.57	-2.61	-2.54	0.00	-2.78	-2.57	0.00	0.00	-2.91	0.00	-2.51
TCGA-85-8481-10A-01D-2323-08_LUSC	-2.55	-2.57	-2.51	-4.29	-2.64	-2.69	-2.70	-2.74	-4.59	-3.22	-2.54	-2.66	-2.55	-2.49	0.00	0.00	-2.48
TCGA-85-8580-10A-01D-2395-08_LUSC	-2.51	-2.77	-2.78	-2.92	-2.53	-2.64	-2.68	-2.61	-2.58	0.00	-2.93	-2.72	0.00	-4.59	-3.05	-2.76	-2.59
TCGA-85-8582-10A-01D-2395-08_LUSC	-2.67	-2.78	-2.79	-2.98	-2.57	-2.71	-2.68	-2.71	-2.75	-3.39	-2.76	-2.81	-2.86	-2.74	0.00	-2.77	-2.65
TCGA-85-8584-10A-01D-2395-08_LUSC	-2.57	-2.79	-2.77	-2.91	-2.53	-2.58	-2.66	-2.59	-2.64	-4.22	-2.84	-2.73	0.00	-4.52	0.00	-2.61	-2.55
TCGA-85-8664-10A-01D-2395-08_LUSC	-2.58	-3.82	-3.91	-2.61	-2.58	-2.58	-2.64	-2.64	-2.52	0.00	0.00	0.00	0.00	-4.52	0.00	-2.61	-2.54
TCGA-85-8666-10A-01D-2395-08_LUSC	-2.64	-2.81	-2.78	-2.94	-2.55	-2.72	-2.65	-2.51	-2.52	0.00	-2.82	-2.73	-4.10	0.00	-3.16	-2.79	-2.58
TCGA-85-A4CL-10A-01D-A26K-08_LUSC	-2.52	-2.79	-2.74	-2.80	-2.49	-2.57	-2.59	-2.63	-2.59	0.00	-2.84	-2.69	0.00	0.00	0.00	-2.60	-2.49
TCGA-85-A4CN-10A-01D-A24F-08_LUSC	-2.50	-2.61	-2.62	-2.83	-2.58	-2.69	-2.55	-2.45	-2.50	0.00	-3.79	-3.92	0.00	0.00	0.00	-2.55	-2.44
TCGA-85-A4JB-10A-01D-A25L-08_LUSC	-2.67	-2.72	-2.76	-3.04	-2.51	-2.71	-2.66	-2.56	-2.61	0.00	-2.90	-2.77	0.00	-3.97	-3.13	-2.83	-2.55
TCGA-85-A4JC-10A-01D-A25A-08_LUSC	-2.61	-2.74	-2.65	0.00	-2.64	-2.66	-2.65	-2.63	-2.74	-3.27	-2.68	-2.69	-2.86	-2.78	-3.06	0.00	-2.58
TCGA-85-A4PA-10A-01D-A25A-08_LUSC	-2.62	-2.73	-2.76	-2.88	-2.52	-2.69	-2.65	-2.67	-2.78	-3.36	-2.74	-2.78	-2.80	-2.77	0.00	-2.80	-2.57
TCGA-85-A4QQ-10A-01D-A25L-08_LUSC	-2.57	-3.73	-3.90	-2.66	-2.55	-2.62	-2.58	-2.60	-2.50	0.00	-4.50	-4.20	0.00	-4.50	0.00	-2.62	-2.53
TCGA-85-A4QR-10A-01D-A25A-08_LUSC	-2.40	-2.60	-2.58	-2.72	-2.59	-3.49	-2.63	-2.56	-2.61	0.00	0.00	-4.09	0.00	-2.55	0.00	-2.59	-2.54
TCGA-85-A50M-10A-01D-A25L-08_LUSC	-2.55	0.00	0.00	-2.81	-2.55	-2.57	-2.61	-2.52	-2.56	0.00	-4.54	0.00	-4.54	-4.54	-3.04	-2.73	-2.52
TCGA-85-A50Z-10A-01D-A25L-08_LUSC	-2.47	0.00	0.00	-2.77	-2.48	-2.61	-2.61	-2.69	-2.65	0.00	-4.44	0.00	0.00	-2.65	0.00	-2.61	-2.55
TCGA-85-A510-10A-01D-A26K-08_LUSC	-2.41	-4.16	-3.86	-2.70	-2.47	-2.49	-2.52	-2.50	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.42
TCGA-85-A511-10A-01D-A25L-08_LUSC	-2.49	-3.88	-4.18	-2.80	-2.53	-2.59	-2.63	-2.50	-2.57	0.00	-4.18	0.00	-4.48	-3.78	0.00	-2.47	-2.49
TCGA-85-A512-10A-01D-A26K-08_LUSC	-2.48	-2.76	-2.69	-2.80	-2.62	-2.64	-2.50	-2.53	-2.45	0.00	0.00	0.00	0.00	0.00	-3.07	-2.73	-2.46
TCGA-85-A513-10A-01D-A26K-08_LUSC	-2.45	-4.24	0.00	-2.66	-2.53	-2.54	-2.59	-2.59	-4.06	-3.16	-2.69	-2.58	-4.24	-2.54	0.00	-4.54	-2.53
TCGA-85-A53L-10A-01D-A26K-08_LUSC	-2.51	0.00	0.00	-2.61	-2.49	-2.56	-2.53	-2.50	-2.61	-3.35	-2.86	0.00	-2.75	-2.64	-3.07	-3.76	-2.46
TCGA-85-A5B5-10A-01D-A26K-08_LUSC	-2.55	-2.78	-2.74	-2.97	-2.48	-2.59	-2.60	-2.54	-2.75	-3.41	-2.77	-2.62	-4.56	-2.67	0.00	-2.75	-2.55
TCGA-86-6562-10A-01D-1753-08_LUAD	-2.51	0.00	-4.17	-2.68	-2.45	-2.50	-2.52	-2.50	-2.44	0.00	0.00	-4.47	-4.17	0.00	-3.04	-2.81	-2.40
TCGA-86-6851-10A-01D-1946-08_LUAD	-2.39	-4.55	-4.55	-2.53	-2.46	-2.48	-2.51	-2.54	-2.56	-4.55	-4.55	0.00	0.00	0.00	0.00	-2.54	-2.39
TCGA-86-7701-10A-01D-2167-08_LUAD	-2.38	-2.79	-2.70	-2.64	-2.61	-2.53	-2.46	-2.64	-2.41	0.00	0.00	-4.47	0.00	0.00	0.00	-2.54	-2.34
TCGA-86-7711-10A-01D-2063-08_LUAD	-2.56	-2.74	-2.82	-2.94	-2.50	-2.53	-2.52	-2.62	-2.50	0.00	-3.02	-2.76	-4.52	-4.52	-3.22	-2.86	-2.49
TCGA-86-7713-10A-01D-2063-08_LUAD	-2.42	-2.71	-2.70	-2.82	-2.64	-2.63	-2.57	-2.40	-2.47	-4.53	0.00	0.00	0.00	-4.23	-3.06	-2.68	-2.48
TCGA-86-7714-10A-01D-2167-08_LUAD	-2.47	-2.81	-2.78	0.00	-2.54	-2.53	-2.59	-2.69	-2.46	0.00	-2.92	0.00	-2.91	0.00	-3.08	-2.75	-2.42
TCGA-86-7953-10A-01D-2184-08_LUAD	-2.50	-4.48	0.00	-2.56	-2.50	-2.53	-2.57	-2.70	-2.63	-3.34	-2.94	-4.48	-2.79	-2.58	0.00	-2.78	-2.45
TCGA-86-7954-10A-01D-2184-08_LUAD	-2.40	-2.49	-2.49	-4.36	-4.36	-3.89	-2.49	-2.47	-2.43	0.00	-4.36	0.00	0.00	-4.36	-2.81	-3.89	-2.36
TCGA-86-7955-10A-01D-2184-08_LUAD	-2.55	-4.46	0.00	-2.70	-2.49	-2.60	-2.60	-2.62	-2.70	-3.18	-2.77	0.00	-2.77	-2.58	0.00	-2.69	-2.46
TCGA-86-8054-10A-01D-2238-08_LUAD	-2.38	-4.38	-4.38	-2.59	-2.37	-2.53	-2.52	-2.65	-2.52	0.00	-4.38	0.00	0.00	-2.54	0.00	-2.57	-2.39
TCGA-86-8055-10A-01D-2238-08_LUAD	-2.48	-4.50	0.00	-2.70	-2.47	-2.53	-2.51	-2.47	-2.41	0.00	-4.20	0.00	0.00	-4.20	0.00	-2.56	-2.46
TCGA-86-8056-10A-01D-2238-08_LUAD	-2.61	-2.80	-2.75	-2.89	-2.54	-2.65	-2.68	-2.59	-2.73	-3.25	-2.70	-2.75	-2.91	-2.72	-3.07	0.00	-2.51
TCGA-86-8073-10A-01D-2238-08_LUAD	-2.57	-2.71	-2.73	-2.80	-2.61	-2.64	-2.56	-2.53	-2.65	-3.29	-2.78	0.00	-2.77	-2.61	-2.99	0.00	-2.45
TCGA-86-8074-10A-01D-2238-08_LUAD	-2.56	-2.64	-2.64	-4.57	-2.67	-2.69	-2.60	-2.54	-2.69	-3.31	-2.72	-2.62	0.00	-2.66	-3.01	-4.57	-2.51
TCGA-86-8075-10A-01D-2238-08_LUAD	-2.66	-2.80	-2.65	-2.94	-2.47	-2.64	-2.71	-2.70	-2.70	-3.43	-2.70	-2.61	0.00	-2.70	0.00	-2.77	-2.54
TCGA-86-8076-10A-01D-2238-08_LUAD	-2.41	-4.40	-4.40	-2.61	-2.44	-2.51	-2.54	-2.71	-2.56	0.00	0.00	-4.40	0.00	-2.50	0.00	-2.64	-2.47
TCGA-86-8278-10A-01D-2284-08_LUAD	-2.46	-2.62	-2.56	-2.84	-2.60	-2.60	-2.48	-2.48	-2.41	0.00	0.00	0.00	0.00	0.00	-3.07	-2.69	-2.42
TCGA-86-8279-10A-01D-2284-08_LUAD	-2.43	0.00	0.00	-2.68	-2.45	-2.48	-2.49	-2.47	-2.43	0.00	0.00	0.00	0.00	0.00	-3.09	-2.68	-2.42
TCGA-86-8280-10A-01D-2284-08_LUAD	-2.37	0.00	0.00	-2.49	-2.41	-2.53	-2.56	-2.71	-2.48	0.00	0.00	0.00	0.00	-2.54	0.00	-2.60	-2.38
TCGA-86-8281-10A-01D-2284-08_LUAD	-2.45	-2.76	-2.58	-2.72	-2.54	-2.59	-2.47	-2.46	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.39
TCGA-86-8358-10A-01D-2323-08_LUAD	-2.60	-2.77	-2.70	-2.92	-2.46	-2.60	-2.60	-2.53	-2.64	0.00	-2.98	-2.69	0.00	0.00	0.00	-2.49	-2.49
TCGA-86-8359-10A-01D-2323-08_LUAD	-2.49	-4.39	0.00	-2.72	-2.51	-2.51	-2.57	-2.51	-2.67	-3.29	-2.87	-4.21	-2.77	-2.61	0.00	-2.76	-2.44
TCGA-86-8585-10A-01D-2393-08_LUAD	-2.58	-2.65	-2.66	-2.78	-2.66	-2.66	-2.60	-2.49	-2.49	0.00	-3.94	-3.76	0.00	0.00	-3.03	-2.71	-2.49
TCGA-86-8668-10A-01D-2393-08_LUAD	-2.56	-2.56	-2.56	-3.67	-3.51	-3.61	-2.56	-2.47	-2.42	0.00	0.00	-4.04	-4.21	-3.81	0.00	-2.67	-2.52
TCGA-86-8669-10A-01D-2393-08_LUAD	-2.60	-3.67	-3.73	-2.84	-2.55	-2.56	-2.59	-2.54	-2.58	-4.57	-4.10	-3.73	-4.57	-4.10	0.00	-2.61	-2.55
TCGA-86-8671-10A-01D-2393-08_LUAD	-2.58	-2.77	-2.81	-2.99	-2.55	-2.71	-2.68	-2.67	-2.63	-3.85	-2.86	-2.75	-4.33	-3.63	0.00	-2.52	-2.63
TCGA-86-8672-10A-01D-2393-08_LUAD	-2.73	-2.85	-2.84	-3.00	-2.60	-2.77	-2.72	-2.70	-2.80	-3.30	-2.78	-2.71	-3.87	-2.84	0.00	-2.80	-2.69
TCGA-86-8673-10A-01D-2393-08_LUAD	-2.54	-2.69	-2.67	-2.86	-2.64	-2.66	-2.58	-2.53	-2.50	-3.86	-4.26	-4.56	-3.96	-3.86	0.00	-2.43	-2.52
TCGA-86-8674-10A-01D-2393-08_LUAD	-2.51	0.00	0.00	-2.55	-2.47	-2.47	-2.53	-2.52	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.38
TCGA-86-A456-10A-01D-A24F-08_LUAD	-2.58	-4.46	-3.85	-2.77	-2.57	-2.57	-2.62	-2.55	-2.60	-4.15	-4.15	-3.98	-4.15	-3.85	-3.13	-2.82	-2.50
TCGA-86-A4D0-10A-01D-A24F-08_LUAD	-2.55	-3.71	-3.45	-2.78	-2.51	-2.55	-2.56	-2.48	-2.45	0.00	-4.41	-3.71	-4.41	-3.71	0.00	-2.55	-2.49
TCGA-86-A4JF-10A-01D-A24P-08_LUAD	-2.61	0.00	-3.93	-2.67	-2.58	-2.62	-2.61	-2.43	-2.46	-4.53	-3.93	0.00	-3.93	-3.93	-3.07	-2.73	-2.54
TCGA-86-A4P7-10A-01D-A24P-08_LUAD	-2.53	-2.52	-2.54	-4.46	-3.76	-3.76	-2.57	-2.43	-2.53	0.00	0.00	0.00	-4.46	0.00	-3.00	-2.65	-2.47
TCGA-86-A4P8-10A-01D-A24P-08_LUAD	-2.66	0.00	-4.23	-2.65	-2.63	-2.65	-2.67	-2.58	-2.73	-3.35	-2.88	0.00	-2.79	-2.72	0.00	-2.79	-2.57
TCGA-87-5896-10A-01D-1696-08_GBM	-2.52	-2.66	-2.63	-2.86	-2.66	-2.65	-2.56	-2.52	-2.46	0.00	0.00	0.00	-4.45	-3.75	-3.02	-2.74	-2.42
TCGA-90-6837-10A-01D-1945-08_LUSC	-2.64	-2.82	-2.87	-2.97	-2.60	-2.77	-2.62	-2.55	-2.85	-3.31	-2.82	-2.78	-2.96	-2.82	-3.27	-4.39	-2.60
TCGA-90-7766-10A-01D-2122-08_LUSC	-2.54	-2.72	-2.66	-2.89	-2.63	-2.72	-2.60	-2.54	-2.62	-3.29	-2.85	0.00	-2.73	-2.65	-3.14	-3.74	-2.52
TCGA-90-7767-10A-01D-2122-08_LUSC	-2.52	-2.65	-2.77	-2.83	-2.66	-2.71	-2.60	-2.53	-2.66	-3.35	-2.86	0.00	-2.74	-2.73	-3.20	-4.02	-2.43
TCGA-90-7769-10A-01D-2122-08_LUSC	-2.53	-4.50	0.00	-2.55	-2.53	-2.57	-2.59	-2.46	-2.43	0.00	0.00	-4.50	0.00	-4.20	-3.10	-2.72	-2.47
TCGA-90-7964-10A-01D-2184-08_LUSC	-2.37	-4.13	-4.43	-2.55	-2.50	-2.49	-2.53	-2.52	-2.40	0.00	0.00	0.00	0.00	-4.13	0.00	-2.39	-2.41
TCGA-90-A4ED-10A-01D-A25A-08_LUSC	-2.51	-2.68	-2.70	-2.88	-2.69	-2.71	-2.60	-2.60	-2.65	-3.44	-2.85	0.00	-2.77	-2.73	0.00	-2.73	-2.56
TCGA-90-A4EE-10B-01D-A25A-08_LUSC	-2.45	-2.65	-2.62	-2.87	-2.60	-2.72	-2.55	-2.42	-2.44	0.00	-4.14	-4.44	0.00	0.00	-2.91	-2.64	-2.43

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-90-A59Q-10A-01D-A26K-08_LUSC	-2.47	-4.43	0.00	-2.69	-2.49	-2.52	-2.57	-2.52	-2.53	-4.43	-4.43	0.00	-4.43	-4.43	0.00	-2.46	-2.41
TCGA-91-6828-10A-01D-1855-08_LUAD	-2.50	0.00	0.00	-2.61	-2.55	-2.58	-2.59	-2.56	-2.46	0.00	0.00	0.00	0.00	-4.57	-3.11	-2.83	-2.51
TCGA-91-6840-10A-01D-1946-08_LUAD	-2.55	-2.60	-2.58	-4.55	-2.70	-2.70	-2.58	-2.50	-2.49	-3.40	-2.92	-2.75	0.00	-4.55	-3.19	-2.79	-2.45
TCGA-91-7771-10A-01D-2167-08_LUAD	-2.41	0.00	-4.48	-2.61	-2.53	-2.58	-2.53	-2.41	-2.42	0.00	0.00	0.00	0.00	-4.00	-2.96	-2.68	-2.45
TCGA-91-8496-10A-01D-2393-08_LUAD	-2.43	0.00	0.00	-2.65	-2.50	-2.51	-2.54	-2.53	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.64	-2.47
TCGA-91-8497-10A-01D-2393-08_LUAD	-2.66	-2.93	-2.81	-3.01	-2.78	-2.81	-2.66	-2.55	-2.81	-3.24	-2.87	0.00	-2.83	-2.73	-3.13	-3.61	-2.61
TCGA-91-8499-10A-01D-2393-08_LUAD	-2.50	0.00	-4.61	-2.80	-2.62	-2.65	-2.66	-2.45	-2.51	0.00	0.00	-4.61	0.00	-4.61	0.00	-2.44	-2.55
TCGA-91-A4BC-10A-01D-A24F-08_LUAD	-2.66	-2.81	-2.82	-2.97	-2.52	-2.70	-2.65	-2.68	-2.69	-3.39	-2.76	-2.70	0.00	-2.74	0.00	-2.77	-2.63
TCGA-91-A4BD-10A-01D-A24F-08_LUAD	-2.66	-2.77	-2.73	-2.97	-2.52	-2.64	-2.69	-2.69	-2.73	-3.33	-2.72	-2.75	-2.77	-2.71	0.00	-2.80	-2.60
TCGA-92-7340-10A-01D-2042-08_LUSC	-2.58	-4.54	0.00	-2.63	-2.61	-2.60	-2.60	-2.61	-2.78	-3.31	-2.88	0.00	-2.72	-2.71	0.00	-2.77	-2.51
TCGA-92-7341-10A-01D-2042-08_LUSC	-2.47	-2.49	-2.50	-4.13	-3.96	0.00	-2.54	-2.51	-2.48	0.00	-4.44	-4.44	0.00	-4.44	0.00	-2.47	-2.37
TCGA-92-8063-10A-01D-2244-08_LUSC	-2.58	-2.77	-2.77	-2.82	-2.45	-2.55	-2.62	-2.62	-2.61	-3.36	-2.77	-2.66	-2.76	-2.67	-3.11	-4.17	-2.56
TCGA-92-8064-10A-01D-2244-08_LUSC	-2.48	0.00	0.00	-2.66	-2.48	-2.43	-2.49	-2.54	-2.37	0.00	0.00	0.00	0.00	-4.07	-2.91	-2.63	-2.44
TCGA-92-8065-10A-01D-2244-08_LUSC	-2.48	-3.92	0.00	-2.50	-2.39	-2.46	-2.49	-2.59	-2.38	0.00	0.00	0.00	0.00	-4.39	0.00	-2.52	-2.39
TCGA-93-7347-10A-01D-2184-08_LUAD	-2.32	0.00	0.00	-2.60	-2.43	-2.49	-2.53	-2.55	-2.48	0.00	0.00	0.00	0.00	0.00	-2.92	-4.44	-2.42
TCGA-93-7348-10A-01D-2036-08_LUAD	-2.48	-2.62	-2.71	-2.79	-2.63	-2.65	-2.52	-2.56	-2.56	0.00	0.00	-4.47	0.00	-4.17	0.00	-2.56	-2.43
TCGA-93-8067-10A-01D-2284-08_LUAD	-2.51	0.00	0.00	-2.64	-2.52	-2.50	-2.52	-2.64	-2.63	-3.22	-2.94	-4.55	-2.75	-2.60	0.00	-2.74	-2.47
TCGA-93-A4JN-10A-01D-A24P-08_LUAD	-2.67	-3.82	-3.82	-2.73	-2.45	-2.65	-2.72	-2.71	-2.74	-3.26	-2.83	0.00	-2.79	-2.76	0.00	-2.78	-2.62
TCGA-93-A4JO-10A-01D-A24P-08_LUAD	-2.43	0.00	-4.48	-2.75	-2.59	-2.61	-2.61	-2.38	-2.44	0.00	-4.48	0.00	0.00	0.00	0.00	-2.41	-2.53
TCGA-93-A4JP-10A-01D-A24P-08_LUAD	-2.60	-4.10	-3.98	-2.87	-2.61	-2.66	-2.63	-2.55	-2.52	0.00	-4.28	0.00	-3.98	-3.88	-3.06	-2.73	-2.61
TCGA-93-A4JQ-10A-01D-A24P-08_LUAD	-2.65	-2.71	-2.76	-2.90	-2.68	-2.72	-2.74	-2.77	-2.77	0.00	-2.77	0.00	-2.75	-2.73	0.00	-2.73	-2.60
TCGA-94-7033-10A-01D-1946-08_LUSC	-2.60	-2.87	-2.77	-2.88	-2.51	-2.62	-2.60	-2.52	-2.55	-3.48	-2.93	-2.79	-4.66	0.00	-3.23	-2.84	-2.54
TCGA-94-7557-10A-01D-2122-08_LUSC	-2.62	-2.78	-2.81	-2.94	-2.50	-2.60	-2.60	-2.63	-2.59	0.00	-2.91	-2.71	0.00	0.00	-2.98	-3.96	-2.54
TCGA-94-7943-10A-01D-2184-08_LUSC	-2.51	0.00	0.00	-2.67	-2.47	-2.49	-2.47	-2.50	-2.48	0.00	0.00	0.00	0.00	-4.40	0.00	-2.39	-2.42
TCGA-94-8035-10A-01D-2244-08_LUSC	-2.34	-2.69	0.00	-2.83	-2.41	-2.52	-2.56	-2.41	-2.45	0.00	0.00	0.00	0.00	0.00	-3.05	-2.61	-2.49
TCGA-94-8490-10A-01D-2323-08_LUSC	-2.42	0.00	-4.55	-2.53	-2.53	-2.48	-2.56	-2.42	-2.41	0.00	0.00	0.00	0.00	-4.55	-3.02	-2.75	-2.40
TCGA-94-8491-10A-01D-2323-08_LUSC	-2.37	-2.45	-2.45	0.00	0.00	0.00	-2.44	-2.48	-2.40	0.00	0.00	0.00	0.00	0.00	-2.89	0.00	-2.29
TCGA-94-A4VJ-10A-01D-A25A-08_LUSC	-2.52	0.00	0.00	-2.62	-2.47	-2.54	-2.54	-2.54	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.41
TCGA-94-A5I4-10A-01D-A26K-08_LUSC	-2.42	-4.53	-4.23	-2.67	-2.50	-2.57	-2.53	-2.48	-2.44	0.00	-4.53	-4.05	0.00	0.00	0.00	-2.42	-2.46
TCGA-94-A5I6-10A-01D-A27N-08_LUSC	-2.58	-2.72	-2.72	-2.90	-2.69	-2.73	-2.63	-2.51	-2.68	-3.29	-2.97	0.00	-2.72	-2.72	-3.06	0.00	-2.56
TCGA-95-7039-10A-01D-1946-08_LUAD	-2.52	-4.42	-4.42	-2.72	-2.42	-2.52	-2.52	-2.47	-2.50	0.00	0.00	0.00	0.00	0.00	-3.06	-2.62	-2.42
TCGA-95-7043-10A-01D-1946-08_LUAD	-2.48	0.00	0.00	-2.65	-2.36	-2.48	-2.57	-2.45	-2.41	0.00	0.00	0.00	0.00	0.00	-3.08	-2.69	-2.41
TCGA-95-7562-10B-01D-2238-08_LUAD	-2.47	-4.48	0.00	-2.52	-2.51	-2.55	-2.50	-2.51	-2.43	0.00	0.00	0.00	0.00	-4.01	-3.01	-2.64	-2.49
TCGA-95-7567-10A-01D-2063-08_LUAD	-2.55	-2.66	-2.67	-2.81	-2.65	-2.67	-2.59	-2.42	-2.44	0.00	0.00	0.00	0.00	0.00	-2.99	-2.69	-2.47
TCGA-95-7944-10A-01D-2184-08_LUAD	-2.61	-2.83	-2.76	-2.88	-2.49	-2.58	-2.66	-2.68	-2.72	-3.42	-2.72	-2.73	-2.91	-2.74	0.00	-2.83	-2.53
TCGA-95-7947-10A-01D-2184-08_LUAD	-2.47	-2.65	-2.68	-2.79	-2.62	-2.58	-2.55	-2.50	-2.52	0.00	-4.42	0.00	0.00	0.00	-3.01	-2.62	-2.44
TCGA-95-7948-10A-01D-2184-08_LUAD	-2.63	-2.73	-2.69	-2.84	-2.48	-2.58	-2.62	-2.63	-2.52	0.00	-2.96	-2.71	0.00	-4.55	0.00	-2.47	-2.54
TCGA-95-8039-10A-01D-2238-08_LUAD	-2.50	-4.44	0.00	-2.70	-2.45	-2.47	-2.53	-2.47	-2.41	0.00	0.00	0.00	0.00	0.00	-3.00	-2.62	-2.42
TCGA-95-8494-10A-01D-2323-08_LUAD	-2.59	-2.75	-2.72	0.00	-2.51	-2.58	-2.63	-2.58	-2.80	-3.54	-2.81	-2.76	-2.80	-2.73	0.00	-2.86	-2.52
TCGA-95-A4VK-10A-01D-A25L-08_LUAD	-2.58	-4.54	0.00	-2.67	-2.57	-2.59	-2.61	-2.59	-2.53	0.00	-3.94	-4.07	-4.24	-4.07	0.00	-2.49	-2.55
TCGA-95-A4VN-10A-01D-A25L-08_LUAD	-2.60	-4.57	-4.57	-2.69	-2.60	-2.60	-2.65	-2.66	-2.70	-3.21	-2.92	-4.10	-2.81	-2.72	0.00	-2.78	-2.58
TCGA-95-A4VP-10A-01D-A25L-08_LUAD	-2.46	-4.19	-3.79	-2.76	-2.50	-2.60	-2.55	-2.56	-2.54	0.00	-4.02	-3.79	0.00	0.00	-3.03	-2.74	-2.49
TCGA-96-7544-10A-01D-2042-08_LUSC	-2.53	0.00	-4.53	-2.74	-2.56	-2.57	-2.66	-2.56	-2.64	-3.33	-2.86	-4.53	-2.74	-2.68	0.00	-2.70	-2.52
TCGA-96-7545-10A-01D-2042-08_LUSC	-2.49	0.00	-4.47	-2.75	-2.36	-2.61	-2.55	-2.58	-2.41	0.00	0.00	-4.47	0.00	0.00	0.00	-2.55	-2.40
TCGA-96-8169-10A-01D-2293-08_LUSC	-2.60	0.00	-4.50	-2.54	-2.49	-2.52	-2.55	-2.48	-2.43	0.00	-4.20	-4.20	0.00	0.00	-2.96	-2.72	-2.42
TCGA-96-8170-10A-01D-2293-08_LUSC	-2.49	-2.62	-2.63	-2.77	-2.56	-2.58	-2.53	-2.46	-2.39	0.00	0.00	0.00	0.00	-4.42	-3.02	-2.71	-2.38
TCGA-96-A4JK-10A-01D-A25A-08_LUSC	-2.49	-2.76	-2.63	-2.81	-2.63	-2.70	-2.53	-2.53	-2.54	0.00	-3.98	-3.98	-3.98	-3.62	0.00	-2.55	-2.42
TCGA-96-A4JL-10A-01D-A25A-08_LUSC	-2.42	-4.27	0.00	-2.63	-2.57	-2.57	-2.61	-2.47	-2.75	-3.27	-2.84	-4.57	-2.83	-2.72	-3.06	-4.27	-2.54
TCGA-97-7546-10A-01D-2036-08_LUAD	-2.56	-2.73	-2.69	-2.89	-2.66	-2.70	-2.64	-2.50	-2.59	0.00	0.00	-4.50	-3.90	-3.90	-3.01	-2.71	-2.49
TCGA-97-7547-10A-01D-2036-08_LUAD	-2.60	0.00	-4.57	-2.63	-2.63	-2.64	-2.64	-2.61	-2.69	-3.53	-2.92	-4.10	-2.89	-2.72	0.00	-2.77	-2.53
TCGA-97-7552-10A-01D-2036-08_LUAD	-2.53	-4.23	-4.23	-2.61	-2.55	-2.60	-2.55	-2.53	-2.56	0.00	0.00	0.00	-4.54	-4.54	0.00	-2.41	-2.50
TCGA-97-7553-10A-01D-2036-08_LUAD	-2.53	-2.74	-2.72	-2.93	-2.54	-2.63	-2.60	-2.58	-2.71	-3.39	-2.76	-2.72	-2.80	-2.74	-3.15	-4.59	-2.57
TCGA-97-7554-10A-01D-2036-08_LUAD	-2.51	0.00	0.00	-2.83	-2.54	-2.59	-2.59	-2.53	-2.73	-3.56	-2.95	0.00	-2.71	-2.68	-3.09	0.00	-2.45
TCGA-97-7937-10A-01D-2167-08_LUAD	-2.46	0.00	0.00	-2.61	-2.48	-2.50	-2.49	-2.60	-4.50	-3.10	-2.73	0.00	-2.68	-2.48	0.00	-4.20	-2.43
TCGA-97-7938-10A-01D-2167-08_LUAD	-2.47	0.00	0.00	-2.68	-2.56	-2.51	-2.56	-2.66	-2.73	-3.30	-2.86	0.00	-2.86	-2.69	0.00	-2.76	-2.53
TCGA-97-7941-10A-01D-2184-08_LUAD	-2.48	-4.42	-4.42	-2.54	-2.47	-2.51	-2.58	-2.47	-2.52	0.00	0.00	0.00	0.00	-4.42	-2.97	-2.61	-2.41
TCGA-97-8171-10A-01D-2284-08_LUAD	-2.48	-2.64	-2.66	-2.82	-2.57	-2.63	-2.50	-2.49	-2.49	0.00	0.00	0.00	0.00	-4.51	-3.03	-2.75	-2.41
TCGA-97-8172-10A-01D-2284-08_LUAD	-2.53	-2.74	-2.69	-2.84	-2.61	-2.61	-2.56	-2.57	-2.59	-3.25	-2.89	0.00	-2.76	-2.61	-3.14	0.00	-2.43
TCGA-97-8174-10A-01D-2284-08_LUAD	-2.48	-2.73	-2.66	-2.85	-2.67	-2.67	-2.50	-2.55	-2.57	-3.29	-3.01	0.00	-2.71	-2.60	0.00	-2.88	-2.43
TCGA-97-8175-10A-01D-2284-08_LUAD	-2.49	-2.74	-2.69	-2.83	-2.61	-2.63	-2.50	-2.56	-2.63	-3.42	-2.97	0.00	-2.74	-2.57	0.00	-2.76	-2.40
TCGA-97-8176-10B-01D-2393-08_LUAD	-2.45	0.00	0.00	-2.73	-2.51	-2.49	-2.53	-2.45	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.44
TCGA-97-8177-10A-01D-2284-08_LUAD	-2.49	-4.50	0.00	-2.67	-2.48	-2.47	-2.52	-2.52	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.44
TCGA-97-8179-10A-01D-2284-08_LUAD	-2.46	0.00	0.00	-2.54	-2.44	-2.46	-2.49	-2.57	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.39
TCGA-97-8547-10A-01D-2393-08_LUAD	-2.56	-3.91	-3.91	-2.82	-2.57	-2.60	-2.56	-2.59	-2.62	-4.51	-4.03	-4.21	-3.73	-3.60	0.00	-2.43	-2.57
TCGA-97-8552-10A-01D-2393-08_LUAD	-2.44	-2.64	-2.61	-2.86	-2.62	-2.65	-2.57	-2.49	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.45
TCGA-97-A4LX-10A-01D-A24P-08_LUAD	-2.64	-2.76	-2.75	-2.93	-2.53	-2.67	-2.68	-2.58	-2.58	0.00	-2.91	-2.77	-3.68	-4.11	-3.14	-2.77	-2.68
TCGA-97-A4M0-10A-01D-A24P-08_LUAD	-2.55	0.00	-4.50	-2.78	-2.54	-2.57	-2.62	-2.49	-2.75	-3.46	-2.89	0.00	-2.77	-2.67	0.00	-2.77	-2.52
TCGA-97-A4M1-10A-01D-A24P-08_LUAD	-2.66	-2.77	-2.77	-2.95	-2.57	-2.68	-2.70	-2.59	-2.75	-3.45	-2.74	-2.77	-2.86	-2.72	0.00	-2.87	-2.63
TCGA-97-A4M2-10A-01D-A24P-08_LUAD	-2.67	-2.74	-2.72	-2.92	-2.77	-2.72	-2.70	-2.53	-2.70	-3.40	-2.83	0.00	-2.81	-2.75	-3.15	-4.07	-2.60
TCGA-97-A4M3-10A-01D-A24P-08_LUAD	-2.60	0.00	-4.04	-2.62	-2.58	-2.64	-2.63	-2.41	-2.48	0.00	0.00	0.00	0.00	0.00	-3.09	-2.66	-2.54
TCGA-97-A4M5-10A-01D-A24P-08_LUAD	-2.57	-2.66	-2.65	-2.82	-2.64	-2.67	-2.65	-2.74	-2.64	0.00	-2.85	0.00	-2.73	-2.65	0.00	-2.71	-2.51
TCGA-97-A4M6-10A-01D-A24P-08_LUAD	-2.63	-2.65	-2.72	-4.05	-2.63	-2.63	-2.62	-2.69	-3.93	-3.21	-2.63	-2.77	-2.64	-2.65	0.00	-4.53	-2.59
TCGA-97-A4M7-10A-01D-A24P-08_LUAD	-2.60	-3.95	-4.08	-2.90	-2.61	-2.65	-2.65	-2.51	-2.50	0.00	-4.55	-4.55	0.00	-4.25	-3.06	-2.72	-2.58
TCGA-98-7454-10A-01D-2042-08_LUSC	-2.48	0.00	-4.50	-2.55	-2.50	-2.59	-2.57	-2.57	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.46
TCGA-98-8020-10A-01D-2244-08_LUSC	-2.49	-2.71	-2.70	-2.85	-2.45	-2.42	-2.57	-2.59	-2.46	-4.47	-2.89	-2.66	0.00	0.00	0.00	-2.64	-2.45
TCGA-98-8021-10A-01D-2244-08_LUSC	-2.40	0.00	0.00	-2.42	-2.36	-2.38	-2.54	-2.65	-2.47	0.00	0.00	0.00	0.00	0.00	-2.88	0.00	-2.41
TCGA-98-8022-10A-01D-2244-08_LUSC	-2.43	0.00	0.00	-2.49	-2.44	-2.44	-2.45	-2.49	-2.51	0.00	0.00	-4.06	0.00	-4.36	0.00	-2.41	-2.37
TCGA-98-8023-10A-01D-2244-08_LUSC	-2.50	0.00	0.00	-2.73	-2.53	-2.48	-2.56	-2.58	-2.67	-3.23	-2.91	0.00	-2.83	-2.59	0.00	-2.63	-2.44
TCGA-98-A538-10A-01D-A25L-08_LUSC	-2.54	0.00	-4.23	-2.79	-2.57	-2.56	-2.60	-2.49	-2.55	0.00	0.00	0.00	0.00	0.00	-3.07	-2.74	-2.48
TCGA-98-A539-10A-01D-A25L-08_LUSC	-2.57	0.00	0.00	-2.64	-2.59	-2.59	-2.59	-2.53	-2.52	0.00	0.00	-4.49	0.00	0.00	-3.00	-2.71	-2.48
TCGA-98-A53A-10A-01D-A25L-08_LUSC	-2.52	-2.68	-2.64	-2.86	-2.62	-2.66	-2.59	-2.43	-2.49	0.00	-4.17	-3.87	0.00	-4.47	-3.08	-3.70	-2.58
TCGA-98-A53B-10A-01D-A25L-08_LUSC	-2.59	-2.68	-2.65	-3.00	-2.68	-2.72	-2.62	-2.54	-2.60	0.00	-4.53	-4.23	0.00	-4.23	0.00	-2.46	-2.53
TCGA-98-A53C-10A-01D-A25L-08_LUSC	-2.63	-2.71	-2.75	-3.02	-2.81	-2.79	-2.64	-2.64	-2.85	-3.35	-2.87	0.00	-2.88	-2.70	0.00	-2.74	-2.51
TCGA-98-A53D-10A-01D-A25L-08_LUSC	-2.46	0.00	0.00	-2.66	-2.55	-2.60	-2.62	-2.47	-2.57	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.53
TCGA-98-A53H-10A-01D-A25L-08_LUSC	-2.60	-2.75	-2.76	-2.96	-2.76	-2.76	-2.65	-2.51	-2.77	-3.39	-2.84	-3.72	-2.78	-2.77	0.00	-2.87	-2.51
TCGA-98-A53I-10A-01D-A25L-08_LUSC	-2.46	-2.75	-2.73	-2.94	-2.67	-2.77	-2.59	-2.59	-2.70	-3.39	-2.87	0.00	-2.73	-2.72	0.00	-2.75	-2.54
TCGA-98-A53J-10A-01D-A26K-08_LUSC	-2.52	0.00	0.00	-2.59	-2.50	-2.52	-2.50	-2.54	-2.50	-4.47	-4.47	0.00	-3.99	-3.69	0.00	-2.53	-2.44
TCGA-99-7458-10A-01D-2036-08_LUAD	-2.53	0.00	-4.57	-2.63	-2.52	-2.56	-2.56	-2.53	-2.68	-3.29	-2.84	0.00	-2.76	-2.62	-3.02	-4.09	-2.51
TCGA-99-8025-10A-01D-2238-08_LUAD	-2.47	0.00	0.00	-2.65	-2.43	-2.49	-2.53	-2.53	-2.43	0.00	0.00	0.00	-4.43	0.00	-2.96	-2.70	-2.43
TCGA-99-8028-10A-01D-2238-08_LUAD	-2.57	0.00	-4.52	-2.56	-2.49	-2.53	-2.57	-2.44	-2.45	0.00	0.00	-4.22	0.00	0.00	-2.93	-2.70	-2.44
TCGA-99-8032-10A-01D-2238-08_LUAD	-2.49	0.00	0.00	-2.67	-2.49	-2.53	-2.54	-2.47	-2.40	0.00	-4.48	0.00	0.00	-4.48	-2.96	-2.64	-2.42
TCGA-99-8033-10A-01D-2238-08_LUAD	-2.47	0.00	-4.49	-2.52	-2.50	-2.48	-2.54	-2.42	-2.45	0.00	0.00	0.00	0.00	-4.49	0.00	-2.36	-2.49
TCGA-A1-A0SB-10B-01D-A142-09_BRCA	-3.08	-2.78	-2.90	-3.16	-2.79	-2.89	-2.59	-2.70	-4.54	-3.34	-2.64	-2.82	-2.88	-2.65	0.00	0.00	-2.74
TCGA-A1-A0SD-10A-01D-A110-09_BRCA	-2.73	-2.44	-2.44	-4.42	0.00	-4.12	-2.43	-2.51	-2.34	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.60
TCGA-A1-A0SE-10A-03D-A099-09_BRCA	-3.11	-2.88	-2.89	-3.21	-2.68	-2.75	-2.66	-2.80	0.00	-3.45	-2.65	-2.75	-2.93	-2.75	0.00	0.00	-2.85
TCGA-A1-A0SF-10B-01D-A142-09_BRCA	-2.96	-2.77	-2.90	-3.29	-2.64	-2.74	-2.74	-2.80	-2.66	0.00	-3.03	-2.92	0.00	0.00	-3.19	-3.03	-2.84

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-A1-A0SG-10B-01D-A17G-09_BRCA	-2.99	-2.68	-2.71	0.00	-2.88	-2.86	-2.71	-2.80	-2.94	-3.44	-2.69	-2.87	-2.87	-2.80	0.00	-2.90	-2.89
TCGA-A1-A0SH-10A-03D-A099-09_BRCA	-3.23	-2.94	-3.00	-3.33	-2.75	-2.81	-2.71	-2.93	-5.11	-3.29	-2.76	-2.85	-2.95	-2.72	0.00	0.00	-2.97
TCGA-A1-A0SI-10B-01D-A142-09_BRCA	-2.96	0.00	-4.52	-3.01	-2.66	-2.76	-2.64	-2.80	-2.93	-3.48	-2.96	-3.01	0.00	-2.91	-3.22	0.00	-2.84
TCGA-A1-A0SJ-10A-02D-A099-09_BRCA	-2.97	0.00	-4.83	-2.94	-2.54	-2.64	-2.62	-2.71	-2.58	0.00	-2.92	-2.79	0.00	-4.83	-2.97	0.00	-2.77
TCGA-A1-A0SK-10A-03D-A099-09_BRCA	-2.72	0.00	0.00	-2.86	-2.48	-2.47	-2.38	-2.53	-2.43	0.00	0.00	0.00	0.00	0.00	-2.86	0.00	-2.57
TCGA-A1-A0SM-10A-02D-A10G-09_BRCA	-2.86	-2.78	-2.76	-3.13	-2.53	-2.70	-2.67	-2.59	-2.56	0.00	-2.91	-2.77	0.00	0.00	-3.13	-2.84	-2.80
TCGA-A1-A0SN-10B-01D-A142-09_BRCA	-2.94	-4.48	0.00	-2.90	-2.56	-2.58	-2.53	-2.59	-2.55	0.00	0.00	-4.48	0.00	0.00	-3.21	-2.82	-2.59
TCGA-A1-A0SO-10A-03D-A099-09_BRCA	-3.05	-2.82	-2.84	-3.24	-2.60	-2.78	-2.66	-2.79	-2.80	-3.49	-2.74	-2.86	-2.93	-2.86	0.00	-2.95	-2.89
TCGA-A1-A0SP-10A-02D-A099-09_BRCA	-3.03	-2.84	-2.84	-3.19	-2.63	-2.73	-2.62	-2.69	-2.69	0.00	-2.99	-2.84	0.00	0.00	0.00	-2.63	-2.85
TCGA-A2-A04N-10A-01D-A110-09_BRCA	-2.89	0.00	0.00	-2.73	-2.58	-2.61	-2.57	-2.63	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.67
TCGA-A2-A04R-10B-01D-A10G-09_BRCA	-2.97	-2.76	-2.79	-3.18	-2.71	-2.71	-2.68	-2.76	-2.82	-3.41	-2.74	0.00	-2.70	-2.89	-3.22	-4.23	-2.81
TCGA-A2-A04U-10A-01D-A110-09_BRCA	-2.88	0.00	0.00	-2.77	-2.59	-2.59	-2.54	-2.58	-2.59	0.00	0.00	0.00	0.00	0.00	-2.99	-2.78	-2.70
TCGA-A2-A04W-10A-01D-A110-09_BRCA	-2.90	0.00	0.00	-2.96	-2.59	-2.61	-2.49	-2.58	-2.56	0.00	0.00	0.00	0.00	0.00	-3.03	-2.82	-2.76
TCGA-A2-A0CK-10A-01D-A22A-09_BRCA	-2.87	-2.61	-2.60	-3.94	-2.61	-2.61	-2.62	-2.63	-2.69	-3.81	-2.64	-2.59	-3.94	-2.78	0.00	-2.97	-2.70
TCGA-A2-A0CL-10A-01D-A110-09_BRCA	-2.90	-2.71	-2.58	0.00	-2.60	-2.56	-2.56	-2.60	-2.57	-4.89	-2.60	-2.69	-2.78	-4.41	-3.17	-2.93	-2.68
TCGA-A2-A0CO-10A-01D-A22A-09_BRCA	-2.97	-2.85	-2.82	-3.44	-2.54	-2.67	-2.59	-2.64	-2.65	-3.36	-2.69	-2.79	-2.88	-2.80	0.00	-2.98	-2.63
TCGA-A2-A0CR-10A-01D-A22A-09_BRCA	-2.83	-4.08	-4.08	-3.01	-2.46	-2.57	-2.50	-2.61	-2.38	-4.39	-4.39	-3.91	0.00	0.00	-2.84	0.00	-2.59
TCGA-A2-A0CS-10A-01D-A110-09_BRCA	-2.94	0.00	0.00	-3.02	-2.54	-2.64	-2.54	-2.61	-2.75	-3.32	-2.77	-4.78	-2.76	-2.75	0.00	-2.73	-2.69
TCGA-A2-A0CV-10A-01D-A110-09_BRCA	-2.94	0.00	0.00	-2.70	-2.58	-2.53	-2.46	-2.58	-2.36	0.00	0.00	0.00	0.00	0.00	-3.05	-2.78	-2.69
TCGA-A2-A0CW-10A-01D-A110-09_BRCA	-2.74	-2.74	-2.75	-3.04	-2.69	-2.69	-2.54	-2.61	-2.50	0.00	0.00	0.00	0.00	0.00	-2.88	0.00	-2.73
TCGA-A2-A0D3-10A-01D-A110-09_BRCA	-2.91	-2.72	-2.69	-3.00	-2.71	-2.77	-2.69	-2.88	0.00	-3.43	-2.66	-2.57	0.00	-2.59	0.00	0.00	-2.76
TCGA-A2-A0EN-10A-01D-A099-09_BRCA	-2.92	-2.69	-2.69	-3.11	-2.81	-2.75	-2.58	-2.55	-2.72	-3.31	-2.88	0.00	-2.77	-2.75	0.00	-2.82	-2.74
TCGA-A2-A0EP-10A-01D-A22X-09_BRCA	-2.81	-4.18	-4.18	-3.02	-2.54	-2.56	-2.50	-2.51	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.60
TCGA-A2-A0ES-10A-01D-A110-09_BRCA	-2.99	-2.57	-2.54	0.00	-2.82	-2.83	-2.58	-2.66	0.00	-3.32	-2.61	-2.46	0.00	-2.62	0.00	-4.84	-2.69
TCGA-A2-A0EW-10A-01D-A110-09_BRCA	-2.80	-2.68	-2.64	-3.05	-2.67	-2.64	-2.52	-2.49	-2.44	0.00	0.00	0.00	0.00	0.00	-2.99	-2.71	-2.64
TCGA-A2-A0ST-10A-01D-A099-09_BRCA	-2.88	0.00	-4.26	-2.80	-2.61	-2.56	-2.52	-2.64	-2.68	-3.34	-2.77	-2.68	0.00	-2.69	0.00	-2.73	-2.69
TCGA-A2-A0SU-10A-01D-A099-09_BRCA	-3.00	0.00	0.00	-2.94	-2.59	-2.69	-2.59	-2.66	-2.82	-3.45	-2.96	-4.87	-2.84	-2.85	-3.36	0.00	-2.72
TCGA-A2-A0SX-10A-01D-A099-09_BRCA	-2.86	0.00	-4.81	-2.80	-2.52	-2.54	-2.46	-2.52	-2.46	0.00	0.00	0.00	0.00	0.00	-3.14	-2.80	-2.61
TCGA-A2-A0SY-10A-01D-A099-09_BRCA	-2.89	-2.69	-2.65	-3.00	-2.67	-2.71	-2.54	-2.67	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.68
TCGA-A2-A0T0-10A-01D-A099-09_BRCA	-3.15	-2.76	-2.81	-3.23	-2.62	-2.77	-2.62	-2.91	-2.65	0.00	-3.34	-2.83	0.00	0.00	0.00	-2.96	-2.79
TCGA-A2-A0T1-10A-01D-A099-09_BRCA	-2.90	-2.62	-2.59	0.00	-2.82	-2.77	-2.62	-2.74	-2.71	-3.41	-2.70	-2.60	0.00	-2.76	0.00	-2.83	-2.77
TCGA-A2-A0T2-10A-01D-A099-09_BRCA	-3.04	0.00	0.00	-2.97	-2.72	-2.66	-2.58	-2.58	-2.90	-3.24	-2.89	0.00	-2.77	-2.78	0.00	-2.89	-2.85
TCGA-A2-A0T3-10A-01D-A110-09_BRCA	-2.93	-2.80	-2.72	-3.08	-2.55	-2.63	-2.63	-2.65	-2.52	0.00	-2.95	-2.83	0.00	0.00	0.00	-2.57	-2.76
TCGA-A2-A0T4-10A-01D-A099-09_BRCA	-2.95	-2.72	-2.71	-3.11	-2.72	-2.79	-2.58	-2.65	-2.62	0.00	0.00	0.00	0.00	0.00	-3.07	-2.79	-2.78
TCGA-A2-A0T5-10A-01D-A099-09_BRCA	-2.96	-2.86	-2.89	-3.12	-2.65	-2.73	-2.76	-2.80	-2.87	-3.38	-2.84	-2.77	-4.85	-2.88	0.00	-3.07	-2.92
TCGA-A2-A0T6-10A-01D-A099-09_BRCA	-2.76	0.00	0.00	-2.85	-2.51	-2.46	-2.47	-2.57	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.62
TCGA-A2-A0T7-10A-01D-A099-09_BRCA	-2.92	0.00	-4.78	-3.02	-2.62	-2.67	-2.64	-2.58	-2.74	-3.38	-2.83	0.00	-2.75	-2.73	-3.08	0.00	-2.76
TCGA-A2-A0YC-10A-01D-A10G-09_BRCA	-2.83	-2.68	-2.67	-3.07	-2.75	-2.79	-2.50	-2.53	-2.45	0.00	0.00	0.00	0.00	0.00	-3.00	-2.78	-2.67
TCGA-A2-A0YD-10A-01D-A10G-09_BRCA	-2.85	0.00	0.00	-2.87	-2.55	-2.60	-2.54	-2.63	-2.48	0.00	0.00	0.00	0.00	-4.66	0.00	-2.58	-2.70
TCGA-A2-A0YE-10A-01D-A10G-09_BRCA	-2.81	0.00	-4.76	-2.78	-2.60	-2.63	-2.55	-2.49	-2.50	-4.76	0.00	-4.46	-4.16	-4.16	-3.08	-2.80	-2.67
TCGA-A2-A0YF-10A-01D-A10G-09_BRCA	-3.19	-2.75	-2.76	-3.25	-2.61	-2.63	-2.62	-2.85	-2.69	0.00	-3.03	-4.13	-2.90	-4.61	-3.50	-3.18	-2.80
TCGA-A2-A0YG-10A-01D-A10G-09_BRCA	-2.89	0.00	0.00	-2.82	-2.57	-2.55	-2.46	-2.67	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.67	-2.66
TCGA-A2-A0YH-10A-01D-A10G-09_BRCA	-2.91	0.00	0.00	-2.72	-2.59	-2.59	-2.50	-2.55	-2.48	0.00	0.00	0.00	0.00	-4.68	0.00	-2.48	-2.66
TCGA-A2-A0YI-10A-01D-A10M-09_BRCA	-2.86	0.00	0.00	-2.97	-2.53	-2.59	-2.54	-2.67	-2.56	0.00	0.00	0.00	0.00	0.00	-2.98	-2.79	-2.70
TCGA-A2-A0YJ-10A-01D-A10G-09_BRCA	-2.99	-2.76	-2.63	-3.08	-2.82	-2.72	-2.52	-2.77	-2.46	0.00	0.00	0.00	0.00	-4.39	-3.34	-3.06	-2.70
TCGA-A2-A0YK-10A-01D-A117-09_BRCA	-2.91	0.00	-4.59	-2.89	-2.53	-2.53	-2.46	-2.60	-2.49	0.00	0.00	0.00	-4.89	-4.89	0.00	-2.59	-2.58
TCGA-A2-A0YL-10A-01D-A10G-09_BRCA	-2.86	-4.74	0.00	-2.95	-2.59	-2.62	-2.55	-2.61	-2.68	-3.44	-2.76	0.00	-2.72	-2.73	0.00	-2.85	-2.71
TCGA-A2-A0YM-10A-01D-A10G-09_BRCA	-2.94	-2.90	-2.82	-3.17	-2.59	-2.71	-2.67	-2.69	-2.86	-3.43	-2.76	-2.71	0.00	-2.92	0.00	-2.96	-2.81
TCGA-A2-A0YT-10A-01D-A10G-09_BRCA	-2.90	-2.68	-2.66	-3.08	-2.71	-2.67	-2.58	-2.42	-2.45	0.00	0.00	0.00	0.00	0.00	-3.00	-2.74	-2.70
TCGA-A2-A1FV-10A-01D-A13O-09_BRCA	-2.84	0.00	0.00	-2.93	-2.62	-2.61	-2.57	-2.59	-2.54	0.00	0.00	0.00	0.00	0.00	-3.00	-2.83	-2.72
TCGA-A2-A1FW-10A-01D-A13O-09_BRCA	-2.84	-2.80	-2.88	-3.13	-2.82	-2.82	-2.62	-2.59	-2.54	0.00	-4.23	0.00	0.00	0.00	-3.01	-2.87	-2.72
TCGA-A2-A1FX-10A-01D-A13O-09_BRCA	-2.87	-2.67	-2.74	-2.97	-2.79	-2.74	-2.60	-2.59	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.65	-2.70
TCGA-A2-A1FZ-10A-01D-A14G-09_BRCA	-3.10	-2.67	-2.66	-4.58	-2.95	-2.86	-2.61	-2.70	-2.85	-3.37	-2.73	-2.74	0.00	-2.90	0.00	-3.02	-2.79
TCGA-A2-A1G0-10A-01D-A13O-09_BRCA	-2.93	0.00	0.00	-2.89	-2.56	-2.57	-2.49	-2.60	-2.51	0.00	0.00	0.00	0.00	0.00	-3.22	-2.89	-2.69
TCGA-A2-A1G1-10A-01D-A13O-09_BRCA	-2.98	-2.63	-2.84	0.00	-2.69	-2.64	-2.65	-2.73	-2.60	0.00	-2.96	-2.82	0.00	0.00	-3.12	-3.02	-2.74
TCGA-A2-A1G6-10A-01D-A13O-09_BRCA	-2.95	0.00	0.00	-2.97	-2.67	-2.64	-2.60	-2.71	-2.83	-3.51	-2.91	0.00	-2.82	-2.82	0.00	-2.98	-2.83
TCGA-A2-A259-10A-01D-A16D-09_BRCA	-2.91	0.00	0.00	-2.77	-2.62	-2.60	-2.61	-2.65	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.64	-2.70
TCGA-A2-A25A-10A-01D-A16D-09_BRCA	-2.87	0.00	0.00	-2.80	-2.60	-2.69	-2.49	-2.60	-2.61	0.00	0.00	0.00	0.00	0.00	0.00	-2.74	-2.72
TCGA-A2-A25B-10A-01D-A167-09_BRCA	-2.96	0.00	0.00	-2.83	-2.56	-2.53	-2.56	-2.61	-2.55	0.00	0.00	0.00	0.00	0.00	-2.83	0.00	-2.67
TCGA-A2-A25C-10A-01D-A167-09_BRCA	-2.83	0.00	0.00	-2.86	-2.67	-2.67	-2.65	-2.60	-2.58	0.00	0.00	0.00	-4.41	0.00	0.00	-2.64	-2.77
TCGA-A2-A25D-10A-01D-A16D-09_BRCA	-3.05	-4.74	0.00	-2.93	-2.57	-2.63	-2.55	-2.72	-2.54	-4.74	0.00	0.00	0.00	-4.74	0.00	-2.64	-2.78
TCGA-A2-A25E-10A-01D-A167-09_BRCA	-2.98	0.00	0.00	-2.82	-2.63	-2.71	-2.58	-2.68	-2.59	0.00	0.00	0.00	0.00	0.00	0.00	-2.73	-2.77
TCGA-A2-A25F-10A-01D-A167-09_BRCA	-2.98	-2.78	-2.80	-3.16	-2.91	-2.92	-2.60	-2.73	-2.59	0.00	0.00	0.00	0.00	0.00	-3.21	-3.07	-2.69
TCGA-A2-A3KC-10A-01D-A20S-09_BRCA	-2.78	-2.67	-2.78	-3.30	-2.75	-2.63	-2.59	-2.87	-2.60	0.00	-2.87	0.00	-2.78	-2.78	-2.89	-3.78	-2.54
TCGA-A2-A3KD-10A-01D-A20S-09_BRCA	-2.85	-2.73	-2.79	-3.11	-2.72	-2.77	-2.57	-2.59	-2.62	-3.67	-2.90	-4.15	-2.78	-2.76	0.00	-2.84	-2.57
TCGA-A2-A3XS-10A-01D-A22X-09_BRCA	-2.85	-2.71	-2.81	-3.24	-2.55	-2.58	-2.61	-2.55	-2.50	0.00	-2.88	-4.60	-2.82	-4.12	0.00	-2.59	-2.66
TCGA-A2-A3XT-10A-01D-A22X-09_BRCA	-2.73	-2.63	-2.57	-3.34	-2.61	-2.54	-2.49	-2.41	-2.32	-4.15	-3.61	-4.45	-3.98	-4.45	0.00	-2.69	-2.66
TCGA-A2-A3XU-10A-01D-A22X-09_BRCA	-2.87	-2.73	-2.73	-3.29	-2.49	-2.59	-2.57	-2.53	-2.45	0.00	-2.96	-2.75	0.00	0.00	-3.03	-2.77	-2.64
TCGA-A2-A3XV-10A-01D-A23C-09_BRCA	-2.71	-3.78	0.00	-2.97	-2.54	-2.55	-2.52	-2.59	-2.53	0.00	-4.48	0.00	-4.48	0.00	0.00	-2.53	-2.60
TCGA-A2-A3XW-10A-01D-A23C-09_BRCA	-2.86	-4.03	-4.20	-2.95	-2.55	-2.57	-2.46	-2.54	-2.61	-3.55	-2.82	0.00	-2.79	-2.75	0.00	-2.76	-2.61
TCGA-A2-A3XX-10A-01D-A23C-09_BRCA	-2.82	-4.56	-2.76	-3.31	-2.61	-2.60	-2.60	-2.62	-2.52	0.00	-2.81	-4.26	-2.71	0.00	-2.88	-4.56	-2.69
TCGA-A2-A3XY-10A-01D-A23C-09_BRCA	-2.85	-2.70	-2.78	-3.32	-2.48	-2.56	-2.59	-2.60	-2.51	0.00	-2.85	0.00	-2.74	-4.10	-3.04	-2.88	-2.64
TCGA-A2-A3XZ-10A-01D-A23C-09_BRCA	-2.81	-4.14	-4.01	-2.93	-2.48	-2.62	-2.54	-2.62	-2.49	-4.14	-4.14	-4.14	-4.01	0.00	-3.00	-2.74	-2.70
TCGA-A2-A3Y0-10A-01D-A23C-09_BRCA	-2.66	-3.79	0.00	-2.81	-2.44	-2.47	-2.47	-2.42	-2.39	-4.39	-4.09	-4.39	0.00	-4.39	0.00	-2.85	-2.63
TCGA-A2-A4RW-10A-01D-A25Q-09_BRCA	-2.82	-4.46	-3.86	-3.16	-2.54	-2.53	-2.48	-2.51	-2.64	-3.50	-2.94	-2.78	0.00	-2.79	0.00	-2.87	-2.67
TCGA-A2-A4RX-10A-01D-A25Q-09_BRCA	-2.75	-3.89	-4.19	-2.98	-2.57	-2.61	-2.54	-2.59	-2.43	0.00	-3.89	-4.50	-4.50	-3.89	-2.93	-2.82	-2.64
TCGA-A2-A4RY-10A-01D-A25Q-09_BRCA	-2.75	-2.74	-2.79	-3.48	-2.75	-2.74	-2.56	-2.63	-2.62	-3.45	-2.94	0.00	-2.74	-2.72	0.00	-2.78	-2.65
TCGA-A2-A4S0-10A-01D-A25Q-09_BRCA	-2.92	-3.53	-4.00	-2.99	-2.48	-2.55	-2.56	-2.50	-2.42	-4.30	-4.13	-3.91	-4.30	-3.65	-3.06	-2.79	-2.63
TCGA-A2-A4S1-10A-01D-A25Q-09_BRCA	-2.63	-2.75	-2.72	-3.15	-2.78	-2.70	-2.52	-2.58	-2.49	-4.54	0.00	-4.54	0.00	-4.54	0.00	-2.56	-2.60
TCGA-A2-A4S2-10A-01D-A25Q-09_BRCA	-2.70	0.00	0.00	-3.03	-2.52	-2.48	-2.50	-2.47	-2.47	0.00	0.00	0.00	-3.83	-4.23	-2.95	-2.72	-2.54
TCGA-A2-A4S3-10A-01D-A25Q-09_BRCA	-2.80	-3.95	-3.95	-3.01	-2.47	-2.47	-2.45	-2.49	-2.45	0.00	0.00	-4.43	0.00	0.00	-2.83	-3.83	-2.57
TCGA-A4-7286-10A-01D-2136-08_KIRP	-2.44	-2.71	-2.69	-2.88	-2.70	-2.73	-2.58	-2.58	-2.67	-3.20	-2.87	-3.72	-2.81	-2.65	-3.07	-4.56	-2.48
TCGA-A4-7287-10A-01D-2136-08_KIRP	-2.50	-4.48	-3.71	-2.60	-2.54	-2.56	-2.59	-2.49	-2.57	0.00	0.00	0.00	-4.48	-4.48	0.00	-2.42	-2.53
TCGA-A4-7583-10A-01D-2136-08_KIRP	-2.47	-2.64	-2.65	-2.77	-2.64	-2.65	-2.54	-2.45	-2.52	-4.46	0.00	0.00	-4.46	0.00	0.00	-2.39	-2.39
TCGA-A4-7584-10A-01D-2136-08_KIRP	-2.49	-4.21	-3.73	-2.59	-2.49	-2.55	-2.55	-2.55	-2.54	-4.51	-4.51	-4.51	-4.21	-4.51	0.00	-2.53	-2.39
TCGA-A4-7732-10A-01D-2136-08_KIRP	-2.38	-3.90	-3.81	-2.75	-2.53	-2.54	-2.56	-2.46	-2.42	0.00	-4.50	0.00	0.00	0.00	-2.99	-2.68	-2.45
TCGA-A4-7734-10A-01D-2136-08_KIRP	-2.61	-4.26	-3.96	-2.77	-2.61	-2.58	-2.63	-2.66	-2.73	-3.28	-2.83	-4.56	-2.79	-2.65	0.00	-2.71	-2.50
TCGA-A4-7828-10A-01D-2136-08_KIRP	-2.58	-2.62	-2.61	-4.07	-2.68	-2.67	-2.64	-2.50	-2.59	0.00	-2.88	-2.72	0.00	0.00	-3.07	-2.71	-2.54
TCGA-A4-7915-10A-01D-2201-08_KIRP	-2.56	-4.54	0.00	-2.79	-2.54	-2.59	-2.58	-2.51	-2.56	0.00	0.00	0.00	0.00	0.00	-3.04	-2.70	-2.49
TCGA-A4-7996-10A-01D-2201-08_KIRP	-2.54	0.00	0.00	-2.72	-2.53	-2.56	-2.55	-2.48	-2.47	0.00	-4.53	0.00	0.00	-4.05	0.00	-2.37	-2.46
TCGA-A4-7997-10A-01D-2201-08_KIRP	-2.44	0.00	0.00	-2.72	-2.54	-2.52	-2.55	-2.52	-2.52	0.00	0.00	0.00	-4.50	0.00	-2.99	-2.72	-2.47
TCGA-A4-8098-10A-01D-2396-08_KIRP	-2.56	-4.49	0.00	-2.84	-2.54	-2.57	-2.61	-2.57	-2.51	0.00	0.00	-4.01	0.00	-4.19	-3.01	-2.69	-2.46
TCGA-A4-8310-10A-01D-2396-08_KIRP	-2.58	-2.74	-2.68	-2.96	-2.69	-2.68	-2.64	-2.47	-2.52	0.00	-4.50	-4.03	0.00	0.00	0.00	-2.39	-2.51
TCGA-A4-8311-10A-01D-2396-08_KIRP	-2.39	-2.64	-2.63	-2.80	-2.62	-2.66	-2.58	-2.58	-2.54	0.00	0.00	-4.46	-3.98	-3.85	-2.88	0.00	-2.48
TCGA-A4-8312-10A-01D-2396-08_KIRP	-2.55	-4.21	-3.74	-2.63	-2.48	-2.60	-2.59	-2.51	-2.60	0.00	-4.51	-4.51	0.00	0.00	-2.93	-3.91	-2.57
TCGA-A4-8515-10A-01D-2396-08_KIRP	-2.68	-4.16	-4.16	-2.89	-2.52	-2.65	-2.67	-2.71	-2.81	-3.17	-2.79	-2.70	0.00	-2.71	0.00	-2.80	-2.61

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-A4-8517-10A-01D-2396-08_KIRP	-2.48	0.00	0.00	-2.62	-2.44	-2.54	-2.52	-2.53	-2.82	-3.60	-2.93	0.00	-2.78	-2.59	0.00	-2.76	-2.43
TCGA-A4-8518-10A-01D-2396-08_KIRP	-2.47	-2.68	-2.71	-2.83	-2.71	-2.75	-2.54	-2.45	-2.72	-3.30	-2.91	0.00	-2.77	-2.65	0.00	-2.73	-2.42
TCGA-A4-8630-10A-01D-2396-08_KIRP	-2.72	-2.77	-2.76	-3.00	-2.56	-2.67	-2.73	-2.62	-2.76	-3.30	-2.79	-2.77	-2.78	-2.74	0.00	-2.86	-2.64
TCGA-A4-A48D-10A-01D-A25F-10_KIRP	-2.46	-2.57	-2.66	-2.82	-2.41	-2.35	-2.37	-2.46	-2.36	0.00	-2.88	-2.62	0.00	-4.34	-3.04	-2.79	-2.39
TCGA-A4-A4ZT-10A-01D-A26P-10_KIRP	-2.48	-2.65	-2.57	-2.81	-2.42	-2.38	-2.41	-2.52	-2.55	-3.55	-2.54	-2.60	-2.73	-2.50	0.00	-2.59	-2.50
TCGA-A4-A57E-10A-01D-A26P-10_KIRP	-2.48	-2.61	-2.64	-2.85	-2.43	-2.37	-2.39	-2.36	-2.36	0.00	-2.78	-2.69	0.00	0.00	0.00	-2.39	-2.50
TCGA-A4-A5DU-10A-01D-A28G-10_KIRP	-2.46	-2.70	-2.68	-2.83	-2.49	-2.35	-2.38	-2.44	-2.56	-3.85	-2.58	-2.39	-4.32	-2.63	0.00	-2.58	-2.49
TCGA-A4-A5XZ-10A-01D-A31X-10_KIRP	-2.41	0.00	0.00	-2.64	-2.51	-2.44	-2.31	-2.39	-2.57	-3.54	-2.91	-2.59	-4.14	-2.68	0.00	-2.66	-2.37
TCGA-A4-A6HP-10A-01D-A31X-10_KIRP	-2.42	0.00	0.00	-2.51	-2.53	-2.36	-2.26	-2.39	-2.57	-3.40	-2.92	0.00	-2.64	-2.83	0.00	-2.66	-2.43
TCGA-A5-A0G1-10A-01D-A122-09_UCEC	-2.87	0.00	-4.93	-2.82	-2.64	-2.66	-2.63	-2.73	-2.77	-3.49	-2.92	-2.77	0.00	-2.80	0.00	-2.83	-2.85
TCGA-A5-A0GG-10A-01D-A122-09_UCEC	-2.83	-2.74	-2.78	-3.00	-2.67	-2.75	-2.60	-2.64	-2.49	-3.86	-3.59	-3.40	0.00	-3.47	0.00	-2.65	-2.75
TCGA-A5-A0GQ-10A-01D-A122-09_UCEC	-2.85	0.00	-4.93	-2.83	-2.67	-2.61	-2.56	-2.54	-2.58	0.00	0.00	0.00	0.00	0.00	-3.06	-2.84	-2.72
TCGA-A5-A0GR-10A-01D-A122-09_UCEC	-2.99	-2.88	-2.82	-3.19	-2.57	-2.64	-2.69	-2.64	-2.61	0.00	-2.89	-2.83	0.00	-4.98	-3.14	-2.97	-2.86
TCGA-A5-A0R6-10A-01D-A10B-09_UCEC	-2.87	-2.65	-2.63	-2.84	-2.74	-2.69	-2.49	-2.54	-2.43	0.00	0.00	0.00	0.00	0.00	-3.16	-2.84	-2.67
TCGA-A5-A0R7-10A-01D-A10B-09_UCEC	-2.89	-2.72	-2.73	-3.13	-2.73	-2.74	-2.65	-2.65	-2.70	-3.48	-2.77	0.00	-2.76	-2.75	0.00	-2.77	-2.82
TCGA-A5-A0R8-10A-01D-A10B-09_UCEC	-2.92	0.00	0.00	-2.81	-2.55	-2.65	-2.59	-2.62	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.65	-2.71
TCGA-A5-A0R9-10A-01D-A10B-09_UCEC	-2.91	-2.80	-2.78	-3.13	-2.55	-2.75	-2.69	-2.76	-2.74	-3.44	-2.76	-2.69	0.00	-2.77	0.00	-2.84	-2.82
TCGA-A5-A0RA-10A-01D-A10B-09_UCEC	-2.85	-2.54	-2.53	0.00	0.00	0.00	-2.51	-2.54	-2.67	-3.30	-2.70	0.00	-2.68	-2.63	-3.14	0.00	-2.68
TCGA-A5-A0VO-10A-01D-A10G-09_UCEC	-2.92	-2.82	-2.79	-3.13	-2.56	-2.72	-2.69	-2.71	-2.78	-3.43	-2.68	-2.79	-2.79	-2.84	0.00	-2.92	-2.82
TCGA-A5-A0VP-10A-01D-A10B-09_UCEC	-2.98	-2.75	-2.80	-3.18	-2.56	-2.68	-2.62	-2.57	-2.55	0.00	-2.96	-2.80	0.00	-4.80	-3.14	-2.85	-2.84
TCGA-A5-A0VQ-10A-01D-A10B-09_UCEC	-2.80	-2.61	-2.64	-3.03	-2.74	-2.70	-2.53	-2.56	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.62	-2.69
TCGA-A5-A1OF-10A-01D-A14G-09_UCEC	-2.88	-2.73	-2.73	-3.48	-2.80	-2.80	-2.47	-2.58	-2.39	0.00	0.00	0.00	0.00	0.00	-2.99	-2.83	-2.55
TCGA-A5-A1OG-10A-01D-A14G-09_UCEC	-2.91	-4.73	0.00	-3.02	-2.63	-2.68	-2.63	-2.62	-2.77	-3.22	-2.84	0.00	-2.82	-2.79	-3.16	0.00	-2.75
TCGA-A5-A1OH-10A-01D-A22A-09_UCEC	-2.77	-3.77	-4.55	-3.00	-2.59	-2.57	-2.56	-2.52	-2.51	-4.08	-4.25	-4.55	-4.08	0.00	0.00	-2.50	-2.59
TCGA-A5-A1OJ-10A-01D-A14G-09_UCEC	-2.76	-4.36	-4.36	-2.94	-2.50	-2.49	-2.43	-2.48	-2.36	0.00	0.00	0.00	0.00	0.00	-2.85	-2.76	-2.54
TCGA-A5-A1OK-10A-01D-A14K-09_UCEC	-2.73	0.00	0.00	-3.02	-2.49	-2.77	-2.54	-2.57	-4.45	-3.31	-2.61	-2.75	-2.70	-2.52	0.00	-4.15	-2.63
TCGA-A5-A2K2-10A-01D-A18P-09_UCEC	-2.75	-2.67	-2.71	-3.21	-2.76	-2.73	-2.46	-2.54	-2.45	0.00	-4.42	0.00	-4.42	0.00	0.00	-2.60	-2.61
TCGA-A5-A2K3-10A-01D-A17W-09_UCEC	-2.84	0.00	-4.54	-3.04	-2.55	-2.56	-2.59	-2.62	-2.74	-3.42	-2.92	0.00	-2.79	-2.71	0.00	-2.87	-2.68
TCGA-A5-A2K4-10B-01D-A18P-09_UCEC	-2.80	-4.18	-4.00	-2.99	-2.54	-2.57	-2.57	-2.48	-2.65	-3.36	-2.82	-4.18	-2.79	-2.68	0.00	-2.81	-2.64
TCGA-A5-A2K5-10A-01D-A17W-09_UCEC	-2.75	-2.71	-2.81	-3.27	-2.82	-2.75	-2.55	-2.60	-4.48	-3.33	-2.66	-4.48	-2.58	-2.60	0.00	0.00	-2.66
TCGA-A5-A2K7-10A-01D-A17W-09_UCEC	-2.77	-2.66	-2.70	-3.50	-2.73	-2.67	-2.64	-2.77	-2.61	-4.40	-2.79	-4.40	-2.67	-2.64	-2.88	-4.40	-2.59
TCGA-A5-A3LO-10A-01D-A22A-09_UCEC	-2.79	-2.57	-2.61	0.00	-2.92	-2.72	-2.51	-2.64	-2.73	-3.31	-2.66	-2.87	-2.87	-2.79	0.00	-2.83	-2.63
TCGA-A5-A3LP-10A-01D-A22A-09_UCEC	-2.85	-2.66	-2.75	-3.24	-2.65	-2.69	-2.54	-2.48	-2.42	0.00	0.00	0.00	-4.52	0.00	0.00	-2.44	-2.61
TCGA-A6-2671-10A-01D-1408-10_COAD	-2.59	0.00	0.00	-2.60	-2.50	-2.60	-2.40	-2.70	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.43
TCGA-A6-2674-10A-01D-A270-10_COAD	-2.46	0.00	-3.97	-2.57	-2.42	-2.32	-2.32	-2.39	-2.40	0.00	0.00	0.00	0.00	-4.27	0.00	-2.39	-2.42
TCGA-A6-2675-10A-01D-1719-10_COAD	-2.46	-4.63	-4.63	-2.57	-2.40	-2.43	-2.37	-2.45	-2.30	0.00	0.00	0.00	0.00	0.00	-3.14	-2.90	-2.36
TCGA-A6-2677-10A-01D-A270-10_COAD	-2.57	-2.48	-2.60	0.00	-2.56	-2.45	-2.45	-2.51	0.00	-3.35	-2.43	-2.37	-2.81	-2.45	0.00	0.00	-2.57
TCGA-A6-2684-10A-01D-A270-10_COAD	-2.49	-2.64	-2.77	-2.86	-2.65	-2.62	-2.39	-2.41	-3.82	-3.34	-2.67	-4.12	-2.43	-2.39	0.00	0.00	-2.47
TCGA-A6-3809-10A-01D-A270-10_COAD	-2.53	-2.55	-2.47	0.00	-2.72	-2.69	-2.28	-2.31	-2.77	-3.32	-2.55	-2.86	-2.89	-2.60	-3.09	0.00	-2.47
TCGA-A6-3810-10A-01D-A270-10_COAD	-2.35	-2.56	-2.63	-2.66	-2.66	-2.52	-2.29	-2.36	-2.31	0.00	-4.16	0.00	-3.86	0.00	0.00	-2.31	-2.39
TCGA-A6-4105-10A-01D-1771-10_COAD	-2.55	0.00	0.00	-2.81	-2.49	-2.45	-2.55	-2.66	-2.66	-3.26	-2.94	0.00	-2.85	-2.79	0.00	-2.70	-2.47
TCGA-A6-5656-10A-01D-A270-10_COAD	-2.37	0.00	0.00	-2.56	-2.52	-2.38	-2.30	-2.40	-2.75	-3.37	-3.01	0.00	-2.68	-2.48	0.00	-2.66	-2.44
TCGA-A6-5657-10A-01D-1650-10_COAD	-2.57	0.00	-2.67	-2.96	-2.46	-2.52	-2.37	-2.53	-2.46	0.00	-2.92	0.00	-2.78	0.00	-3.22	0.00	-2.64
TCGA-A6-5659-10A-01D-1650-10_COAD	-2.43	0.00	0.00	-2.66	-2.44	-2.65	-2.36	-2.50	-2.32	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.36
TCGA-A6-5662-10A-01D-1650-10_COAD	-2.50	0.00	-4.39	-2.77	-2.46	-2.45	-2.37	-2.50	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.63	-2.41
TCGA-A6-5664-10A-01D-1835-10_COAD	-2.42	0.00	0.00	-2.71	-2.59	-2.50	-2.52	-2.48	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-3.43	-2.48
TCGA-A6-5665-10A-01D-1650-10_COAD	-2.58	0.00	0.00	-2.71	-2.50	-2.51	-2.39	-2.58	-2.36	0.00	0.00	0.00	0.00	-4.64	0.00	-2.64	-2.38
TCGA-A6-5666-10A-01D-1650-10_COAD	-2.52	0.00	0.00	-2.67	-2.48	-2.53	-2.42	-2.54	-2.42	0.00	0.00	0.00	0.00	0.00	-3.04	-2.92	-2.48
TCGA-A6-6137-10A-01D-1806-10_COAD	-2.51	0.00	0.00	-2.67	-2.50	-2.51	-2.44	-2.55	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.43
TCGA-A6-6138-10A-01D-1771-10_COAD	-2.55	-2.64	-2.62	0.00	-2.86	-2.89	-2.40	-2.50	-2.51	-3.45	-3.23	-2.83	0.00	0.00	-3.25	-2.81	-2.54
TCGA-A6-6141-10A-01D-1771-10_COAD	-2.50	-2.73	-2.82	-2.80	-2.75	-2.59	-2.67	-2.71	-2.68	0.00	-2.99	0.00	-2.80	-2.79	0.00	-2.86	-2.44
TCGA-A6-6142-10A-01D-1771-10_COAD	-2.55	0.00	0.00	-2.59	-2.52	-2.58	-2.44	-2.59	-2.44	0.00	0.00	0.00	0.00	-4.30	0.00	-2.58	-2.47
TCGA-A6-6648-10A-01D-1771-10_COAD	-2.51	-2.88	-2.75	-2.86	-2.88	-2.88	-2.42	-2.71	-2.63	-3.21	-2.93	0.00	-2.91	-2.78	0.00	-2.96	-2.55
TCGA-A6-6649-10A-01D-1771-10_COAD	-2.58	0.00	0.00	-2.86	-2.65	-2.63	-2.55	-2.75	-2.85	-3.42	-3.01	0.00	-3.25	-2.88	0.00	-2.81	-2.59
TCGA-A6-6650-10A-01D-1771-10_COAD	-2.67	0.00	0.00	-2.73	-2.63	-2.44	-2.47	-2.65	-2.45	0.00	0.00	0.00	0.00	-4.05	-3.09	0.00	-2.44
TCGA-A6-6651-10A-01D-1835-10_COAD	-2.44	-3.10	-4.05	-2.88	-2.48	-2.56	-2.53	-2.67	-2.73	-3.45	-3.10	0.00	-3.35	-2.60	0.00	-2.91	-2.42
TCGA-A6-6652-10A-01D-1771-10_COAD	-2.50	-2.93	0.00	-2.89	-2.79	-2.89	-2.62	-2.95	-2.62	0.00	-2.91	0.00	-2.93	-2.79	0.00	-2.66	-2.39
TCGA-A6-6653-10A-01D-1771-10_COAD	-2.41	-2.55	-2.41	0.00	0.00	-4.26	-2.63	-2.71	-2.61	0.00	-2.98	-4.26	-2.83	-2.60	0.00	-2.70	-2.42
TCGA-A6-6654-10A-01D-1835-10_COAD	-2.59	0.00	0.00	-2.73	-2.59	-2.49	-2.57	-2.57	-2.45	0.00	0.00	0.00	0.00	0.00	-3.26	-2.75	-2.55
TCGA-A6-6780-10A-01D-A270-10_COAD	-2.53	0.00	0.00	-2.53	-2.59	-2.56	-2.33	-2.37	0.00	-3.15	-2.71	0.00	-2.47	-2.58	0.00	0.00	-2.53
TCGA-A6-6781-10A-01D-1924-10_COAD	-2.63	-4.07	0.00	-2.78	-2.60	-2.68	-2.56	-2.54	-2.86	-3.20	-3.12	0.00	-3.10	-2.98	0.00	-2.87	-2.56
TCGA-A6-6782-10A-01D-1835-10_COAD	-2.61	-2.75	-2.96	-3.05	-2.70	-2.83	-2.41	-2.57	-2.66	-3.23	-3.00	-2.83	0.00	-3.00	-3.05	0.00	-2.50
TCGA-A6-A565-10A-01D-A28G-10_COAD	-2.53	0.00	0.00	-2.73	-2.28	-2.26	-2.37	-2.52	-2.38	0.00	-2.48	0.00	-2.39	-4.40	-2.74	0.00	-2.50
TCGA-A6-A566-10A-01D-A28G-10_COAD	-2.49	0.00	-4.28	-2.54	-2.32	-2.25	-2.25	-2.35	-2.26	0.00	0.00	0.00	-4.28	0.00	0.00	-2.24	-2.39
TCGA-A6-A567-10A-01D-A28G-10_COAD	-2.49	-2.66	-2.70	-3.04	-2.68	-2.43	-2.37	-2.35	-2.41	0.00	-2.57	-2.57	-2.73	0.00	-3.12	-2.77	-2.46
TCGA-A6-A56B-10A-01D-A28G-10_COAD	-2.48	0.00	-4.32	-2.80	-2.35	-2.30	-2.33	-2.45	-2.31	0.00	-2.77	0.00	-2.60	0.00	-2.71	-4.32	-2.43
TCGA-A6-A5ZU-10A-01D-A28G-10_COAD	-2.40	0.00	-2.55	-2.83	-2.32	-2.33	-2.32	-2.44	-2.32	0.00	-2.86	0.00	-2.59	0.00	-2.69	-4.05	-2.49
TCGA-A7-A0DA-10A-01D-A110-09_BRCA	-2.81	-4.95	-4.95	-2.81	-2.51	-2.55	-2.49	-2.63	-2.48	0.00	-4.64	0.00	-4.95	0.00	-3.12	-2.76	-2.66
TCGA-A7-A0DB-10A-02D-A272-09_BRCA	-2.93	-2.71	-2.87	-3.36	-2.51	-2.55	-2.54	-2.62	-2.67	-3.42	-2.72	-2.78	-2.88	-2.79	-3.10	-4.53	-2.71
TCGA-A7-A13D-10A-02D-A12Q-09_BRCA	-2.93	0.00	-4.65	-2.91	-2.60	-2.65	-2.67	-2.60	-2.67	0.00	-2.88	-2.80	0.00	-4.65	-3.08	-2.93	-2.79
TCGA-A7-A13E-10A-01D-A12Q-09_BRCA	-2.79	-2.64	-2.67	-2.98	-2.62	-2.70	-2.54	-2.60	-2.55	0.00	0.00	0.00	0.00	0.00	-2.85	-4.65	-2.64
TCGA-A7-A13F-10A-01D-A12Q-09_BRCA	-2.94	-2.88	-2.85	-3.22	-2.59	-2.69	-2.68	-2.67	-2.87	-3.64	-2.72	-2.70	0.00	-2.79	-3.18	0.00	-2.82
TCGA-A7-A13H-10A-01D-A22A-09_BRCA	-2.75	0.00	-4.21	-3.08	-2.52	-2.54	-2.53	-2.49	-2.38	0.00	-4.51	0.00	0.00	-4.03	0.00	-2.56	-2.51
TCGA-A7-A26E-10A-01D-A167-09_BRCA	-2.99	-4.69	0.00	-3.17	-2.51	-2.69	-2.68	-2.69	-4.21	-3.35	-2.70	-2.94	-2.79	-2.77	0.00	0.00	-2.88
TCGA-A7-A26F-10A-01D-A167-09_BRCA	-2.95	0.00	0.00	-2.93	-2.55	-2.54	-2.43	-2.65	-2.53	0.00	0.00	0.00	0.00	0.00	-2.97	-2.97	-2.68
TCGA-A7-A26G-10A-01D-A167-09_BRCA	-2.82	-2.64	-4.49	-3.15	-2.74	-2.75	-2.74	-2.81	-2.71	0.00	-2.85	0.00	-2.69	-2.75	0.00	-2.76	-2.64
TCGA-A7-A26H-10A-01D-A167-09_BRCA	-3.02	-2.69	-2.88	-3.20	-2.70	-2.82	-2.58	-2.69	-2.52	0.00	0.00	0.00	0.00	0.00	-3.18	-2.96	-2.72
TCGA-A7-A26I-10A-01D-A167-09_BRCA	-3.08	-2.79	-2.81	-3.04	-2.80	-2.75	-2.55	-2.73	-2.51	0.00	0.00	0.00	-4.57	0.00	0.00	-2.65	-2.74
TCGA-A7-A26J-10A-01D-A167-09_BRCA	-2.94	-4.54	0.00	-2.82	-2.51	-2.59	-2.54	-2.60	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.77
TCGA-A7-A2KD-10A-01D-A21Q-09_BRCA	-2.80	-2.72	-3.79	-2.99	-2.49	-2.68	-2.51	-2.60	-2.48	0.00	-4.09	-4.09	-3.79	-3.91	0.00	-2.64	-2.60
TCGA-A7-A3IY-10A-01D-A21Q-09_BRCA	-2.68	-3.68	-4.07	-2.93	-2.50	-2.55	-2.47	-2.54	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.54
TCGA-A7-A3IZ-10A-01D-A20S-09_BRCA	-2.81	-3.89	-3.89	-3.19	-2.61	-2.53	-2.46	-2.57	-4.06	-3.36	-2.66	-4.06	-2.66	-2.57	0.00	-3.89	-2.57
TCGA-A7-A3J0-10A-01D-A20S-09_BRCA	-2.75	-2.76	-2.66	-3.33	-2.79	-2.76	-2.42	-2.57	-2.37	-4.02	-4.02	-4.02	-3.85	-4.02	-2.86	0.00	-2.47
TCGA-A7-A3J1-10A-01D-A20S-09_BRCA	-2.85	0.00	-3.78	-3.03	-2.47	-2.52	-2.51	-2.60	-2.35	0.00	0.00	0.00	-3.78	-4.26	0.00	-2.61	-2.59
TCGA-A7-A3RF-10A-01D-A22A-09_BRCA	-2.81	-4.34	-3.87	-3.13	-2.59	-2.60	-2.59	-2.57	-2.65	-3.44	-2.80	0.00	-2.78	-2.76	0.00	-2.83	-2.68
TCGA-A7-A425-10A-01D-A243-09_BRCA	-2.77	-3.20	-3.34	-3.06	-2.60	-2.54	-2.46	-2.53	-2.42	-4.04	-3.74	-3.64	-3.56	-3.50	0.00	-2.85	-2.54
TCGA-A7-A426-10A-01D-A243-09_BRCA	-2.82	-2.67	-2.72	-3.16	-2.74	-2.81	-2.51	-2.57	-2.60	-3.35	-2.81	-2.77	-4.20	-2.78	0.00	-2.76	-2.59
TCGA-A7-A4SA-10A-01D-A25Q-09_BRCA	-2.91	-2.74	-2.76	-3.23	-2.52	-2.57	-2.54	-2.50	-2.46	0.00	-2.88	-2.80	-4.05	-4.05	-2.92	-2.82	-2.67
TCGA-A7-A4SB-10A-01D-A25Q-09_BRCA	-2.84	-2.59	-2.67	-4.54	-2.70	-2.81	-2.58	-2.67	-2.69	-3.40	-2.72	-2.79	-2.82	-2.85	0.00	-2.90	-2.68
TCGA-A7-A4SC-10A-01D-A25Q-09_BRCA	-2.82	-4.14	0.00	-2.94	-2.49	-2.52	-2.47	-2.52	-2.41	-4.44	0.00	0.00	-4.44	0.00	-3.01	-2.79	-2.59
TCGA-A7-A4SD-10A-01D-A25Q-09_BRCA	-2.77	-3.66	-3.80	-3.03	-2.41	-2.49	-2.55	-2.55	-2.45	-4.20	-4.03	0.00	-4.03	-3.80	-2.80	-4.50	-2.61
TCGA-A7-A4SE-10A-01D-A25Q-09_BRCA	-2.83	-4.17	-4.34	-2.99	-2.50	-2.61	-2.57	-2.65	-2.48	0.00	-4.64	-4.64	0.00	-4.34	-2.90	0.00	-2.63
TCGA-A7-A4SF-10A-01D-A25Q-09_BRCA	-2.72	-2.72	-2.66	-3.20	-2.67	-2.65	-2.56	-2.47	-2.39	-4.50	-4.20	-4.20	-4.50	-4.20	-2.93	-2.72	-2.59
TCGA-A7-A56D-10A-01D-A27P-09_BRCA	-2.78	-2.73	-2.78	-3.26	-2.60	-2.57	-2.61	-2.65	-2.46	0.00	-2.68	-2.62	0.00	0.00	-2.86	-4.49	-2.58
TCGA-A7-A5ZV-10A-01D-A28E-09_BRCA	-2.83	-4.45	0.00	-3.11	-2.43	-2.43	-2.47	-2.46	-2.30	0.00	0.00	-4.45	0.00	0.00	-2.95	-2.71	-2.54
TCGA-A7-A5ZW-10A-01D-A29N-09_BRCA	-2.92	0.00	-4.22	-3.03	-2.51	-2.53	-2.49	-2.50	-2.56	-3.52	-2.89	-4.52	-2.78	0.00	-2.90	-4.22	-2.73

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-A7-A5ZX-10A-01D-A29N-09_BRCA	-2.83	-2.73	-2.75	-3.35	-2.54	-2.57	-2.65	-2.54	-2.54	0.00	-2.91	-2.84	0.00	0.00	0.00	-2.55	-2.65
TCGA-A8-A075-10B-01D-A099-09_BRCA	-2.82	-4.73	0.00	-2.76	-2.60	-2.60	-2.49	-2.56	-2.55	0.00	0.00	0.00	-4.73	0.00	-3.07	-2.84	-2.73
TCGA-A8-A07R-10B-01D-A047-09_BRCA	-2.94	0.00	-4.96	-3.10	-2.70	-2.70	-2.71	-2.74	-2.81	-3.51	-2.89	0.00	-2.90	-2.87	0.00	-2.96	-2.86
TCGA-A8-A097-10A-01D-A047-09_BRCA	-2.90	0.00	0.00	-3.05	-2.62	-2.68	-2.65	-2.72	-2.54	0.00	0.00	0.00	0.00	-4.90	0.00	-2.69	-2.81
TCGA-AC-A23C-10A-01D-A167-09_BRCA	-2.94	-2.74	-2.86	-3.14	-2.78	-2.78	-2.56	-2.76	-2.51	0.00	0.00	0.00	0.00	0.00	-3.14	-2.92	-2.72
TCGA-AC-A23E-10A-01D-A159-09_BRCA	-2.88	-2.81	-2.80	-3.26	-2.59	-2.70	-2.66	-2.75	-2.90	-3.33	-2.75	-2.78	-2.84	-2.83	0.00	-2.93	-2.84
TCGA-AC-A2B8-10A-01D-A17D-09_BRCA	-2.92	0.00	0.00	-2.95	-2.62	-2.57	-2.62	-2.70	-2.82	-3.39	-2.93	0.00	-2.87	-2.81	0.00	-2.94	-2.74
TCGA-AC-A2QH-10A-01D-A18P-09_BRCA	-2.88	-2.60	-2.67	0.00	-2.85	-2.78	-2.56	-2.62	-2.60	0.00	-2.84	-2.83	0.00	0.00	0.00	-2.68	-2.80
TCGA-AC-A2QI-10A-01D-A19Y-09_BRCA	-3.00	-3.71	-3.89	-2.99	-2.59	-2.55	-2.52	-2.46	-2.44	-4.49	-3.89	-4.49	-3.65	-3.45	-3.49	-2.64	-2.60
TCGA-AC-A3BB-10A-01D-A19Y-09_BRCA	-2.86	-4.39	-4.09	-2.91	-2.54	-2.56	-2.50	-2.61	-2.32	0.00	-4.09	-4.09	-4.39	0.00	0.00	-3.31	-2.54
TCGA-AC-A3HN-10A-01D-A20S-09_BRCA	-2.74	-4.28	-3.98	-3.11	-2.52	-2.48	-2.48	-2.45	-2.39	-4.28	-3.80	-3.68	0.00	-4.28	-2.98	-3.00	-2.51
TCGA-AC-A3QP-10B-01D-A22X-09_BRCA	-2.81	-2.78	-2.83	-3.23	-2.55	-2.65	-2.66	-2.62	-2.76	-3.44	-2.72	-2.88	-2.78	-2.84	0.00	-2.89	-2.64
TCGA-AC-A3TM-10A-01D-A22A-09_BRCA	-2.77	-2.58	-2.53	0.00	-3.39	-3.25	-2.44	-2.56	-2.59	-3.59	-2.76	0.00	-2.84	-2.76	-3.01	-3.99	-2.58
TCGA-AC-A3TN-10A-01D-A22A-09_BRCA	-2.92	-4.48	-4.48	-3.03	-2.60	-2.53	-2.40	-2.48	-2.63	-3.25	-3.08	-4.00	-2.80	-2.69	-3.02	0.00	-2.61
TCGA-AC-A3W5-10A-01D-A22A-09_BRCA	-2.74	-4.47	-4.17	-2.98	-2.47	-2.56	-2.54	-2.60	-2.49	-4.17	-4.17	-4.17	-4.17	-3.99	-2.74	-3.62	-2.54
TCGA-AC-A3W6-10A-01D-A22A-09_BRCA	-2.73	-2.73	0.00	-3.31	-2.52	-2.59	-2.57	-2.57	-2.64	-3.45	-2.87	0.00	-2.83	-2.85	0.00	-2.82	-2.61
TCGA-AC-A3W7-10A-01D-A22A-09_BRCA	-2.90	-2.61	-2.88	-3.20	-2.57	-2.59	-2.57	-2.70	-3.91	-3.38	-2.57	-2.78	-2.63	-2.59	0.00	-4.61	-2.65
TCGA-AC-A3YI-10A-01D-A23C-09_BRCA	-2.83	-2.62	-2.68	0.00	-2.54	-2.59	-2.50	-2.57	-2.64	-3.57	-2.71	-2.79	-2.73	-2.71	0.00	-2.75	-2.62
TCGA-AC-A3YJ-10A-01D-A22X-09_BRCA	-2.89	-4.62	-4.62	-3.02	-2.59	-2.59	-2.58	-2.60	-2.62	-3.54	-2.86	-4.32	-2.72	-2.72	0.00	-2.77	-2.64
TCGA-AC-A5EH-10A-01D-A28E-09_BRCA	-2.87	-2.66	-2.79	-3.44	-2.53	-2.53	-2.49	-2.51	-2.43	0.00	-2.86	-2.67	-4.44	0.00	0.00	-2.51	-2.66
TCGA-AC-A5EI-10A-01D-A27P-09_BRCA	-2.72	-2.69	-2.61	-3.50	-2.68	-2.62	-2.48	-2.39	-2.36	0.00	0.00	-4.40	0.00	0.00	0.00	-2.38	-2.55
TCGA-AC-A5XS-10A-01D-A29N-09_BRCA	-2.74	-4.16	0.00	-3.08	-2.53	-2.49	-2.51	-2.61	-2.41	-4.46	0.00	0.00	0.00	-4.46	0.00	-2.53	-2.59
TCGA-AC-A5XU-10A-01D-A28E-09_BRCA	-2.78	-4.01	-2.67	-3.23	-2.66	-2.75	-2.48	-2.52	-2.38	0.00	-4.48	0.00	-4.48	0.00	-2.87	-2.77	-2.61
TCGA-AC-A62V-10A-01D-A31U-09_BRCA	-2.85	0.00	-2.67	-3.21	-2.61	-2.67	-2.59	-2.75	-2.48	0.00	-2.79	0.00	-2.67	-2.62	-2.85	0.00	-2.44
TCGA-AC-A62X-10A-01D-A29N-09_BRCA	-2.78	0.00	-4.49	-3.13	-2.58	-2.59	-2.57	-2.61	-2.66	-3.45	-2.86	0.00	-2.78	-2.69	-2.97	0.00	-2.68
TCGA-AC-A62Y-10A-01D-A29N-09_BRCA	-2.71	-2.68	-2.70	-3.36	-2.74	-2.66	-2.52	-2.56	-2.36	0.00	-4.14	-4.44	0.00	0.00	-2.72	0.00	-2.61
TCGA-AD-5900-10A-01D-1650-10_COAD	-2.48	0.00	0.00	-2.69	-2.40	-2.48	-2.42	-2.56	-2.30	0.00	0.00	0.00	0.00	0.00	-3.29	-2.82	-2.32
TCGA-AD-6548-10A-01D-1835-10_COAD	-2.45	0.00	0.00	-2.55	-2.43	-2.64	-2.31	-2.66	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.39
TCGA-AD-6888-10A-01D-1924-10_COAD	-2.67	0.00	0.00	-2.70	-2.59	-2.49	-2.41	-2.55	-2.75	-3.14	-2.95	-2.88	-2.95	-2.89	-3.11	0.00	-2.51
TCGA-AD-6889-10A-01D-1924-10_COAD	-2.45	-2.48	-2.45	0.00	0.00	0.00	-2.38	-2.51	-2.39	0.00	0.00	0.00	0.00	0.00	-2.86	0.00	-2.34
TCGA-AD-6890-10A-01D-1924-10_COAD	-2.48	-2.68	-2.84	-2.76	-2.68	-2.82	-2.53	-2.69	-2.41	0.00	0.00	-3.93	0.00	0.00	-3.19	-2.65	-2.41
TCGA-AD-6895-10A-01D-1924-10_COAD	-2.55	0.00	0.00	-2.66	-2.51	-2.50	-2.53	-2.59	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.62	-2.47
TCGA-AD-6899-10A-01D-1924-10_COAD	-2.48	-2.71	-3.00	-2.84	-2.82	-2.84	-2.45	-2.65	-2.52	0.00	0.00	0.00	0.00	0.00	-2.97	-2.84	-2.43
TCGA-AD-6901-10A-01D-1924-10_COAD	-2.45	0.00	0.00	-2.72	-2.56	-2.59	-2.39	-2.63	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.36
TCGA-AD-6963-10A-01D-1924-10_COAD	-2.53	0.00	0.00	-2.66	-2.66	-2.61	-2.47	-2.53	-2.67	-3.37	-3.04	0.00	-2.87	-2.81	0.00	-2.90	-2.32
TCGA-AD-6964-10A-01D-1924-10_COAD	-2.54	-2.56	-2.62	0.00	-2.85	-2.81	-2.47	-2.65	0.00	-3.18	-2.58	-2.87	-2.75	-2.58	0.00	0.00	-2.53
TCGA-AD-6965-10A-01D-1924-10_COAD	-2.44	0.00	-4.31	-2.55	-2.57	-2.63	-2.45	-2.57	-2.38	0.00	-4.01	0.00	0.00	-4.31	0.00	-2.80	-2.48
TCGA-AD-A5EK-10A-01D-A28G-10_COAD	-2.36	0.00	-2.49	-2.83	-2.57	-2.41	-2.25	-2.36	-2.30	0.00	-2.68	-2.54	-4.29	0.00	-2.70	0.00	-2.36
TCGA-AF-2687-10A-01D-1733-10_READ	-2.56	0.00	0.00	-2.75	-2.55	-2.63	-2.48	-2.63	-2.34	0.00	-4.13	0.00	0.00	0.00	0.00	-2.76	-2.43
TCGA-AF-2690-10A-01D-1733-10_READ	-2.64	0.00	-4.45	-2.93	-2.54	-2.54	-2.48	-2.52	-2.43	0.00	0.00	0.00	0.00	0.00	-3.25	-2.85	-2.40
TCGA-AF-2693-10A-01D-1733-10_READ	-2.64	-2.81	-2.74	-3.30	-2.68	-2.67	-2.42	-2.58	-2.72	-3.57	-3.18	0.00	-2.82	-2.76	-3.41	0.00	-2.42
TCGA-AF-3911-10A-01D-1733-10_READ	-2.55	0.00	0.00	-2.75	-2.55	-2.52	-2.36	-2.55	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.41
TCGA-AF-4110-10A-01D-1733-10_READ	-2.57	0.00	0.00	-2.76	-2.45	-2.62	-2.44	-2.62	-2.41	0.00	0.00	0.00	0.00	0.00	-3.45	-2.89	-2.42
TCGA-AF-5654-10A-01D-1657-10_READ	-2.63	-2.70	-2.67	-2.91	-2.48	-2.59	-2.50	-2.61	-2.45	0.00	-3.09	-2.82	-4.16	0.00	0.00	-2.65	-2.49
TCGA-AG-3591-10A-01D-1733-10_READ	-2.63	-2.71	-2.82	-3.00	-2.83	-2.77	-2.40	-2.61	-2.62	-3.38	-2.83	0.00	-2.73	-2.67	0.00	-3.17	-2.42
TCGA-AG-3592-10A-01D-1733-10_READ	-2.52	-4.11	0.00	-2.73	-2.58	-2.49	-2.47	-2.65	-2.55	-3.30	-3.13	0.00	-2.84	-2.84	0.00	-3.01	-2.41
TCGA-AG-4021-10A-01D-1733-10_READ	-2.62	-2.72	-2.69	-3.01	-2.77	-2.91	-2.46	-2.63	-2.63	-3.29	-3.08	0.00	-2.81	-2.73	0.00	-3.01	-2.45
TCGA-AH-6544-10A-01D-1826-10_READ	-2.59	-2.90	-2.81	-2.94	-2.90	-2.79	-2.57	-2.64	-2.71	-3.34	-2.98	0.00	-2.95	-2.83	0.00	-2.74	-2.51
TCGA-AH-6897-10A-01D-1924-10_READ	-2.55	0.00	0.00	-2.73	-2.47	-2.43	-2.51	-2.58	-2.48	0.00	0.00	0.00	0.00	-4.16	0.00	-2.51	-2.40
TCGA-AH-6903-10A-01D-1924-10_READ	-2.63	-2.98	-2.88	-2.98	-2.59	-2.62	-2.61	-2.67	-2.75	-3.39	-3.04	-2.55	0.00	-2.88	0.00	-2.98	-2.53
TCGA-AJ-A23M-10A-01D-A159-09_UCEC	-3.04	-2.65	-2.67	-2.95	-2.78	-2.77	-2.51	-2.58	-2.47	0.00	0.00	0.00	0.00	-3.84	-3.07	-2.83	-2.64
TCGA-AJ-A23N-10A-01D-A22A-09_UCEC	-2.81	-2.78	-2.84	-3.25	-2.74	-2.77	-2.60	-2.58	-2.53	0.00	-4.10	0.00	-4.10	0.00	0.00	-2.63	-2.66
TCGA-AJ-A23O-10A-01D-A159-09_UCEC	-2.74	0.00	0.00	-2.86	-2.50	-2.51	-2.44	-2.55	-2.43	0.00	-4.40	0.00	0.00	-4.40	-2.71	-4.40	-2.56
TCGA-AJ-A2QK-10A-01D-A18P-09_UCEC	-2.83	-2.66	-2.62	0.00	-2.68	-2.65	-2.64	-2.57	-2.74	-3.38	-2.64	-2.63	0.00	-2.69	-3.00	-4.01	-2.72
TCGA-AJ-A2QL-10A-01D-A18P-09_UCEC	-2.69	-2.58	-2.61	-3.23	-2.65	-3.69	-2.58	-2.64	-2.54	-4.46	-4.16	-4.46	-4.16	-2.60	-2.90	0.00	-2.51
TCGA-AJ-A2QM-10A-01D-A18P-09_UCEC	-2.74	-3.99	-4.17	-2.98	-2.54	-2.53	-2.53	-2.50	-2.38	0.00	0.00	-4.47	-4.47	-4.47	-2.96	-2.68	-2.60
TCGA-AJ-A2QN-10A-01D-A18P-09_UCEC	-2.90	-2.78	-2.84	-3.40	-2.58	-2.61	-2.62	-2.61	-2.49	0.00	-2.88	-2.79	0.00	0.00	-3.05	-2.88	-2.74
TCGA-AJ-A2QO-10A-01D-A18P-09_UCEC	-2.72	-4.46	-4.16	-2.96	-2.51	-2.51	-2.51	-2.57	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.59
TCGA-AJ-A3BD-10A-01D-A19Y-09_UCEC	-2.80	0.00	-4.52	-2.93	-2.51	-2.52	-2.52	-2.45	-2.39	-4.22	0.00	0.00	0.00	-4.22	0.00	-2.46	-2.63
TCGA-AJ-A3BF-10A-01D-A20S-09_UCEC	-2.85	-2.57	-2.61	0.00	-2.63	-2.72	-2.59	-2.49	-2.50	0.00	-2.84	-2.76	0.00	0.00	-3.04	-2.74	-2.65
TCGA-AJ-A3BG-10A-01D-A19Y-09_UCEC	-2.84	-4.04	-4.52	-3.00	-2.55	-2.60	-2.58	-2.60	-2.65	-3.48	-2.87	-4.22	-2.85	-2.75	0.00	-2.82	-2.69
TCGA-AJ-A3BH-10A-01D-A19Y-09_UCEC	-2.88	-2.83	-2.94	-3.31	-2.57	-2.63	-2.69	-2.58	-2.80	-3.61	-2.70	-2.72	0.00	-2.81	0.00	-2.89	-2.74
TCGA-AJ-A3BI-10A-01D-A20S-09_UCEC	-2.64	-4.11	-3.94	-2.94	-2.48	-2.53	-2.46	-2.62	-2.45	0.00	0.00	-4.41	0.00	0.00	-2.74	-3.81	-2.52
TCGA-AJ-A3BK-10A-01D-A19Y-09_UCEC	-2.86	-2.67	-2.70	-3.23	-2.61	-2.70	-2.46	-2.58	-2.48	0.00	0.00	0.00	0.00	0.00	-2.72	-4.18	-2.58
TCGA-AJ-A3EJ-10A-01D-A19Y-09_UCEC	-2.80	-4.60	-3.90	-3.02	-2.54	-2.55	-2.50	-2.52	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.67
TCGA-AJ-A3EL-10A-01D-A20S-09_UCEC	-2.88	-3.85	-4.06	-3.14	-2.61	-2.51	-2.61	-2.64	-2.76	-3.46	-2.93	-2.82	-4.28	-2.88	0.00	-2.76	-2.68
TCGA-AJ-A3I9-10A-01D-A22A-09_UCEC	-2.67	-4.06	-3.84	-2.96	-2.54	-2.49	-2.48	-2.50	-2.43	0.00	0.00	0.00	0.00	-4.54	-2.92	-2.83	-2.65
TCGA-AJ-A3IA-10A-01D-A20S-09_UCEC	-2.83	-2.76	-2.79	-3.15	-2.69	-2.69	-2.56	-2.51	-2.47	-4.11	-4.11	0.00	-3.98	-4.28	-3.05	-2.71	-2.72
TCGA-AJ-A3NC-10A-01D-A22A-09_UCEC	-2.83	-3.94	-4.54	-3.02	-2.60	-2.55	-2.53	-2.57	-2.68	-3.54	-2.80	0.00	-2.79	-2.75	0.00	-2.74	-2.64
TCGA-AJ-A3NE-10A-01D-A22A-09_UCEC	-2.66	-2.51	-2.52	-4.41	-3.63	-3.63	-2.43	-2.43	-2.31	0.00	0.00	-4.11	0.00	0.00	0.00	-2.43	-2.56
TCGA-AJ-A3NF-10A-01D-A22A-09_UCEC	-2.69	-3.81	-3.81	-2.99	-2.54	-2.56	-2.47	-2.58	-2.43	-4.51	0.00	-4.51	-4.20	-3.81	-2.88	-3.66	-2.64
TCGA-AJ-A3NG-10A-01D-A22A-09_UCEC	-2.83	-4.47	-3.99	-3.26	-2.52	-2.60	-2.58	-2.69	-2.78	-3.42	-2.85	0.00	-2.87	-2.75	0.00	-2.81	-2.65
TCGA-AJ-A3NH-10A-01D-A22A-09_UCEC	-2.68	-4.21	-4.21	-2.92	-2.50	-2.49	-2.40	-2.60	-2.47	0.00	0.00	-4.52	0.00	0.00	-2.80	-4.04	-2.63
TCGA-AJ-A3OJ-10A-01D-A22A-09_UCEC	-2.78	-4.09	-4.39	-3.11	-2.52	-2.51	-2.50	-2.48	-2.60	-3.28	-2.93	0.00	-2.76	-2.64	0.00	-2.81	-2.59
TCGA-AJ-A3OK-10A-01D-A22A-09_UCEC	-2.75	0.00	0.00	-3.01	-2.51	-2.51	-2.47	-2.51	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.57
TCGA-AJ-A3OL-10A-01D-A22A-09_UCEC	-2.85	-2.77	-2.87	-3.32	-2.57	-2.59	-2.60	-2.68	-2.56	0.00	-2.89	-2.83	0.00	0.00	0.00	-2.67	-2.68
TCGA-AJ-A3QS-10A-01D-A22A-09_UCEC	-2.95	-2.52	-2.68	0.00	-2.68	-2.68	-2.64	-2.65	-2.43	0.00	-2.69	-2.89	-2.90	0.00	-3.06	-2.94	-2.70
TCGA-AJ-A3TW-10A-01D-A22A-09_UCEC	-2.69	-2.53	-2.55	0.00	-2.86	-2.97	-2.60	-2.61	-2.46	0.00	-2.79	-2.86	0.00	0.00	-3.25	-2.91	-2.70
TCGA-AJ-A5DV-10A-01D-A27P-09_UCEC	-2.57	-2.61	-2.71	-3.25	-2.62	-2.68	-2.44	-2.42	-2.35	0.00	0.00	0.00	0.00	-4.37	-2.93	0.00	-2.68
TCGA-AJ-A5DW-10A-01D-A27P-09_UCEC	-2.74	-2.66	-2.68	-3.22	-2.65	-2.60	-2.61	-2.72	-2.56	0.00	-2.75	0.00	-2.74	-2.66	0.00	-2.66	-2.64
TCGA-AK-3426-10A-01D-1251-10_KIRC	-2.95	0.00	0.00	-2.82	-2.56	-2.55	-2.52	-2.74	-2.50	0.00	0.00	0.00	0.00	-4.87	0.00	-2.77	-2.71
TCGA-AK-3427-10A-01D-0966-08_KIRC	-2.56	-2.74	-2.73	-2.98	-2.64	-2.73	-2.72	-2.72	-2.73	0.00	-2.90	0.00	-2.78	-2.69	-3.08	-4.67	-2.51
TCGA-AK-3429-10A-01D-1251-10_KIRC	-3.02	0.00	0.00	-2.84	-2.59	-2.53	-2.53	-2.66	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.71
TCGA-AK-3430-10A-01D-1251-10_KIRC	-3.01	0.00	0.00	-2.88	-2.69	-2.59	-2.56	-2.66	-2.80	-3.19	-3.04	0.00	-2.78	-2.82	0.00	-3.09	-2.71
TCGA-AK-3436-10A-01D-1251-10_KIRC	-3.06	-2.41	-2.45	0.00	0.00	-4.75	-2.68	-3.13	0.00	-3.05	-2.87	0.00	-2.57	-2.49	0.00	0.00	-2.75
TCGA-AK-3440-10A-01D-0966-08_KIRC	-2.65	-2.85	-2.72	-3.05	-2.77	-2.82	-2.69	-2.55	-2.81	-3.33	-2.85	0.00	-2.78	-2.81	0.00	-2.82	-2.63
TCGA-AK-3443-10A-01D-0966-08_KIRC	-2.60	0.00	-4.36	-2.70	-2.57	-2.66	-2.68	-2.59	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.55
TCGA-AK-3444-10A-01D-0966-08_KIRC	-2.46	-2.74	-2.76	-3.01	-2.67	-2.67	-2.62	-2.49	-2.59	0.00	-4.65	0.00	-4.65	0.00	0.00	-2.55	-2.48
TCGA-AK-3447-10A-01D-0966-08_KIRC	-2.61	0.00	0.00	-2.91	-2.64	-2.62	-2.64	-2.64	-2.76	-3.40	-2.91	0.00	-2.79	-2.71	0.00	-2.74	-2.54
TCGA-AK-3451-10A-01D-1251-10_KIRC	-3.05	0.00	-4.58	-2.86	-2.65	-2.62	-2.44	-2.59	-2.52	-3.08	0.00	0.00	0.00	0.00	-3.18	0.00	-2.70
TCGA-AK-3453-10A-01D-0966-08_KIRC	-2.57	-2.81	-2.79	-2.96	-2.73	-2.75	-2.69	-2.61	-2.75	-3.38	-2.96	0.00	-2.83	-2.76	0.00	-2.76	-2.57
TCGA-AK-3455-10A-01D-0966-08_KIRC	-2.53	-2.56	-2.61	-4.27	-4.27	-4.09	-2.60	-2.45	-2.53	0.00	0.00	0.00	0.00	0.00	-3.07	-2.67	-2.50
TCGA-AK-3456-10A-01D-1251-10_KIRC	-2.88	-2.70	-2.64	-3.03	-2.88	-2.79	-2.47	-2.67	-2.47	0.00	0.00	0.00	0.00	0.00	-3.04	0.00	-2.66
TCGA-AK-3458-10A-01D-1501-10_KIRC	-3.21	-2.66	-2.71	-3.27	-2.56	-2.66	-2.57	-2.86	-2.88	-3.18	-3.00	-2.66	0.00	-2.87	0.00	-3.26	-2.67
TCGA-AK-3465-10A-01D-0966-08_KIRC	-2.51	-4.63	0.00	-2.86	-2.51	-2.57	-2.64	-2.59	-2.58	0.00	0.00	-4.63	0.00	-4.63	-3.09	-2.75	-2.51
TCGA-AL-3466-10A-01D-1252-08_KIRP	-2.59	0.00	0.00	-2.81	-2.58	-2.54	-2.66	-2.56	-2.57	0.00	0.00	0.00	0.00	-4.23	-3.12	-2.75	-2.56

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-AL-3467-10A-01D-1252-08_KIRP	-2.49	0.00	-4.67	-2.83	-2.58	-2.52	-2.64	-2.46	-2.50	0.00	0.00	0.00	-4.67	-4.20	0.00	-2.41	-2.53
TCGA-AL-3468-10A-01D-1252-08_KIRP	-2.63	-2.75	-2.74	-4.51	-2.66	-2.63	-2.79	-2.59	-2.60	0.00	-2.90	-2.69	0.00	0.00	-3.17	-2.89	-2.67
TCGA-AL-3472-10A-01D-1252-08_KIRP	-2.52	-2.74	-2.75	-2.91	-2.69	-2.70	-2.64	-2.42	-2.50	0.00	0.00	0.00	0.00	0.00	-3.13	-2.71	-2.51
TCGA-AL-3473-10A-01D-1252-08_KIRP	-2.45	0.00	-4.34	-2.84	-2.55	-2.53	-2.62	-2.55	-2.48	-4.64	-4.64	0.00	0.00	-4.34	0.00	-2.60	-2.52
TCGA-AL-7173-10A-01D-2136-08_KIRP	-2.55	-2.67	-2.63	-2.87	-2.70	-2.60	-2.57	-2.45	-2.51	0.00	0.00	-4.45	0.00	0.00	-3.01	-2.64	-2.50
TCGA-AL-A5DJ-10A-01D-A26P-10_KIRP	-2.48	0.00	0.00	-2.55	-2.46	-2.32	-2.32	-2.43	0.00	-3.60	-2.59	0.00	-2.38	-2.34	0.00	0.00	-2.48
TCGA-AN-A04C-10A-01D-A047-09_BRCA	-2.86	0.00	-4.28	-2.84	-2.61	-2.66	-2.66	-2.62	-2.64	-4.88	0.00	-4.40	0.00	-4.18	-3.09	-2.80	-2.79
TCGA-AN-A0FY-10A-01D-A047-09_BRCA	-2.89	0.00	-4.48	-2.97	-2.62	-2.73	-2.60	-2.62	-2.57	0.00	0.00	-4.96	0.00	0.00	-3.19	-2.87	-2.87
TCGA-AN-A0XL-10A-01D-A10M-09_BRCA	-2.95	-2.83	-2.89	-3.10	-2.55	-2.79	-2.60	-2.75	-2.65	0.00	-3.06	-2.99	0.00	0.00	0.00	-2.83	-2.91
TCGA-AN-A0XN-10A-01D-A10G-09_BRCA	-2.98	-2.74	-2.74	-3.21	-2.59	-2.60	-2.52	-2.73	-2.51	0.00	-3.01	-2.70	-4.48	0.00	-3.17	-2.91	-2.73
TCGA-AN-A0XO-10A-01D-A10G-09_BRCA	-2.92	-2.72	-2.69	0.00	-3.31	-2.73	-2.55	-2.50	-2.88	-3.21	-2.50	-2.98	-2.90	-2.94	-3.34	0.00	-2.78
TCGA-AN-A0XP-10A-01D-A10G-09_BRCA	-2.86	-3.39	-3.65	-2.82	-2.54	-2.59	-2.54	-2.56	-2.54	0.00	-3.95	-3.42	-4.65	0.00	0.00	-2.50	-2.66
TCGA-AN-A0XR-10A-01D-A117-09_BRCA	-2.97	-2.81	-2.91	-3.29	-2.57	-2.74	-2.63	-2.68	-2.81	-3.35	-2.66	-2.85	-2.89	-2.90	0.00	-2.99	-2.83
TCGA-AN-A0XS-10A-01D-A10G-09_BRCA	-2.91	-2.67	-2.68	-3.05	-2.72	-2.74	-2.46	-2.54	-2.39	0.00	0.00	0.00	0.00	-4.72	-3.04	-2.77	-2.73
TCGA-AN-A0XT-10A-01D-A10G-09_BRCA	-2.75	-4.37	0.00	-2.88	-2.55	-2.57	-2.54	-2.48	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.68
TCGA-AN-A0XU-10A-01D-A10G-09_BRCA	-2.97	-2.86	-2.86	-3.18	-2.64	-2.76	-2.75	-2.65	-2.86	-3.54	-2.76	-2.73	-4.22	-2.89	-3.13	0.00	-2.82
TCGA-AN-A0XV-10A-01D-A10G-09_BRCA	-3.05	-2.69	-2.66	-3.05	-2.52	-2.63	-2.58	-2.86	-2.51	0.00	-3.13	-2.79	0.00	0.00	-3.23	0.00	-2.75
TCGA-AN-A0XW-10A-01D-A10G-09_BRCA	-2.91	-2.71	-2.71	-3.10	-2.58	-2.70	-2.56	-2.78	-2.51	0.00	-3.12	-2.78	0.00	-4.66	-3.23	-3.05	-2.76
TCGA-AO-A03M-10A-01D-A10M-09_BRCA	-2.89	-2.77	-2.76	-3.13	-2.75	-2.77	-2.67	-2.70	0.00	-3.25	-2.60	-2.73	-2.81	-2.71	0.00	0.00	-2.82
TCGA-AO-A03N-10A-01D-A10M-09_BRCA	-2.81	-2.49	-2.46	0.00	0.00	0.00	-2.50	-2.64	-2.41	0.00	0.00	0.00	0.00	0.00	-2.84	0.00	-2.65
TCGA-AO-A03U-10A-01D-A10M-09_BRCA	-3.15	0.00	0.00	-2.99	-2.65	-2.66	-2.65	-2.87	-2.75	-3.28	-3.18	0.00	-2.79	-2.75	0.00	-3.23	-2.82
TCGA-AO-A03V-10A-01D-A110-09_BRCA	-2.90	0.00	0.00	-2.94	-2.57	-2.63	-2.58	-2.62	-2.73	-3.30	-2.78	0.00	-2.82	-2.76	0.00	-2.87	-2.79
TCGA-AO-A0JG-10A-01D-A099-09_BRCA	-2.91	-2.56	-2.52	0.00	0.00	0.00	-2.53	-2.50	-2.49	0.00	0.00	0.00	0.00	0.00	-3.10	-2.76	-2.76
TCGA-AO-A124-10A-01D-A10M-09_BRCA	-3.05	-2.80	-2.76	-3.20	-2.57	-2.70	-2.65	-2.82	-2.77	-3.45	-2.81	-2.84	-2.84	-2.86	0.00	-3.07	-2.83
TCGA-AO-A125-10A-01D-A10M-09_BRCA	-2.99	-2.72	-2.74	-3.13	-2.55	-2.65	-2.62	-2.65	-2.45	0.00	-2.84	0.00	-2.75	-4.75	-3.16	-2.85	-2.68
TCGA-AO-A126-10A-01D-A10M-09_BRCA	-2.91	0.00	0.00	-2.96	-2.61	-2.58	-2.56	-2.52	-2.44	0.00	0.00	0.00	0.00	0.00	-3.09	-2.77	-2.69
TCGA-AO-A128-10A-01D-A10M-09_BRCA	-2.72	0.00	-4.75	-2.75	-2.50	-2.46	-2.41	-2.44	-2.46	0.00	0.00	-4.75	-4.75	0.00	0.00	-2.36	-2.69
TCGA-AO-A129-10A-01D-A10M-09_BRCA	-2.93	0.00	0.00	-2.75	-2.60	-2.61	-2.49	-2.64	-2.57	0.00	0.00	0.00	0.00	0.00	-2.86	0.00	-2.68
TCGA-AO-A12A-10A-01D-A110-09_BRCA	-2.85	-2.49	-2.59	0.00	-2.66	-2.72	-2.50	-2.64	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.62	-2.66
TCGA-AO-A12B-10A-01D-A10M-09_BRCA	-2.87	-2.69	-2.68	-3.00	-2.67	-2.77	-2.66	-2.90	-2.75	0.00	-2.86	-2.78	0.00	-2.76	0.00	-2.85	-2.69
TCGA-AO-A12D-10A-01D-A110-09_BRCA	-2.83	0.00	0.00	-2.80	-2.53	-2.50	-2.46	-2.66	-2.49	0.00	-4.88	-4.88	0.00	-4.88	0.00	-2.57	-2.72
TCGA-AO-A12E-10A-01D-A10M-09_BRCA	-2.85	0.00	0.00	-2.73	-2.61	-2.61	-2.53	-2.57	-2.57	0.00	0.00	0.00	0.00	0.00	-3.07	-2.82	-2.78
TCGA-AO-A12F-10A-01D-A110-09_BRCA	-2.98	-2.64	-2.74	-3.06	-2.67	-2.75	-2.63	-3.00	-2.71	0.00	-2.91	-4.65	-2.72	-2.79	-3.31	0.00	-2.60
TCGA-AO-A12G-10A-01D-A10M-09_BRCA	-3.14	-2.65	-2.75	-3.01	-2.74	-2.83	-2.57	-2.92	-2.59	0.00	0.00	0.00	-4.71	0.00	-3.19	0.00	-2.69
TCGA-AO-A12H-10A-01D-A110-09_BRCA	-2.93	-4.88	-2.80	-3.08	-2.79	-2.87	-2.70	-2.66	-2.73	-3.45	-2.85	-4.58	-2.85	-2.76	-3.25	-4.58	-2.80
TCGA-AO-A1KO-10A-01D-A13O-09_BRCA	-2.89	-2.70	-2.70	-3.12	-2.71	-2.77	-2.56	-2.57	-2.57	0.00	0.00	0.00	0.00	0.00	-3.16	-2.79	-2.70
TCGA-AO-A1KR-10A-01D-A142-09_BRCA	-3.04	-2.83	-2.90	-3.18	-2.61	-2.64	-2.67	-2.71	-2.62	0.00	-3.14	-2.85	0.00	0.00	-3.26	-2.95	-2.78
TCGA-AO-A1KT-10A-01D-A188-09_BRCA	-2.87	-2.64	-2.74	0.00	-2.87	-2.79	-2.62	-2.64	-2.66	0.00	0.00	0.00	0.00	0.00	-3.07	-2.84	-2.75
TCGA-AP-A059-10A-01D-A122-09_UCEC	-3.05	-2.94	-2.90	-3.25	-2.60	-2.68	-2.72	-2.67	-2.59	0.00	-2.93	-2.79	0.00	-5.07	0.00	-2.73	-2.88
TCGA-AP-A05O-10A-01D-A122-09_UCEC	-2.97	0.00	-4.93	-3.04	-2.69	-2.64	-2.65	-2.72	-4.93	-3.32	-2.72	0.00	-2.64	-2.65	0.00	0.00	-2.75
TCGA-AP-A0LE-10A-01D-A10B-09_UCEC	-2.99	0.00	0.00	-2.95	-2.51	-2.60	-2.57	-2.59	-2.47	0.00	0.00	0.00	0.00	0.00	-3.10	-2.88	-2.72
TCGA-AP-A0LF-10A-01D-A122-09_UCEC	-2.89	-2.73	-2.72	-3.04	-2.75	-2.75	-2.73	-2.75	-2.79	0.00	-2.81	0.00	-2.75	-2.73	0.00	-2.88	-2.72
TCGA-AP-A0LL-10A-01D-A10B-09_UCEC	-2.83	0.00	-4.73	-2.95	-2.59	-2.58	-2.57	-2.60	-2.41	0.00	0.00	0.00	0.00	-4.73	0.00	-2.61	-2.68
TCGA-AP-A0LM-10A-01D-A122-09_UCEC	-3.01	-2.90	-2.74	0.00	-2.76	-2.72	-2.74	-2.69	-2.66	0.00	-2.71	-2.82	-2.94	0.00	-3.19	-3.03	-2.87
TCGA-AP-A0LP-10A-01D-A10B-09_UCEC	-2.89	0.00	0.00	-2.88	-2.54	-2.60	-2.48	-2.66	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.67	-2.67
TCGA-AP-A0LQ-10A-01D-A10B-09_UCEC	-3.02	-2.68	-2.68	-5.01	-2.69	-2.74	-2.67	-2.73	-5.01	-3.39	-2.52	-2.51	-5.01	-2.72	0.00	0.00	-2.81
TCGA-AP-A0LS-10B-01D-A14G-09_UCEC	-2.70	-2.58	-2.65	-3.22	-2.61	-2.77	-2.68	-2.86	-2.61	0.00	-2.79	0.00	-2.68	-2.72	-2.96	-4.39	-2.55
TCGA-AP-A1DH-10A-01D-A135-09_UCEC	-2.82	-2.56	-2.59	0.00	-2.73	-2.70	-2.56	-2.57	-2.47	-4.50	-2.81	-2.68	0.00	-4.20	-2.97	-2.81	-2.61
TCGA-AP-A1DK-10A-01D-A135-09_UCEC	-2.62	-4.33	-3.86	-2.95	-2.38	-2.56	-2.57	-2.64	-2.48	-4.33	-4.33	-3.86	0.00	-2.64	0.00	-2.63	-2.64
TCGA-AP-A1DM-10A-01D-A135-09_UCEC	-2.70	-3.87	-4.10	-2.94	-2.59	-2.61	-2.50	-2.49	-2.46	0.00	0.00	-4.27	-4.27	-4.10	-2.99	-2.87	-2.62
TCGA-AP-A1DO-10A-01D-A135-09_UCEC	-2.93	-2.86	-2.80	-3.24	-2.57	-2.64	-2.72	-2.64	-2.71	-3.49	-2.71	-2.81	-2.87	-2.83	-3.07	-4.61	-2.72
TCGA-AP-A1DP-10A-01D-A135-09_UCEC	-2.72	-2.41	-2.49	0.00	0.00	0.00	-2.43	-2.54	-2.43	0.00	-4.14	-3.96	-4.44	-4.14	-2.69	-4.44	-2.51
TCGA-AP-A1DQ-10A-01D-A135-09_UCEC	-3.04	0.00	0.00	-2.90	-2.66	-2.65	-2.45	-2.80	-2.60	0.00	0.00	0.00	0.00	-4.65	-3.29	-2.96	-2.77
TCGA-AP-A1DR-10A-01D-A135-09_UCEC	-2.89	-2.60	-2.55	0.00	-2.70	-2.74	-2.49	-2.56	-2.39	0.00	-2.84	0.00	-2.74	0.00	-2.96	-2.82	-2.63
TCGA-AP-A1DV-10A-01D-A135-09_UCEC	-2.67	-2.73	-2.64	-3.03	-2.65	-2.65	-2.63	-2.80	-2.60	0.00	-2.73	-4.39	-2.63	-2.60	0.00	-2.68	-2.58
TCGA-AP-A1E0-10A-01D-A135-09_UCEC	-2.66	0.00	0.00	-3.11	-2.48	-2.52	-2.48	-2.48	-2.40	0.00	-4.06	0.00	-3.89	-4.36	0.00	-2.49	-2.49
TCGA-AP-A1E1-10A-01D-A135-09_UCEC	-2.74	-2.74	-2.71	-3.24	-2.78	-2.70	-2.52	-2.54	-2.64	-3.66	-2.94	0.00	-2.71	-2.77	0.00	-2.72	-2.58
TCGA-AP-A1E3-10A-01D-A135-09_UCEC	-2.79	0.00	-4.01	-3.09	-2.56	-2.55	-2.50	-2.66	-4.19	-3.32	-2.67	-4.49	-2.57	-2.56	0.00	0.00	-2.60
TCGA-AP-A1E4-10A-01D-A135-09_UCEC	-2.82	-2.81	-2.84	-3.24	-2.62	-2.70	-2.73	-2.62	-2.78	-3.71	-2.75	-2.74	-4.41	-2.81	0.00	-2.89	-2.77
TCGA-AP-A3K1-10A-01D-A20S-09_UCEC	-2.69	-2.58	-2.58	-3.17	-2.52	-4.38	-2.56	-2.62	-2.53	0.00	-4.38	-4.38	0.00	-2.57	-2.85	-3.90	-2.64
TCGA-AP-A5FX-10A-01D-A27P-09_UCEC	-2.81	-4.74	-2.80	-3.27	-2.58	-2.70	-2.71	-2.55	-2.60	0.00	-2.84	0.00	-2.78	-4.44	-3.05	-2.84	-2.74
TCGA-AQ-A04H-10A-01D-A10M-09_BRCA	-2.96	-2.81	-2.74	-3.12	-2.55	-2.69	-2.63	-2.72	-2.60	0.00	-3.03	-2.76	0.00	0.00	-3.36	-2.88	-2.85
TCGA-AQ-A04L-10A-01D-A12J-09_BRCA	-3.36	0.00	0.00	-3.36	-3.12	-3.06	-3.04	-3.13	-3.12	-3.81	-3.56	0.00	-3.46	-3.31	0.00	0.00	-3.13
TCGA-AQ-A0Y5-10A-01D-A17G-09_BRCA	-3.05	-2.86	-2.82	-3.18	-2.59	-2.67	-2.69	-2.80	0.00	-3.30	-2.64	-2.66	0.00	-2.71	0.00	0.00	-2.88
TCGA-AQ-A1H2-10A-01D-A13O-09_BRCA	-3.02	0.00	0.00	-3.01	-2.68	-2.74	-2.71	-2.69	-2.83	-3.34	-2.87	0.00	-2.88	-2.96	0.00	-3.04	-2.81
TCGA-AQ-A1H3-10A-01D-A188-09_BRCA	-2.91	0.00	0.00	-2.70	-2.44	-2.59	-2.51	-2.52	-2.71	-3.20	-2.82	0.00	-2.76	-2.80	0.00	-2.87	-2.63
TCGA-AQ-A54N-10A-01D-A25Q-09_BRCA	-2.96	-2.70	-2.73	-3.34	-2.53	-2.53	-2.57	-2.49	-2.40	-4.51	-2.90	-2.73	-4.51	-4.21	0.00	-2.56	-2.65
TCGA-AQ-A54O-10A-01D-A25Q-09_BRCA	-2.85	-4.65	-4.35	-3.09	-2.57	-2.67	-2.51	-2.59	-2.50	-3.50	-3.09	0.00	-2.80	-4.35	-3.00	-2.93	-2.73
TCGA-AR-A0TP-10A-01D-A099-09_BRCA	-2.96	0.00	0.00	-2.92	-2.71	-2.69	-2.61	-2.73	-2.87	-3.42	-2.90	0.00	-2.82	-2.82	0.00	-2.86	-2.78
TCGA-AR-A0TQ-10A-01D-A099-09_BRCA	-3.17	0.00	-4.21	-2.77	-2.58	-2.62	-2.56	-2.91	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.83	-2.71
TCGA-AR-A0TR-10A-01D-A099-09_BRCA	-3.00	-2.66	-2.64	-4.71	-2.86	-2.84	-2.68	-2.59	-2.80	-3.39	-2.66	-2.84	-2.86	-2.80	0.00	-2.89	-2.79
TCGA-AR-A0TS-10A-01D-A110-09_BRCA	-2.88	-2.60	-2.63	-3.03	-2.63	-2.62	-2.42	-2.54	-2.53	0.00	0.00	0.00	0.00	0.00	-3.08	-2.73	-2.64
TCGA-AR-A0TT-10A-01D-A099-09_BRCA	-2.94	0.00	-4.44	-2.88	-2.52	-2.56	-2.46	-2.57	-2.43	0.00	0.00	0.00	-4.44	-4.74	-3.10	-2.82	-2.64
TCGA-AR-A0TU-10A-01D-A10G-09_BRCA	-3.15	0.00	-4.61	-3.00	-2.69	-2.68	-2.61	-2.80	-2.83	-3.25	-3.15	-4.31	-2.89	-2.86	0.00	-3.25	-2.73
TCGA-AR-A0TV-10A-01D-A099-09_BRCA	-2.77	0.00	0.00	-2.71	-2.51	-2.53	-2.51	-2.55	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.65
TCGA-AR-A0TW-10A-01D-A099-09_BRCA	-3.04	0.00	0.00	-2.83	-2.78	-2.62	-2.62	-2.86	-2.92	-3.12	-3.32	0.00	-2.87	-2.80	0.00	-3.17	-2.66
TCGA-AR-A0TX-10A-01D-A099-09_BRCA	-2.77	0.00	-4.65	-2.71	-2.52	-2.53	-2.49	-2.47	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.67
TCGA-AR-A0TY-10A-01D-A110-09_BRCA	-2.95	0.00	0.00	-2.93	-2.74	-2.73	-2.67	-2.65	-2.85	-3.59	-2.93	0.00	-2.86	-2.88	-3.12	0.00	-2.88
TCGA-AR-A0TZ-10A-01D-A099-09_BRCA	-2.89	0.00	-4.79	-2.70	-2.41	-2.68	-2.58	-2.80	-2.56	0.00	0.00	0.00	-4.79	-2.63	0.00	-2.88	-2.74
TCGA-AR-A0U0-10A-01D-A10G-09_BRCA	-2.81	-4.28	-4.59	-2.72	-2.57	-2.58	-2.52	-2.56	-2.46	0.00	0.00	0.00	0.00	-4.59	-3.04	-2.81	-2.66
TCGA-AR-A0U1-10A-01D-A110-09_BRCA	-2.89	-4.17	-4.87	-2.97	-2.52	-2.55	-2.58	-2.70	-2.56	0.00	0.00	-4.57	0.00	0.00	-3.34	-2.99	-2.71
TCGA-AR-A0U2-10A-01D-A10G-09_BRCA	-2.80	-4.58	0.00	-2.95	-2.57	-2.55	-2.54	-2.60	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.70
TCGA-AR-A0U3-10A-01D-A10G-09_BRCA	-2.98	-4.63	-4.33	-2.99	-2.59	-2.62	-2.58	-2.68	-2.49	-4.63	-4.63	0.00	-4.63	-4.03	0.00	-2.69	-2.74
TCGA-AR-A0U4-10A-01D-A10G-09_BRCA	-2.86	-2.65	-2.67	-3.12	-2.73	-2.79	-2.50	-2.61	-2.46	0.00	0.00	0.00	0.00	0.00	-3.14	-2.87	-2.66
TCGA-AR-A1AH-10A-01D-A12B-09_BRCA	-2.93	-2.81	-2.81	-3.22	-2.75	-2.88	-2.59	-2.58	-2.54	0.00	0.00	0.00	0.00	0.00	-3.15	-2.90	-2.68
TCGA-AR-A1AI-10A-01D-A12Q-09_BRCA	-3.03	-2.95	-2.80	-3.22	-2.85	-2.87	-2.65	-2.66	-2.90	-3.25	-2.75	0.00	-2.69	-2.92	0.00	-2.97	-2.97
TCGA-AR-A1AJ-10A-01D-A12Q-09_BRCA	-2.91	0.00	0.00	-2.83	-2.61	-2.66	-2.61	-2.54	-2.56	0.00	0.00	0.00	0.00	-4.90	-3.07	-2.79	-2.76
TCGA-AR-A1AK-10A-01D-A12Q-09_BRCA	-2.87	0.00	-4.91	-2.84	-2.60	-2.61	-2.59	-2.59	-2.63	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.73
TCGA-AR-A1AL-10A-01D-A12Q-09_BRCA	-2.89	-2.75	-2.75	-3.08	-2.80	-2.75	-2.61	-2.62	-2.48	0.00	0.00	0.00	0.00	0.00	-3.16	-2.82	-2.78
TCGA-AR-A1AM-10A-01D-A22A-09_BRCA	-2.77	-2.45	-2.56	-3.86	-3.30	-3.30	-2.44	-2.52	-2.42	-4.04	-3.74	-3.74	-3.86	-3.34	0.00	-2.80	-2.51
TCGA-AR-A1AN-10A-01D-A12Q-09_BRCA	-2.92	-2.75	-2.75	-3.04	-2.80	-2.78	-2.53	-2.63	-2.49	0.00	0.00	0.00	0.00	0.00	-3.18	-2.90	-2.72
TCGA-AR-A1AO-10A-01D-A12Q-09_BRCA	-2.95	-2.79	0.00	-3.11	-2.53	-2.61	-2.63	-2.56	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.80
TCGA-AR-A1AP-10A-01D-A12Q-09_BRCA	-2.83	0.00	0.00	-2.85	-2.55	-2.60	-2.55	-2.60	-2.47	0.00	0.00	0.00	0.00	0.00	-2.87	0.00	-2.69
TCGA-AR-A1AQ-10A-01D-A12Q-09_BRCA	-2.95	-2.92	-2.86	-3.27	-2.61	-2.75	-2.62	-2.52	-2.71	-3.66	-2.89	-2.84	-4.99	0.00	-2.87	0.00	-2.92
TCGA-AR-A1AR-10A-01D-A135-09_BRCA	-2.98	-2.87	-2.85	-3.21	-2.77	-2.81	-2.64	-2.64	-2.77	-3.61	-2.81	0.00	-2.78	-2.83	0.00	-2.82	-2.77
TCGA-AR-A1AS-10A-01D-A12Q-09_BRCA	-3.06	-2.94	-2.94	-3.20	-2.66	-2.72	-2.74	-2.73	-2.90	-3.54	-2.66	-2.84	-2.91	-2.89	0.00	-3.02	-2.90

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-AR-A1AT-10A-01D-A12Q-09_BRCA	-3.02	-2.94	-2.95	-3.21	-2.63	-2.75	-2.80	-2.73	-2.97	-3.59	-2.74	-2.74	-5.06	-2.89	-3.19	0.00	-2.92
TCGA-AR-A1AU-10A-01D-A12Q-09_BRCA	-2.89	0.00	0.00	-2.78	-2.57	-2.65	-2.61	-2.63	-2.61	0.00	0.00	0.00	0.00	0.00	-2.90	-4.86	-2.77
TCGA-AR-A1AV-10A-01D-A12Q-09_BRCA	-2.97	-2.79	-2.83	-3.13	-2.58	-2.71	-2.70	-2.77	-2.56	0.00	-2.93	-2.82	0.00	-4.61	0.00	-2.79	-2.80
TCGA-AR-A1AW-10A-01D-A12Q-09_BRCA	-2.89	-4.66	-4.66	-2.68	-2.56	-4.18	-2.59	-2.73	-2.58	0.00	0.00	-4.66	0.00	-2.60	0.00	-3.06	-2.70
TCGA-AR-A1AX-10A-01D-A12Q-09_BRCA	-2.98	0.00	-4.58	-2.86	-2.65	-2.71	-2.59	-2.60	-2.82	-3.50	-2.88	0.00	-2.83	-2.83	0.00	-2.80	-2.84
TCGA-AR-A1AY-10A-01D-A12Q-09_BRCA	-2.87	0.00	0.00	-2.97	-2.61	-2.56	-2.57	-2.68	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.68
TCGA-AR-A24H-10A-01D-A167-09_BRCA	-2.92	-2.68	-2.71	-3.19	-2.81	-2.74	-2.57	-2.67	-2.63	0.00	0.00	0.00	0.00	0.00	-2.83	0.00	-2.70
TCGA-AR-A24K-10A-01D-A167-09_BRCA	-2.93	0.00	0.00	-2.98	-2.61	-2.73	-2.59	-2.67	-2.65	0.00	0.00	0.00	0.00	0.00	0.00	-2.69	-2.66
TCGA-AR-A24L-10A-01D-A167-09_BRCA	-3.02	0.00	0.00	-2.82	-2.67	-2.70	-2.70	-2.70	-2.88	-3.35	-2.92	0.00	-2.83	-2.81	-3.10	-4.43	-2.84
TCGA-AR-A24M-10A-01D-A167-09_BRCA	-2.94	0.00	0.00	-3.14	-2.64	-2.56	-2.51	-2.62	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.67
TCGA-AR-A24N-10A-01D-A167-09_BRCA	-2.90	-2.82	-2.84	-3.18	-2.59	-2.65	-2.60	-2.64	-2.65	0.00	-2.93	-2.84	0.00	0.00	0.00	-2.62	-2.74
TCGA-AR-A24O-10A-01D-A167-09_BRCA	-3.09	-2.79	-2.87	-3.15	-2.62	-2.72	-2.63	-2.60	-2.60	0.00	-3.03	-2.82	0.00	0.00	-3.20	-2.90	-2.81
TCGA-AR-A24P-10A-01D-A167-09_BRCA	-2.85	-2.71	-2.79	-3.00	-2.76	-2.74	-2.49	-2.52	-2.51	0.00	0.00	0.00	0.00	0.00	-3.11	-2.87	-2.67
TCGA-AR-A24Q-10A-01D-A167-09_BRCA	-2.83	0.00	0.00	-2.82	-2.56	-2.62	-2.53	-2.62	-2.54	0.00	0.00	0.00	0.00	0.00	-3.09	-2.87	-2.69
TCGA-AR-A24R-10A-01D-A167-09_BRCA	-2.84	-2.69	-2.69	-3.10	-2.79	-2.72	-2.57	-2.78	-2.72	0.00	-2.74	-2.75	0.00	-2.73	-3.00	0.00	-2.68
TCGA-AR-A24S-10A-01D-A167-09_BRCA	-2.87	0.00	-4.53	-2.86	-2.61	-2.55	-2.50	-2.58	-2.58	-4.53	0.00	0.00	0.00	0.00	0.00	-2.54	-2.66
TCGA-AR-A24T-10A-01D-A167-09_BRCA	-3.01	0.00	0.00	-2.93	-2.62	-2.60	-2.54	-2.61	-2.85	-3.31	-2.93	-2.80	0.00	-2.80	0.00	-2.80	-2.67
TCGA-AR-A24U-10A-01D-A167-09_BRCA	-2.88	-4.53	0.00	-2.87	-2.67	-2.68	-2.58	-2.70	-2.59	0.00	0.00	0.00	-4.53	0.00	-3.23	-3.03	-2.66
TCGA-AR-A24V-10A-01D-A167-09_BRCA	-2.83	0.00	0.00	-2.80	-2.61	-2.60	-2.52	-2.61	-2.53	0.00	0.00	0.00	0.00	0.00	-3.05	-2.89	-2.67
TCGA-AR-A24W-10A-01D-A167-09_BRCA	-2.91	0.00	0.00	-2.92	-2.70	-2.60	-2.54	-2.65	-2.61	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.62
TCGA-AR-A24X-10A-01D-A167-09_BRCA	-2.84	-2.75	-2.86	-3.16	-2.84	-2.76	-2.55	-2.67	-2.84	-3.35	-2.93	0.00	-2.82	-2.77	0.00	-2.97	-2.71
TCGA-AR-A24Z-10A-01D-A167-09_BRCA	-2.94	-4.48	0.00	-2.85	-2.62	-2.67	-2.61	-2.60	-2.59	0.00	0.00	0.00	0.00	-4.48	0.00	-2.57	-2.71
TCGA-AR-A250-10A-01D-A167-09_BRCA	-2.91	-2.81	-2.86	-3.10	-2.75	-2.81	-2.53	-2.62	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.68	-2.70
TCGA-AR-A251-10A-01D-A167-09_BRCA	-3.01	0.00	0.00	-2.81	-2.57	-2.65	-2.51	-2.61	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.72	-2.67
TCGA-AR-A252-10A-01D-A167-09_BRCA	-2.88	-2.73	-2.81	-3.10	-2.91	-2.81	-2.57	-2.57	-2.60	0.00	-4.42	0.00	0.00	0.00	0.00	-2.70	-2.69
TCGA-AR-A254-10A-01D-A167-09_BRCA	-2.84	0.00	0.00	-2.91	-2.63	-2.63	-2.51	-2.70	-2.62	0.00	-4.50	-4.50	0.00	0.00	0.00	-2.68	-2.62
TCGA-AR-A255-10A-01D-A167-09_BRCA	-2.90	0.00	0.00	-3.10	-2.62	-2.73	-2.67	-2.69	-2.91	-3.49	-2.97	0.00	-2.97	-2.98	0.00	-2.94	-2.77
TCGA-AR-A256-10A-01D-A167-09_BRCA	-3.13	-2.94	-3.00	-3.39	-2.70	-2.80	-2.74	-2.80	-2.70	-4.71	-3.11	-2.98	0.00	0.00	0.00	-2.81	-2.86
TCGA-AR-A2LE-10A-01D-A17W-09_BRCA	-2.85	-2.71	-2.67	-2.99	-2.74	-4.52	-2.67	-2.89	-2.73	0.00	0.00	0.00	0.00	-2.72	-2.98	0.00	-2.82
TCGA-AR-A2LH-10A-01D-A18P-09_BRCA	-2.95	0.00	0.00	-2.87	-2.54	-2.60	-2.50	-2.53	-2.52	0.00	0.00	0.00	0.00	0.00	-3.05	-2.82	-2.71
TCGA-AR-A2LJ-10A-01D-A19Y-09_BRCA	-2.85	-2.68	-2.81	-3.26	-2.80	-2.78	-2.50	-2.70	-2.62	-3.48	-2.95	0.00	-2.82	-2.72	0.00	-2.81	-2.62
TCGA-AR-A2LK-10A-01D-A17W-09_BRCA	-2.74	-4.54	0.00	-2.80	-2.50	-2.65	-2.45	-2.55	-2.44	0.00	0.00	-4.54	-4.54	-4.24	0.00	-2.54	-2.56
TCGA-AR-A2LL-10A-01D-A17W-09_BRCA	-2.97	0.00	0.00	-2.99	-2.65	-2.62	-2.66	-2.60	-2.81	-3.38	-2.98	0.00	-2.87	-2.82	0.00	-2.94	-2.76
TCGA-AR-A2LM-10A-01D-A17W-09_BRCA	-2.99	-2.81	-2.84	-3.16	-2.64	-2.73	-2.68	-2.69	-2.70	0.00	-2.98	-2.82	0.00	0.00	-3.20	-2.93	-2.82
TCGA-AR-A2LN-10A-01D-A18P-09_BRCA	-3.01	0.00	-4.31	-2.90	-2.62	-2.59	-2.54	-2.57	-2.58	0.00	0.00	0.00	-4.61	0.00	0.00	-2.57	-2.71
TCGA-AR-A2LO-10A-01D-A18P-09_BRCA	-3.05	0.00	-4.15	-2.96	-2.66	-2.70	-2.65	-2.66	-2.62	-4.62	0.00	-4.62	0.00	0.00	-3.12	-2.87	-2.73
TCGA-AR-A2LQ-10A-01D-A18P-09_BRCA	-3.14	-2.94	-3.01	-3.29	-2.69	-2.69	-2.69	-2.79	-2.94	-3.44	-2.72	-2.93	-2.93	-2.96	-3.24	0.00	-2.82
TCGA-AR-A2LR-10A-01D-A18P-09_BRCA	-3.11	-4.80	0.00	-3.13	-2.64	-2.73	-2.67	-2.68	0.00	-3.39	-2.70	-2.89	-2.79	-2.76	0.00	0.00	-2.79
TCGA-AR-A5QM-10A-01D-A27P-09_BRCA	-2.82	0.00	0.00	-3.07	-2.61	-2.60	-2.57	-2.55	-2.64	-3.57	-2.83	-4.47	-2.78	-2.71	0.00	-2.75	-2.59
TCGA-AR-A5QN-10A-01D-A28E-09_BRCA	-2.76	-4.44	-4.44	-3.06	-2.53	-2.48	-2.39	-2.51	-2.43	0.00	0.00	0.00	0.00	0.00	-2.81	0.00	-2.60
TCGA-AR-A5QP-10A-01D-A28E-09_BRCA	-2.74	-2.74	-2.78	-3.18	-2.55	-2.57	-2.53	-2.54	-2.36	0.00	-2.95	-2.74	0.00	0.00	-3.01	-2.81	-2.68
TCGA-AR-A5QQ-10A-01D-A28E-09_BRCA	-2.80	0.00	-4.47	-2.82	-2.49	-2.52	-2.48	-2.51	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.54
TCGA-AS-3777-10A-01D-0966-08_KIRC	-2.62	0.00	-4.36	-2.88	-2.58	-2.64	-2.68	-2.56	-2.56	0.00	0.00	0.00	0.00	-4.36	-3.10	-2.69	-2.59
TCGA-AS-3778-10A-01D-0966-08_KIRC	-2.59	-4.57	0.00	-2.83	-2.55	-2.55	-2.61	-2.61	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.51
TCGA-AT-A5NU-10A-01D-A28G-10_KIRP	-2.44	-2.58	-2.59	-2.86	-2.54	-2.39	-2.17	-2.29	-2.32	0.00	0.00	0.00	0.00	0.00	0.00	-2.27	-2.35
TCGA-AU-3779-10A-01D-1719-10_COAD	-2.58	0.00	0.00	-2.63	-2.37	-2.39	-2.31	-2.42	-2.30	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.35
TCGA-AU-6004-10A-01D-1719-10_COAD	-2.54	0.00	0.00	-2.70	-2.36	-2.31	-2.26	-2.52	-2.24	0.00	0.00	0.00	0.00	0.00	0.00	-2.65	-2.28
TCGA-AW-A1PO-10A-01D-A159-09_UCEC	-2.62	-4.23	-4.23	-2.91	-2.37	-2.56	-2.60	-2.69	-2.64	0.00	-4.23	-3.75	-3.93	-2.49	0.00	-2.71	-2.65
TCGA-AX-A06D-10A-01D-A122-09_UCEC	-2.92	-2.73	-2.68	0.00	-2.77	-2.77	-2.66	-2.70	-2.55	0.00	-2.86	-2.75	0.00	0.00	0.00	-2.67	-2.84
TCGA-AX-A06H-10A-01D-A122-09_UCEC	-2.82	-2.77	-2.71	-3.15	-2.73	-2.72	-2.59	-2.57	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.74
TCGA-AX-A06L-10A-01D-A122-09_UCEC	-2.96	-4.62	0.00	-2.98	-2.68	-2.67	-2.64	-2.75	-4.92	-3.40	-2.71	0.00	-2.68	-2.64	0.00	0.00	-2.76
TCGA-AX-A0IS-10B-01D-A10M-09_UCEC	-2.95	0.00	0.00	-3.01	-2.58	-2.60	-2.53	-2.60	-2.59	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.68
TCGA-AX-A0IU-10A-01D-A10B-09_UCEC	-2.93	-2.71	-2.72	-3.15	-2.53	-2.61	-2.61	-2.74	-2.57	0.00	-2.97	-2.80	0.00	-4.55	-3.22	-2.96	-2.73
TCGA-AX-A0IZ-10A-01D-A122-09_UCEC	-2.87	-2.73	-2.75	-3.10	-2.70	-2.76	-2.60	-2.63	-2.59	0.00	0.00	0.00	0.00	-4.85	-2.96	0.00	-2.71
TCGA-AX-A1C4-10A-01D-A135-09_UCEC	-2.87	-2.82	-2.81	-3.55	-2.56	-2.63	-2.62	-2.66	-4.51	-3.43	-2.60	-2.68	-2.81	-2.64	0.00	-4.51	-2.71
TCGA-AX-A1C5-10A-01D-A135-09_UCEC	-2.65	-4.05	-4.05	-3.01	-2.47	-2.47	-2.42	-2.62	-2.37	0.00	0.00	0.00	-4.35	-4.05	0.00	-2.43	-2.54
TCGA-AX-A1C7-10A-01D-A135-09_UCEC	-3.02	0.00	0.00	-2.85	-2.65	-2.60	-2.52	-2.70	-2.54	0.00	0.00	0.00	0.00	0.00	-3.27	-2.95	-2.71
TCGA-AX-A1C8-10A-01D-A135-09_UCEC	-2.99	-2.57	-2.65	0.00	-2.93	-2.90	-2.58	-2.77	-2.61	0.00	-3.10	-2.91	0.00	0.00	-3.18	-3.04	-2.71
TCGA-AX-A1C9-10A-01D-A135-09_UCEC	-2.68	-2.56	-2.70	-3.21	-2.64	-2.67	-2.68	-2.94	-2.54	0.00	-2.78	0.00	-2.68	-2.57	-2.97	0.00	-2.53
TCGA-AX-A1CA-10A-01D-A135-09_UCEC	-2.85	-2.72	-2.72	-3.11	-2.72	-2.74	-2.58	-2.65	-2.61	0.00	0.00	0.00	0.00	-4.72	-2.92	0.00	-2.64
TCGA-AX-A1CC-10A-01D-A135-09_UCEC	-2.93	0.00	0.00	-2.81	-2.81	-2.57	-2.45	-2.53	-2.54	0.00	0.00	0.00	0.00	0.00	-3.35	-3.17	-2.60
TCGA-AX-A1CE-10A-01D-A135-09_UCEC	-2.66	-2.59	-2.58	-3.38	-2.64	-2.57	-2.41	-2.67	-2.29	0.00	0.00	0.00	0.00	-4.42	0.00	-2.56	-2.53
TCGA-AX-A1CN-10A-01D-A135-09_UCEC	-2.77	-2.68	-2.74	-3.26	-2.67	-2.68	-2.45	-2.46	-2.47	0.00	0.00	-4.13	0.00	0.00	0.00	-2.41	-2.56
TCGA-AX-A1CP-10A-01D-A135-09_UCEC	-3.03	0.00	0.00	-2.77	-2.64	-2.63	-2.58	-2.64	-2.66	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.74
TCGA-AX-A2H7-10A-01D-A18P-09_UCEC	-2.89	-2.85	-2.93	-3.40	-2.63	-2.70	-2.58	-2.68	-3.93	-3.31	-2.64	-2.91	-2.77	-2.71	0.00	-4.40	-2.78
TCGA-AX-A2HF-10A-01D-A17D-09_UCEC	-2.93	-2.74	-2.76	-3.06	-2.80	-2.84	-2.55	-2.67	-2.53	0.00	0.00	0.00	0.00	0.00	-2.99	-2.85	-2.71
TCGA-AX-A2HG-10A-01D-A17D-09_UCEC	-2.73	-2.40	-2.45	-4.38	-4.38	-3.68	-2.41	-2.39	-2.27	0.00	-4.38	0.00	0.00	0.00	0.00	-2.34	-2.52
TCGA-AX-A2HH-10A-01D-A17D-09_UCEC	-2.90	-2.65	-2.75	-3.31	-2.76	-2.72	-2.51	-2.55	-4.49	-3.31	-2.60	-2.76	-2.75	-2.48	0.00	-4.19	-2.61
TCGA-AX-A2HJ-10A-01D-A17D-09_UCEC	-2.73	-4.38	0.00	-3.10	-2.47	-2.45	-2.47	-2.51	-2.38	0.00	0.00	-4.38	0.00	0.00	-2.75	-4.07	-2.54
TCGA-AX-A2HK-10A-01D-A17D-09_UCEC	-2.69	-2.62	-2.72	-3.23	-2.64	-2.52	-2.47	-2.53	-2.35	0.00	-3.87	-4.35	-4.35	-3.75	-2.89	-2.70	-2.50
TCGA-AX-A2IN-10A-01D-A17W-09_UCEC	-2.82	-2.68	-2.80	-3.27	-2.70	-2.66	-2.51	-2.53	-2.46	0.00	0.00	0.00	-4.08	-4.38	-2.84	-2.80	-2.52
TCGA-AX-A2IO-10A-01D-A17W-09_UCEC	-2.73	-4.27	0.00	-2.95	-2.53	-2.55	-2.60	-2.51	-2.64	-3.53	-2.82	0.00	-2.75	-2.70	-2.96	-4.09	-2.65
TCGA-AX-A3FS-10A-01D-A22A-09_UCEC	-2.69	-3.52	-3.76	-2.97	-2.56	-2.52	-2.45	-2.57	-2.40	-4.37	-3.89	0.00	-4.37	0.00	0.00	-2.63	-2.58
TCGA-AX-A3FT-10A-01D-A22A-09_UCEC	-2.73	-4.45	0.00	-2.92	-2.53	-2.52	-2.51	-2.50	-2.56	0.00	0.00	-4.45	0.00	0.00	0.00	-2.50	-2.69
TCGA-AX-A3FV-10A-01D-A22A-09_UCEC	-2.81	-2.65	-2.60	-3.38	-2.61	-2.68	-2.48	-2.46	-2.38	-4.38	-4.08	0.00	-4.38	-4.38	-2.93	-2.69	-2.53
TCGA-AX-A3FW-10A-01D-A22A-09_UCEC	-2.86	0.00	-3.69	-3.09	-2.50	-2.46	-2.45	-2.47	-2.52	0.00	-4.47	0.00	0.00	-4.47	0.00	-2.49	-2.57
TCGA-AX-A3FX-10A-01D-A22A-09_UCEC	-2.76	-4.50	0.00	-3.14	-2.49	-2.54	-2.54	-2.46	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.64
TCGA-AX-A3FZ-10A-01D-A22A-09_UCEC	-2.79	-4.24	-4.24	-3.04	-2.54	-2.62	-2.48	-2.51	-2.44	0.00	0.00	0.00	0.00	-4.07	-3.01	-2.78	-2.64
TCGA-AX-A3G1-10A-01D-A22A-09_UCEC	-2.82	-3.85	-3.97	-3.15	-2.57	-2.58	-2.56	-2.58	-3.30	-3.37	-2.76	-2.94	-2.92	-2.63	0.00	-3.45	-2.63
TCGA-AX-A3G3-10A-01D-A20S-09_UCEC	-2.82	-2.71	-2.79	-3.39	-2.79	-2.73	-2.57	-2.60	-3.99	-3.39	-2.66	-4.47	-2.62	-2.53	0.00	-3.87	-2.60
TCGA-AX-A3G4-10A-01D-A20S-09_UCEC	-2.72	-2.69	-2.71	-3.21	-2.68	-2.70	-2.48	-2.47	-2.33	0.00	-4.14	-4.44	0.00	0.00	-2.98	-2.71	-2.61
TCGA-AX-A3G6-10A-01D-A20S-09_UCEC	-2.77	0.00	-4.45	-3.00	-2.50	-2.54	-2.54	-2.53	-2.37	0.00	0.00	-4.45	0.00	0.00	-2.95	-2.76	-2.57
TCGA-AX-A3G7-10A-01D-A20S-09_UCEC	-2.70	-4.03	-4.03	-3.01	-2.48	-2.52	-2.47	-2.50	-2.44	0.00	0.00	0.00	0.00	-4.20	-2.95	-2.73	-2.62
TCGA-AX-A3G8-10A-01D-A22A-09_UCEC	-3.00	-2.78	-2.72	-3.24	-2.83	-2.75	-2.54	-2.66	-2.59	-3.39	-2.80	0.00	-2.77	-2.81	0.00	-2.92	-2.56
TCGA-AX-A3G9-10A-01D-A22A-09_UCEC	-2.72	-2.56	-2.55	0.00	-4.18	-4.48	-2.64	-2.75	-3.88	-3.58	-2.51	-2.70	-2.66	-2.52	0.00	-4.48	-2.65
TCGA-AX-A3GB-10A-01D-A22A-09_UCEC	-2.86	-2.68	-2.72	-3.49	-2.51	-2.62	-2.55	-2.59	-2.47	0.00	-2.72	-2.73	0.00	0.00	-3.21	-2.88	-2.62
TCGA-AX-A3GI-10A-01D-A20S-09_UCEC	-2.84	0.00	-4.60	-2.98	-2.54	-2.57	-2.58	-2.47	-2.47	0.00	0.00	0.00	0.00	0.00	-2.85	-2.71	-2.59
TCGA-AY-5543-10A-01D-1650-10_COAD	-2.46	-2.57	0.00	-2.97	-2.57	-2.60	-2.48	-2.81	-2.48	0.00	-2.86	0.00	-2.78	-2.61	-3.24	0.00	-2.36
TCGA-AY-6197-10A-01D-1719-10_COAD	-2.38	0.00	0.00	-2.68	-2.44	-2.42	-2.35	-2.42	-2.28	0.00	0.00	0.00	0.00	0.00	-3.01	-2.91	-2.34
TCGA-AZ-4315-10A-01D-1408-10_COAD	-2.56	0.00	0.00	-2.82	-2.45	-2.47	-2.44	-2.56	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.65	-2.50
TCGA-AZ-4323-10A-01D-1835-10_COAD	-2.44	0.00	0.00	-2.67	-2.51	-2.53	-2.51	-2.59	-2.70	-3.38	-3.00	0.00	-2.83	-3.08	0.00	-2.83	-2.47
TCGA-AZ-4616-10A-01D-1835-10_COAD	-2.44	0.00	0.00	-2.41	-2.45	-2.73	-2.63	-2.76	-2.56	0.00	0.00	0.00	0.00	-2.51	0.00	-2.73	-2.65
TCGA-AZ-4681-10A-01D-1408-10_COAD	-2.53	0.00	0.00	-2.61	-2.50	-2.58	-2.40	-2.63	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.72	-2.38
TCGA-AZ-4682-10A-01D-1408-10_COAD	-2.63	0.00	0.00	-2.69	-2.62	-2.80	-2.72	-2.89	-4.21	-3.17	-2.87	0.00	-2.68	-2.78	0.00	0.00	-2.48
TCGA-AZ-5403-10A-01D-1650-10_COAD	-2.58	0.00	-4.50	-2.75	-2.51	-2.52	-2.38	-2.52	-2.37	0.00	0.00	0.00	0.00	-4.50	-3.30	-3.06	-2.44
TCGA-B0-5399-10A-01D-1501-10_KIRC	-2.96	-3.98	-3.89	-2.77	-2.56	-2.53	-2.56	-2.64	-2.42	-4.04	-4.41	0.00	-4.29	-3.98	-3.42	-2.91	-2.64

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-B0-5698-10A-01D-1669-08_KIRC	-2.44	-2.48	-2.46	0.00	-4.50	-4.20	-2.49	-2.38	-2.42	0.00	-4.50	0.00	0.00	-4.20	-3.03	-2.69	-2.36
TCGA-B1-5398-10A-01D-1589-08_KIRP	-2.51	-4.53	0.00	-2.57	-2.51	-2.55	-2.53	-2.59	-2.54	0.00	0.00	-4.53	0.00	-4.53	0.00	-2.56	-2.44
TCGA-B1-7332-10A-01D-2136-08_KIRP	-2.58	-2.74	-2.71	-2.93	-2.57	-2.57	-2.66	-2.61	-2.51	0.00	-2.84	-2.77	-4.58	0.00	-2.98	-4.11	-2.53
TCGA-B1-A47M-10A-01D-A25F-10_KIRP	-2.39	0.00	-4.20	-2.52	-2.42	-2.20	-2.30	-2.38	-2.36	0.00	0.00	0.00	0.00	0.00	-2.71	0.00	-2.38
TCGA-B1-A47N-10A-01D-A25F-10_KIRP	-2.45	-2.63	-2.62	-2.96	-2.35	-2.36	-2.31	-2.35	-2.36	0.00	-2.82	-2.55	0.00	0.00	0.00	-2.33	-2.40
TCGA-B1-A47O-10A-01D-A25F-10_KIRP	-2.41	0.00	0.00	-2.67	-2.44	-2.33	-2.34	-2.50	-2.50	-3.40	-2.82	0.00	-2.60	-2.55	0.00	-2.69	-2.30
TCGA-B1-A654-10A-01D-A31X-10_KIRP	-2.40	0.00	-2.54	-2.69	-2.64	-2.47	-2.24	-2.36	-2.30	0.00	0.00	0.00	0.00	-4.03	-2.64	0.00	-2.35
TCGA-B1-A655-10A-01D-A31X-10_KIRP	-2.44	-2.40	-2.66	0.00	-2.72	-2.57	-2.41	-2.35	0.00	-3.36	-2.80	0.00	-2.48	-2.31	0.00	0.00	-2.36
TCGA-B1-A656-10A-01D-A31X-10_KIRP	-2.39	-2.35	-2.44	-3.87	-4.17	0.00	-2.31	-2.40	-2.55	-3.27	-2.81	0.00	-2.62	-2.65	-2.92	-4.17	-2.41
TCGA-B1-A657-10A-01D-A31X-10_KIRP	-2.39	0.00	0.00	-2.63	-2.35	-2.31	-2.27	-2.37	-2.24	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.47
TCGA-B2-3923-10A-01D-1458-08_KIRC	-2.48	-2.60	-2.55	0.00	-4.10	0.00	-2.51	-2.52	-2.50	0.00	0.00	0.00	0.00	0.00	-2.91	0.00	-2.46
TCGA-B2-3924-10A-01D-1458-08_KIRC	-2.63	-2.80	-2.79	-2.97	-2.49	-2.60	-2.72	-2.58	-2.54	0.00	-2.97	-2.77	0.00	-4.71	0.00	-2.50	-2.59
TCGA-B2-4098-10A-01D-1458-08_KIRC	-2.56	-4.65	-4.17	-2.84	-2.54	-2.56	-2.63	-2.62	-2.49	0.00	0.00	-4.65	-3.95	-4.17	0.00	-2.58	-2.53
TCGA-B2-4099-10A-01D-1458-08_KIRC	-2.56	-4.41	0.00	-2.93	-2.61	-2.66	-2.67	-2.66	-2.75	-3.46	-2.88	-2.73	0.00	-2.74	0.00	-2.78	-2.57
TCGA-B2-5633-10A-01D-1535-10_KIRC	-2.97	0.00	-4.54	-2.63	-2.46	-2.58	-2.50	-2.64	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.62	-2.70
TCGA-B2-5635-10A-01D-A270-10_KIRC	-2.41	-2.68	-2.59	-2.87	-2.65	-2.64	-2.40	-2.44	-2.41	0.00	0.00	0.00	0.00	0.00	-2.76	0.00	-2.45
TCGA-B2-5636-10A-01D-1535-10_KIRC	-2.98	0.00	-4.73	-2.69	-2.50	-2.64	-2.49	-2.63	-2.62	-3.28	0.00	0.00	0.00	-4.43	0.00	-2.73	-2.75
TCGA-B2-5639-10A-01D-1535-10_KIRC	-2.92	0.00	0.00	-2.59	-2.53	-2.44	-2.49	-2.64	-2.46	0.00	0.00	0.00	0.00	0.00	-3.29	-3.00	-2.68
TCGA-B2-5641-10A-01D-1535-10_KIRC	-2.95	0.00	-4.67	-2.70	-2.53	-2.56	-2.49	-2.63	-2.39	0.00	0.00	0.00	0.00	-4.67	-3.47	-3.03	-2.66
TCGA-B2-A4SR-10A-01D-A25V-10_KIRC	-2.55	0.00	0.00	-2.78	-2.54	-2.55	-2.49	-2.68	-2.42	0.00	0.00	0.00	0.00	0.00	-3.13	-2.77	-2.48
TCGA-B3-3925-10A-01D-1458-08_KIRP	-2.64	-4.34	0.00	-2.89	-2.66	-2.67	-2.71	-2.56	-2.71	-3.69	-3.03	-4.64	-2.86	-2.71	-3.17	0.00	-2.61
TCGA-B3-4103-10A-01D-1458-08_KIRP	-2.56	0.00	-4.32	-2.78	-2.55	-2.54	-2.58	-2.49	-2.55	0.00	0.00	0.00	-4.62	0.00	0.00	-2.58	-2.49
TCGA-B3-4104-10A-01D-1458-08_KIRP	-2.59	-4.63	0.00	-2.70	-2.57	-2.60	-2.62	-2.50	-2.56	-4.63	0.00	0.00	-4.63	0.00	0.00	-2.48	-2.56
TCGA-B3-8121-10A-01D-2396-08_KIRP	-2.58	-4.57	-2.73	-2.89	-2.49	-2.68	-2.67	-2.69	-2.65	0.00	-2.91	0.00	-2.75	-4.09	-2.99	0.00	-2.56
TCGA-B4-5377-10A-01D-1501-10_KIRC	-2.90	0.00	-4.59	-2.83	-2.54	-2.60	-2.59	-2.65	-2.48	0.00	0.00	0.00	0.00	0.00	-3.30	-2.97	-2.72
TCGA-B4-5378-10A-01D-1501-10_KIRC	-2.96	0.00	0.00	-2.97	-2.59	-2.56	-2.52	-2.69	-2.54	0.00	0.00	0.00	0.00	0.00	-3.06	0.00	-2.63
TCGA-B4-5832-10A-01D-1669-08_KIRC	-2.54	0.00	0.00	-2.63	-2.54	-2.55	-2.58	-2.57	-2.59	-3.31	-2.99	-4.59	-2.77	-2.73	0.00	-2.76	-2.44
TCGA-B4-5834-10A-02D-1669-08_KIRC	-2.46	-2.69	-2.66	-2.82	-2.65	-2.60	-2.55	-2.52	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.38
TCGA-B4-5835-10A-01D-1669-08_KIRC	-2.50	-2.74	-2.72	-2.92	-2.47	-2.60	-2.62	-2.56	-2.50	0.00	-2.99	-2.75	-4.59	-3.99	-3.18	-2.77	-2.47
TCGA-B4-5836-10A-01D-1669-08_KIRC	-2.54	-2.72	0.00	-2.91	-2.49	-2.54	-2.65	-2.62	-2.73	-3.30	-3.08	0.00	-2.79	-2.72	0.00	-2.75	-2.42
TCGA-B4-5838-10A-01D-1669-08_KIRC	-2.56	-2.59	-2.54	-4.28	-2.71	-2.70	-2.58	-2.55	-2.48	0.00	-2.90	-2.71	0.00	0.00	0.00	-2.50	-2.47
TCGA-B4-5843-10A-01D-1669-08_KIRC	-2.46	0.00	0.00	-2.60	-2.51	-2.50	-2.58	-2.58	-2.43	0.00	0.00	0.00	0.00	-4.55	0.00	-2.52	-2.43
TCGA-B4-5844-10A-01D-1669-08_KIRC	-2.57	-2.81	-2.76	-2.95	-2.52	-2.62	-2.60	-2.63	-2.72	-3.34	-2.76	-2.63	-4.62	-2.69	0.00	-2.90	-2.46
TCGA-B5-A0JN-10A-01D-A10O-09_UCEC	-3.06	-2.90	-2.88	-3.13	-2.68	-2.86	-2.55	-2.73	-2.63	0.00	-2.89	0.00	-2.88	0.00	0.00	-2.65	-2.87
TCGA-B5-A0JS-10A-01D-A10O-09_UCEC	-3.00	-2.78	-2.78	-3.13	-2.59	-2.71	-2.68	-2.63	-2.78	-3.47	-2.63	-2.81	-2.83	-2.85	0.00	-2.90	-2.77
TCGA-B5-A0JT-10A-01D-A122-09_UCEC	-2.93	0.00	0.00	-2.79	-2.68	-2.67	-2.55	-2.61	-2.61	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.74
TCGA-B5-A0JU-10A-01D-A14G-09_UCEC	-2.82	-2.75	-2.80	-3.22	-2.45	-2.59	-2.54	-2.63	-2.48	0.00	-2.88	0.00	-2.82	0.00	-2.80	0.00	-2.62
TCGA-B5-A0JX-10B-01D-A14K-09_UCEC	-2.75	-2.67	-2.64	-3.17	-2.63	-2.63	-2.49	-2.59	-2.40	0.00	0.00	0.00	-4.45	0.00	0.00	-2.51	-2.58
TCGA-B5-A0JY-10A-01D-A10O-09_UCEC	-2.79	0.00	0.00	-2.76	-2.60	-2.57	-2.52	-2.48	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.69
TCGA-B5-A0K2-10A-01D-A10B-09_UCEC	-2.91	-2.72	-2.73	-3.12	-2.75	-2.75	-2.62	-2.68	-2.73	-3.43	-2.79	0.00	-2.79	-2.79	0.00	-2.87	-2.78
TCGA-B5-A0K7-10A-02D-A10B-09_UCEC	-2.80	-2.63	-2.63	-2.98	-2.66	-2.73	-2.51	-2.60	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.68
TCGA-B5-A0K8-10B-01D-A14K-09_UCEC	-3.07	-2.90	-2.89	-3.14	-2.63	-2.67	-2.62	-2.72	-2.92	-3.28	-2.75	-2.82	-2.90	-2.81	-3.30	-4.68	-2.77
TCGA-B5-A0K9-10A-02D-A10B-09_UCEC	-2.80	0.00	-4.76	-2.89	-2.51	-2.54	-2.50	-2.52	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.67
TCGA-B5-A0KB-10A-01D-A14G-09_UCEC	-2.93	-4.56	0.00	-3.16	-2.43	-2.62	-2.51	-2.58	-2.47	-3.41	-2.95	0.00	-2.86	0.00	-2.87	-2.95	-2.71
TCGA-B5-A11E-10A-01D-A10M-09_UCEC	-2.91	0.00	0.00	-2.74	-2.52	-2.56	-2.50	-2.78	-2.45	0.00	0.00	0.00	0.00	-4.65	-3.24	-2.91	-2.70
TCGA-B5-A11F-10A-01D-A10M-09_UCEC	-3.04	-2.91	-2.89	-3.28	-2.66	-2.79	-2.71	-2.71	-2.81	-3.66	-2.78	-2.72	-4.75	-2.89	0.00	-2.92	-2.89
TCGA-B5-A11G-10A-01D-A122-09_UCEC	-2.83	0.00	0.00	-3.00	-2.58	-2.64	-2.55	-2.51	-2.56	0.00	0.00	-4.85	0.00	0.00	-2.94	-2.77	-2.72
TCGA-B5-A11H-10B-01D-A122-09_UCEC	-2.98	-2.85	-2.84	-3.18	-2.62	-2.74	-2.68	-2.71	-2.81	-3.60	-2.76	-2.72	0.00	-2.83	0.00	-2.92	-2.83
TCGA-B5-A11I-10A-01D-A10M-09_UCEC	-2.87	0.00	0.00	-2.97	-2.61	-2.60	-2.58	-2.60	-2.59	0.00	-2.85	-4.88	-2.77	-4.88	-3.26	0.00	-2.94
TCGA-B5-A11J-10A-01D-A122-09_UCEC	-2.92	-2.75	-2.74	-3.04	-2.75	-2.76	-2.60	-2.55	-2.52	0.00	0.00	0.00	0.00	-4.88	-3.11	-2.85	-2.73
TCGA-B5-A11L-10A-01D-A13O-09_UCEC	-2.85	-2.66	-2.71	-3.34	-2.70	-2.70	-2.56	-2.56	-2.66	-3.29	-2.90	-4.52	-2.74	-2.75	-2.95	-4.21	-2.63
TCGA-B5-A11M-10A-01D-A122-09_UCEC	-3.00	-2.79	-2.83	0.00	-2.80	-2.84	-2.66	-2.70	-2.84	-3.44	-2.86	0.00	-2.78	-2.79	0.00	-2.88	-2.87
TCGA-B5-A11N-10A-01D-A122-09_UCEC	-2.83	0.00	-4.84	-2.95	-2.58	-2.66	-2.55	-2.46	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.77
TCGA-B5-A11O-10A-01D-A122-09_UCEC	-2.82	0.00	-4.87	-2.93	-2.65	-2.62	-2.57	-2.51	-2.50	0.00	0.00	0.00	0.00	0.00	-3.07	-2.78	-2.74
TCGA-B5-A11P-10A-01D-A14G-09_UCEC	-2.80	-2.56	-2.55	0.00	-2.69	-2.72	-2.53	-2.59	-2.49	0.00	-2.88	-2.64	0.00	0.00	-2.78	-4.42	-2.58
TCGA-B5-A11Q-10A-01D-A122-09_UCEC	-2.87	0.00	0.00	-3.03	-2.67	-2.70	-2.65	-2.61	-2.52	0.00	0.00	0.00	0.00	0.00	-3.06	-2.82	-2.76
TCGA-B5-A11R-10A-01D-A122-09_UCEC	-2.98	0.00	0.00	-2.86	-2.52	-2.66	-2.67	-2.62	-2.54	0.00	0.00	0.00	-4.86	-4.86	0.00	-2.59	-2.77
TCGA-B5-A11S-10A-01D-A122-09_UCEC	-2.91	-2.86	-2.83	-3.24	-2.62	-2.71	-2.63	-2.57	-2.58	0.00	-2.84	-2.85	0.00	-4.97	-3.13	-2.85	-2.85
TCGA-B5-A11U-10A-01D-A122-09_UCEC	-2.84	0.00	0.00	-3.03	-2.59	-2.61	-2.62	-2.49	-2.59	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.80
TCGA-B5-A11V-10A-01D-A10M-09_UCEC	-3.05	0.00	-4.51	-2.92	-2.74	-2.58	-2.67	-2.66	-2.81	-3.59	-2.78	0.00	-2.86	-2.92	-3.21	0.00	-2.93
TCGA-B5-A11W-10A-01D-A122-09_UCEC	-2.89	-4.56	-4.86	-2.85	-2.61	-2.62	-2.60	-2.56	-2.61	0.00	0.00	0.00	0.00	0.00	-3.12	-2.81	-2.77
TCGA-B5-A11X-10A-01D-A10M-09_UCEC	-2.97	-2.80	-2.80	-3.21	-2.60	-2.74	-2.69	-2.79	-2.66	0.00	-2.92	-2.81	0.00	0.00	-3.10	-2.84	-2.87
TCGA-B5-A11Y-10A-01D-A10M-09_UCEC	-2.99	-2.86	-2.80	-3.29	-2.60	-2.62	-2.57	-2.68	-2.57	0.00	-2.88	-2.77	0.00	0.00	0.00	-2.56	-2.74
TCGA-B5-A11Z-10A-01D-A10M-09_UCEC	-2.89	-2.80	-4.96	-3.25	-2.78	-2.84	-2.57	-2.56	-2.74	-3.54	-2.79	-2.76	0.00	-2.84	-3.11	0.00	-2.72
TCGA-B5-A121-10A-01D-A122-09_UCEC	-2.85	0.00	0.00	-2.87	-2.57	-2.52	-2.48	-2.58	-2.35	0.00	0.00	0.00	0.00	0.00	-3.14	-2.74	-2.65
TCGA-B5-A1MR-10A-01D-A14G-09_UCEC	-2.78	-2.56	-2.58	0.00	-2.86	-2.79	-2.57	-2.62	-2.51	0.00	-2.93	-2.74	0.00	0.00	-2.97	-2.94	-2.65
TCGA-B5-A1MS-10A-01D-A22A-09_UCEC	-2.68	-4.08	-4.26	-3.07	-2.50	-2.50	-2.54	-2.49	-2.43	0.00	0.00	0.00	0.00	0.00	-3.01	-2.80	-2.63
TCGA-B5-A1MU-10A-01D-A13O-09_UCEC	-3.05	-4.57	0.00	-2.87	-2.58	-2.54	-2.51	-2.53	-2.57	0.00	0.00	0.00	0.00	0.00	-3.00	-2.87	-2.70
TCGA-B5-A1MV-10A-01D-A14G-09_UCEC	-2.89	-2.80	-2.73	-3.42	-2.56	-2.60	-2.56	-2.54	-2.58	0.00	-2.93	-2.89	0.00	0.00	0.00	-2.56	-2.72
TCGA-B5-A1MW-10A-01D-A17D-09_UCEC	-2.79	0.00	-4.53	-3.03	-2.52	-2.56	-2.54	-2.62	-2.65	-3.42	-2.80	-4.23	-2.76	-2.72	0.00	-2.82	-2.65
TCGA-B5-A1MX-10A-01D-A142-09_UCEC	-2.70	0.00	-4.16	-2.76	-2.51	-2.53	-2.51	-2.48	-2.37	0.00	0.00	0.00	0.00	-4.46	-2.89	-2.69	-2.60
TCGA-B5-A1MY-10A-01D-A142-09_UCEC	-3.15	-3.00	-3.00	-3.20	-2.76	-2.74	-2.79	-2.84	0.00	-3.13	-2.64	-2.78	-2.75	-2.77	0.00	0.00	-2.78
TCGA-B5-A1MZ-10A-01D-A142-09_UCEC	-2.88	-2.72	-2.87	-3.43	-2.56	-2.56	-2.53	-2.52	-2.68	-3.31	-2.57	-2.78	-2.81	-2.74	0.00	-2.87	-2.62
TCGA-B5-A1N2-10A-01D-A142-09_UCEC	-2.73	-2.72	-4.12	-3.19	-2.79	-2.70	-2.60	-2.65	-2.69	0.00	-2.77	0.00	-2.78	-2.71	-3.14	0.00	-2.59
TCGA-B5-A3F9-10A-01D-A22A-09_UCEC	-2.84	0.00	-4.04	-2.88	-2.53	-2.53	-2.52	-2.48	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.59
TCGA-B5-A3FA-10A-01D-A19Y-09_UCEC	-2.83	-4.22	-3.92	-2.94	-2.48	-2.55	-2.51	-2.73	-2.59	-3.40	-2.99	-2.71	-4.52	-2.61	0.00	-3.03	-2.58
TCGA-B5-A3FB-10A-01D-A19Y-09_UCEC	-2.84	0.00	-2.77	-3.30	-2.58	-2.57	-2.56	-2.74	-2.46	0.00	-2.64	-2.77	-2.79	0.00	-2.88	-4.58	-2.69
TCGA-B5-A3FC-10A-01D-A22A-09_UCEC	-2.81	-4.63	-4.63	-3.07	-2.45	-2.61	-2.56	-2.55	-2.46	0.00	0.00	0.00	0.00	0.00	-2.80	-2.77	-2.65
TCGA-B5-A3FD-10A-01D-A19Y-09_UCEC	-2.80	-2.65	-4.44	-3.33	-2.65	-2.75	-2.63	-2.74	-2.55	0.00	-2.79	0.00	-2.65	-2.68	-2.86	0.00	-2.54
TCGA-B5-A3FH-10A-01D-A19Y-09_UCEC	-2.80	-2.67	-2.67	-3.15	-2.74	-2.66	-2.48	-2.61	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.55
TCGA-B5-A3S1-10A-01D-A22A-09_UCEC	-2.76	-2.82	-2.81	-3.21	-2.69	-2.75	-2.44	-2.60	-2.45	-4.03	0.00	-4.03	-4.33	-3.63	-2.91	-2.82	-2.65
TCGA-B5-A5OC-10A-01D-A27P-09_UCEC	-2.67	-2.74	-2.74	-3.22	-2.62	-2.64	-2.48	-2.51	-2.36	0.00	-2.77	0.00	-2.77	0.00	0.00	-2.67	-2.72
TCGA-B5-A5OD-10A-01D-A31U-09_UCEC	-2.77	0.00	0.00	-2.99	-2.40	-2.48	-2.43	-2.54	-2.33	0.00	0.00	0.00	0.00	0.00	-2.67	0.00	-2.46
TCGA-B5-A5OE-10A-01D-A31U-09_UCEC	-2.83	0.00	0.00	-2.91	-2.40	-2.54	-2.48	-2.44	-2.37	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.50
TCGA-B6-A0I1-10A-01D-A21Q-09_BRCA	-2.82	-2.76	-2.71	-3.21	-2.53	-2.60	-2.49	-2.57	-2.60	-3.31	-2.69	0.00	-2.49	-2.72	0.00	-4.39	-2.77
TCGA-B6-A0IH-10A-01D-A110-09_BRCA	-2.87	-4.09	-4.32	-2.87	-2.55	-2.51	-2.50	-2.57	-2.48	0.00	-4.79	-4.32	0.00	0.00	0.00	-2.62	-2.69
TCGA-B6-A0RH-10A-01D-A110-09_BRCA	-3.01	-2.76	-2.75	-3.13	-2.48	-2.65	-2.51	-2.69	-2.57	0.00	-2.88	-2.72	-4.39	-4.57	-3.28	-2.89	-2.72
TCGA-B6-A0RL-10A-01D-A099-09_BRCA	-2.92	-2.69	-2.73	-3.11	-2.77	-2.77	-2.56	-2.61	-2.70	-3.45	-2.64	0.00	-2.57	-2.80	-3.22	-4.77	-2.73
TCGA-B6-A0RM-10A-01D-A099-09_BRCA	-2.99	-2.86	-2.85	-3.16	-2.62	-2.74	-2.66	-2.62	-2.62	-4.84	-2.92	-2.90	0.00	0.00	0.00	-2.62	-2.81
TCGA-B6-A0RN-10A-01D-A099-09_BRCA	-2.84	-2.65	0.00	-2.98	-2.66	-2.68	-2.50	-2.56	-2.42	0.00	0.00	0.00	0.00	0.00	-2.99	-2.79	-2.65
TCGA-B6-A0RO-10A-01D-A099-09_BRCA	-3.00	0.00	0.00	-2.92	-2.59	-2.71	-2.61	-2.82	-2.85	-3.35	-3.02	-2.77	-4.65	-2.90	0.00	-3.03	-2.81
TCGA-B6-A0RP-10A-01D-A099-09_BRCA	-2.94	0.00	0.00	-2.93	-2.62	-2.66	-2.56	-2.83	-2.50	0.00	0.00	0.00	0.00	-4.67	0.00	-2.82	-2.82
TCGA-B6-A0RQ-10A-01D-A110-09_BRCA	-2.74	0.00	-4.81	-2.74	-2.58	-2.54	-2.53	-2.55	-2.70	-3.41	-2.73	0.00	-2.72	-2.72	0.00	-2.80	-2.73
TCGA-B6-A0RT-10A-01D-A099-09_BRCA	-2.85	0.00	0.00	-2.80	-2.55	-2.63	-2.54	-2.67	-2.70	-3.45	-2.76	-4.81	-2.70	-2.77	-3.18	0.00	-2.79
TCGA-B6-A0RU-10A-01D-A099-09_BRCA	-2.98	0.00	-4.77	-3.03	-2.71	-2.72	-2.70	-2.71	-2.84	-3.43	-2.98	-2.84	0.00	-2.82	0.00	-2.91	-2.84
TCGA-B6-A0RV-10A-01D-A099-09_BRCA	-2.86	0.00	0.00	-2.92	-2.59	-2.56	-2.52	-2.56	-2.53	0.00	0.00	0.00	0.00	-4.73	-3.05	-2.76	-2.73

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-B6-A0WS-10A-01D-A110-09_BRCA	-2.90	0.00	-4.69	-2.99	-2.59	-2.66	-2.60	-2.72	-2.60	0.00	0.00	0.00	0.00	0.00	-3.17	-3.01	-2.75
TCGA-B6-A0WT-10A-01D-A10G-09_BRCA	-2.99	0.00	0.00	-2.78	-2.53	-2.56	-2.53	-2.69	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.67	-2.77
TCGA-B6-A0WV-10A-01D-A10G-09_BRCA	-2.97	-2.82	-2.87	-3.11	-2.84	-2.81	-2.63	-2.60	-2.82	-3.49	-2.89	0.00	-2.80	-2.83	0.00	-2.84	-2.82
TCGA-B6-A0WW-10A-01D-A10G-09_BRCA	-2.91	0.00	-4.98	-3.04	-2.63	-2.67	-2.68	-2.62	-2.66	0.00	0.00	0.00	0.00	-4.68	-3.12	-2.85	-2.86
TCGA-B6-A0WX-10A-01D-A10G-09_BRCA	-2.98	-2.74	-2.77	-3.19	-2.56	-2.66	-2.62	-2.68	-2.54	0.00	-2.89	-4.39	-2.77	-4.57	0.00	-2.68	-2.72
TCGA-B6-A0WY-10A-01D-A10G-09_BRCA	-3.04	-2.74	-2.68	-3.06	-2.83	-2.83	-2.52	-2.82	-2.52	0.00	0.00	-4.47	0.00	0.00	-3.20	-4.17	-2.70
TCGA-B6-A0WZ-10A-01D-A10G-09_BRCA	-3.04	0.00	0.00	-2.82	-2.51	-2.55	-2.49	-2.81	-2.51	-4.56	0.00	0.00	0.00	0.00	-2.90	0.00	-2.68
TCGA-B6-A0X0-10A-01D-A110-09_BRCA	-2.79	-2.69	-2.65	-3.04	-2.68	-2.67	-2.65	-2.74	0.00	-3.37	-2.48	0.00	-2.55	-2.57	0.00	0.00	-2.70
TCGA-B6-A0X1-10A-01D-A117-09_BRCA	-3.05	-2.67	-2.65	0.00	-2.63	-2.62	-2.67	-2.76	-2.67	0.00	-2.81	-2.67	0.00	0.00	0.00	-2.69	-2.76
TCGA-B6-A0X4-10A-01D-A10G-09_BRCA	-3.12	0.00	0.00	-2.97	-2.68	-2.55	-2.59	-2.68	-2.49	0.00	0.00	0.00	0.00	0.00	-3.33	-2.98	-2.77
TCGA-B6-A0X5-10A-01D-A10G-09_BRCA	-3.07	-2.56	-2.56	0.00	-2.87	-2.85	-2.58	-2.88	-2.75	-3.27	-2.77	-2.83	-2.81	-2.89	0.00	0.00	-2.78
TCGA-B6-A0X7-10A-01D-A10M-09_BRCA	-2.96	-2.70	-2.71	0.00	-2.67	-2.69	-2.68	-2.79	-2.87	-3.54	-2.61	-2.66	-2.86	-2.83	0.00	-2.89	-2.75
TCGA-B6-A1KN-10A-01D-A188-09_BRCA	-3.00	-2.75	-2.89	-3.05	-2.81	-2.84	-2.54	-2.59	-2.51	0.00	0.00	0.00	0.00	-4.48	-3.27	-2.84	-2.62
TCGA-B6-A2IU-10A-01D-A18P-09_BRCA	-2.82	-2.62	-2.66	-3.05	-2.80	-2.72	-2.45	-2.45	-2.46	0.00	0.00	0.00	0.00	0.00	-3.18	-2.82	-2.53
TCGA-B6-A3ZX-10A-01D-A23C-09_BRCA	-2.71	-4.12	0.00	-3.02	-2.47	-2.46	-2.45	-2.47	-2.36	-4.42	-3.82	-4.12	-4.12	-3.82	-2.94	-2.87	-2.53
TCGA-B6-A400-10A-01D-A23C-09_BRCA	-2.76	-4.49	-4.49	-2.98	-2.56	-2.53	-2.54	-2.59	-2.45	0.00	-4.49	0.00	0.00	0.00	-2.76	-3.79	-2.59
TCGA-B6-A401-10A-01D-A23C-09_BRCA	-2.88	-2.76	-2.83	-3.24	-2.51	-2.62	-2.56	-2.63	-2.77	-3.47	-2.70	-2.88	-2.83	-2.80	-3.05	-4.58	-2.69
TCGA-B6-A402-10A-01D-A23C-09_BRCA	-2.84	-2.68	-2.73	-3.19	-2.53	-2.62	-2.59	-2.60	-2.52	0.00	-2.97	-2.87	-4.53	0.00	-3.10	-2.94	-2.64
TCGA-B6-A408-10A-01D-A243-09_BRCA	-2.70	-2.58	-2.74	-3.01	-2.62	-2.66	-2.45	-2.43	-2.36	0.00	-4.38	-4.38	0.00	-4.38	0.00	-2.86	-2.60
TCGA-B6-A409-10A-01D-A243-09_BRCA	-2.81	-4.44	-4.44	-3.26	-2.79	-2.55	-2.50	-2.62	-2.47	0.00	-3.02	-3.96	-2.79	-3.96	-2.87	-3.74	-2.65
TCGA-B6-A40B-10A-01D-A23C-09_BRCA	-2.82	-3.89	0.00	-2.97	-2.53	-2.51	-2.55	-2.49	-2.41	-4.19	-4.49	-3.79	0.00	0.00	0.00	-2.48	-2.54
TCGA-B6-A40C-10A-01D-A23C-09_BRCA	-2.77	-2.66	-2.67	-3.51	-2.66	-2.75	-2.43	-2.53	-2.33	0.00	-4.35	-4.35	-4.05	-4.35	0.00	-2.54	-2.59
TCGA-B7-5816-10A-01D-1600-08_STAD	-2.53	-2.73	-2.68	-2.88	-2.66	-2.64	-2.55	-2.55	-2.57	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.45
TCGA-B7-5818-10A-01D-1600-08_STAD	-2.60	-2.82	-2.78	-2.99	-2.46	-2.62	-2.66	-2.71	-2.52	0.00	-2.96	-2.73	0.00	0.00	0.00	-2.67	-2.61
TCGA-B7-A5TI-10A-01D-A31J-08_STAD	-2.58	-2.63	-2.60	0.00	-2.64	-2.71	-2.62	-2.55	-2.69	-3.30	-2.73	-2.68	0.00	-2.71	-3.11	0.00	-2.56
TCGA-B7-A5TJ-10A-01D-A31J-08_STAD	-2.62	-2.69	-2.68	-4.57	-2.68	-2.70	-2.68	-2.69	-2.68	-3.27	-2.71	-2.77	-2.80	-2.73	0.00	-2.82	-2.59
TCGA-B7-A5TK-10A-01D-A31J-08_STAD	-2.47	0.00	0.00	-2.55	-2.48	-2.52	-2.53	-2.62	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.48
TCGA-B7-A5TN-10A-01D-A31J-08_STAD	-2.64	-2.69	-2.71	-2.92	-2.49	-2.67	-2.65	-2.69	-2.52	0.00	-2.86	-2.72	0.00	0.00	0.00	-2.68	-2.59
TCGA-B8-4146-10A-01D-1669-08_KIRC	-2.59	-2.73	-2.72	-2.99	-2.48	-2.59	-2.59	-2.62	-2.47	0.00	-2.97	-2.73	0.00	-4.65	0.00	-2.66	-2.51
TCGA-B8-4148-10A-01D-1251-10_KIRC	-2.81	0.00	0.00	-2.75	-2.57	-2.48	-2.56	-2.70	-2.81	-3.27	-3.03	0.00	-2.73	-2.80	0.00	-2.89	-2.64
TCGA-B8-4151-10A-01D-1251-10_KIRC	-3.00	-2.58	-2.63	-3.06	-2.88	-2.74	-2.45	-2.63	-2.53	0.00	0.00	0.00	0.00	0.00	-3.31	-2.91	-2.63
TCGA-B8-4619-10A-01D-1251-10_KIRC	-2.96	-2.65	-2.65	-3.01	-2.77	-2.81	-2.57	-2.84	-2.51	0.00	0.00	0.00	0.00	-4.85	0.00	-2.76	-2.70
TCGA-B8-4620-10A-01D-1251-10_KIRC	-2.98	0.00	0.00	-2.81	-2.56	-2.57	-2.54	-2.66	-2.48	0.00	0.00	0.00	0.00	0.00	-3.32	-2.84	-2.66
TCGA-B8-4621-10A-01D-1501-10_KIRC	-2.95	-4.01	-4.48	-2.81	-2.59	-2.55	-2.52	-2.64	-2.48	-4.48	0.00	0.00	0.00	-4.78	-3.42	-2.83	-2.63
TCGA-B8-5158-10A-01D-1421-08_KIRC	-2.49	0.00	-4.66	-2.66	-2.49	-2.57	-2.55	-2.53	-2.63	0.00	0.00	0.00	-4.66	0.00	0.00	-2.45	-2.51
TCGA-B8-5159-10A-01D-1421-08_KIRC	-2.52	-2.82	-2.75	-2.98	-2.71	-2.73	-2.63	-2.70	-2.76	-3.43	-2.92	-2.72	0.00	-2.78	0.00	-2.78	-2.53
TCGA-B8-5162-10A-01D-1421-08_KIRC	-2.51	-2.76	-2.72	-2.98	-2.66	-2.67	-2.59	-2.58	-2.71	-3.37	-2.92	0.00	-2.72	-2.69	0.00	-2.76	-2.52
TCGA-B8-5163-10A-01D-1421-08_KIRC	-2.47	-2.61	-2.54	0.00	0.00	-4.57	-2.53	-2.50	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.47
TCGA-B8-5164-10A-01D-1421-08_KIRC	-2.54	-2.77	-2.76	-3.01	-2.68	-2.71	-2.65	-2.61	-2.72	-3.43	-3.02	0.00	-2.88	-2.74	0.00	-2.81	-2.51
TCGA-B8-5165-10A-01D-1421-08_KIRC	-2.52	0.00	-4.62	-2.67	-2.47	-2.49	-2.60	-2.62	-2.46	0.00	0.00	0.00	0.00	-4.14	0.00	-2.62	-2.52
TCGA-B8-5545-10A-01D-1669-08_KIRC	-2.49	-4.55	-4.55	-2.72	-2.55	-2.55	-2.55	-2.39	-2.43	0.00	0.00	0.00	0.00	0.00	-3.04	-2.70	-2.47
TCGA-B8-5546-10A-01D-1535-10_KIRC	-3.10	-2.68	-2.75	-3.15	-2.55	-2.69	-2.58	-2.73	-2.59	0.00	-3.10	-2.87	0.00	-4.83	0.00	-2.79	-2.78
TCGA-B8-5549-10A-01D-1535-10_KIRC	-3.11	0.00	-4.68	-2.77	-2.58	-2.58	-2.57	-2.90	-2.85	-3.05	-3.11	0.00	-2.79	-2.75	0.00	-3.01	-2.66
TCGA-B8-5550-10A-01D-1535-10_KIRC	-2.95	0.00	-4.75	-2.70	-2.54	-2.54	-2.56	-2.65	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.64	-2.61
TCGA-B8-5551-10A-01D-1535-10_KIRC	-2.91	0.00	0.00	-2.78	-2.56	-2.50	-2.50	-2.67	-2.49	0.00	0.00	0.00	0.00	-4.43	-3.18	0.00	-2.60
TCGA-B8-5552-10A-01D-1669-08_KIRC	-2.45	0.00	-4.60	-2.60	-2.58	-2.56	-2.56	-2.54	-2.64	-3.45	-2.92	0.00	-2.74	-2.67	-3.09	0.00	-2.41
TCGA-B8-5553-10A-01D-1535-10_KIRC	-2.94	0.00	-4.85	-2.71	-2.53	-2.53	-2.46	-2.73	-2.50	0.00	0.00	0.00	0.00	-4.37	-3.14	0.00	-2.59
TCGA-B8-A54D-10A-01D-A25V-10_KIRC	-2.37	-2.46	-2.49	-2.78	-2.53	-2.44	-2.29	-2.41	-2.32	0.00	0.00	0.00	0.00	0.00	-2.71	0.00	-2.33
TCGA-B8-A54E-10A-01D-A25V-10_KIRC	-2.43	-2.59	-2.56	-2.80	-2.35	-2.30	-2.34	-2.40	-2.35	0.00	-2.75	-2.58	0.00	0.00	-2.97	-2.63	-2.43
TCGA-B8-A54F-10A-01D-A25V-10_KIRC	-2.36	-2.40	-2.48	-2.74	-2.77	-2.41	-2.27	-2.27	-2.34	0.00	0.00	0.00	0.00	0.00	0.00	-2.26	-2.38
TCGA-B8-A54G-10A-01D-A25V-10_KIRC	-2.35	0.00	-2.47	-2.82	-2.63	-2.33	-2.24	-2.31	-2.28	0.00	0.00	0.00	0.00	0.00	-2.73	-2.47	-2.32
TCGA-B9-4114-10A-01D-1252-08_KIRP	-2.62	0.00	0.00	-2.78	-2.58	-2.58	-2.67	-2.66	-2.55	0.00	0.00	0.00	-4.73	-4.73	0.00	-2.60	-2.57
TCGA-B9-4115-10A-01D-1252-08_KIRP	-2.53	-3.67	-3.67	-2.69	-2.54	-2.56	-2.62	-2.58	-2.51	0.00	-3.71	-4.67	-3.67	-3.71	-2.96	-4.37	-2.54
TCGA-B9-4116-10A-01D-1252-08_KIRP	-2.64	-2.88	-2.82	-3.03	-2.57	-2.61	-2.73	-2.57	-2.57	0.00	-2.96	-4.76	-2.86	-4.76	-3.12	-2.77	-2.65
TCGA-B9-4117-10A-01D-1252-08_KIRP	-2.50	-2.72	-2.72	-2.88	-2.41	-2.53	-2.72	-2.77	-2.66	0.00	-2.71	0.00	-2.61	-2.66	-3.04	0.00	-2.50
TCGA-B9-4617-10A-01D-1252-08_KIRP	-2.59	0.00	0.00	-2.72	-2.44	-2.60	-2.61	-2.50	-2.52	0.00	0.00	0.00	-4.67	-4.36	-3.11	-2.78	-2.53
TCGA-B9-5155-10A-01D-1589-08_KIRP	-2.55	-2.66	-2.70	-2.84	-2.58	-2.68	-2.67	-2.75	-2.65	0.00	-2.82	-4.03	-2.67	-2.67	0.00	-2.67	-2.46
TCGA-B9-5156-10A-01D-1589-08_KIRP	-2.58	-2.62	-2.58	-4.09	-2.65	-2.68	-2.58	-2.59	-2.55	0.00	-2.91	-2.63	0.00	-4.09	-2.93	-4.27	-2.52
TCGA-B9-7268-10A-01D-2136-08_KIRP	-2.60	-2.82	-2.78	-2.90	-2.48	-2.61	-2.57	-2.52	-2.62	-3.34	-2.87	-2.70	0.00	0.00	-3.09	-2.76	-2.57
TCGA-B9-A44B-10A-01D-A25F-10_KIRP	-2.42	0.00	0.00	-2.67	-2.36	-2.29	-2.30	-2.37	-2.30	0.00	0.00	0.00	-4.32	-4.01	-2.87	-2.56	-2.26
TCGA-B9-A5W7-10A-01D-A31X-10_KIRP	-2.43	0.00	-2.85	-2.85	-2.63	-2.52	-2.42	-2.51	-2.62	-3.50	-2.67	0.00	-2.50	-2.65	-3.16	0.00	-2.40
TCGA-B9-A5W8-10A-01D-A28G-10_KIRP	-2.52	-2.35	-2.61	-4.39	-2.51	-2.34	-2.29	-2.41	-2.60	0.00	-2.54	-2.38	0.00	0.00	-2.85	-2.62	-2.49
TCGA-B9-A5W9-10A-01D-A28G-10_KIRP	-2.36	-3.81	0.00	-2.69	-2.36	-2.32	-2.27	-2.36	-2.30	0.00	0.00	0.00	0.00	0.00	-3.06	-2.50	-2.35
TCGA-B9-A69E-10A-01D-A31X-10_KIRP	-2.45	-2.62	-2.66	-2.76	-2.62	-2.51	-2.53	-2.51	-2.63	-3.66	-2.68	-2.79	-2.60	-2.76	0.00	-2.69	-2.42
TCGA-BA-4074-10A-01D-1434-08_HNSC	-2.54	-2.73	-2.67	-2.91	-2.62	-2.69	-2.60	-2.51	-2.49	0.00	-4.60	0.00	0.00	0.00	-3.05	-2.68	-2.57
TCGA-BA-4075-10A-01D-1434-08_HNSC	-2.54	0.00	0.00	-2.64	-2.57	-2.58	-2.58	-2.57	-2.54	-4.57	0.00	0.00	0.00	-4.26	-2.87	-4.57	-2.54
TCGA-BA-4076-10A-01D-1434-08_HNSC	-2.57	-2.69	-2.72	-4.66	-2.73	-2.73	-2.69	-2.67	-2.71	-3.41	-2.75	-2.62	0.00	-2.73	0.00	-2.75	-2.63
TCGA-BA-4077-10A-01D-1434-08_HNSC	-2.58	-2.81	-2.79	-2.99	-2.52	-2.63	-2.62	-2.61	-2.64	0.00	-2.97	-2.69	-4.63	-4.33	-3.00	-4.63	-2.63
TCGA-BA-4078-10A-01D-1434-08_HNSC	-2.45	0.00	0.00	-2.82	-2.54	-2.40	-2.57	-2.50	-2.51	0.00	0.00	-4.26	0.00	0.00	0.00	-2.44	-2.56
TCGA-BA-5149-10A-01D-1512-08_HNSC	-2.44	-2.75	-2.72	-2.99	-2.69	-2.77	-2.65	-2.47	-2.52	0.00	-4.65	-4.35	0.00	-4.35	-3.09	-2.73	-2.60
TCGA-BA-5151-10A-01D-1434-08_HNSC	-2.62	0.00	-4.64	-2.96	-2.61	-2.67	-2.71	-2.55	-2.72	-3.41	-2.91	0.00	-2.80	-2.71	0.00	-2.76	-2.53
TCGA-BA-5152-10A-01D-1870-08_HNSC	-2.55	-2.79	-2.71	-2.95	-2.74	-2.74	-2.64	-2.51	-2.76	-3.31	-2.78	0.00	-2.81	-2.73	0.00	-2.79	-2.51
TCGA-BA-5153-10A-01D-1434-08_HNSC	-2.56	-2.69	-2.68	-2.91	-2.67	-2.69	-2.60	-2.58	-2.60	0.00	0.00	0.00	0.00	-4.58	0.00	-2.59	-2.51
TCGA-BA-5555-10A-01D-1512-08_HNSC	-2.69	-2.85	-2.85	-3.08	-2.60	-2.71	-2.78	-2.77	-2.66	0.00	-3.06	-2.79	-4.71	-4.71	-3.04	-4.40	-2.74
TCGA-BA-5556-10A-01D-1512-08_HNSC	-2.64	-4.30	-4.60	-2.70	-2.63	-2.64	-2.67	-2.51	-2.64	0.00	0.00	0.00	0.00	-4.60	0.00	-2.46	-2.60
TCGA-BA-5557-10A-01D-1512-08_HNSC	-2.59	-4.58	-4.28	-2.87	-2.60	-2.63	-2.65	-2.52	-2.58	0.00	0.00	0.00	-4.58	0.00	-3.06	-2.76	-2.56
TCGA-BA-5558-10A-01D-1512-08_HNSC	-2.55	-4.54	-3.94	-2.61	-2.55	-2.57	-2.60	-2.57	-2.53	0.00	0.00	-4.54	-4.24	-3.84	0.00	-2.44	-2.49
TCGA-BA-5559-10A-01D-1512-08_HNSC	-2.49	-4.62	0.00	-2.90	-2.61	-2.64	-2.62	-2.54	-2.73	-3.41	-2.84	-4.62	-2.83	-2.72	0.00	-2.80	-2.56
TCGA-BA-6868-10A-01D-1912-08_HNSC	-2.64	-2.75	-2.77	-2.97	-2.54	-2.70	-2.68	-2.61	-2.72	-3.40	-2.73	-2.80	-2.81	-2.73	-3.13	-4.30	-2.55
TCGA-BA-6869-10A-01D-1870-08_HNSC	-2.51	-2.70	-2.74	-2.82	-2.70	-2.72	-2.54	-2.46	-2.47	0.00	0.00	0.00	0.00	0.00	-3.00	-2.74	-2.50
TCGA-BA-6870-10A-01D-1870-08_HNSC	-2.43	-4.22	0.00	-2.56	-2.50	-2.49	-2.55	-2.41	-2.51	0.00	-4.52	0.00	0.00	0.00	-2.94	0.00	-2.55
TCGA-BA-6871-10A-01D-1870-08_HNSC	-2.47	0.00	0.00	-2.68	-2.50	-2.59	-2.54	-2.59	-2.46	0.00	0.00	0.00	0.00	-4.55	0.00	-2.57	-2.46
TCGA-BA-6872-10A-01D-1870-08_HNSC	-2.40	-4.59	0.00	-2.73	-2.59	-2.53	-2.52	-2.48	-2.56	0.00	-4.59	-4.59	0.00	0.00	0.00	-2.61	-2.47
TCGA-BA-6873-10A-01D-1870-08_HNSC	-2.55	0.00	0.00	-2.74	-2.59	-2.58	-2.62	-2.63	-2.72	-3.32	-2.81	-4.62	-2.79	-2.68	0.00	-2.81	-2.50
TCGA-BA-7269-10A-01D-2013-08_HNSC	-2.64	0.00	0.00	-2.68	-2.61	-2.63	-2.64	-2.60	-2.73	-3.28	-2.87	0.00	-2.71	-2.70	0.00	-2.83	-2.62
TCGA-BA-A4IF-10A-01D-A25Y-08_HNSC	-2.67	-2.79	-2.73	-2.98	-2.57	-2.64	-2.68	-2.62	-2.60	-4.62	-2.79	-2.78	-4.32	-4.14	0.00	-2.51	-2.62
TCGA-BA-A4IG-10A-01D-A25Y-08_HNSC	-2.53	-4.18	-4.48	-2.59	-2.60	-2.55	-2.56	-2.49	-2.50	0.00	-4.18	-4.18	-4.48	-4.00	0.00	-2.45	-2.51
TCGA-BA-A4IH-10A-01D-A25Y-08_HNSC	-2.54	0.00	0.00	-2.80	-2.56	-2.54	-2.63	-2.53	-2.53	-4.50	-4.50	0.00	-4.02	-4.02	0.00	-2.46	-2.50
TCGA-BA-A4II-10A-01D-A25Y-08_HNSC	-2.46	-2.75	-2.73	-2.96	-2.53	-2.61	-2.62	-2.54	-2.57	0.00	-2.84	-2.82	-4.53	-4.23	-3.09	-2.71	-2.51
TCGA-BA-A6D8-10A-01D-A31J-08_HNSC	-2.49	0.00	0.00	-2.73	-2.52	-2.55	-2.54	-2.54	-2.52	0.00	0.00	0.00	0.00	0.00	-2.88	0.00	-2.50
TCGA-BA-A6DA-10A-01D-A31J-08_HNSC	-2.55	0.00	0.00	-2.56	-2.50	-2.52	-2.53	-2.45	-2.40	0.00	0.00	0.00	0.00	-4.13	0.00	-2.35	-2.45
TCGA-BA-A6DB-10A-01D-A30H-08_HNSC	-2.61	-2.76	-2.72	-2.90	-2.49	-2.61	-2.61	-2.55	-2.67	0.00	-2.94	-2.64	0.00	-4.64	0.00	-2.50	-2.50
TCGA-BA-A6DD-10A-01D-A31J-08_HNSC	-2.51	-2.79	-2.65	-2.83	-2.61	-2.67	-2.55	-2.50	-2.51	0.00	0.00	0.00	0.00	0.00	-3.10	-2.73	-2.48
TCGA-BA-A6DE-10A-01D-A31J-08_HNSC	-2.59	0.00	0.00	-2.77	-2.56	-2.55	-2.59	-2.59	-2.69	-3.41	-2.82	0.00	-2.71	-2.62	0.00	-2.73	-2.47
TCGA-BA-A6DF-10A-01D-A30H-08_HNSC	-2.46	0.00	-4.58	-2.60	-2.51	-2.51	-2.57	-2.61	-4.58	-3.14	-2.67	0.00	-2.62	-2.51	0.00	0.00	-2.46
TCGA-BA-A6DG-10A-01D-A30H-08_HNSC	-2.52	-2.74	-2.71	-2.88	-2.65	-2.74	-2.58	-2.54	-2.73	-3.39	-2.94	0.00	-2.79	-2.65	0.00	-2.72	-2.50

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BA-A6DI-10A-01D-A30H-08_HNSC	-2.51	-2.69	-2.64	-2.86	-2.68	-2.66	-2.57	-2.64	-2.64	-3.22	-2.79	0.00	-2.74	-2.67	0.00	-2.74	-2.47
TCGA-BA-A6DJ-10A-01D-A30H-08_HNSC	-2.54	-2.59	-2.51	0.00	-2.65	-2.65	-2.69	-2.71	-2.67	0.00	-2.60	-2.67	-2.74	-2.67	0.00	-2.81	-2.43
TCGA-BA-A6DL-10A-01D-A30H-08_HNSC	-2.49	0.00	0.00	-2.66	-2.44	-2.48	-2.48	-2.52	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.43
TCGA-BB-4217-10A-01D-2078-08_HNSC	-2.54	0.00	-3.84	-2.57	-2.55	-2.47	-2.59	-2.59	-2.55	-4.44	0.00	0.00	0.00	-4.44	-2.95	0.00	-2.51
TCGA-BB-4223-10A-01D-1434-08_HNSC	-2.65	-2.76	-2.77	-2.99	-2.74	-2.68	-2.61	-2.55	-2.58	-3.40	0.00	0.00	0.00	0.00	0.00	-2.64	-2.52
TCGA-BB-4224-10A-01D-1434-08_HNSC	-2.63	0.00	-4.65	-2.92	-2.65	-2.65	-2.69	-2.70	-2.76	-3.27	-2.93	0.00	-2.80	-2.73	0.00	-2.74	-2.60
TCGA-BB-4225-10A-01D-1434-08_HNSC	-2.52	-4.52	-4.22	-2.59	-2.51	-2.56	-2.58	-2.52	-2.71	-3.24	-2.95	-4.52	-2.76	-2.69	-3.03	-4.52	-2.44
TCGA-BB-4227-10A-01D-1870-08_HNSC	-2.48	-2.72	-2.70	-2.76	-2.66	-2.66	-2.53	-2.43	-2.48	0.00	0.00	-4.55	0.00	0.00	-3.03	-2.68	-2.43
TCGA-BB-4228-10A-01D-1434-08_HNSC	-2.61	-2.73	-2.70	-2.95	-2.68	-2.70	-2.60	-2.47	-2.60	-3.31	-4.61	0.00	0.00	-4.61	-2.99	-2.73	-2.62
TCGA-BB-7861-10A-01D-2229-08_HNSC	-2.46	0.00	0.00	-2.69	-2.42	-2.49	-2.46	-2.60	-2.37	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.41
TCGA-BB-7862-10A-01D-2229-08_HNSC	-2.57	-2.68	-2.78	-2.88	-2.51	-2.58	-2.54	-2.65	-2.46	0.00	-2.89	-2.71	0.00	0.00	0.00	-2.60	-2.45
TCGA-BB-7863-10A-01D-2229-08_HNSC	-2.62	-2.69	-2.71	0.00	-2.61	-2.55	-2.63	-2.58	-2.69	-3.29	-2.64	-2.59	-2.85	-2.68	-3.15	0.00	-2.50
TCGA-BB-7864-10A-01D-2229-08_HNSC	-2.53	0.00	0.00	-2.63	-2.47	-2.51	-2.50	-2.53	-2.75	-3.23	-2.93	0.00	-2.74	-2.62	0.00	-2.76	-2.48
TCGA-BB-7866-10A-01D-2229-08_HNSC	-2.50	0.00	0.00	-2.52	-2.45	-2.49	-2.50	-2.48	-2.41	0.00	0.00	0.00	0.00	-4.52	-2.97	-2.77	-2.41
TCGA-BB-7870-10A-01D-2229-08_HNSC	-2.48	0.00	-4.52	-2.62	-2.51	-2.51	-2.53	-2.48	-2.43	0.00	0.00	0.00	0.00	0.00	-3.06	-2.77	-2.44
TCGA-BB-7871-10A-01D-2229-08_HNSC	-2.44	-2.68	-2.63	-2.80	-2.66	-2.63	-2.51	-2.51	-2.47	0.00	0.00	0.00	0.00	-4.49	-3.07	-2.70	-2.40
TCGA-BB-7872-10A-01D-2229-08_HNSC	-2.40	-2.69	-2.68	-2.75	-2.54	-2.53	-2.66	-2.75	-2.59	0.00	-2.88	-4.42	-2.67	-2.55	0.00	-2.70	-2.38
TCGA-BB-8596-10A-01D-2394-08_HNSC	-2.51	-2.66	0.00	-2.83	-2.61	-2.64	-2.62	-2.64	-2.72	0.00	-2.74	0.00	-2.70	-2.70	0.00	-2.64	-2.47
TCGA-BB-8601-10A-01D-2394-08_HNSC	-2.62	-2.79	-2.70	-2.97	-2.51	-2.66	-2.63	-2.57	-2.54	0.00	-2.79	-2.72	0.00	0.00	-3.08	-2.78	-2.57
TCGA-BC-4073-10A-01D-A12Z-10_LIHC	-2.54	-2.75	-2.70	-2.96	-2.48	-2.46	-2.35	-2.60	-2.36	0.00	-3.10	-2.75	0.00	0.00	-3.40	0.00	-2.49
TCGA-BC-A217-10A-01D-A152-10_LIHC	-2.53	-2.61	-2.60	0.00	0.00	0.00	-2.56	-2.67	-2.66	-3.22	-2.75	0.00	-2.83	-2.79	0.00	-2.85	-2.49
TCGA-BC-A3KF-10A-01D-A20W-10_LIHC	-2.38	-2.61	-2.49	-2.85	-2.64	-2.61	-2.26	-2.41	-2.55	-3.27	-2.73	0.00	-2.65	-2.53	0.00	-2.63	-2.28
TCGA-BC-A3KG-10A-01D-A20W-10_LIHC	-2.61	0.00	0.00	-2.83	-2.64	-2.64	-2.53	-2.65	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.55
TCGA-BC-A5W4-10A-01D-A28X-10_LIHC	-2.37	0.00	0.00	-2.48	-2.37	-2.31	-2.29	-2.24	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.32	-2.41
TCGA-BC-A69H-10A-01D-A30V-10_LIHC	-2.48	-2.36	-2.35	-4.21	-4.21	-4.21	-2.37	-2.38	-2.55	-3.51	-2.90	0.00	-2.71	-2.60	-3.06	0.00	-2.39
TCGA-BC-A69I-10A-01D-A30V-10_LIHC	-2.49	-4.13	0.00	-2.64	-2.37	-2.36	-2.31	-2.37	-2.29	0.00	-4.13	0.00	0.00	0.00	-3.09	-2.60	-2.36
TCGA-BF-A1PU-10A-01D-A19A-08_SKCM	-2.53	-2.70	-2.75	-2.87	-2.68	-2.70	-2.61	-2.53	-2.63	-3.49	-2.86	0.00	-2.86	-2.66	0.00	-2.79	-2.51
TCGA-BF-A1PV-10A-01D-A19A-08_SKCM	-2.42	0.00	0.00	-2.50	-2.65	-2.69	-2.51	-2.58	-2.80	-3.42	-3.07	0.00	-3.07	-2.89	-3.18	-4.32	-2.39
TCGA-BF-A1PX-10A-01D-A19A-08_SKCM	-2.43	0.00	-4.40	-2.59	-2.52	-2.53	-2.54	-2.57	-2.86	-3.40	-3.08	0.00	-2.90	-2.72	0.00	-2.73	-2.40
TCGA-BF-A1PZ-10A-01D-A19A-08_SKCM	-2.49	-2.57	-2.51	-4.16	-2.81	-2.87	-2.66	-2.59	-2.63	0.00	-3.14	-2.93	0.00	-4.16	-3.28	-2.81	-2.41
TCGA-BF-A1Q0-10A-01D-A19A-08_SKCM	-2.46	-4.49	0.00	-2.68	-2.46	-2.52	-2.54	-2.40	-2.46	0.00	0.00	0.00	0.00	-4.49	0.00	-2.37	-2.40
TCGA-BF-A3DJ-10A-02D-A20D-08_SKCM	-2.57	-2.72	-2.74	-2.82	-2.44	-2.55	-2.64	-2.57	-2.53	0.00	-3.01	-2.73	0.00	0.00	-3.07	-2.73	-2.39
TCGA-BF-A3DL-10A-02D-A20D-08_SKCM	-2.48	-2.65	-2.63	-2.79	-2.58	-2.58	-2.52	-2.47	-2.49	0.00	0.00	-4.45	0.00	0.00	-3.00	-2.65	-2.40
TCGA-BF-A3DM-10A-02D-A20D-08_SKCM	-2.53	0.00	0.00	-2.58	-2.46	-2.49	-2.51	-2.47	-2.44	0.00	0.00	-4.41	0.00	-4.11	0.00	-2.47	-2.44
TCGA-BF-A3DN-10A-01D-A20D-08_SKCM	-2.59	-2.75	-2.71	-2.91	-2.44	-2.58	-2.63	-2.58	-2.56	0.00	-2.79	-2.69	0.00	0.00	0.00	-2.42	-2.47
TCGA-BF-A5EO-10A-01D-A27N-08_SKCM	-2.59	0.00	0.00	-2.67	-2.59	-2.63	-2.61	-2.58	-2.63	-3.47	-2.88	0.00	-2.71	-2.65	0.00	-2.79	-2.53
TCGA-BF-A5EP-10A-01D-A27N-08_SKCM	-2.54	0.00	-4.46	-2.73	-2.58	-2.55	-2.52	-2.50	-2.43	0.00	0.00	0.00	0.00	-4.16	0.00	-2.59	-2.49
TCGA-BF-A5EQ-10A-01D-A27N-08_SKCM	-2.53	0.00	0.00	-2.51	-2.48	-2.53	-2.52	-2.58	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.49
TCGA-BF-A5ER-10A-01D-A27N-08_SKCM	-2.45	-2.62	-2.63	0.00	-2.65	-2.68	-2.60	-2.65	-2.64	0.00	-2.79	-2.68	0.00	0.00	0.00	-2.64	-2.56
TCGA-BF-A5ES-10A-01D-A27N-08_SKCM	-2.51	-4.44	-4.44	-2.77	-2.53	-2.56	-2.54	-2.48	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.46
TCGA-BG-A0M0-10A-01D-A10B-09_UCEC	-2.99	-2.84	-2.81	-3.20	-2.65	-2.79	-2.76	-2.72	0.00	-3.44	-2.64	-2.69	-2.85	-2.73	0.00	0.00	-2.90
TCGA-BG-A0M3-10A-01D-A127-09_UCEC	-2.85	0.00	0.00	-2.66	-2.49	-2.64	-2.65	-2.88	-2.61	0.00	0.00	0.00	0.00	-2.69	0.00	-2.86	-2.79
TCGA-BG-A0M8-10A-01D-A10O-09_UCEC	-2.89	0.00	0.00	-2.77	-2.65	-2.60	-2.53	-2.46	-2.39	0.00	0.00	0.00	0.00	0.00	-3.04	-2.76	-2.74
TCGA-BG-A0M9-10A-01D-A10B-09_UCEC	-3.02	-2.75	-2.74	-3.07	-2.53	-2.70	-2.66	-2.75	-2.64	0.00	-2.90	-2.78	-4.70	0.00	0.00	-2.64	-2.76
TCGA-BG-A0MG-10A-01D-A10B-09_UCEC	-2.90	-2.74	-2.80	-3.03	-2.77	-2.79	-2.60	-2.68	-2.62	0.00	0.00	0.00	0.00	0.00	-3.13	-2.83	-2.74
TCGA-BG-A0MK-10A-01D-A19Y-09_UCEC	-2.73	0.00	0.00	-2.97	-2.41	-2.47	-2.50	-2.43	-2.38	0.00	0.00	0.00	0.00	0.00	-2.91	0.00	-2.63
TCGA-BG-A0MQ-10A-02D-A10B-09_UCEC	-2.85	0.00	0.00	-3.05	-2.59	-2.61	-2.54	-2.70	-2.71	-3.41	-2.84	0.00	-2.68	-2.75	0.00	-2.85	-2.71
TCGA-BG-A0MU-10A-02D-A10B-09_UCEC	-2.92	0.00	-4.69	-2.87	-2.56	-2.55	-2.51	-2.60	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.62	-2.67
TCGA-BG-A0RY-10A-02D-A10B-09_UCEC	-2.83	-2.56	-2.58	0.00	0.00	0.00	-2.57	-2.54	-2.54	0.00	0.00	0.00	0.00	0.00	-2.97	-2.77	-2.68
TCGA-BG-A0VV-10A-01D-A122-09_UCEC	-2.94	-2.87	-2.87	-3.22	-2.57	-2.67	-2.69	-2.61	-2.59	0.00	-2.91	-2.83	0.00	0.00	-3.19	-2.84	-2.81
TCGA-BG-A0VW-10A-01D-A122-09_UCEC	-2.93	-2.79	-2.82	-3.20	-2.59	-2.70	-2.70	-2.69	-2.69	0.00	-2.94	-2.83	0.00	0.00	0.00	-2.77	-2.86
TCGA-BG-A0VX-10A-01D-A122-09_UCEC	-2.91	0.00	-4.83	-2.80	-2.63	-2.66	-2.62	-2.70	-2.59	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.71
TCGA-BG-A0VZ-10A-02D-A117-09_UCEC	-3.08	-2.86	-2.92	-3.17	-2.68	-2.78	-2.62	-2.73	-2.69	-3.29	-3.25	-2.90	0.00	0.00	0.00	-2.88	-2.83
TCGA-BG-A0W1-10A-01D-A117-09_UCEC	-2.98	-2.89	-2.87	-3.28	-2.88	-2.87	-2.69	-2.70	-2.88	-3.59	-2.86	0.00	-2.87	-2.86	0.00	-2.87	-2.86
TCGA-BG-A0YU-10A-01D-A10M-09_UCEC	-2.99	-4.55	0.00	-2.89	-2.73	-2.72	-2.64	-2.73	0.00	-3.44	-2.71	-2.82	-2.82	-2.72	0.00	0.00	-2.83
TCGA-BG-A0YV-10A-01D-A10M-09_UCEC	-2.85	-2.70	-2.73	-3.04	-2.74	-2.74	-2.72	-2.81	-2.74	0.00	-2.86	0.00	-2.74	-2.74	0.00	-2.76	-2.69
TCGA-BG-A186-10A-01D-A12J-09_UCEC	-2.84	-2.66	-2.52	-4.73	0.00	-4.73	-2.47	-2.56	-2.43	-4.73	-4.73	-4.73	0.00	0.00	-2.79	-4.73	-2.64
TCGA-BG-A187-10A-01D-A12J-09_UCEC	-2.98	0.00	0.00	-2.86	-2.52	-2.63	-2.54	-2.63	-2.86	-3.37	-2.69	-2.90	-2.85	-2.84	-3.26	0.00	-2.84
TCGA-BG-A18A-10A-01D-A12J-09_UCEC	-2.91	0.00	0.00	-2.94	-2.62	-2.57	-2.57	-2.54	-2.72	-3.39	-2.77	-2.71	-4.84	-2.76	0.00	-2.81	-2.70
TCGA-BG-A18B-10A-01D-A12J-09_UCEC	-2.97	0.00	-4.87	-3.01	-2.64	-2.64	-2.58	-2.70	-2.70	-3.42	-2.83	-4.87	-2.77	-2.83	0.00	-2.79	-2.78
TCGA-BG-A18C-10A-01D-A12J-09_UCEC	-2.87	-2.77	-2.79	-3.10	-2.74	-2.73	-2.60	-2.58	-2.52	-4.87	0.00	0.00	0.00	-4.87	-2.88	0.00	-2.74
TCGA-BG-A220-10A-01D-A159-09_UCEC	-2.66	0.00	0.00	-3.02	-2.38	-2.41	-2.46	-2.50	-2.46	0.00	0.00	0.00	0.00	0.00	-2.95	-2.77	-2.53
TCGA-BG-A221-10A-01D-A159-09_UCEC	-2.74	-2.65	-2.68	-3.23	-2.66	-2.65	-2.51	-2.53	-2.60	-3.46	-2.71	-4.16	-2.69	-2.73	-3.01	0.00	-2.65
TCGA-BG-A222-10A-01D-A159-09_UCEC	-2.69	-4.44	-4.44	-2.90	-2.53	-2.50	-2.44	-2.53	-2.46	0.00	-4.44	-4.14	0.00	-4.44	0.00	-2.40	-2.60
TCGA-BG-A2AE-10A-01D-A16D-09_UCEC	-2.97	-2.77	-2.84	-3.13	-2.86	-2.78	-2.57	-2.69	-2.76	-3.29	-2.94	0.00	-2.80	-2.82	0.00	-2.89	-2.75
TCGA-BG-A2L7-10A-01D-A18P-09_UCEC	-2.86	-2.62	-2.63	0.00	-2.68	-2.64	-2.60	-2.65	-2.52	0.00	-2.74	-2.68	-3.82	-4.29	-2.89	-4.59	-2.65
TCGA-BG-A3PP-10A-01D-A22A-09_UCEC	-2.82	-2.79	-2.73	-3.30	-2.48	-2.58	-2.57	-2.55	-2.46	0.00	-2.98	-2.79	0.00	-4.53	0.00	-2.54	-2.65
TCGA-BH-A0AV-10A-01D-A110-09_BRCA	-2.95	-2.75	-2.61	-4.85	-2.77	-2.78	-2.59	-2.58	-2.46	0.00	-2.84	0.00	-2.78	0.00	-3.17	-2.90	-2.70
TCGA-BH-A0B0-10A-01D-A110-09_BRCA	-2.95	-2.62	-2.73	-3.05	-2.71	-2.74	-2.67	-2.82	-2.65	0.00	-2.81	-4.77	-2.74	-2.73	0.00	-2.75	-2.66
TCGA-BH-A0B6-10A-01D-A19Y-09_BRCA	-2.77	-2.71	-2.93	-3.21	-2.76	-2.83	-2.52	-2.43	-2.67	-3.45	-2.95	0.00	-2.81	-2.77	0.00	-2.88	-2.53
TCGA-BH-A0B7-10A-01D-A110-09_BRCA	-2.95	0.00	-4.99	-2.91	-2.73	-2.81	-2.77	-2.66	-2.69	0.00	0.00	-4.69	0.00	-4.99	0.00	-2.61	-2.97
TCGA-BH-A0BC-10A-01D-A099-09_BRCA	-2.86	-2.68	-2.64	-3.05	-2.65	-2.68	-2.51	-2.59	-2.50	0.00	0.00	0.00	0.00	0.00	-2.97	-2.77	-2.72
TCGA-BH-A0BG-10A-01D-A110-09_BRCA	-2.71	-3.40	-3.54	-2.66	-3.44	-2.49	-2.41	-2.47	-2.49	0.00	-3.74	0.00	-4.14	-3.74	0.00	-2.72	-2.55
TCGA-BH-A0BL-10A-01D-A110-09_BRCA	-2.85	-2.85	-2.83	-3.18	-2.84	-2.83	-2.66	-2.57	-2.83	-3.58	-2.81	0.00	-2.82	-2.84	0.00	-2.86	-2.83
TCGA-BH-A0BO-10A-01D-A12B-09_BRCA	-3.01	-2.88	-2.88	-3.31	-2.59	-2.70	-2.64	-2.74	-2.64	0.00	-3.05	-2.82	0.00	-5.11	-3.20	-2.96	-2.84
TCGA-BH-A0BP-10A-01D-A110-09_BRCA	-2.94	-2.84	-2.84	-3.21	-2.57	-2.58	-2.59	-2.59	-2.59	0.00	-2.84	-2.75	0.00	0.00	-3.14	-2.77	-2.77
TCGA-BH-A0BQ-10A-01D-A110-09_BRCA	-2.95	-2.78	-2.66	-3.09	-2.74	-2.81	-2.59	-2.52	-2.73	-3.40	-2.70	-4.78	-2.67	-2.80	0.00	-2.83	-2.74
TCGA-BH-A0BR-10A-01D-A110-09_BRCA	-2.84	-4.66	0.00	-2.92	-2.56	-2.57	-2.54	-2.61	-2.53	0.00	-4.36	0.00	-4.66	-4.66	0.00	-2.57	-2.72
TCGA-BH-A0BW-10A-01D-A110-09_BRCA	-2.98	-3.99	-4.10	-2.80	-2.50	-2.62	-2.58	-2.74	-2.55	0.00	-4.94	-3.99	0.00	0.00	-3.28	-3.03	-2.76
TCGA-BH-A0C1-10A-01D-A12B-09_BRCA	-2.98	-2.82	-2.85	-3.20	-2.83	-2.80	-2.69	-2.77	-2.82	-3.47	-2.89	0.00	-2.83	-2.84	0.00	-2.90	-2.78
TCGA-BH-A0C7-10A-01D-A110-09_BRCA	-3.07	-2.85	-2.84	-3.32	-2.61	-2.68	-2.70	-2.80	-2.90	-3.49	-2.87	-2.70	0.00	-2.84	-3.21	0.00	-2.86
TCGA-BH-A0DE-10A-02D-A110-09_BRCA	-2.90	0.00	0.00	-2.81	-2.59	-2.64	-2.60	-2.74	-2.55	0.00	-4.64	0.00	0.00	0.00	0.00	-2.73	-2.71
TCGA-BH-A0DH-10A-01D-A099-09_BRCA	-2.95	-2.71	-2.72	-3.09	-2.75	-2.79	-2.57	-2.52	-2.63	0.00	0.00	0.00	0.00	0.00	-3.02	-2.80	-2.77
TCGA-BH-A0DL-10A-01D-A110-09_BRCA	-2.90	-2.70	-2.70	-3.14	-2.68	-2.71	-2.51	-2.58	-2.75	-3.40	-2.75	-4.86	-2.75	-2.71	-3.07	0.00	-2.72
TCGA-BH-A0DQ-10A-01D-A099-09_BRCA	-2.89	-2.78	-2.71	-2.98	-2.77	-2.80	-2.59	-2.69	-2.61	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.70
TCGA-BH-A0DX-10A-02D-A110-09_BRCA	-2.89	-2.77	-2.77	-3.19	-2.49	-2.54	-2.57	-2.72	-2.57	0.00	-2.84	-2.72	-4.95	0.00	0.00	-2.57	-2.78
TCGA-BH-A0E9-10A-01D-A110-09_BRCA	-2.79	0.00	0.00	-3.02	-2.57	-2.53	-2.46	-2.66	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.66
TCGA-BH-A0EA-10A-01D-A110-09_BRCA	-2.99	-2.74	-2.72	-3.14	-2.54	-2.62	-2.59	-2.70	-2.59	-4.98	-2.86	-2.76	0.00	-4.67	-2.95	-4.20	-2.71
TCGA-BH-A0EI-10A-01D-A110-09_BRCA	-2.86	0.00	0.00	-2.89	-2.56	-2.58	-2.54	-2.44	-2.42	0.00	0.00	0.00	0.00	0.00	-3.03	-2.74	-2.63
TCGA-BH-A0H5-10A-01D-A110-09_BRCA	-2.86	-3.32	-3.30	-2.78	-2.54	-2.56	-2.43	-2.62	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.62	-2.61
TCGA-BH-A0HI-10A-01D-A099-09_BRCA	-3.11	-2.87	-2.82	-3.24	-2.59	-2.73	-2.65	-2.73	-2.86	-3.47	-2.69	-2.81	-2.86	-2.89	0.00	-2.92	-2.87
TCGA-BH-A0HN-10A-01D-A099-09_BRCA	-2.90	0.00	0.00	-2.82	-2.66	-2.67	-2.60	-2.62	-2.72	-3.43	-2.87	0.00	-2.69	-2.77	-3.06	0.00	-2.74
TCGA-BH-A0HP-10A-01D-A099-09_BRCA	-2.97	0.00	0.00	-2.82	-2.70	-2.69	-2.69	-2.62	-2.60	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.85
TCGA-BH-A0RX-10A-01D-A099-09_BRCA	-2.99	-2.78	-2.82	-3.15	-2.87	-2.79	-2.58	-2.63	-2.76	-3.38	-2.81	-4.70	-2.75	-2.80	0.00	-2.94	-2.74
TCGA-BH-A0W4-10A-01D-A10G-09_BRCA	-3.12	-2.78	-2.72	-3.27	-2.67	-2.73	-2.60	-2.88	-2.86	-3.29	-2.92	-2.89	-2.84	-2.85	0.00	-3.12	-2.77
TCGA-BH-A0W5-10A-01D-A117-09_BRCA	-2.84	0.00	0.00	-2.97	-2.63	-2.65	-2.58	-2.60	-2.71	-3.42	-2.73	0.00	-2.71	-2.76	0.00	-2.79	-2.73

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BH-A0W7-10A-01D-A110-09_BRCA	-2.98	-2.76	-2.77	-3.26	-2.51	-2.66	-2.59	-2.68	-2.62	0.00	-3.01	-2.77	0.00	0.00	-3.30	-2.92	-2.80
TCGA-BH-A0WA-10A-01D-A117-09_BRCA	-2.89	-2.70	-2.70	-3.09	-2.74	-2.73	-2.64	-2.67	-2.72	-3.43	-2.83	0.00	-2.73	-2.74	0.00	-2.75	-2.77
TCGA-BH-A18G-10A-01D-A12B-09_BRCA	-3.07	-2.77	-2.78	-5.13	-2.73	-2.74	-2.72	-2.74	-2.90	-3.60	-2.67	-2.62	-5.13	-2.92	0.00	-3.00	-2.87
TCGA-BH-A18H-10A-01D-A12B-09_BRCA	-2.97	-2.84	-2.84	-3.22	-2.60	-2.77	-2.68	-2.69	-2.73	0.00	-2.97	-2.88	0.00	0.00	-3.18	-2.95	-2.88
TCGA-BH-A18I-10A-01D-A12B-09_BRCA	-2.98	-4.82	0.00	-2.86	-2.51	-2.64	-2.57	-2.64	-2.75	-3.50	-2.84	-2.81	0.00	-2.75	0.00	-2.87	-2.73
TCGA-BH-A201-10A-01D-A14K-09_BRCA	-3.04	-2.85	-2.74	-3.14	-2.83	-2.85	-2.62	-2.75	-2.89	-3.35	-2.76	0.00	-2.71	-2.80	0.00	-2.95	-2.89
TCGA-BH-A202-10A-01D-A14K-09_BRCA	-2.87	0.00	-4.42	-2.77	-2.57	-2.58	-2.54	-2.57	-2.58	0.00	0.00	0.00	0.00	-4.72	0.00	-2.46	-2.78
TCGA-BH-A28O-10A-01D-A22A-09_BRCA	-2.91	-3.89	-4.11	-3.22	-2.54	-2.59	-2.55	-2.51	-2.60	-3.63	-3.04	-2.92	-4.59	-4.59	0.00	-2.65	-2.73
TCGA-BH-A28Q-10A-01D-A16D-09_BRCA	-2.90	0.00	0.00	-2.91	-2.57	-2.62	-2.62	-2.72	-2.64	-4.66	0.00	-4.66	0.00	0.00	0.00	-2.72	-2.66
TCGA-BH-A2L8-10A-01D-A18P-09_BRCA	-2.88	-4.26	0.00	-2.78	-2.54	-2.60	-2.57	-2.59	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.71
TCGA-BH-A42T-10A-01D-A243-09_BRCA	-2.85	-2.80	-2.95	-3.39	-2.48	-2.57	-2.58	-2.58	-2.50	0.00	-2.95	-2.81	0.00	0.00	-2.85	-4.39	-2.68
TCGA-BH-A42U-10A-01D-A243-09_BRCA	-2.72	-3.96	-3.96	-2.98	-2.40	-2.46	-2.53	-2.49	-2.36	-4.44	-3.84	0.00	-4.44	-4.44	-2.83	-2.82	-2.55
TCGA-BH-A42V-10A-01D-A243-09_BRCA	-2.72	-3.84	-3.84	-3.03	-2.55	-2.48	-2.47	-2.54	-2.36	0.00	-4.01	-3.71	0.00	-3.84	-3.06	-2.79	-2.54
TCGA-BH-A5IZ-10A-01D-A27P-09_BRCA	-2.83	-2.67	-2.73	-3.31	-2.49	-2.71	-2.53	-2.60	-2.39	0.00	-2.95	-2.68	-4.42	0.00	-3.10	-2.78	-2.59
TCGA-BH-A5J0-10A-01D-A27P-09_BRCA	-2.72	-2.71	-2.80	-3.32	-2.68	-2.46	-2.59	-2.57	-2.52	0.00	-4.47	-3.99	0.00	-4.47	-2.79	-4.17	-2.61
TCGA-BI-A0VR-10A-01D-A10S-08_CESC	-2.57	0.00	0.00	-2.62	-2.56	-2.61	-2.61	-2.47	-2.58	0.00	-4.53	0.00	0.00	-4.53	-3.04	-2.73	-2.50
TCGA-BI-A0VS-10A-01D-A10S-08_CESC	-2.59	-2.77	-2.80	-3.01	-2.52	-2.65	-2.68	-2.63	-2.59	0.00	-2.99	-2.73	0.00	-4.63	0.00	-2.52	-2.57
TCGA-BI-A20A-10A-01D-A14W-08_CESC	-2.51	0.00	0.00	-2.67	-2.52	-2.49	-2.50	-2.41	-2.48	0.00	-4.46	-4.16	0.00	-4.16	-3.06	-2.75	-2.41
TCGA-BJ-A0YZ-10A-01D-A10S-08_THCA	-2.55	0.00	-4.59	-2.67	-2.57	-2.59	-2.63	-2.51	-2.65	0.00	0.00	0.00	-4.29	-4.29	0.00	-2.42	-2.51
TCGA-BJ-A0Z0-10A-01D-A10S-08_THCA	-2.68	-2.82	-2.81	-3.02	-2.54	-2.69	-2.74	-2.67	-2.76	-3.41	-2.80	-2.78	-2.84	-2.76	0.00	-2.78	-2.60
TCGA-BJ-A0Z2-10A-01D-A10S-08_THCA	-2.43	0.00	0.00	-2.67	-2.61	-2.62	-2.65	-2.50	-2.54	0.00	0.00	0.00	-4.57	-4.57	-3.03	-2.67	-2.52
TCGA-BJ-A0Z3-10A-01D-A13W-08_THCA	-2.56	-2.72	-2.74	-2.95	-2.46	-2.53	-2.64	-2.57	-2.74	-3.36	-2.79	-2.53	0.00	-2.69	0.00	-2.86	-2.44
TCGA-BJ-A0Z9-10A-01D-A10S-08_THCA	-2.65	-2.82	-2.78	-3.03	-2.55	-2.70	-2.68	-2.60	-2.68	0.00	-2.90	-2.78	-4.65	-4.65	0.00	-2.50	-2.58
TCGA-BJ-A0ZA-10A-02D-A10S-08_THCA	-2.48	0.00	-4.62	-2.90	-2.62	-2.62	-2.71	-2.67	-2.73	-3.51	-2.96	-4.14	-2.77	-2.72	0.00	-2.76	-2.57
TCGA-BJ-A0ZB-10A-01D-A10S-08_THCA	-2.57	-2.72	-2.69	-2.95	-2.69	-2.69	-2.78	-2.79	-2.66	0.00	-2.81	0.00	-2.74	-2.69	0.00	-2.76	-2.58
TCGA-BJ-A0ZC-10A-01D-A13W-08_THCA	-2.47	-4.41	-4.23	-2.72	-2.42	-2.48	-2.48	-2.55	-2.42	0.00	-4.71	-4.71	-4.71	0.00	-3.03	-2.77	-2.36
TCGA-BJ-A0ZE-10A-01D-A10S-08_THCA	-2.56	0.00	-4.27	-2.69	-2.56	-2.62	-2.57	-2.60	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.55
TCGA-BJ-A0ZF-10A-01D-A10S-08_THCA	-2.52	-2.56	-2.55	0.00	-4.21	0.00	-2.57	-2.46	-2.53	0.00	0.00	-4.51	0.00	-4.51	-3.00	-2.62	-2.49
TCGA-BJ-A0ZG-10A-01D-A10S-08_THCA	-2.57	0.00	-4.16	-2.72	-2.63	-2.69	-2.67	-2.68	-2.72	-3.36	-2.90	0.00	-2.82	-2.74	0.00	-2.73	-2.53
TCGA-BJ-A0ZH-10A-01D-A10S-08_THCA	-2.60	0.00	-4.61	-2.74	-2.50	-2.62	-2.69	-2.52	-2.76	-3.38	-2.92	0.00	-2.82	-2.73	0.00	-2.71	-2.58
TCGA-BJ-A0ZJ-10A-01D-A10S-08_THCA	-2.48	-4.62	0.00	-2.84	-2.65	-2.66	-2.67	-2.51	-2.72	-3.32	-2.88	0.00	-2.75	-2.77	0.00	-2.76	-2.53
TCGA-BJ-A18Y-10A-01D-A13W-08_THCA	-2.43	-2.67	-2.61	-2.88	-2.64	-2.64	-2.51	-2.51	-2.36	0.00	0.00	0.00	0.00	-4.66	-3.03	-2.76	-2.36
TCGA-BJ-A18Z-10A-01D-A13W-08_THCA	-2.45	-2.67	-2.68	-2.84	-2.57	-2.62	-2.62	-2.69	-2.60	0.00	-2.97	0.00	-2.67	-2.56	0.00	-2.68	-2.29
TCGA-BJ-A190-10A-01D-A13W-08_THCA	-2.38	-2.69	-2.66	-2.84	-2.67	-2.68	-2.44	-2.50	-2.44	0.00	-4.68	0.00	0.00	-4.20	-3.13	-2.77	-2.36
TCGA-BJ-A191-10A-01D-A13W-08_THCA	-2.50	-2.65	-2.60	0.00	-2.51	-2.53	-2.61	-2.70	-4.51	-3.22	-2.63	-2.47	-2.89	-2.53	0.00	-4.34	-2.47
TCGA-BJ-A192-10A-01D-A13W-08_THCA	-2.42	0.00	-4.64	-2.60	-2.43	-2.47	-2.51	-2.52	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.36
TCGA-BJ-A28R-10A-01D-A16O-08_THCA	-2.57	0.00	-4.62	-2.83	-2.68	-2.62	-2.60	-2.52	-2.76	-3.30	-2.82	0.00	-2.79	-2.69	0.00	-2.76	-2.52
TCGA-BJ-A28S-10A-01D-A19M-08_THCA	-2.55	-2.68	-2.70	-2.84	-2.64	-2.71	-2.56	-2.61	0.00	-3.27	-2.64	-4.47	-2.63	-2.48	0.00	0.00	-2.47
TCGA-BJ-A28T-10A-01D-A16O-08_THCA	-2.50	-2.66	-2.66	-2.80	-2.65	-2.71	-2.58	-2.41	-2.45	0.00	0.00	0.00	0.00	0.00	-3.04	-2.67	-2.48
TCGA-BJ-A28V-10A-01D-A19M-08_THCA	-2.64	-2.89	-2.79	-2.98	-2.46	-2.55	-2.55	-2.48	-2.58	-3.55	-2.83	-2.67	0.00	-4.66	-3.23	-2.93	-2.59
TCGA-BJ-A28W-10A-01D-A17V-08_THCA	-2.62	-2.82	-2.80	-2.90	-2.54	-2.67	-2.66	-2.59	-2.71	-3.42	-2.72	-2.73	-2.83	-2.76	0.00	-2.75	-2.64
TCGA-BJ-A28X-10A-01D-A22D-08_THCA	-2.56	-2.66	-2.65	0.00	-2.63	-2.67	-2.59	-2.47	-2.63	-3.47	-2.87	-2.70	0.00	0.00	0.00	-2.40	-2.56
TCGA-BJ-A28Z-10A-01D-A16O-08_THCA	-2.65	-2.80	-2.77	-2.94	-2.57	-2.70	-2.72	-2.58	-2.80	-3.42	-2.78	-2.81	-2.84	-2.80	0.00	-2.82	-2.70
TCGA-BJ-A290-10A-01D-A17V-08_THCA	-2.58	-2.64	-2.59	-4.10	-2.69	-2.77	-2.68	-2.60	-2.75	-3.46	-2.67	-2.78	-2.78	-2.67	0.00	-2.82	-2.55
TCGA-BJ-A2N7-10A-01D-A18F-08_THCA	-2.49	0.00	0.00	-2.73	-2.55	-2.49	-2.54	-2.47	-2.43	0.00	0.00	0.00	0.00	-4.47	0.00	-2.44	-2.44
TCGA-BJ-A2N8-10A-01D-A18F-08_THCA	-2.59	0.00	0.00	-2.58	-2.56	-2.61	-2.62	-2.51	-2.69	-3.28	-2.89	0.00	-2.76	-2.69	-3.15	0.00	-2.48
TCGA-BJ-A2N9-10A-01D-A18F-08_THCA	-2.47	-2.70	-2.62	-2.87	-2.65	-2.65	-2.53	-2.57	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.45
TCGA-BJ-A2NA-10A-01D-A19M-08_THCA	-2.61	-2.66	-2.65	-3.76	-2.55	-2.63	-2.54	-2.63	-2.85	-3.30	-2.71	-2.65	-2.88	-2.74	0.00	-2.86	-2.54
TCGA-BJ-A2P4-10A-01D-A18F-08_THCA	-2.56	0.00	0.00	-2.62	-2.58	-2.56	-2.65	-2.60	-2.65	-3.55	-2.91	0.00	-2.72	-2.71	0.00	-2.77	-2.52
TCGA-BJ-A3EZ-10A-01D-A202-08_THCA	-2.56	0.00	0.00	-2.60	-2.55	-2.60	-2.66	-2.47	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.50
TCGA-BJ-A3F0-10A-01D-A202-08_THCA	-2.52	-2.67	-2.60	-2.75	-2.59	-2.68	-2.53	-2.45	-2.42	0.00	0.00	0.00	0.00	-4.43	-2.91	-2.68	-2.45
TCGA-BJ-A3PR-10A-01D-A21Z-08_THCA	-2.39	-2.69	-2.67	-2.75	-2.60	-2.63	-2.55	-2.51	-2.51	0.00	-4.49	0.00	0.00	0.00	-3.06	-2.69	-2.46
TCGA-BJ-A3PT-10A-01D-A21Z-08_THCA	-2.50	-2.66	-2.64	-2.78	-2.60	-2.61	-2.51	-2.49	-2.50	0.00	0.00	0.00	0.00	0.00	-3.03	-2.63	-2.48
TCGA-BJ-A3PU-10A-01D-A21Z-08_THCA	-2.56	-2.67	-2.65	-2.81	-2.62	-2.63	-2.57	-2.46	-2.53	0.00	0.00	-4.20	0.00	-4.51	-2.97	-2.68	-2.48
TCGA-BJ-A45C-10A-01D-A23U-08_THCA	-2.41	-2.65	-2.68	-2.87	-2.46	-2.48	-2.44	-2.55	-2.42	0.00	-2.89	0.00	-2.71	0.00	0.00	-2.76	-2.49
TCGA-BJ-A45D-10A-01D-A23U-08_THCA	-2.58	-2.78	-2.67	-2.85	-2.46	-2.62	-2.58	-2.55	-2.60	0.00	-2.85	-2.73	0.00	0.00	0.00	-2.59	-2.56
TCGA-BJ-A45E-10A-01D-A23U-08_THCA	-2.65	-2.80	-2.81	-2.97	-2.58	-2.59	-2.60	-2.58	-3.53	-3.11	-2.57	-2.78	-2.68	-2.62	0.00	-3.96	-2.56
TCGA-BJ-A45F-10A-01D-A23U-08_THCA	-2.48	-2.49	-2.48	0.00	-2.57	-2.66	-2.51	-2.48	-2.42	-4.65	-2.89	-2.71	0.00	0.00	-3.01	-2.75	-2.38
TCGA-BJ-A45G-10A-01D-A23U-08_THCA	-2.68	-2.82	-2.77	-3.03	-2.56	-2.68	-2.74	-2.69	-2.79	-3.42	-2.76	-2.69	-4.60	-2.77	0.00	-2.77	-2.67
TCGA-BJ-A45H-10A-01D-A23U-08_THCA	-2.37	-2.76	-2.67	-2.81	-2.65	-2.69	-2.51	-2.57	-2.69	-3.38	-2.83	0.00	-2.80	-2.65	0.00	-2.77	-2.38
TCGA-BJ-A45I-10A-01D-A23U-08_THCA	-2.52	-4.02	-4.20	-2.79	-2.55	-2.62	-2.61	-2.50	-2.55	0.00	0.00	0.00	0.00	-4.50	0.00	-2.59	-2.52
TCGA-BJ-A45J-10A-01D-A23U-08_THCA	-2.52	-2.68	-2.64	-2.89	-2.61	-2.62	-2.54	-2.45	-2.49	-4.40	0.00	-3.70	0.00	-3.80	0.00	-2.46	-2.50
TCGA-BJ-A45K-10A-01D-A23U-08_THCA	-2.50	0.00	0.00	-2.71	-2.54	-2.49	-2.57	-2.41	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.36	-2.44
TCGA-BJ-A4O8-10A-01D-A25A-08_THCA	-2.58	-2.66	-2.63	-2.79	-2.65	-2.72	-2.57	-2.49	-2.50	0.00	-4.41	-3.93	0.00	0.00	-3.01	-2.71	-2.53
TCGA-BJ-A4O9-10A-01D-A25A-08_THCA	-2.57	0.00	-4.39	-2.81	-2.71	-2.60	-2.67	-2.49	-2.73	-3.43	-2.77	-4.39	-2.79	-2.84	0.00	-2.66	-2.54
TCGA-BK-A0CA-10A-02D-A272-09_UCEC	-2.84	-4.75	-4.15	-3.06	-2.67	-2.64	-2.57	-2.56	-2.68	-3.57	-2.79	0.00	-2.78	-2.78	0.00	-2.83	-2.72
TCGA-BK-A0CC-10A-02D-A272-09_UCEC	-2.91	-3.75	-3.88	-3.10	-2.51	-2.49	-2.45	-2.33	-2.42	0.00	0.00	0.00	-4.35	-4.35	-2.97	-2.79	-2.51
TCGA-BK-A139-10A-01D-A272-09_UCEC	-2.91	0.00	0.00	-2.98	-2.71	-2.70	-2.62	-2.47	-2.53	0.00	-4.32	0.00	-4.49	0.00	-2.99	-2.80	-2.71
TCGA-BK-A13B-10A-01D-A22A-09_UCEC	-2.87	0.00	-2.71	-3.28	-2.54	-2.56	-2.55	-2.56	-2.45	0.00	-2.99	0.00	-2.69	0.00	-2.99	-2.87	-2.57
TCGA-BK-A13C-10A-01D-A122-09_UCEC	-2.89	0.00	-4.93	-2.86	-2.54	-2.53	-2.54	-2.53	-2.45	0.00	0.00	0.00	0.00	-4.93	-3.17	-2.79	-2.69
TCGA-BK-A26L-10A-01D-A16D-09_UCEC	-2.74	-2.55	-2.57	0.00	0.00	0.00	-2.54	-2.48	-2.55	0.00	0.00	0.00	0.00	0.00	-3.00	-2.82	-2.63
TCGA-BK-A4ZD-10A-01D-A27P-09_UCEC	-2.62	-2.62	-4.40	-3.28	-2.62	-2.62	-2.70	-2.59	-2.65	0.00	-2.79	0.00	-2.60	-2.68	0.00	-2.69	-2.58
TCGA-BK-A56F-10A-01D-A27P-09_UCEC	-2.67	0.00	0.00	-2.96	-2.52	-2.47	-2.54	-2.48	-2.45	0.00	-4.49	0.00	0.00	0.00	-2.85	-2.72	-2.60
TCGA-BL-A0C8-10A-01D-A10S-08_BLCA	-2.60	0.00	-4.59	-2.64	-2.54	-2.62	-2.61	-2.49	-2.60	-4.59	0.00	0.00	0.00	0.00	0.00	-2.41	-2.55
TCGA-BL-A13I-10A-01D-A271-08_BLCA	-2.48	0.00	0.00	-2.77	-2.53	-2.52	-2.53	-2.38	-2.42	0.00	0.00	0.00	0.00	-4.09	0.00	-2.42	-2.48
TCGA-BL-A13J-10A-01D-A271-08_BLCA	-2.53	0.00	0.00	-2.60	-2.57	-2.55	-2.58	-2.47	-2.59	0.00	0.00	0.00	0.00	-4.43	0.00	-2.42	-2.49
TCGA-BL-A5ZZ-10A-01D-A30H-08_BLCA	-2.41	-2.64	-2.63	-2.79	-2.60	-2.56	-2.48	-2.52	-2.40	0.00	0.00	0.00	0.00	0.00	-2.82	0.00	-2.38
TCGA-BM-6198-10A-01D-1733-10_READ	-2.54	-2.58	-2.84	-4.44	-2.57	-2.54	-2.46	-2.67	-4.14	-3.12	-2.64	-2.90	-2.62	-2.64	0.00	0.00	-2.46
TCGA-BR-6452-10A-01D-1800-08_STAD	-2.35	-4.43	-4.43	-2.51	-2.40	-2.63	-2.57	-2.74	-2.62	0.00	-4.43	0.00	0.00	-2.61	0.00	-2.65	-2.43
TCGA-BR-6455-10A-01D-1800-08_STAD	-2.64	-2.79	-2.69	-2.94	-2.77	-2.77	-2.64	-2.67	-2.71	-3.20	-2.73	-4.33	-2.71	-2.73	0.00	-2.83	-2.60
TCGA-BR-6456-10A-01D-1800-08_STAD	-2.51	-2.66	-2.69	-2.84	-2.58	-2.68	-2.53	-2.50	-2.48	-4.51	-4.51	-3.81	-4.03	-4.51	0.00	-2.42	-2.48
TCGA-BR-6457-10A-01D-1800-08_STAD	-2.58	-2.73	-2.73	-2.88	-2.53	-2.66	-2.66	-2.54	-2.64	-4.59	-2.86	-2.72	0.00	0.00	0.00	-2.50	-2.58
TCGA-BR-6458-10A-01D-1800-08_STAD	-2.58	0.00	-4.09	-2.73	-2.63	-2.62	-2.63	-2.49	-2.70	-3.42	-2.86	0.00	-2.75	-2.71	0.00	-2.75	-2.52
TCGA-BR-6563-10A-01D-2053-08_STAD	-2.57	-2.76	-2.71	-2.86	-2.44	-2.58	-2.56	-2.57	-2.66	-3.27	-2.76	-2.62	0.00	-2.70	-3.06	0.00	-2.55
TCGA-BR-6564-10A-01D-1882-08_STAD	-2.48	0.00	0.00	-2.61	-2.53	-2.60	-2.56	-2.54	-2.52	0.00	0.00	0.00	0.00	0.00	-3.04	-2.67	-2.41
TCGA-BR-6565-10A-01D-1800-08_STAD	-2.40	-2.73	-2.63	-2.83	-2.63	-2.66	-2.55	-2.47	-2.52	0.00	0.00	0.00	-4.52	-4.21	-3.04	-2.72	-2.49
TCGA-BR-6566-10A-01D-1800-08_STAD	-2.66	-2.76	-2.63	-2.90	-2.70	-2.76	-2.62	-2.54	-2.59	-3.48	-2.83	0.00	-2.76	0.00	0.00	-2.63	-2.57
TCGA-BR-6705-10A-01D-1882-08_STAD	-2.55	-4.59	0.00	-2.62	-2.54	-2.59	-2.56	-2.58	-2.49	-4.28	0.00	-4.59	-4.28	-3.98	0.00	-2.64	-2.43
TCGA-BR-6706-10A-01D-1882-08_STAD	-2.56	-2.70	-2.62	-2.83	-2.63	-2.63	-2.55	-2.55	-2.60	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.45
TCGA-BR-6707-10A-01D-1882-08_STAD	-2.55	-2.60	-2.64	0.00	-2.71	-2.70	-2.74	-2.83	-2.76	0.00	-2.70	-2.71	-2.82	-2.71	0.00	-2.73	-2.55
TCGA-BR-6709-10A-01D-1882-08_STAD	-2.46	-2.75	-2.70	-2.82	-2.69	-2.66	-2.63	-2.48	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.46
TCGA-BR-6710-10A-01D-1882-08_STAD	-2.62	-2.80	-2.79	-2.98	-2.54	-2.64	-2.67	-2.57	-2.60	0.00	-2.93	-2.72	0.00	0.00	0.00	-2.50	-2.57
TCGA-BR-6801-10A-01D-1882-08_STAD	-2.49	-2.71	-2.63	-2.89	-2.65	-2.67	-2.56	-2.42	-2.49	0.00	0.00	-4.12	0.00	-4.59	-3.02	-2.76	-2.47
TCGA-BR-6802-10A-01D-1882-08_STAD	-2.50	-2.68	-2.59	-2.79	-2.62	0.00	-2.64	-2.60	-4.20	-3.27	-2.73	0.00	-2.70	-2.50	0.00	-4.50	-2.57
TCGA-BR-6803-10A-01D-1882-08_STAD	-2.57	0.00	0.00	-2.61	-2.57	-2.61	-2.61	-2.59	-2.70	-3.38	-2.87	0.00	-2.79	-2.71	0.00	-2.82	-2.48
TCGA-BR-6852-10A-01D-1882-08_STAD	-2.60	-2.83	-2.74	-2.94	-2.50	-2.67	-2.69	-2.67	-2.82	-3.35	-2.78	-2.64	0.00	-2.73	0.00	-2.83	-2.53

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BR-7196-10A-01D-2053-08_STAD	-2.48	-2.57	-2.53	0.00	-2.62	-2.65	-2.52	-2.63	-2.52	0.00	-2.84	-2.69	0.00	0.00	0.00	-2.59	-2.48
TCGA-BR-7197-10A-01D-2201-08_STAD	-2.55	-2.68	-2.74	-2.90	-2.70	-2.73	-2.56	-2.68	-2.74	-3.31	-2.85	-2.64	0.00	-2.71	0.00	-2.75	-2.52
TCGA-BR-7703-10A-01D-2053-08_STAD	-2.36	-2.61	-2.65	-2.74	-2.57	-2.59	-2.50	-2.49	-2.39	-4.38	0.00	-4.08	0.00	-4.08	0.00	-2.53	-2.43
TCGA-BR-7704-10A-01D-2053-08_STAD	-2.53	-2.62	-2.67	-2.84	-2.60	-2.61	-2.54	-2.51	-2.60	-3.39	-2.90	-2.64	0.00	-2.58	0.00	-2.66	-2.45
TCGA-BR-7707-10A-01D-2053-08_STAD	-2.42	-2.47	-2.47	-4.35	-3.57	-3.57	-2.49	-2.44	-2.32	0.00	-4.35	-4.35	0.00	0.00	-2.94	-2.56	-2.40
TCGA-BR-7715-10A-01D-2053-08_STAD	-2.56	-2.70	-2.75	-2.81	-2.39	-2.53	-2.58	-2.64	-2.59	0.00	-2.90	-2.66	0.00	-4.47	0.00	-2.40	-2.48
TCGA-BR-7716-10A-01D-2053-08_STAD	-2.48	-2.62	-2.65	-2.71	-2.57	-2.51	-2.44	-2.51	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.36
TCGA-BR-7717-10A-01D-2053-08_STAD	-2.54	0.00	0.00	-2.54	-2.49	-2.51	-2.54	-2.54	-2.67	-3.23	-2.84	0.00	-2.75	-2.70	0.00	-2.72	-2.44
TCGA-BR-7722-10A-01D-2201-08_STAD	-2.51	-2.66	-2.71	-2.72	-2.58	-2.61	-2.48	-2.52	-2.42	0.00	0.00	-4.48	0.00	-4.48	0.00	-2.53	-2.37
TCGA-BR-7723-10A-01D-2053-08_STAD	-2.58	-2.72	-2.65	-2.85	-2.68	-2.73	-2.51	-2.62	-2.70	-3.16	-2.72	0.00	-2.71	-2.62	0.00	-2.72	-2.49
TCGA-BR-7851-10A-01D-2201-08_STAD	-2.54	-2.78	-2.77	-2.82	-2.46	-2.57	-2.61	-2.57	-2.49	0.00	-2.96	-2.79	0.00	-4.59	-3.14	-2.82	-2.46
TCGA-BR-7901-10A-01D-2201-08_STAD	-2.40	-2.72	-2.71	-2.74	-2.61	-2.63	-2.63	-2.76	-2.56	0.00	-2.85	-4.52	-2.79	-2.60	0.00	-2.74	-2.34
TCGA-BR-7957-10A-01D-2201-08_STAD	-2.50	-2.85	-2.73	-2.83	-2.49	-2.56	-2.58	-2.61	-2.59	0.00	-3.02	-2.70	0.00	0.00	-3.09	-2.73	-2.48
TCGA-BR-7958-10A-01D-2340-08_STAD	-2.53	-2.64	-2.65	-2.78	-2.54	0.00	-2.61	-2.69	0.00	-3.16	-2.80	0.00	-2.67	-2.52	0.00	0.00	-2.56
TCGA-BR-7959-10A-01D-2340-08_STAD	-2.50	-4.63	0.00	-2.57	-2.50	-2.61	-2.53	-2.57	-2.50	0.00	0.00	0.00	0.00	-4.33	0.00	-2.65	-2.51
TCGA-BR-8058-10A-01D-2340-08_STAD	-2.51	-2.69	-2.70	-2.75	-2.45	-2.53	-2.54	-2.58	-2.45	0.00	-2.94	-2.73	0.00	0.00	0.00	-2.56	-2.48
TCGA-BR-8059-10A-01D-2340-08_STAD	-2.48	0.00	0.00	-2.73	-2.50	-2.53	-2.59	-2.47	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.44	-2.50
TCGA-BR-8060-10A-01D-2340-08_STAD	-2.58	0.00	0.00	-2.63	-2.58	-2.62	-2.66	-2.53	-2.73	-3.35	-2.92	0.00	-2.73	-2.72	0.00	-2.78	-2.55
TCGA-BR-8077-10A-01D-2340-08_STAD	-2.57	0.00	0.00	-2.83	-2.50	-2.62	-2.61	-2.66	-2.70	-3.36	-2.81	-2.73	0.00	-2.67	0.00	-2.80	-2.51
TCGA-BR-8078-10A-01D-2340-08_STAD	-2.42	0.00	0.00	-2.49	-2.45	-2.61	-2.63	-2.64	-2.63	0.00	0.00	0.00	0.00	-2.53	0.00	-2.63	-2.50
TCGA-BR-8080-10A-01D-2340-08_STAD	-2.42	0.00	-4.54	-2.58	-2.51	-2.53	-2.53	-2.55	-2.61	-3.39	-3.02	0.00	-2.73	-2.70	-3.12	0.00	-2.47
TCGA-BR-8081-10A-01D-2340-08_STAD	-2.51	-4.56	0.00	-2.73	-2.50	-2.57	-2.58	-2.46	-2.50	0.00	0.00	-4.56	0.00	0.00	0.00	-2.40	-2.48
TCGA-BR-8284-10A-01D-2340-08_STAD	-2.61	0.00	-4.64	-2.63	-2.53	-2.61	-2.60	-2.56	-2.72	-3.31	-2.92	0.00	-2.74	-2.67	0.00	-2.75	-2.57
TCGA-BR-8285-10A-01D-2340-08_STAD	-2.56	-2.59	-2.59	-4.52	0.00	0.00	-2.59	-2.49	-2.65	-3.31	-2.76	0.00	-2.75	-2.64	-2.94	0.00	-2.49
TCGA-BR-8286-10A-01D-2340-08_STAD	-2.45	-2.79	-2.74	-2.90	-2.52	-2.64	-2.65	-2.54	-2.56	0.00	-2.88	-2.74	0.00	-4.36	-3.05	-2.82	-2.58
TCGA-BR-8289-10A-01D-2340-08_STAD	-2.43	-3.27	-3.54	-2.50	-2.45	-2.54	-2.58	-2.62	-2.50	0.00	-3.54	-3.35	0.00	-2.59	0.00	-2.78	-2.48
TCGA-BR-8291-10A-01D-2340-08_STAD	-2.51	-2.66	-2.72	-2.88	-2.62	-2.64	-2.56	-2.45	-2.56	-3.43	-2.95	0.00	-2.76	-2.65	0.00	-2.95	-2.42
TCGA-BR-8295-10A-01D-2340-08_STAD	-2.36	0.00	0.00	-2.74	-2.49	-2.68	-2.57	-2.55	-2.47	0.00	0.00	-4.56	0.00	0.00	0.00	-2.57	-2.47
TCGA-BR-8296-10A-01D-2340-08_STAD	-2.50	0.00	-4.59	-2.75	-2.53	-2.56	-2.55	-2.51	-2.46	0.00	0.00	0.00	0.00	0.00	-3.08	-2.69	-2.49
TCGA-BR-8297-10A-01D-2340-08_STAD	-2.35	0.00	0.00	-2.40	-2.33	-2.56	-2.56	-2.65	-2.58	0.00	0.00	0.00	0.00	-2.51	0.00	-2.56	-2.42
TCGA-BR-8360-10A-01D-2340-08_STAD	-2.65	-2.72	-2.71	0.00	-2.65	-2.62	-2.64	-2.51	-2.53	0.00	-2.74	-2.61	0.00	0.00	-3.11	-2.80	-2.63
TCGA-BR-8361-10A-01D-2340-08_STAD	-2.56	-2.71	0.00	-2.87	-2.65	-2.72	-2.55	-2.68	-2.64	-3.26	-2.88	0.00	-2.75	-2.65	0.00	-2.73	-2.51
TCGA-BR-8362-10A-01D-2340-08_STAD	-2.61	-2.74	-2.76	-2.86	-2.47	-2.63	-2.62	-2.54	-2.54	0.00	-3.03	-2.72	-4.50	-4.20	-3.11	-2.74	-2.55
TCGA-BR-8363-10A-01D-2341-08_STAD	-2.49	-2.75	-2.76	-3.00	-2.51	-2.68	-2.69	-2.54	-2.58	0.00	-2.88	-2.84	0.00	0.00	-3.13	-2.79	-2.59
TCGA-BR-8364-10A-01D-2341-08_STAD	-2.59	-2.65	-2.58	0.00	-2.51	-2.57	-2.61	-2.58	0.00	-3.17	-2.54	-2.54	-2.93	-2.54	0.00	0.00	-2.48
TCGA-BR-8365-10A-01D-2341-08_STAD	-2.63	-2.67	-2.61	0.00	-2.61	-2.66	-2.68	-2.64	-2.75	-3.32	-2.72	-2.57	-3.97	-2.73	0.00	-2.83	-2.58
TCGA-BR-8366-10A-01D-2341-08_STAD	-2.53	-2.71	-2.64	-2.83	-2.66	-2.69	-2.63	-2.62	-2.69	-3.33	-2.80	0.00	-2.77	-2.70	0.00	-2.71	-2.52
TCGA-BR-8367-10A-01D-2341-08_STAD	-2.62	-2.73	-2.71	-2.87	-2.53	-2.59	-2.62	-2.63	-2.54	0.00	-2.91	-2.72	0.00	-4.61	0.00	-2.46	-2.54
TCGA-BR-8368-10A-01D-2341-08_STAD	-2.53	0.00	0.00	-2.75	-2.57	-2.54	-2.63	-2.48	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.50
TCGA-BR-8369-10A-01D-2341-08_STAD	-2.59	0.00	0.00	-2.64	-2.55	-2.59	-2.63	-2.66	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.53
TCGA-BR-8370-10A-01D-2341-08_STAD	-2.53	-2.69	-2.69	-2.81	-2.44	-2.68	-2.67	-2.75	-2.65	0.00	-2.83	-2.67	0.00	-2.60	-3.01	0.00	-2.56
TCGA-BR-8371-10A-01D-2341-08_STAD	-2.59	-2.80	-2.79	-2.87	-2.47	-2.65	-2.64	-2.59	-2.55	0.00	-2.88	-2.75	0.00	0.00	-3.15	-2.78	-2.57
TCGA-BR-8372-10A-01D-2341-08_STAD	-2.51	0.00	-4.58	-2.60	-2.46	-2.58	-2.57	-2.52	-2.56	0.00	0.00	0.00	-4.58	-4.58	0.00	-2.42	-2.50
TCGA-BR-8373-10A-01D-2341-08_STAD	-2.53	0.00	0.00	-2.63	-2.54	-2.55	-2.59	-2.58	-2.57	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.32
TCGA-BR-8380-10A-01D-2341-08_STAD	-2.41	0.00	-4.29	-2.68	-2.46	-2.58	-2.57	-2.58	-2.65	-3.24	-2.89	0.00	-2.77	-2.67	0.00	-2.66	-2.43
TCGA-BR-8381-10A-01D-2394-08_STAD	-2.48	0.00	0.00	-2.48	-2.41	-2.55	-2.61	-2.59	-2.54	-4.39	0.00	0.00	0.00	-2.54	0.00	-2.62	-2.48
TCGA-BR-8382-10A-01D-2394-08_STAD	-2.61	-2.69	-2.69	-2.91	-2.48	-2.64	-2.63	-2.48	-2.52	0.00	-2.86	-2.75	-4.23	-3.93	0.00	-2.53	-2.56
TCGA-BR-8384-10A-01D-2394-08_STAD	-2.71	-2.77	-2.76	-2.95	-2.56	-2.68	-2.72	-2.71	-2.82	-3.38	-2.82	-2.72	-4.61	-2.82	0.00	-2.81	-2.65
TCGA-BR-8483-10A-01D-2394-08_STAD	-2.66	-2.78	-2.77	-2.98	-2.55	-2.68	-2.70	-2.47	-2.58	-3.38	-2.97	-2.82	0.00	-4.03	-3.10	-2.83	-2.63
TCGA-BR-8484-10A-01D-2394-08_STAD	-2.56	-3.84	0.00	-2.65	-2.61	-2.64	-2.60	-2.58	-2.61	0.00	-4.54	0.00	-4.24	-3.94	0.00	-2.59	-2.54
TCGA-BR-8485-10A-01D-2394-08_STAD	-2.66	-2.79	-2.74	-2.87	-2.56	-2.67	-2.67	-2.58	-2.80	-3.34	-2.72	-2.71	-4.61	-2.72	0.00	-2.83	-2.65
TCGA-BR-8486-10A-01D-2394-08_STAD	-2.63	-2.67	-2.67	-2.86	-2.45	-2.64	-2.77	-2.72	-2.62	0.00	-2.88	-2.69	0.00	-2.64	-3.08	-3.93	-2.65
TCGA-BR-8487-10A-01D-2394-08_STAD	-2.50	-2.50	-2.51	-3.96	-3.60	-3.84	-2.52	-2.53	-2.52	0.00	-3.84	-3.96	0.00	-4.44	-2.90	-3.96	-2.46
TCGA-BR-8588-10A-01D-2394-08_STAD	-2.63	-2.81	-2.71	-2.96	-2.58	-2.72	-2.70	-2.67	-2.66	0.00	-2.89	-2.79	0.00	0.00	0.00	-2.50	-2.62
TCGA-BR-8589-10A-01D-2394-08_STAD	-2.59	-2.64	-2.61	0.00	-2.68	-2.69	-2.62	-2.52	-2.51	0.00	-2.78	-2.64	-4.25	-4.07	0.00	-2.48	-2.61
TCGA-BR-8590-10A-01D-2394-08_STAD	-2.56	-2.69	-2.65	-2.81	-2.67	-2.67	-2.57	-2.53	-2.47	0.00	-4.51	0.00	-4.51	-4.03	0.00	-2.42	-2.51
TCGA-BR-8591-10A-01D-2394-08_STAD	-2.63	-3.75	-3.83	-2.82	-2.59	-2.57	-2.63	-2.42	-2.48	-4.53	-3.57	-3.75	-4.53	-3.83	-2.94	-2.67	-2.47
TCGA-BR-8592-10A-01D-2394-08_STAD	-2.48	-2.76	-2.73	-2.84	-2.65	-2.60	-2.48	-2.62	-2.76	-3.25	-2.80	0.00	-2.75	-2.68	0.00	-2.76	-2.40
TCGA-BR-8676-10A-01D-2394-08_STAD	-2.63	-2.72	-2.73	-2.94	-2.54	-2.67	-2.65	-2.58	-2.55	0.00	-2.85	-2.76	0.00	-4.28	-3.12	-2.84	-2.59
TCGA-BR-8677-10A-01D-2394-08_STAD	-2.62	-2.73	-2.70	-2.83	-2.67	-2.73	-2.65	-2.59	-2.72	-3.24	-2.86	-4.57	-2.76	-2.70	-3.07	-4.09	-2.57
TCGA-BR-8678-10A-01D-2394-08_STAD	-2.55	-4.04	-4.22	-2.59	-2.59	-2.58	-2.63	-2.57	-2.58	0.00	-3.92	-3.62	-4.52	-3.82	-3.06	-2.72	-2.51
TCGA-BR-8679-10A-01D-2394-08_STAD	-2.58	-2.69	-2.66	-2.78	-2.62	-2.65	-2.58	-2.52	-2.56	0.00	-4.51	0.00	0.00	0.00	-3.09	-2.67	-2.54
TCGA-BR-8680-10A-01D-2394-08_STAD	-2.71	-2.86	-2.80	-2.91	-2.60	-2.70	-2.70	-2.55	-2.76	-3.35	-2.95	-2.81	-3.72	-3.47	-3.17	-2.88	-2.73
TCGA-BR-8682-10A-01D-2394-08_STAD	-2.59	-2.69	-2.67	-2.91	-2.67	-2.67	-2.65	-2.60	-3.48	-3.13	-2.75	-3.78	-2.66	-2.62	0.00	-3.66	-2.54
TCGA-BR-8683-10A-01D-2394-08_STAD	-2.54	-2.65	-2.65	-2.88	-2.64	-2.64	-2.36	-2.60	-2.47	0.00	0.00	0.00	-4.51	0.00	0.00	-2.59	-2.51
TCGA-BR-8686-10A-01D-2394-08_STAD	-2.39	-2.46	-2.47	-4.22	0.00	0.00	-2.42	-2.50	-2.37	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.31
TCGA-BR-8687-10A-01D-2394-08_STAD	-2.58	0.00	0.00	-2.80	-2.60	-2.59	-2.58	-2.45	-2.49	-3.30	-4.53	0.00	0.00	0.00	-3.01	-2.70	-2.57
TCGA-BR-8690-10A-01D-2394-08_STAD	-2.68	-2.72	-2.69	-2.93	-2.72	-2.77	-2.67	-2.62	-2.78	-3.23	-2.88	0.00	-2.79	-2.72	0.00	-2.69	-2.57
TCGA-BR-A44T-10A-01D-A24F-08_STAD	-2.46	-2.72	-2.71	-2.80	-2.64	-2.72	-2.61	-2.54	-2.54	0.00	0.00	0.00	0.00	-4.41	-2.96	-2.67	-2.49
TCGA-BR-A44U-10A-01D-A24F-08_STAD	-2.36	-2.70	-2.68	-2.86	-2.65	-2.65	-2.59	-2.60	-2.52	0.00	0.00	0.00	0.00	0.00	-2.92	0.00	-2.55
TCGA-BR-A452-10A-01D-A25E-08_STAD	-2.55	0.00	0.00	-2.82	-2.59	-2.57	-2.58	-2.53	-2.47	0.00	0.00	0.00	0.00	-4.51	-3.05	-2.78	-2.52
TCGA-BR-A453-10A-01D-A24F-08_STAD	-2.60	0.00	-4.00	-2.60	-2.55	-2.59	-2.62	-2.56	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.51
TCGA-BR-A4CQ-10A-01D-A25E-08_STAD	-2.66	-2.79	-2.80	-2.97	-2.57	-2.67	-2.69	-2.74	-2.75	-3.47	-2.75	-2.67	0.00	-2.77	0.00	-2.77	-2.67
TCGA-BR-A4CR-10A-01D-A24F-08_STAD	-2.62	-2.77	-2.75	-2.98	-2.51	-2.66	-2.67	-2.56	-2.75	-3.42	-2.73	-2.66	0.00	-2.72	0.00	-2.79	-2.58
TCGA-BR-A4CS-10A-01D-A24F-08_STAD	-2.48	-2.60	-2.58	-2.82	-2.61	0.00	-2.61	-2.59	-2.57	0.00	0.00	0.00	0.00	-2.58	-2.88	-4.40	-2.50
TCGA-BR-A4IU-10A-01D-A25E-08_STAD	-2.49	-2.59	-2.62	-2.75	-2.56	-2.66	-2.48	-2.47	-2.45	0.00	0.00	0.00	0.00	0.00	-3.00	-2.62	-2.40
TCGA-BR-A4IV-10A-01D-A25E-08_STAD	-2.64	-2.77	-2.64	-2.96	-2.69	-2.72	-2.66	-2.49	-2.73	-3.06	-2.76	0.00	-2.73	-2.82	-3.06	-3.88	-2.52
TCGA-BR-A4IY-10A-01D-A25E-08_STAD	-2.44	0.00	0.00	-2.72	-2.54	-2.59	-2.57	-2.56	-2.62	-3.32	-2.90	0.00	-2.81	-2.70	-3.06	-3.82	-2.54
TCGA-BR-A4IZ-10A-01D-A25E-08_STAD	-2.50	-2.69	-2.68	-2.81	-2.67	-2.64	-2.56	-2.42	-2.41	0.00	0.00	0.00	0.00	0.00	-3.05	-2.67	-2.45
TCGA-BR-A4J1-10A-01D-A25E-08_STAD	-2.52	-2.72	-2.74	-2.87	-2.66	-2.72	-2.60	-2.52	-2.64	-3.33	-2.83	0.00	-2.74	-2.66	-3.06	-4.21	-2.49
TCGA-BR-A4J2-10A-01D-A25E-08_STAD	-2.69	-2.68	-2.72	0.00	-2.74	-2.73	-2.65	-2.52	-2.67	-3.33	-2.88	-2.77	0.00	-4.61	-3.03	0.00	-2.59
TCGA-BR-A4J4-10A-01D-A25E-08_STAD	-2.61	0.00	-4.59	-2.90	-2.65	-2.65	-2.67	-2.55	-2.71	-3.36	-2.80	-2.76	0.00	-2.70	-3.04	0.00	-2.65
TCGA-BR-A4J5-10A-01D-A25E-08_STAD	-2.40	0.00	0.00	-2.61	-2.56	-2.59	-2.56	-2.47	-2.48	0.00	0.00	0.00	0.00	-4.48	-3.12	-2.70	-2.49
TCGA-BR-A4J6-10A-01D-A25E-08_STAD	-2.50	-2.68	-2.64	-2.80	-2.61	-2.58	-2.52	-2.55	-2.46	0.00	-3.96	0.00	-4.44	0.00	0.00	-2.58	-2.38
TCGA-BR-A4J7-10A-01D-A25E-08_STAD	-2.51	-2.68	-2.64	-2.84	-2.60	-2.66	-2.64	-2.64	-4.46	-3.22	-2.66	-4.46	-2.57	-2.55	0.00	0.00	-2.46
TCGA-BR-A4J8-10A-01D-A25E-08_STAD	-2.51	-3.88	-3.58	-2.80	-2.51	-2.56	-2.52	-2.57	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.47
TCGA-BR-A4J9-10A-01D-A25E-08_STAD	-2.62	-2.76	-2.76	-2.90	-2.54	-2.61	-2.61	-2.64	-2.74	-3.30	-2.72	-2.65	-3.68	-2.74	-3.12	-3.74	-2.56
TCGA-BR-A4PD-10A-01D-A25E-08_STAD	-2.72	-2.71	-2.68	-4.61	-2.72	-2.67	-2.70	-2.63	-2.76	-3.57	-2.69	-2.65	0.00	-2.82	-3.11	0.00	-2.61
TCGA-BR-A4PE-10A-01D-A25E-08_STAD	-2.51	-2.68	-2.68	-2.84	-2.69	-2.64	-2.54	-2.57	-2.55	0.00	0.00	0.00	0.00	-4.56	-2.91	0.00	-2.47
TCGA-BR-A4PF-10A-01D-A25E-08_STAD	-2.64	0.00	0.00	-2.82	-2.65	-2.70	-2.68	-2.66	-2.84	-3.42	-2.83	-2.79	0.00	-2.76	0.00	-2.76	-2.65
TCGA-BR-A4QI-10A-01D-A25E-08_STAD	-2.47	-2.47	-2.52	-3.75	-3.67	-3.50	-2.51	-2.43	-2.37	0.00	0.00	0.00	0.00	-4.45	0.00	-2.32	-2.42
TCGA-BR-A4QL-10A-01D-A25E-08_STAD	-2.58	-2.62	-2.59	-4.18	-2.64	-2.63	-2.69	-2.72	-3.58	-3.31	-2.55	-2.57	-2.78	-2.55	0.00	-3.64	-2.47
TCGA-BR-A4QM-10A-01D-A25E-08_STAD	-2.47	-2.65	-2.68	-2.75	-2.49	-2.68	-2.47	-2.43	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.40	-2.49
TCGA-BS-A0T9-10C-01D-A12J-09_UCEC	-2.88	0.00	-4.86	-3.00	-2.54	-2.59	-2.58	-2.63	-2.51	0.00	0.00	0.00	0.00	-4.38	-2.89	0.00	-2.70
TCGA-BS-A0TA-10A-01D-A10B-09_UCEC	-3.23	-2.73	-2.79	-3.21	-2.92	-2.86	-2.63	-2.96	-2.88	-3.29	-3.10	0.00	-2.91	-2.89	0.00	-3.17	-2.82
TCGA-BS-A0TC-10A-01D-A10B-09_UCEC	-3.07	-2.89	-2.95	-3.00	-2.79	-2.76	-2.77	-2.87	-2.65	0.00	-3.12	-2.89	0.00	0.00	-3.50	-3.11	-2.90

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BS-A0TD-10A-01D-A10B-09_UCEC	-3.04	0.00	0.00	-2.75	-2.61	-2.67	-2.56	-2.73	-2.54	0.00	0.00	0.00	0.00	0.00	-3.27	-3.10	-2.74
TCGA-BS-A0TE-10A-01D-A10B-09_UCEC	-2.89	0.00	0.00	-2.93	-2.60	-2.62	-2.63	-2.77	-2.59	0.00	0.00	0.00	0.00	0.00	0.00	-2.72	-2.78
TCGA-BS-A0TG-10A-01D-A14K-09_UCEC	-3.03	0.00	-4.99	-3.07	-2.66	-2.72	-2.75	-2.75	-2.64	0.00	0.00	0.00	0.00	0.00	0.00	-2.75	-2.88
TCGA-BS-A0TI-10A-01D-A10B-09_UCEC	-3.04	-2.70	-2.74	-3.10	-2.83	-2.79	-2.80	-3.03	-4.90	-3.38	-2.65	0.00	-2.56	-2.53	0.00	0.00	-2.67
TCGA-BS-A0TJ-10A-01D-A10B-09_UCEC	-2.86	-4.84	0.00	-2.80	-2.51	-2.52	-2.45	-2.61	-2.48	0.00	-4.84	0.00	0.00	0.00	0.00	-2.59	-2.58
TCGA-BS-A0U5-10A-01D-A10G-09_UCEC	-2.94	0.00	-4.79	-3.00	-2.60	-2.62	-2.58	-2.69	0.00	-3.31	-2.67	-4.79	-2.61	-2.63	0.00	0.00	-2.73
TCGA-BS-A0U7-10A-01D-A10B-09_UCEC	-2.99	-2.84	-2.76	-3.20	-2.59	-2.69	-2.74	-2.62	-2.61	0.00	-3.02	-2.86	0.00	0.00	0.00	-2.62	-2.83
TCGA-BS-A0U8-10A-01D-A10B-09_UCEC	-2.88	-2.85	-2.86	-3.23	-2.61	-2.71	-2.70	-2.64	-2.81	-3.53	-2.65	-2.82	-2.86	-2.81	0.00	-2.88	-2.87
TCGA-BS-A0U9-10A-01D-A10M-09_UCEC	-3.07	-2.77	-2.79	-3.16	-2.58	-2.68	-2.66	-2.71	-2.77	0.00	-2.95	-2.78	-4.88	0.00	-3.20	-2.88	-2.79
TCGA-BS-A0UA-10A-01D-A122-09_UCEC	-2.86	-2.73	-2.72	-3.06	-2.74	-2.72	-2.60	-2.63	-2.55	0.00	0.00	0.00	0.00	0.00	-3.04	-2.75	-2.76
TCGA-BS-A0UF-10A-01D-A10B-09_UCEC	-2.93	0.00	0.00	-3.00	-2.67	-2.66	-2.63	-2.67	0.00	-3.36	-2.75	-2.67	0.00	-2.69	0.00	0.00	-2.82
TCGA-BS-A0UJ-10A-01D-A127-09_UCEC	-2.92	0.00	0.00	-2.76	-2.66	-2.63	-2.53	-2.85	-2.52	0.00	0.00	0.00	0.00	0.00	-3.30	-3.00	-2.71
TCGA-BS-A0UL-10A-01D-A10G-09_UCEC	-2.83	0.00	0.00	-2.92	-2.55	-2.57	-2.59	-2.66	-2.71	-3.41	-2.81	-2.75	0.00	-2.75	0.00	-2.82	-2.72
TCGA-BS-A0UM-10A-01D-A10B-09_UCEC	-3.08	-2.86	-2.83	0.00	-2.77	-2.80	-2.83	-2.84	0.00	-3.45	-2.59	-2.67	-2.99	-2.84	0.00	0.00	-2.98
TCGA-BS-A0UT-10A-01D-A10B-09_UCEC	-2.93	0.00	-4.61	-2.87	-2.53	-2.58	-2.53	-2.78	-2.50	0.00	0.00	0.00	0.00	0.00	-3.06	0.00	-2.67
TCGA-BS-A0UV-10A-01D-A10B-09_UCEC	-3.09	0.00	0.00	-3.23	-2.64	-2.75	-2.75	-2.65	-2.79	-3.68	-2.94	-2.96	-5.09	0.00	0.00	-2.70	-2.98
TCGA-BS-A0V4-10A-01D-A14G-09_UCEC	-2.86	-3.94	0.00	-3.10	-2.45	-2.55	-2.51	-2.52	-2.62	-3.46	-2.80	0.00	-2.65	-2.61	0.00	-2.89	-2.58
TCGA-BS-A0V6-10A-01D-A122-09_UCEC	-2.84	0.00	0.00	-2.79	-2.60	-2.65	-2.56	-2.54	-2.54	0.00	0.00	0.00	0.00	-4.88	-3.04	-2.82	-2.70
TCGA-BS-A0V7-10A-01D-A122-09_UCEC	-2.93	-4.07	-4.31	-2.84	-2.61	-2.65	-2.61	-2.61	-2.58	0.00	-4.61	0.00	-4.61	-4.43	-3.07	-2.80	-2.77
TCGA-BS-A0V8-10A-01D-A122-09_UCEC	-2.85	0.00	-4.88	-2.96	-2.62	-2.64	-2.62	-2.50	-2.55	0.00	0.00	0.00	0.00	-4.88	-3.01	-2.78	-2.76
TCGA-BS-A0VI-10A-01D-A14G-09_UCEC	-2.76	-2.54	-2.55	-4.47	-3.78	-4.17	-2.49	-2.48	-2.64	-3.36	-2.81	-2.74	0.00	-2.65	-2.97	0.00	-2.67
TCGA-BS-A0WQ-10A-01D-A10G-09_UCEC	-2.92	-2.67	-2.67	-3.07	-2.70	-2.74	-2.57	-2.63	-2.54	0.00	0.00	0.00	0.00	0.00	-3.14	-2.86	-2.69
TCGA-BT-A0S7-10A-01D-A10S-08_BLCA	-2.56	-2.74	0.00	-2.99	-2.53	-2.62	-2.72	-2.65	-2.67	-3.29	-2.91	0.00	-2.80	-2.71	0.00	-2.73	-2.54
TCGA-BT-A0YX-10A-01D-A10S-08_BLCA	-2.55	0.00	0.00	-2.67	-2.53	-2.65	-2.66	-2.48	-2.51	0.00	0.00	0.00	0.00	-4.31	0.00	-2.50	-2.57
TCGA-BT-A2LB-10A-01D-A18F-08_BLCA	-2.46	-4.51	-4.51	-2.56	-2.57	-2.59	-2.52	-2.45	-2.45	0.00	0.00	0.00	0.00	0.00	-3.07	-2.65	-2.46
TCGA-BT-A2LD-10A-01D-A20D-08_BLCA	-2.49	0.00	-4.50	-2.71	-2.55	-2.55	-2.58	-2.54	-2.60	-3.32	-2.85	0.00	-2.71	-2.61	-3.01	0.00	-2.46
TCGA-BT-A3PH-10A-01D-A21Z-08_BLCA	-2.56	-2.61	-2.60	-4.23	-2.57	-2.66	-2.60	-2.64	-2.49	0.00	-2.73	-2.60	0.00	0.00	0.00	-2.60	-2.48
TCGA-BT-A3PJ-10A-01D-A21Z-08_BLCA	-2.60	-2.68	-2.68	-4.60	-2.66	-2.62	-2.66	-2.55	-2.74	-3.40	-2.68	-2.66	-2.81	-2.68	0.00	-2.75	-2.58
TCGA-BT-A3PK-10A-01D-A21Z-08_BLCA	-2.58	-2.74	-2.73	-2.90	-2.49	-2.57	-2.63	-2.55	-2.53	0.00	-2.90	-2.72	0.00	0.00	0.00	-2.50	-2.54
TCGA-BT-A42B-10A-01D-A23K-08_BLCA	-2.58	-2.63	-2.54	-4.46	-2.69	-2.72	-2.58	-2.61	-2.53	-4.29	-2.82	-2.72	-4.76	-4.46	-3.12	-2.76	-2.50
TCGA-BT-A42C-10A-01D-A23K-08_BLCA	-2.45	-2.49	-2.49	0.00	0.00	0.00	-2.47	-2.42	-2.66	-3.39	-2.93	0.00	-2.75	-2.55	-3.06	0.00	-2.41
TCGA-BT-A42E-10A-01D-A23U-08_BLCA	-2.56	-2.56	-2.59	-4.40	-2.56	-2.66	-2.55	-2.52	-2.45	0.00	-2.82	-2.70	0.00	0.00	-2.95	-2.70	-2.44
TCGA-BT-A42F-10A-01D-A23U-08_BLCA	-2.42	-2.70	-2.68	-2.74	-2.62	-2.61	-2.49	-2.49	-2.39	0.00	-4.54	0.00	0.00	-4.54	0.00	-2.52	-2.40
TCGA-BW-A5NO-10A-01D-A27I-10_LIHC	-2.24	0.00	0.00	-2.41	-2.64	-2.36	-2.35	-2.53	-2.44	0.00	-3.03	0.00	-2.52	-2.37	-2.77	0.00	-2.28
TCGA-BW-A5NP-10A-01D-A27I-10_LIHC	-2.47	0.00	0.00	-2.59	-2.42	-2.33	-2.26	-2.42	-2.63	-3.51	-2.89	-2.50	0.00	-2.54	-2.91	0.00	-2.37
TCGA-BW-A5NQ-10A-01D-A27I-10_LIHC	-2.52	-4.33	0.00	-2.46	-2.35	-2.34	-2.33	-2.31	-2.34	0.00	0.00	0.00	0.00	0.00	-2.97	-2.68	-2.44
TCGA-C4-A0EZ-10A-01D-A10S-08_BLCA	-2.49	-4.64	0.00	-2.74	-2.62	-2.65	-2.69	-2.52	-2.78	-3.56	-2.89	0.00	-2.80	-2.70	0.00	-2.80	-2.57
TCGA-C4-A0F0-10A-01D-A10S-08_BLCA	-2.60	-2.83	-2.77	-3.02	-2.54	-2.69	-2.72	-2.57	-2.58	0.00	-2.95	-2.79	-4.66	-4.18	-3.09	-2.78	-2.64
TCGA-C4-A0F1-10A-01D-A10S-08_BLCA	-2.53	-2.58	-2.57	-4.52	0.00	-4.22	-2.60	-2.42	-2.51	0.00	0.00	0.00	-4.52	0.00	-2.98	-2.65	-2.46
TCGA-C4-A0F6-10A-01D-A10S-08_BLCA	-2.53	-2.69	-2.68	-2.86	-2.63	-2.66	-2.56	-2.48	-2.55	0.00	0.00	0.00	0.00	-4.55	-3.02	-2.72	-2.54
TCGA-C4-A0F7-10A-01D-A10S-08_BLCA	-2.58	-4.58	-4.58	-2.84	-2.56	-2.57	-2.64	-2.52	-2.57	-4.58	0.00	-4.58	0.00	-4.28	0.00	-2.62	-2.55
TCGA-C5-A0TN-10B-01D-A14W-08_CESC	-2.50	-4.44	-4.44	-2.67	-2.49	-2.52	-2.48	-2.52	-2.46	0.00	-4.44	-4.44	0.00	-4.44	-2.99	-4.44	-2.39
TCGA-C5-A1BE-10A-01D-A13W-08_CESC	-2.50	-2.74	-2.68	-2.88	-2.66	-2.66	-2.52	-2.59	-4.42	-3.11	-2.70	-2.69	-2.75	-2.48	0.00	-4.72	-2.43
TCGA-C5-A1BF-10A-01D-A13W-08_CESC	-2.42	-4.69	-4.69	-2.69	-2.42	-2.46	-2.46	-2.48	-2.40	0.00	0.00	-4.21	0.00	-4.38	-3.22	-2.78	-2.34
TCGA-C5-A1BI-10A-01D-A13W-08_CESC	-2.46	-2.72	-2.74	-2.90	-2.65	-2.67	-2.51	-2.56	-2.68	-3.26	-3.06	-4.70	-2.80	-2.61	-3.01	0.00	-2.38
TCGA-C5-A1BJ-10A-01D-A13W-08_CESC	-2.51	-2.60	-2.55	-4.77	-2.65	-2.64	-2.54	-2.56	-2.61	-3.41	-2.80	-2.68	-2.82	-2.68	-3.14	0.00	-2.37
TCGA-C5-A1BK-10A-01D-A13W-08_CESC	-2.49	-2.77	-2.76	-2.93	-2.42	-2.56	-2.50	-2.60	-2.51	0.00	-3.13	-2.69	0.00	0.00	-3.00	0.00	-2.44
TCGA-C5-A1BL-10A-01D-A13W-08_CESC	-2.44	0.00	-4.68	-2.56	-2.47	-2.48	-2.51	-2.51	-2.42	0.00	-4.68	0.00	0.00	-4.20	-3.04	-2.70	-2.33
TCGA-C5-A1BM-10A-01D-A13W-08_CESC	-2.43	-2.64	-2.64	-2.88	-2.59	-2.56	-2.49	-2.52	-2.37	0.00	0.00	-4.65	0.00	-4.65	-2.92	-4.65	-2.37
TCGA-C5-A1BN-10A-01D-A14W-08_CESC	-2.52	-2.65	-2.70	-2.91	-2.65	-2.68	-2.53	-2.62	-2.71	-3.32	-2.96	-4.49	-2.78	-2.62	0.00	-2.78	-2.47
TCGA-C5-A1BQ-10A-01D-A20U-09_CESC	-2.98	-2.87	-2.83	-3.36	-2.60	-2.66	-2.67	-2.60	-2.60	0.00	-2.89	-2.82	-4.62	-4.62	0.00	-2.52	-2.73
TCGA-C5-A1M5-10A-01D-A13W-08_CESC	-2.38	-2.45	-2.43	-4.30	-4.60	-4.60	-2.40	-2.39	-2.34	-4.60	0.00	-4.60	0.00	0.00	-3.10	-2.75	-2.32
TCGA-C5-A1M6-10A-01D-A13W-08_CESC	-2.42	0.00	0.00	-2.72	-2.45	-2.48	-2.52	-2.62	-2.50	0.00	0.00	0.00	0.00	-4.67	0.00	-2.53	-2.37
TCGA-C5-A1M7-10A-01D-A13W-08_CESC	-2.41	-2.69	-2.68	-2.84	-2.63	-2.61	-2.44	-2.55	-2.44	0.00	0.00	-4.59	0.00	-4.59	-2.81	0.00	-2.30
TCGA-C5-A1M8-10A-01D-A13W-08_CESC	-2.47	-2.75	-2.70	-2.89	-2.62	-2.64	-2.47	-2.50	-2.59	-3.61	-3.02	-2.70	-4.35	-2.61	-3.19	0.00	-2.40
TCGA-C5-A1M9-10A-01D-A13W-08_CESC	-2.46	0.00	-4.18	-2.69	-2.46	-2.45	-2.48	-2.57	-2.53	0.00	0.00	0.00	0.00	-4.65	0.00	-2.39	-2.36
TCGA-C5-A1ME-10A-01D-A13W-08_CESC	-2.50	-4.43	0.00	-2.67	-2.49	-2.52	-2.59	-2.57	-2.63	-3.50	-2.95	0.00	-2.86	-2.71	-3.16	-4.43	-2.41
TCGA-C5-A1MF-10A-01D-A13W-08_CESC	-2.46	-4.42	-4.73	-2.59	-2.46	-2.48	-2.55	-2.46	-2.42	0.00	0.00	0.00	0.00	-4.42	0.00	-2.52	-2.36
TCGA-C5-A1MH-10A-01D-A14W-08_CESC	-2.45	-4.46	0.00	-2.69	-2.50	-2.50	-2.51	-2.54	-2.43	0.00	0.00	0.00	-4.46	0.00	0.00	-2.58	-2.42
TCGA-C5-A1MI-10A-01D-A14W-08_CESC	-2.48	-2.68	-2.70	-2.84	-2.61	-2.66	-2.54	-2.50	-2.66	-3.18	-2.84	0.00	-2.69	-2.62	0.00	-2.78	-2.45
TCGA-C5-A1MJ-10A-01D-A14W-08_CESC	-2.65	-2.77	-2.75	-2.95	-2.50	-2.62	-2.58	-2.50	-2.53	-3.40	-2.91	-2.84	0.00	0.00	-3.18	-2.77	-2.61
TCGA-C5-A1MK-10A-01D-A14W-08_CESC	-2.42	-4.49	0.00	-2.64	-2.50	-2.55	-2.57	-2.46	-2.50	0.00	0.00	-4.49	-4.19	-4.19	-3.07	-2.70	-2.50
TCGA-C5-A1ML-10A-01D-A14W-08_CESC	-2.58	0.00	0.00	-2.67	-2.49	-2.55	-2.55	-2.51	-2.65	-3.26	-2.90	0.00	-2.80	-2.61	0.00	-2.71	-2.51
TCGA-C5-A1MN-10A-01D-A14W-08_CESC	-2.43	0.00	-4.51	-2.67	-2.52	-2.55	-2.58	-2.61	-2.65	-3.34	-2.90	0.00	-2.71	-2.63	0.00	-2.80	-2.48
TCGA-C5-A1MP-10A-01D-A14W-08_CESC	-2.55	-2.69	-2.70	-2.91	-2.47	-2.56	-2.62	-2.67	-2.51	0.00	-3.02	-2.72	0.00	-4.51	-3.01	0.00	-2.50
TCGA-C5-A1MQ-10A-01D-A14W-08_CESC	-2.62	-2.76	-2.81	-2.86	-2.51	-2.59	-2.61	-2.63	0.00	-3.27	-2.67	-2.57	-2.80	-2.55	0.00	0.00	-2.47
TCGA-C5-A2LS-10A-01D-A22X-09_CESC	-2.68	0.00	-4.48	-2.92	-2.45	-2.44	-2.50	-2.44	-2.37	0.00	-4.48	-4.48	0.00	0.00	0.00	-2.39	-2.51
TCGA-C5-A2LT-10A-01D-A18J-09_CESC	-2.72	-2.72	-2.74	-3.63	-2.67	-2.71	-2.47	-2.52	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.47
TCGA-C5-A2LV-10A-01D-A18J-09_CESC	-2.76	0.00	0.00	-2.96	-2.45	-2.39	-2.42	-2.56	-2.39	0.00	0.00	0.00	0.00	-4.41	-2.74	-3.93	-2.52
TCGA-C5-A2LX-10A-01D-A18J-09_CESC	-2.70	0.00	0.00	-2.91	-2.51	-2.44	-2.44	-2.52	-2.42	0.00	0.00	0.00	0.00	-4.41	0.00	-2.46	-2.54
TCGA-C5-A2LY-10A-01D-A18J-09_CESC	-2.87	-4.53	0.00	-2.83	-2.57	-2.53	-2.45	-2.51	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.65
TCGA-C5-A2LZ-10B-01D-A20U-09_CESC	-2.92	-2.75	-2.69	0.00	-2.81	-2.84	-2.66	-2.59	-2.78	-3.34	-2.70	-2.88	-2.78	-2.85	-3.16	-3.90	-2.85
TCGA-C5-A2M1-10A-01D-A18J-09_CESC	-2.83	0.00	-4.06	-2.98	-2.52	-2.50	-2.51	-2.65	-2.62	-3.52	-2.93	0.00	-2.71	-2.82	0.00	-2.84	-2.63
TCGA-C5-A2M2-10A-01D-A18J-09_CESC	-2.80	-2.72	-2.78	-3.17	-2.49	-2.62	-2.62	-2.63	-4.21	-3.31	-2.56	-2.56	-2.80	-2.59	0.00	-4.52	-2.65
TCGA-C5-A3HD-10A-01D-A20U-09_CESC	-2.78	-3.83	-4.23	-2.97	-2.57	-2.61	-2.56	-2.63	-2.55	0.00	-3.93	0.00	0.00	-3.76	-3.00	-2.83	-2.63
TCGA-C5-A3HF-10A-01D-A20U-09_CESC	-2.73	-2.78	-2.76	-3.29	-2.77	-2.78	-2.55	-2.54	-2.40	-4.59	-4.59	-3.81	-3.75	-4.29	-3.01	-2.73	-2.68
TCGA-C5-A3HL-10A-01D-A20U-09_CESC	-2.90	-3.96	-3.62	-3.02	-2.61	-2.64	-2.63	-2.57	-2.67	-3.55	-2.95	-4.66	-2.86	-2.78	0.00	-2.89	-2.70
TCGA-C8-A12K-10A-01D-A110-09_BRCA	-2.80	0.00	0.00	-2.83	-2.53	-2.52	-2.51	-2.49	-2.40	0.00	0.00	0.00	0.00	0.00	-2.99	-2.72	-2.63
TCGA-C8-A12L-10A-01D-A110-09_BRCA	-2.93	0.00	-4.52	-2.92	-2.51	-2.55	-2.51	-2.65	-2.47	0.00	0.00	0.00	0.00	-4.83	-2.93	0.00	-2.71
TCGA-C8-A12M-10A-01D-A110-09_BRCA	-3.05	-2.48	-2.52	0.00	0.00	-4.85	-2.48	-2.75	0.00	-3.12	-2.79	-2.51	0.00	-2.53	0.00	0.00	-2.66
TCGA-C8-A12N-10A-01D-A110-09_BRCA	-2.84	0.00	0.00	-2.92	-2.58	-2.58	-2.53	-2.58	-2.43	0.00	0.00	0.00	0.00	-4.75	-3.00	-2.76	-2.76
TCGA-C8-A12O-10A-01D-A110-09_BRCA	-2.84	0.00	0.00	-2.91	-2.56	-2.52	-2.54	-2.62	-2.53	0.00	0.00	-4.63	0.00	0.00	-2.84	0.00	-2.71
TCGA-C8-A12P-10A-01D-A110-09_BRCA	-2.98	0.00	0.00	-2.81	-2.58	-2.52	-2.51	-2.67	-2.70	-3.40	-2.83	0.00	-2.73	-2.80	-3.15	0.00	-2.67
TCGA-C8-A12Q-10A-01D-A110-09_BRCA	-3.00	0.00	-4.38	-3.05	-2.63	-2.69	-2.66	-2.70	-2.80	-3.41	-2.88	0.00	-2.80	-2.80	-3.20	0.00	-2.81
TCGA-C8-A12T-10A-01D-A110-09_BRCA	-2.75	0.00	0.00	-2.88	-2.50	-2.50	-2.50	-2.53	-2.44	0.00	0.00	0.00	0.00	0.00	-2.85	-4.67	-2.69
TCGA-C8-A12U-10A-01D-A110-09_BRCA	-2.98	-2.82	-2.77	-3.22	-2.53	-2.65	-2.68	-2.87	-2.67	0.00	-3.01	-2.75	0.00	0.00	-3.22	-2.98	-2.82
TCGA-C8-A12V-10A-01D-A110-09_BRCA	-2.81	0.00	0.00	-2.86	-2.52	-2.47	-2.50	-2.51	-2.47	0.00	0.00	0.00	0.00	0.00	-2.81	0.00	-2.66
TCGA-C8-A12W-10A-01D-A110-09_BRCA	-2.81	-2.70	-2.72	-3.03	-2.73	-2.82	-2.60	-2.64	-2.50	0.00	0.00	0.00	0.00	0.00	-2.94	0.00	-2.69
TCGA-C8-A12X-10A-01D-A110-09_BRCA	-2.79	0.00	0.00	-2.80	-2.74	-2.50	-2.53	-2.61	-2.41	0.00	0.00	0.00	0.00	0.00	-3.11	-2.78	-2.56
TCGA-C8-A12Y-10A-01D-A12B-09_BRCA	-2.89	0.00	-4.64	-2.98	-2.59	-2.54	-2.49	-2.62	-2.53	0.00	0.00	0.00	0.00	-4.64	0.00	-2.51	-2.80
TCGA-C8-A12Z-10A-01D-A110-09_BRCA	-2.85	0.00	0.00	-2.90	-2.59	-2.58	-2.52	-2.57	-2.39	0.00	0.00	-4.72	0.00	0.00	0.00	-2.48	-2.66
TCGA-C8-A130-10A-01D-A110-09_BRCA	-2.92	0.00	0.00	-2.73	-2.54	-2.58	-2.55	-2.64	-2.52	0.00	0.00	0.00	0.00	0.00	-2.93	0.00	-2.68
TCGA-C8-A131-10A-01D-A110-09_BRCA	-2.96	0.00	0.00	-2.94	-2.59	-2.66	-2.61	-2.63	-2.61	0.00	0.00	0.00	0.00	0.00	-3.06	-2.84	-2.75
TCGA-C8-A132-10A-01D-A110-09_BRCA	-2.86	0.00	0.00	-3.00	-2.62	-2.60	-2.59	-2.59	-2.59	0.00	0.00	0.00	0.00	-4.85	-3.05	-2.84	-2.73
TCGA-C8-A133-10A-01D-A12B-09_BRCA	-3.04	-5.14	-4.84	-3.00	-2.60	-2.65	-2.60	-2.65	-2.81	-3.45	-2.89	-5.14	-2.88	-2.83	0.00	-2.90	-2.77
TCGA-C8-A134-10A-01D-A110-09_BRCA	-2.88	-2.79	-2.75	-3.08	-2.51	-2.62	-2.63	-2.69	-2.62	0.00	-2.78	-2.77	-4.81	-4.81	-2.91	0.00	-2.80

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-C8-A135-10A-02D-A110-09_BRCA	-2.85	0.00	-4.65	-2.99	-2.64	-2.59	-2.64	-2.67	-2.68	-4.95	0.00	0.00	0.00	-4.95	-2.82	0.00	-2.79
TCGA-C8-A137-10A-02D-A110-09_BRCA	-2.78	0.00	-4.63	-2.90	-2.56	-2.53	-2.53	-2.57	-2.51	0.00	0.00	-4.63	0.00	0.00	-2.78	0.00	-2.68
TCGA-C8-A138-10A-01D-A110-09_BRCA	-3.04	-2.72	-2.75	-3.15	-2.64	-2.69	-2.70	-2.67	-2.85	-3.36	-2.67	-2.82	-2.81	-2.95	-3.31	0.00	-2.77
TCGA-C8-A1HE-10A-01D-A13O-09_BRCA	-2.97	0.00	0.00	-2.85	-2.58	-2.56	-2.48	-2.64	-2.60	0.00	0.00	0.00	0.00	0.00	0.00	-2.62	-2.72
TCGA-C8-A1HF-10A-01D-A135-09_BRCA	-2.90	-5.01	0.00	-3.18	-2.64	-2.62	-2.62	-2.62	-2.55	0.00	0.00	-5.01	0.00	0.00	0.00	-2.53	-2.76
TCGA-C8-A1HG-10A-01D-A135-09_BRCA	-2.93	-2.84	-2.84	-3.12	-2.78	-2.81	-2.60	-2.59	-2.60	0.00	0.00	-5.01	0.00	-5.01	-3.11	-2.82	-2.77
TCGA-C8-A1HI-10A-01D-A135-09_BRCA	-2.89	0.00	-5.03	-2.97	-2.63	-2.59	-2.60	-2.62	-2.63	0.00	0.00	0.00	0.00	-5.03	-3.06	-2.83	-2.79
TCGA-C8-A1HJ-10A-01D-A13O-09_BRCA	-3.13	0.00	0.00	-3.02	-2.67	-2.74	-2.65	-2.75	-2.89	-3.38	-3.12	-2.79	0.00	-2.88	0.00	-3.09	-2.81
TCGA-C8-A1HK-10A-01D-A13O-09_BRCA	-2.83	-2.71	-2.80	-3.06	-2.75	-2.73	-2.45	-2.59	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.67	-2.60
TCGA-C8-A1HL-10A-01D-A135-09_BRCA	-2.91	0.00	-5.10	-2.94	-2.67	-2.74	-2.63	-2.71	-2.87	-3.62	-2.89	0.00	-2.87	-2.90	-3.23	0.00	-2.84
TCGA-C8-A1HM-10A-01D-A135-09_BRCA	-2.98	0.00	0.00	-2.87	-2.71	-2.68	-2.67	-2.64	-2.87	-3.67	-2.91	-2.82	0.00	-2.85	-3.09	0.00	-2.82
TCGA-C8-A1HN-10A-01D-A135-09_BRCA	-2.85	0.00	-4.83	-2.98	-2.59	-2.62	-2.51	-2.60	-2.50	-4.83	0.00	0.00	-4.83	0.00	-2.84	0.00	-2.78
TCGA-C8-A1HO-10A-01D-A188-09_BRCA	-2.95	0.00	-4.68	-2.95	-2.64	-2.61	-2.55	-2.52	-2.60	0.00	0.00	-4.68	0.00	0.00	-3.08	-2.81	-2.78
TCGA-C8-A26V-10A-01D-A16D-09_BRCA	-3.05	0.00	0.00	-2.92	-2.54	-2.65	-2.57	-2.55	-2.73	-3.50	-3.12	-2.94	0.00	-4.71	-3.04	-4.71	-2.88
TCGA-C8-A26W-10A-01D-A16D-09_BRCA	-2.90	-4.81	0.00	-2.88	-2.76	-2.72	-2.73	-2.72	-2.79	-3.40	-2.97	0.00	-2.85	-2.91	-3.19	-4.34	-2.83
TCGA-C8-A26X-10A-01D-A16D-09_BRCA	-3.10	-2.85	-2.83	-3.12	-2.63	-2.72	-2.67	-2.75	-2.75	-3.40	-3.03	-2.84	0.00	0.00	-3.01	0.00	-2.81
TCGA-C8-A26Y-10A-01D-A16D-09_BRCA	-2.82	0.00	0.00	-2.85	-2.60	-2.64	-2.60	-2.62	-2.57	0.00	0.00	0.00	0.00	-4.47	-3.09	-2.78	-2.76
TCGA-C8-A26Z-10A-01D-A16D-09_BRCA	-2.86	-2.69	-2.71	-3.03	-2.70	-2.68	-2.56	-2.62	-2.55	0.00	0.00	0.00	-4.53	0.00	-3.09	-2.83	-2.71
TCGA-C8-A273-10A-01D-A16D-09_BRCA	-3.05	-2.81	-2.94	-3.16	-2.65	-2.71	-2.67	-2.68	-2.96	-3.42	-2.86	-2.72	0.00	-2.93	-3.26	0.00	-2.85
TCGA-C8-A274-10A-01D-A16D-09_BRCA	-2.92	0.00	0.00	-2.90	-2.60	-2.69	-2.58	-2.63	-2.74	-3.46	-2.86	0.00	-2.89	-2.81	0.00	-2.86	-2.72
TCGA-C8-A275-10A-01D-A16D-09_BRCA	-2.91	-2.83	-2.82	-3.12	-2.83	-2.88	-2.62	-2.66	-2.80	-3.42	-3.03	-2.88	0.00	-2.79	0.00	-2.91	-2.74
TCGA-C8-A278-10A-01D-A167-09_BRCA	-2.89	0.00	0.00	-3.05	-2.66	-2.66	-2.63	-2.72	-2.89	-3.33	-2.86	0.00	-2.82	-2.83	0.00	-2.99	-2.71
TCGA-C8-A27A-10B-01D-A167-09_BRCA	-2.84	-4.47	0.00	-2.96	-2.64	-2.66	-2.61	-2.64	-2.75	-3.24	-2.98	0.00	-2.90	-2.84	-3.15	0.00	-2.77
TCGA-C8-A27B-10A-01D-A167-09_BRCA	-2.76	-4.29	0.00	-3.12	-2.62	-2.66	-2.47	-2.50	-2.54	-4.29	0.00	-4.29	0.00	0.00	-2.76	-4.29	-2.65
TCGA-C8-A3M7-10A-01D-A21Q-09_BRCA	-2.81	-3.50	-3.33	-3.10	-2.62	-2.55	-2.54	-2.70	-2.57	-3.40	-2.97	-2.73	0.00	-2.79	0.00	-2.89	-2.63
TCGA-C8-A3M8-10A-01D-A20S-09_BRCA	-2.80	-3.70	0.00	-2.98	-2.57	-2.52	-2.49	-2.62	-2.65	-3.44	-2.85	-3.92	-2.96	-2.84	0.00	-2.85	-2.65
TCGA-C9-A47Z-10A-01D-A24F-08_HNSC	-2.45	-4.54	0.00	-2.69	-2.63	-2.60	-2.61	-2.62	-2.71	-3.20	-2.81	0.00	-2.72	-2.67	0.00	-2.81	-2.59
TCGA-C9-A480-10A-01D-A24F-08_HNSC	-2.51	0.00	-4.41	-2.73	-2.53	-2.57	-2.56	-2.60	-2.56	0.00	0.00	0.00	0.00	0.00	-2.88	-4.41	-2.52
TCGA-CA-5796-10A-01D-1650-10_COAD	-2.61	0.00	0.00	-2.69	-2.44	-2.55	-2.37	-2.86	-2.64	-3.38	-3.03	-2.83	0.00	-2.59	-3.41	0.00	-2.48
TCGA-CA-5797-10A-01D-1650-10_COAD	-2.50	0.00	-4.47	-2.81	-2.48	-2.46	-2.37	-2.59	-2.62	-3.13	-2.93	-2.82	0.00	-2.77	-3.32	0.00	-2.36
TCGA-CA-6716-10A-01D-1835-10_COAD	-2.64	-2.99	-2.84	-2.88	-2.56	-2.51	-2.48	-2.63	-2.47	0.00	-3.14	-2.99	0.00	0.00	-3.08	0.00	-2.40
TCGA-CA-6719-10A-01D-1835-10_COAD	-2.55	0.00	0.00	-2.79	-2.52	-2.48	-2.41	-2.77	-2.44	0.00	0.00	0.00	0.00	0.00	-3.12	-4.12	-2.44
TCGA-CC-5258-10A-01D-A12Z-10_LIHC	-2.58	0.00	0.00	-2.71	-2.46	-2.58	-2.31	-2.63	-2.40	0.00	0.00	0.00	0.00	-4.43	-3.17	0.00	-2.32
TCGA-CC-5259-10A-01D-A20W-10_LIHC	-2.35	0.00	0.00	-2.63	-2.34	-2.34	-2.22	-2.39	-2.28	0.00	-4.26	-4.26	0.00	0.00	-2.67	0.00	-2.31
TCGA-CC-5260-10B-01D-A12Z-10_LIHC	-2.51	0.00	-4.18	-2.70	-2.48	-2.41	-2.36	-2.70	-2.34	0.00	0.00	0.00	0.00	-4.48	-3.58	-2.94	-2.31
TCGA-CC-5261-10A-01D-A12Z-10_LIHC	-2.58	0.00	0.00	-2.72	-2.54	-2.46	-2.41	-2.63	-2.60	-3.26	-2.91	-4.16	-2.85	-2.75	0.00	-3.14	-2.37
TCGA-CC-5262-10B-01D-A12Z-10_LIHC	-2.56	0.00	-4.24	-2.83	-2.53	-2.62	-2.52	-2.76	0.00	-3.29	-2.78	-2.79	-2.88	-2.55	0.00	0.00	-2.52
TCGA-CC-5263-10B-01D-A12Z-10_LIHC	-2.51	0.00	0.00	-2.75	-2.47	-2.53	-2.38	-2.68	-2.30	0.00	0.00	0.00	0.00	0.00	-3.53	-2.92	-2.35
TCGA-CC-5264-10A-01D-A12Z-10_LIHC	-2.55	0.00	0.00	-2.89	-2.50	-2.41	-2.36	-2.71	-2.60	-3.25	-3.17	0.00	-3.01	-2.70	0.00	-3.06	-2.37
TCGA-CC-A123-10A-01D-A12Z-10_LIHC	-2.48	0.00	0.00	-2.75	-2.48	-2.51	-2.39	-2.72	-2.67	-3.33	-2.99	0.00	-2.86	-2.82	0.00	-2.93	-2.34
TCGA-CC-A1HT-10A-01D-A12Z-10_LIHC	-2.45	0.00	0.00	-2.75	-2.42	-2.47	-2.39	-2.59	-2.38	0.00	0.00	0.00	0.00	0.00	-2.92	0.00	-2.30
TCGA-CC-A3M9-10A-01D-A20W-10_LIHC	-2.31	0.00	0.00	-2.60	-2.38	-2.27	-2.16	-2.38	-2.15	0.00	0.00	-3.98	0.00	0.00	-3.00	-2.69	-2.27
TCGA-CC-A3MA-10A-01D-A20W-10_LIHC	-2.38	0.00	-4.01	-2.63	-2.41	-2.35	-2.27	-2.47	-2.52	-3.41	-2.93	0.00	-2.62	-2.57	0.00	-2.68	-2.42
TCGA-CC-A3MB-10A-01D-A20W-10_LIHC	-2.36	0.00	0.00	-2.73	-2.31	-2.32	-2.29	-2.45	-2.22	0.00	0.00	0.00	0.00	0.00	-2.75	0.00	-2.32
TCGA-CC-A3MC-10A-01D-A22F-10_LIHC	-2.43	-2.57	-2.69	-2.90	-2.68	-2.79	-2.57	-2.81	-2.47	0.00	-2.92	0.00	-2.69	-2.68	-3.07	0.00	-2.35
TCGA-CC-A5UC-10A-01D-A28X-10_LIHC	-2.38	0.00	0.00	-2.59	-2.37	-2.27	-2.25	-2.37	-2.35	0.00	0.00	0.00	0.00	-3.93	-2.98	-2.59	-2.41
TCGA-CC-A5UD-10A-01D-A28X-10_LIHC	-2.40	0.00	0.00	-2.51	-2.44	-2.30	-2.28	-2.28	-2.48	-3.63	-2.72	-2.52	0.00	-2.52	-2.75	-4.23	-2.46
TCGA-CC-A5UE-10A-01D-A28X-10_LIHC	-2.41	0.00	0.00	-2.58	-2.29	-2.19	-2.26	-2.30	-2.35	0.00	0.00	0.00	0.00	0.00	-2.76	-2.57	-2.37
TCGA-CD-5798-10A-01D-1600-08_STAD	-2.54	-2.78	-2.78	-3.03	-2.69	-2.69	-2.59	-2.66	-2.72	-3.27	-3.03	-2.73	-4.68	-2.69	0.00	-2.81	-2.54
TCGA-CD-5799-10A-01D-1600-08_STAD	-2.52	-4.61	-4.01	-2.62	-2.53	-2.53	-2.58	-2.59	-2.57	0.00	0.00	0.00	-4.61	0.00	-2.95	0.00	-2.54
TCGA-CD-5800-10A-01D-1600-08_STAD	-2.43	0.00	0.00	-2.77	-2.51	-2.54	-2.59	-2.62	-2.54	0.00	0.00	0.00	-4.60	-4.60	-2.98	-4.60	-2.50
TCGA-CD-5801-10A-01D-1600-08_STAD	-2.52	-2.72	-2.70	-2.91	-2.65	-2.68	-2.55	-2.51	-2.51	0.00	0.00	0.00	0.00	0.00	-3.06	-2.72	-2.51
TCGA-CD-5802-10A-01D-1600-08_STAD	-2.56	0.00	-4.36	-2.84	-2.55	-2.54	-2.67	-2.50	-2.50	0.00	-4.66	-4.66	0.00	-4.18	-3.10	-2.72	-2.50
TCGA-CD-5803-10A-01D-1600-08_STAD	-2.50	0.00	-4.32	-2.82	-2.48	-2.53	-2.59	-2.50	-2.45	0.00	0.00	-4.14	-4.62	0.00	-3.10	-2.74	-2.50
TCGA-CD-5804-10A-01D-2053-08_STAD	-2.51	-2.64	-2.66	-2.80	-2.53	-2.57	-2.50	-2.52	-2.39	0.00	0.00	0.00	0.00	0.00	-2.87	-2.61	-2.40
TCGA-CD-5813-10A-01D-1600-08_STAD	-2.54	0.00	0.00	-2.88	-2.54	-2.54	-2.63	-2.55	-2.58	0.00	0.00	0.00	-4.65	-4.65	-3.10	-2.85	-2.54
TCGA-CD-8524-10A-01D-2341-08_STAD	-2.57	0.00	0.00	-2.64	-2.63	-2.58	-2.67	-2.58	-2.68	-3.32	-2.89	0.00	-2.75	-2.68	-3.04	0.00	-2.48
TCGA-CD-8525-10A-01D-2341-08_STAD	-2.41	0.00	-4.59	-2.57	-2.55	-2.58	-2.57	-2.49	-2.48	0.00	0.00	0.00	0.00	-4.59	-3.03	-2.71	-2.48
TCGA-CD-8526-10A-01D-2341-08_STAD	-2.56	-2.75	-2.73	-2.83	-2.68	-2.72	-2.60	-2.59	-2.65	-3.22	-2.95	0.00	-2.73	-2.67	0.00	-2.75	-2.54
TCGA-CD-8527-10A-01D-2341-08_STAD	-2.59	0.00	-4.60	-2.81	-2.58	-2.62	-2.61	-2.65	-2.74	-3.30	-2.86	0.00	-2.78	-2.66	0.00	-2.77	-2.54
TCGA-CD-8528-10A-01D-2341-08_STAD	-2.54	0.00	0.00	-2.63	-2.59	-2.57	-2.64	-2.58	-2.67	-3.33	-2.84	0.00	-2.82	-2.71	-3.00	0.00	-2.51
TCGA-CD-8529-10A-01D-2341-08_STAD	-2.51	-2.71	-2.64	-2.84	-2.64	-2.66	-2.57	-2.61	-2.48	0.00	0.00	0.00	0.00	-4.57	-3.06	-2.64	-2.46
TCGA-CD-8530-10A-01D-2341-08_STAD	-2.59	0.00	-4.32	-2.77	-2.60	-2.57	-2.63	-2.59	-2.69	-3.30	-2.85	-2.75	0.00	-2.66	-3.02	0.00	-2.58
TCGA-CD-8531-10A-01D-2341-08_STAD	-2.55	0.00	0.00	-2.77	-2.62	-2.59	-2.58	-2.54	-2.65	-3.26	-2.84	-2.71	0.00	-2.67	-3.15	0.00	-2.43
TCGA-CD-8532-10A-01D-2341-08_STAD	-2.52	0.00	-4.22	-2.68	-2.49	-2.54	-2.54	-2.60	-2.47	0.00	0.00	0.00	0.00	-4.52	-2.91	0.00	-2.45
TCGA-CD-8533-10A-01D-2341-08_STAD	-2.55	-2.77	-2.71	-2.89	-2.67	-2.72	-2.77	-2.73	-3.67	-3.25	-2.65	-2.56	-3.77	-2.53	0.00	-4.37	-2.45
TCGA-CD-8534-10A-01D-2341-08_STAD	-2.40	0.00	0.00	-2.62	-2.56	-2.57	-2.56	-2.52	-2.67	-3.33	-2.94	0.00	-2.79	-2.68	0.00	-2.93	-2.46
TCGA-CD-8535-10A-01D-2341-08_STAD	-2.50	-2.72	-2.70	-2.75	-2.46	-2.46	-2.59	-2.55	-2.46	0.00	-2.85	-2.70	-4.43	-3.23	0.00	-3.35	-2.44
TCGA-CD-8536-10A-01D-2341-08_STAD	-2.54	0.00	0.00	-2.74	-2.54	-2.54	-2.53	-2.50	-2.51	0.00	0.00	0.00	0.00	0.00	-3.07	-2.71	-2.45
TCGA-CD-A486-10A-01D-A24F-08_STAD	-2.66	-2.79	-2.83	-2.95	-2.54	-2.67	-2.65	-2.62	-2.73	-3.30	-2.71	-2.73	-2.81	-2.72	0.00	-2.80	-2.60
TCGA-CD-A487-10A-01D-A24F-08_STAD	-2.50	-4.45	0.00	-2.79	-2.49	-2.58	-2.54	-2.56	-2.48	0.00	-3.97	-3.67	0.00	-4.15	-2.89	-4.45	-2.46
TCGA-CD-A489-10A-01D-A24F-08_STAD	-2.62	0.00	0.00	-2.83	-2.57	-2.63	-2.60	-2.57	-2.62	-3.32	-2.86	-2.72	0.00	-2.69	-3.04	-4.17	-2.58
TCGA-CD-A48A-10A-01D-A24F-08_STAD	-2.56	-4.47	-4.47	-2.81	-2.57	-2.61	-2.61	-2.53	-2.59	0.00	0.00	0.00	0.00	-4.47	-2.98	-2.66	-2.52
TCGA-CD-A48C-10A-01D-A24F-08_STAD	-2.53	0.00	0.00	-2.79	-2.56	-2.53	-2.59	-2.44	-2.57	0.00	-4.18	-3.88	0.00	-3.78	-3.02	-2.70	-2.56
TCGA-CD-A4MG-10A-01D-A25E-08_STAD	-2.56	0.00	0.00	-2.76	-2.53	-2.60	-2.62	-2.53	-2.58	0.00	0.00	0.00	0.00	0.00	-3.06	-2.77	-2.56
TCGA-CD-A4MH-10A-01D-A25E-08_STAD	-2.62	-2.80	-2.82	-2.99	-2.57	-2.68	-2.66	-2.64	-2.73	-3.53	-2.75	-2.79	-2.90	-2.73	-3.18	-4.10	-2.60
TCGA-CD-A4MI-10A-01D-A25E-08_STAD	-2.39	-4.43	0.00	-2.67	-2.48	-2.50	-2.49	-2.48	-2.47	-4.43	-3.95	0.00	-4.43	-4.13	-2.85	0.00	-2.45
TCGA-CD-A4MJ-10A-01D-A25E-08_STAD	-2.41	-3.77	-3.99	-2.75	-2.50	-2.53	-2.55	-2.46	-2.42	0.00	-4.47	0.00	-3.87	-3.87	-2.93	-2.67	-2.45
TCGA-CE-A13K-10A-01D-A10S-08_THCA	-2.61	-2.77	-2.73	-2.95	-2.72	-2.71	-2.67	-2.56	-4.60	-3.26	-2.76	0.00	-2.66	-2.61	0.00	0.00	-2.56
TCGA-CE-A27D-10A-01D-A17V-08_THCA	-2.46	0.00	0.00	-2.71	-2.50	-2.49	-2.49	-2.53	-2.46	0.00	0.00	0.00	0.00	0.00	-2.94	0.00	-2.47
TCGA-CE-A3MD-10A-01D-A20C-08_THCA	-2.63	-2.70	-2.66	-4.60	-2.73	-2.73	-2.63	-2.57	-2.60	-3.34	-2.98	-2.78	-4.60	0.00	-3.09	-2.77	-2.58
TCGA-CE-A3ME-10A-01D-A20C-08_THCA	-2.45	-4.28	-4.28	-2.63	-2.64	-2.58	-2.65	-2.57	-2.67	-3.22	-2.84	0.00	-2.82	-2.69	-3.12	0.00	-2.54
TCGA-CE-A481-10A-01D-A23U-08_THCA	-2.51	-2.62	-2.62	-2.88	-2.64	-2.63	-2.62	-2.66	-3.66	-3.32	-2.63	-2.65	-2.83	-2.55	0.00	-3.88	-2.42
TCGA-CE-A482-10A-01D-A23U-08_THCA	-2.55	-4.42	0.00	-2.73	-2.54	-2.54	-2.48	-2.47	-2.43	0.00	0.00	0.00	0.00	-4.42	-2.98	-2.67	-2.50
TCGA-CE-A483-10A-01D-A23U-08_THCA	-2.36	-2.72	-2.72	-2.85	-2.64	-2.56	-2.49	-2.61	-2.66	-3.43	-2.84	-2.61	-4.33	-2.60	0.00	-2.78	-2.39
TCGA-CE-A484-10A-01D-A23U-08_THCA	-2.50	0.00	-4.05	-2.72	-2.48	-2.50	-2.54	-2.53	-2.51	0.00	-4.05	-3.65	-4.35	-4.05	-2.87	0.00	-2.43
TCGA-CE-A485-10A-01D-A23U-08_THCA	-2.62	-2.85	-2.84	-2.97	-2.64	-2.68	-2.62	-2.52	-2.75	-3.25	-2.74	-2.67	0.00	-2.80	-3.08	0.00	-2.58
TCGA-CF-A1HR-10A-01D-A13W-08_BLCA	-2.47	0.00	-4.36	-2.64	-2.43	-2.42	-2.53	-2.54	-2.42	0.00	0.00	-4.66	-4.36	0.00	-2.94	0.00	-2.37
TCGA-CF-A1HS-10A-01D-A13W-08_BLCA	-2.44	-2.44	-2.41	-4.62	-4.31	-4.62	-2.41	-2.46	-2.32	0.00	0.00	0.00	0.00	-4.62	-3.06	-2.69	-2.28
TCGA-CF-A27C-10A-01D-A16O-08_BLCA	-2.51	0.00	-4.53	-2.70	-2.47	-2.54	-2.53	-2.59	-2.48	0.00	0.00	0.00	0.00	-4.53	-2.89	0.00	-2.43
TCGA-CF-A3MF-10A-01D-A21A-08_BLCA	-2.50	0.00	-4.46	-2.66	-2.54	-2.59	-2.56	-2.52	-2.59	-3.25	-2.82	-2.71	0.00	-2.65	0.00	-2.66	-2.49
TCGA-CF-A3MG-10A-01D-A20D-08_BLCA	-2.40	-4.19	-4.01	-2.57	-2.53	-2.54	-2.51	-2.48	-2.41	0.00	0.00	-4.49	0.00	-4.49	-3.00	-2.64	-2.53
TCGA-CF-A3MH-10A-01D-A20D-08_BLCA	-2.41	0.00	0.00	-2.66	-2.55	-2.56	-2.61	-2.54	-2.67	-3.23	-2.81	-2.68	0.00	-2.67	-3.04	0.00	-2.42
TCGA-CF-A3MI-10A-01D-A20D-08_BLCA	-2.42	0.00	-4.49	-2.56	-2.57	-2.51	-2.56	-2.63	-2.66	-3.25	-2.86	0.00	-2.91	-2.64	0.00	-2.72	-2.49
TCGA-CF-A47S-10A-01D-A23U-08_BLCA	-2.56	-2.71	-2.63	-2.88	-2.69	-2.63	-2.56	-2.55	-2.60	-3.28	-2.86	-3.95	-2.69	-2.68	-3.01	-4.43	-2.54
TCGA-CF-A47T-10A-01D-A23U-08_BLCA	-2.51	0.00	0.00	-2.70	-2.51	-2.54	-2.52	-2.46	-2.47	0.00	0.00	-4.39	0.00	-4.39	-2.96	-2.66	-2.49

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CF-A47V-10A-01D-A23U-08_BLCA	-2.55	-2.71	-2.66	-2.84	-2.66	-2.66	-2.63	-2.53	-2.64	-3.35	-2.82	0.00	-2.71	-2.59	-3.01	-4.16	-2.52
TCGA-CF-A47W-10A-01D-A23U-08_BLCA	-2.41	-2.61	-2.64	-2.76	-2.60	-2.63	-2.47	-2.40	-2.45	0.00	0.00	0.00	0.00	0.00	-3.00	-2.76	-2.39
TCGA-CF-A47X-10A-01D-A23U-08_BLCA	-2.68	-2.70	-2.78	-2.98	-2.56	-2.68	-2.62	-2.56	-2.54	-3.44	-2.93	-2.85	-4.04	-3.92	-3.16	-2.83	-2.64
TCGA-CF-A47Y-10A-01D-A23U-08_BLCA	-2.43	0.00	-4.62	-2.62	-2.44	-2.44	-2.47	-2.51	-2.42	0.00	0.00	0.00	0.00	0.00	-2.81	0.00	-2.38
TCGA-CF-A5U8-10A-01D-A289-08_BLCA	-2.48	-2.65	-2.68	-2.76	-2.64	-2.69	-2.47	-2.54	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.42
TCGA-CF-A5UA-10A-01D-A289-08_BLCA	-2.53	0.00	-4.57	-2.66	-2.52	-2.47	-2.58	-2.55	-2.47	0.00	0.00	0.00	0.00	0.00	-2.92	0.00	-2.39
TCGA-CG-4300-10A-01D-1158-08_STAD	-2.49	-2.77	-2.70	-2.97	-2.61	-2.70	-2.55	-2.59	-2.50	0.00	0.00	-4.35	0.00	0.00	0.00	-2.57	-2.48
TCGA-CG-4301-10A-01D-1158-08_STAD	-2.58	-2.85	-2.79	-3.06	-2.58	-2.62	-2.65	-2.70	-2.62	-4.79	-3.02	-2.75	0.00	-4.49	-3.26	-2.93	-2.56
TCGA-CG-4304-10A-01D-1158-08_STAD	-2.50	0.00	-4.44	-2.80	-2.50	-2.60	-2.63	-2.62	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.49
TCGA-CG-4305-10A-01D-1158-08_STAD	-2.64	-2.82	-2.79	-3.02	-2.51	-2.63	-2.66	-2.64	-2.82	-3.42	-2.86	-2.87	-2.87	-2.80	0.00	-2.90	-2.57
TCGA-CG-4306-10A-01D-1158-08_STAD	-2.58	-4.66	0.00	-2.90	-2.50	-2.53	-2.60	-2.63	-2.74	-3.30	-2.98	0.00	-2.83	-2.70	0.00	-2.79	-2.50
TCGA-CG-4436-10A-01D-1158-08_STAD	-2.58	0.00	-4.16	-2.87	-2.54	-2.60	-2.64	-2.59	-2.80	-3.48	-2.97	-4.76	-2.84	-2.77	0.00	-2.83	-2.52
TCGA-CG-4437-10A-01D-1800-08_STAD	-2.42	-4.44	0.00	-2.63	-2.47	-2.56	-2.57	-2.64	-2.53	0.00	0.00	0.00	0.00	-2.57	0.00	-2.68	-2.49
TCGA-CG-4438-10A-01D-1158-08_STAD	-2.55	-4.43	-4.73	-2.67	-2.49	-2.54	-2.61	-2.57	-2.59	0.00	0.00	-4.73	0.00	-4.13	0.00	-2.50	-2.50
TCGA-CG-4440-10A-01D-1158-08_STAD	-2.49	0.00	-4.60	-2.77	-2.45	-2.45	-2.57	-2.59	-2.44	0.00	0.00	-4.30	0.00	-4.60	0.00	-2.56	-2.40
TCGA-CG-4441-10A-01D-1800-08_STAD	-2.54	-4.08	-4.55	-2.64	-2.57	-2.57	-2.60	-2.66	-2.67	-3.35	-2.86	-4.55	-2.84	-2.69	0.00	-2.69	-2.44
TCGA-CG-4442-10A-01D-1158-08_STAD	-2.60	-2.82	-2.82	-2.98	-2.51	-2.56	-2.69	-2.56	-2.53	0.00	-2.98	-2.70	-4.40	-4.70	-3.22	-2.85	-2.54
TCGA-CG-4443-10A-01D-1158-08_STAD	-2.55	0.00	0.00	-2.67	-2.50	-2.49	-2.62	-2.63	-2.51	0.00	0.00	0.00	-4.64	-4.64	0.00	-2.54	-2.46
TCGA-CG-4444-10A-01D-1158-08_STAD	-2.54	-2.72	-2.64	-4.42	-2.73	-2.70	-2.67	-2.69	-2.61	0.00	-2.91	-2.73	0.00	-4.72	-3.02	-4.72	-2.56
TCGA-CG-4449-10A-01D-1158-08_STAD	-2.62	-2.85	-2.84	-3.06	-2.52	-2.61	-2.75	-2.64	-2.71	0.00	-3.01	-2.71	0.00	0.00	0.00	-2.61	-2.56
TCGA-CG-4455-10A-01D-1158-08_STAD	-2.55	-4.45	-4.15	-2.69	-2.52	-2.64	-2.61	-2.51	-2.68	0.00	0.00	0.00	-4.45	-4.45	0.00	-2.55	-2.56
TCGA-CG-4460-10A-01D-1158-08_STAD	-2.53	-4.63	-4.63	-2.81	-2.49	-2.53	-2.58	-2.52	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.49
TCGA-CG-4462-10A-01D-1158-08_STAD	-2.53	0.00	0.00	-2.87	-2.54	-2.58	-2.62	-2.55	-2.56	0.00	-4.72	0.00	0.00	0.00	0.00	-2.62	-2.48
TCGA-CG-4465-10A-01D-1158-08_STAD	-2.55	-2.63	-2.60	-4.65	-3.95	-4.35	-2.62	-2.56	-2.64	-3.35	-2.86	0.00	-2.76	-2.68	-3.09	-4.65	-2.47
TCGA-CG-4466-10A-01D-1158-08_STAD	-2.55	-4.70	-4.70	-2.86	-2.52	-2.61	-2.54	-2.55	-2.47	0.00	0.00	0.00	0.00	-4.40	0.00	-2.55	-2.49
TCGA-CG-4469-10A-01D-1158-08_STAD	-2.62	-4.40	-4.71	-2.76	-2.54	-2.57	-2.64	-2.57	-2.72	-3.43	-2.96	0.00	-2.84	-2.73	0.00	-2.76	-2.52
TCGA-CG-4472-10A-01D-1158-08_STAD	-2.47	-4.37	-4.07	-2.86	-2.53	-2.53	-2.63	-2.59	-2.74	-3.47	-3.03	0.00	-2.77	-2.70	0.00	-2.82	-2.54
TCGA-CG-4474-10A-01D-1158-08_STAD	-2.56	-2.77	-2.75	-3.01	-2.68	-2.78	-2.67	-2.52	-2.52	0.00	-4.70	-4.23	-4.70	-3.93	0.00	-2.48	-2.56
TCGA-CG-4475-10A-01D-1158-08_STAD	-2.58	-2.81	-2.72	-4.83	-2.67	-2.64	-2.68	-2.66	-2.81	-3.65	-2.78	-2.45	0.00	-2.80	-3.27	0.00	-2.57
TCGA-CG-4476-10A-01D-1158-08_STAD	-2.40	0.00	-4.68	-2.71	-2.48	-2.54	-2.63	-2.56	-2.52	0.00	0.00	0.00	0.00	0.00	-3.16	-2.73	-2.51
TCGA-CG-4477-10A-01D-1158-08_STAD	-2.48	-2.62	-2.58	0.00	-3.91	-4.69	-2.57	-2.51	-2.56	0.00	0.00	0.00	-4.69	0.00	0.00	-2.63	-2.45
TCGA-CG-5716-10A-01D-1800-08_STAD	-2.52	0.00	-4.54	-2.59	-2.56	-2.56	-2.58	-2.39	-2.33	0.00	0.00	0.00	-4.54	-4.24	-3.09	-2.67	-2.52
TCGA-CG-5717-10A-01D-1600-08_STAD	-2.55	-4.62	-4.62	-2.80	-2.49	-2.52	-2.58	-2.50	-2.50	0.00	0.00	0.00	0.00	0.00	-3.11	-2.78	-2.54
TCGA-CG-5718-10A-01D-1600-08_STAD	-2.61	-4.74	-4.44	-2.75	-2.57	-2.64	-2.72	-2.57	-2.75	-3.44	-2.91	-4.44	-2.82	-2.74	0.00	-2.78	-2.60
TCGA-CG-5719-10A-01D-1600-08_STAD	-2.41	-2.69	-2.60	-2.85	-2.55	0.00	-2.59	-2.64	-2.55	0.00	0.00	0.00	0.00	-2.53	0.00	-2.66	-2.54
TCGA-CH-5737-10A-01D-1576-08_PRAD	-2.56	-4.23	-4.70	-2.84	-2.51	-2.56	-2.65	-2.56	-2.68	-3.34	-2.93	0.00	-2.84	-2.71	0.00	-2.83	-2.47
TCGA-CH-5738-10A-01D-1576-08_PRAD	-2.52	-2.74	-2.73	-4.77	-2.62	-2.63	-2.73	-2.59	-2.83	-3.49	-2.82	-2.52	0.00	-2.76	0.00	-2.88	-2.61
TCGA-CH-5739-10A-01D-1576-08_PRAD	-2.50	-4.67	-4.19	-2.84	-2.57	-2.57	-2.63	-2.58	-2.58	0.00	0.00	-4.67	-4.67	-4.67	0.00	-2.66	-2.51
TCGA-CH-5740-10A-01D-1576-08_PRAD	-2.64	-2.77	-2.80	-3.03	-2.71	-2.76	-2.70	-2.64	-2.66	-3.25	-2.99	0.00	-2.83	-2.73	0.00	-2.75	-2.61
TCGA-CH-5741-10A-01D-1576-08_PRAD	-2.59	-4.66	-4.66	-2.70	-2.57	-2.61	-2.64	-2.54	-2.50	0.00	0.00	-4.66	0.00	-4.66	0.00	-2.63	-2.59
TCGA-CH-5743-10A-01D-1576-08_PRAD	-2.53	0.00	0.00	-2.85	-2.57	-2.58	-2.63	-2.53	-2.56	0.00	0.00	0.00	0.00	-4.67	0.00	-2.60	-2.57
TCGA-CH-5744-10A-01D-1576-08_PRAD	-2.58	0.00	0.00	-2.88	-2.49	-2.62	-2.66	-2.64	-2.75	-3.34	-2.93	0.00	-2.84	-2.74	0.00	-2.79	-2.60
TCGA-CH-5745-10A-01D-1576-08_PRAD	-2.51	-4.64	0.00	-2.65	-2.50	-2.57	-2.60	-2.60	-2.53	0.00	-4.34	0.00	0.00	-4.64	-3.00	-4.17	-2.50
TCGA-CH-5746-10A-01D-1576-08_PRAD	-2.55	-2.73	-2.67	-2.91	-2.68	-2.71	-2.58	-2.58	-2.69	-3.28	-2.84	0.00	-2.80	-2.70	0.00	-2.70	-2.51
TCGA-CH-5748-10A-01D-1576-08_PRAD	-2.62	-2.81	-2.83	-3.01	-2.51	-2.65	-2.69	-2.68	-4.45	-3.31	-2.75	-2.62	-2.85	-2.64	0.00	-4.15	-2.63
TCGA-CH-5750-10A-01D-1576-08_PRAD	-2.56	-4.35	-4.65	-2.68	-2.60	-2.58	-2.65	-2.55	-2.49	0.00	0.00	0.00	0.00	-4.65	0.00	-2.52	-2.55
TCGA-CH-5751-10A-01D-1576-08_PRAD	-2.56	0.00	-4.67	-2.65	-2.54	-2.55	-2.63	-2.49	-2.49	0.00	0.00	0.00	0.00	-4.19	0.00	-2.45	-2.48
TCGA-CH-5752-10A-01D-1576-08_PRAD	-2.57	-2.70	-2.61	-4.73	-2.74	-2.74	-2.66	-2.58	-2.79	-3.39	-2.79	-2.60	0.00	-2.74	0.00	-2.79	-2.59
TCGA-CH-5753-10A-01D-1576-08_PRAD	-2.58	0.00	-4.39	-2.88	-2.63	-2.59	-2.64	-2.50	-2.56	0.00	0.00	-4.69	-4.69	0.00	0.00	-2.44	-2.54
TCGA-CH-5754-10A-01D-1576-08_PRAD	-2.51	-4.63	-4.63	-2.89	-2.56	-2.62	-2.58	-2.58	-2.63	0.00	0.00	0.00	0.00	-4.03	0.00	-2.56	-2.53
TCGA-CH-5788-10A-01D-1576-08_PRAD	-2.55	-4.36	-4.66	-2.80	-2.56	-2.57	-2.60	-2.47	-2.52	-4.66	0.00	0.00	-4.36	-4.18	0.00	-2.46	-2.52
TCGA-CH-5789-10A-01D-1576-08_PRAD	-2.68	-2.82	-2.76	-2.99	-2.58	-2.66	-2.71	-2.53	-2.56	0.00	-3.01	-2.75	0.00	-4.22	-3.18	-2.82	-2.61
TCGA-CH-5790-10A-01D-1576-08_PRAD	-2.59	-2.73	-2.75	-2.88	-2.67	-2.67	-2.62	-2.59	-2.56	0.00	-4.64	0.00	0.00	-3.86	0.00	-2.60	-2.50
TCGA-CH-5791-10A-01D-1576-08_PRAD	-2.47	-4.35	0.00	-2.80	-2.55	-2.58	-2.59	-2.57	-2.60	0.00	0.00	0.00	0.00	-4.65	0.00	-2.59	-2.49
TCGA-CH-5792-10A-01D-1576-08_PRAD	-2.56	-4.29	0.00	-2.67	-2.49	-2.51	-2.64	-2.47	-2.46	0.00	0.00	-4.59	0.00	0.00	-3.11	-2.72	-2.48
TCGA-CH-5794-10A-01D-1577-08_PRAD	-2.61	-4.63	-4.63	-2.75	-2.58	-2.66	-2.69	-2.68	-2.71	-3.31	-2.95	-4.33	-2.74	-2.70	0.00	-2.76	-2.54
TCGA-CI-6621-10A-01D-1826-10_READ	-2.52	0.00	0.00	-2.59	-2.67	-2.59	-2.45	-2.61	-2.41	0.00	0.00	0.00	0.00	0.00	-3.19	-2.84	-2.48
TCGA-CI-6622-10A-01D-1826-10_READ	-2.70	0.00	0.00	-2.81	-2.61	-2.60	-2.57	-2.61	-2.92	-3.12	-3.16	-2.99	-3.10	-2.83	0.00	-3.08	-2.61
TCGA-CI-6624-10A-01D-1826-10_READ	-2.55	0.00	0.00	-2.76	-2.58	-2.61	-2.45	-2.56	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.52
TCGA-CK-4947-10A-01D-1650-10_COAD	-2.54	0.00	-4.52	-2.74	-2.46	-2.56	-2.44	-2.61	-2.65	-3.24	-2.92	0.00	-2.77	-2.71	0.00	-2.93	-2.41
TCGA-CK-4952-10A-01D-1719-10_COAD	-2.42	-2.63	-2.72	-2.95	-2.60	-2.73	-2.25	-2.49	-2.53	-3.40	-3.03	0.00	-2.66	-2.60	0.00	-3.03	-2.29
TCGA-CK-5912-10A-01D-1650-10_COAD	-2.43	-2.33	-2.35	0.00	0.00	0.00	-2.65	-2.80	-2.54	0.00	-2.94	0.00	-2.63	-2.58	0.00	-2.89	-2.38
TCGA-CK-5913-10A-01D-1650-10_COAD	-2.46	-2.64	-2.61	-3.02	-2.62	-2.70	-2.38	-2.56	-2.34	0.00	0.00	0.00	0.00	0.00	-3.36	-3.00	-2.37
TCGA-CK-5915-10A-01D-1650-10_COAD	-2.56	0.00	-4.40	-2.73	-2.49	-2.50	-2.44	-2.76	-2.70	-3.22	-3.25	0.00	-2.85	-2.66	0.00	-2.89	-2.42
TCGA-CK-5916-10A-01D-1650-10_COAD	-2.41	0.00	0.00	-2.66	-2.55	-2.63	-2.40	-2.77	-2.31	0.00	0.00	0.00	0.00	0.00	0.00	-2.62	-2.37
TCGA-CL-5917-10A-01D-1657-10_READ	-2.47	-2.52	-2.47	0.00	-2.73	-2.79	-2.32	-2.77	-2.34	0.00	-3.06	-2.88	0.00	0.00	0.00	-2.73	-2.42
TCGA-CL-5918-10A-01D-1657-10_READ	-2.49	-2.70	-2.58	-2.97	-2.73	-2.68	-2.53	-2.88	-2.53	0.00	-3.03	0.00	-2.84	-2.63	0.00	-2.94	-2.28
TCGA-CM-4743-10A-01D-1719-10_COAD	-2.51	-2.51	-2.58	-2.90	-2.60	-2.61	-2.55	-2.67	-2.50	0.00	-2.75	0.00	-2.58	-2.50	0.00	-2.81	-2.31
TCGA-CM-4746-10A-01D-1408-10_COAD	-2.63	0.00	0.00	-2.63	-2.61	-2.63	-2.60	-2.59	-2.58	0.00	0.00	0.00	0.00	0.00	-3.31	-2.88	-2.63
TCGA-CM-4747-10A-01D-1408-10_COAD	-2.44	0.00	0.00	-2.74	-2.81	-2.57	-2.44	-2.64	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.48
TCGA-CM-4748-10A-01D-1408-10_COAD	-2.63	0.00	0.00	-2.82	-2.63	-2.70	-2.51	-2.71	-2.70	-3.31	-2.95	0.00	-3.04	-2.88	0.00	-2.86	-2.57
TCGA-CM-4752-10A-01D-1408-10_COAD	-2.64	0.00	0.00	-2.73	-2.63	-2.65	-2.65	-2.73	-2.79	-3.27	-3.04	0.00	-2.94	-2.84	0.00	-2.76	-2.55
TCGA-CM-5341-10A-01D-1408-10_COAD	-2.41	0.00	0.00	-2.70	-2.79	-2.57	-2.54	-2.60	-2.81	-3.57	-3.14	0.00	-2.87	-3.04	-3.26	0.00	-2.36
TCGA-CM-5344-10A-01D-1719-10_COAD	-2.46	-2.59	-2.57	-2.91	-2.58	-2.72	-2.26	-2.44	-2.29	0.00	0.00	0.00	-4.56	0.00	-3.02	-2.89	-2.34
TCGA-CM-5348-10A-01D-1719-10_COAD	-2.54	0.00	0.00	-2.66	-2.39	-2.41	-2.38	-2.48	-2.26	0.00	0.00	0.00	0.00	0.00	-3.21	-2.84	-2.38
TCGA-CM-5349-10A-01D-1719-10_COAD	-2.60	-2.72	-2.61	-2.90	-2.42	-2.57	-2.43	-2.55	-2.60	-3.42	-2.72	-2.72	-2.79	-2.71	0.00	-2.99	-2.49
TCGA-CM-5860-10A-01D-1650-10_COAD	-2.53	0.00	0.00	-2.68	-2.52	-2.57	-2.42	-2.76	0.00	-3.13	-2.68	0.00	-2.58	-2.45	0.00	0.00	-2.46
TCGA-CM-5861-10A-01D-1650-10_COAD	-2.46	-2.35	-2.42	0.00	0.00	0.00	-2.32	-2.49	-2.35	0.00	0.00	0.00	0.00	0.00	-3.11	-2.75	-2.34
TCGA-CM-5862-10A-01D-1650-10_COAD	-2.57	-2.41	-2.48	0.00	-2.79	-2.82	-2.41	-2.59	-2.44	0.00	-2.86	-2.64	0.00	0.00	-2.82	0.00	-2.35
TCGA-CM-5864-10A-01D-1650-10_COAD	-2.48	-2.72	-2.74	-3.11	-2.42	-2.42	-2.34	-2.60	-2.42	0.00	-2.98	-2.76	0.00	0.00	0.00	-2.57	-2.35
TCGA-CM-5868-10A-01D-1650-10_COAD	-2.40	-2.36	-2.49	0.00	-2.85	-2.78	-2.39	-2.59	-2.24	0.00	-3.00	-2.83	0.00	0.00	-3.24	-2.97	-2.19
TCGA-CM-6161-10A-01D-1650-10_COAD	-2.70	-2.70	-2.82	-2.99	-2.54	-2.60	-2.59	-2.77	-2.45	0.00	-3.30	-2.78	0.00	0.00	0.00	-2.81	-2.55
TCGA-CM-6163-10A-01D-1650-10_COAD	-2.45	0.00	0.00	-3.00	-2.46	-2.49	-2.40	-2.60	-2.53	-3.26	-2.82	0.00	-2.69	-2.84	0.00	-2.92	-2.37
TCGA-CM-6164-10A-01D-1650-10_COAD	-2.60	-2.72	-2.65	-2.99	-2.69	-2.67	-2.46	-2.77	-2.38	0.00	0.00	-4.55	0.00	0.00	0.00	-2.77	-2.43
TCGA-CM-6165-10A-01D-1650-10_COAD	-2.49	-2.40	-2.37	0.00	0.00	0.00	-2.38	-2.49	-2.26	0.00	0.00	0.00	0.00	0.00	-2.99	0.00	-2.46
TCGA-CM-6166-10A-01D-1650-10_COAD	-2.41	0.00	0.00	-2.70	-2.49	-2.46	-2.40	-2.56	-2.63	-3.30	-3.26	0.00	-2.74	-2.71	0.00	-2.96	-2.47
TCGA-CM-6168-10A-01D-1650-10_COAD	-2.40	-2.81	-2.48	-2.91	-2.67	-2.69	-2.65	-2.75	-2.59	0.00	-2.93	0.00	-2.85	-2.69	0.00	-2.89	-2.35
TCGA-CM-6169-10A-01D-1650-10_COAD	-2.36	0.00	-4.26	-2.72	-2.48	-2.48	-2.33	-2.62	-2.31	0.00	0.00	0.00	0.00	0.00	-3.31	-2.85	-2.29
TCGA-CM-6170-10A-01D-1650-10_COAD	-2.50	0.00	0.00	-2.71	-2.57	-2.64	-2.47	-2.65	-2.48	0.00	0.00	0.00	0.00	0.00	-3.39	-3.14	-2.43
TCGA-CM-6171-10A-01D-1650-10_COAD	-2.51	-2.36	-2.35	0.00	0.00	0.00	-2.38	-2.67	-2.36	0.00	0.00	0.00	0.00	-4.44	-2.91	0.00	-2.35
TCGA-CM-6172-10A-01D-1650-10_COAD	-2.58	-2.82	-2.79	-2.96	-2.76	-2.74	-2.47	-2.66	-2.71	-3.17	-3.08	0.00	-2.89	-2.71	0.00	-3.10	-2.38
TCGA-CM-6674-10A-01D-1835-10_COAD	-2.57	0.00	0.00	-2.71	-2.61	-2.57	-2.51	-2.63	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.63	-2.46
TCGA-CM-6675-10A-01D-1835-10_COAD	-2.57	0.00	-2.85	-2.94	-2.55	-2.60	-2.56	-2.66	-2.49	0.00	-2.98	0.00	-2.90	0.00	-3.13	-3.00	-2.52
TCGA-CM-6676-10A-01D-1835-10_COAD	-2.59	-2.88	-2.81	-3.19	-2.64	-2.56	-2.61	-2.77	-2.53	0.00	-3.26	-2.86	0.00	-4.37	0.00	-2.73	-2.63
TCGA-CM-6677-10A-01D-1835-10_COAD	-2.46	-2.49	-2.42	-4.29	0.00	0.00	-2.51	-2.37	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.39
TCGA-CM-6678-10A-01D-1835-10_COAD	-2.56	0.00	-4.37	-2.96	-2.65	-2.62	-2.55	-2.71	-2.73	-3.26	-2.98	0.00	-2.87	-2.82	0.00	-2.91	-2.46

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CM-6679-10A-01D-1835-10_COAD	-2.51	-2.80	-2.69	-2.91	-2.71	-2.70	-2.67	-2.86	-2.57	0.00	-3.01	0.00	-2.85	-2.64	0.00	-2.87	-2.44
TCGA-CN-4723-10A-01D-1434-08_HNSC	-2.62	-2.70	-2.66	-4.62	-2.69	-2.71	-2.64	-2.55	-2.52	0.00	-2.91	-2.68	-4.62	0.00	0.00	-2.48	-2.54
TCGA-CN-4725-10A-01D-1434-08_HNSC	-2.54	0.00	0.00	-2.79	-2.50	-2.56	-2.62	-2.60	-2.52	0.00	0.00	-4.56	-4.56	-4.56	0.00	-2.56	-2.49
TCGA-CN-4726-10A-01D-1434-08_HNSC	-2.60	0.00	0.00	-2.86	-2.59	-2.61	-2.64	-2.55	-2.54	0.00	0.00	0.00	-4.29	0.00	0.00	-2.61	-2.51
TCGA-CN-4727-10A-01D-1434-08_HNSC	-2.59	0.00	-4.57	-2.62	-2.56	-2.57	-2.59	-2.49	-2.56	0.00	0.00	-4.27	-4.57	0.00	-2.99	-2.63	-2.55
TCGA-CN-4728-10A-01D-1434-08_HNSC	-2.64	-2.81	-2.80	-2.95	-2.52	-2.72	-2.65	-2.60	-2.69	0.00	-2.89	-2.80	0.00	-4.38	-3.13	-2.80	-2.61
TCGA-CN-4729-10A-01D-1434-08_HNSC	-2.51	0.00	0.00	-2.81	-2.52	-2.54	-2.61	-2.47	-2.62	0.00	0.00	-4.56	0.00	0.00	0.00	-2.40	-2.54
TCGA-CN-4730-10A-01D-1434-08_HNSC	-2.56	-2.71	-2.71	-2.94	-2.66	-2.67	-2.60	-2.48	-2.57	0.00	0.00	0.00	0.00	0.00	-2.98	-2.71	-2.52
TCGA-CN-4731-10A-01D-1434-08_HNSC	-2.59	-2.77	-2.78	-2.94	-2.52	-2.66	-2.73	-2.54	-2.62	0.00	-3.01	-2.73	0.00	0.00	0.00	-2.51	-2.62
TCGA-CN-4733-10A-01D-1870-08_HNSC	-2.52	-2.60	-2.59	-2.96	-2.65	-2.76	-2.76	-2.76	-2.71	0.00	-2.73	-2.60	0.00	-2.68	-3.11	-4.66	-2.52
TCGA-CN-4734-10A-01D-1434-08_HNSC	-2.56	-2.77	-2.75	-2.96	-2.55	-2.62	-2.68	-2.54	-2.55	0.00	-2.93	-2.76	0.00	0.00	-3.08	-2.75	-2.59
TCGA-CN-4735-10A-01D-1434-08_HNSC	-2.63	-2.83	-2.79	-3.03	-2.53	-2.70	-2.70	-2.74	-2.78	-3.45	-2.84	-2.66	0.00	-2.80	0.00	-2.77	-2.56
TCGA-CN-4736-10A-01D-1434-08_HNSC	-2.44	-2.66	-2.60	-2.83	-2.64	-2.64	-2.48	-2.49	-2.40	0.00	0.00	0.00	0.00	0.00	-3.00	-2.69	-2.35
TCGA-CN-4737-10A-01D-1434-08_HNSC	-2.63	0.00	-4.67	-2.71	-2.65	-2.65	-2.69	-2.67	-2.76	-3.35	-2.95	-2.72	-4.67	-2.72	0.00	-2.76	-2.58
TCGA-CN-4738-10A-01D-1512-08_HNSC	-2.53	-2.73	-2.68	-2.90	-2.67	-2.68	-2.62	-2.51	-2.53	0.00	0.00	0.00	0.00	0.00	-3.08	-2.68	-2.55
TCGA-CN-4739-10A-01D-1512-08_HNSC	-2.61	-2.76	-2.76	-2.99	-2.51	-2.67	-2.71	-2.56	-2.62	0.00	-3.01	-2.75	0.00	-4.16	-3.07	-2.87	-2.63
TCGA-CN-4740-10A-01D-1434-08_HNSC	-2.63	-2.80	-2.75	-3.00	-2.51	-2.62	-2.72	-2.58	-2.50	0.00	-2.88	-2.73	0.00	-4.34	-3.06	-2.79	-2.58
TCGA-CN-4741-10A-01D-1434-08_HNSC	-2.58	-2.64	-2.65	0.00	-4.59	-4.29	-2.64	-2.52	-2.69	-3.27	-2.79	0.00	-2.80	-2.67	-3.03	-3.99	-2.49
TCGA-CN-4742-10A-01D-1512-08_HNSC	-2.56	0.00	0.00	-2.86	-2.59	-2.59	-2.62	-2.54	-2.67	-3.35	-2.86	-4.60	-2.75	-2.72	-3.19	-4.13	-2.56
TCGA-CN-5355-10A-01D-1434-08_HNSC	-2.61	-4.65	0.00	-2.90	-2.43	-2.58	-2.52	-2.48	-2.67	0.00	-2.82	0.00	-2.68	-4.65	0.00	-2.83	-2.71
TCGA-CN-5356-10A-01D-1434-08_HNSC	-2.53	0.00	0.00	-2.72	-2.50	-2.46	-2.56	-2.46	-2.44	0.00	0.00	-4.49	0.00	0.00	0.00	-2.41	-2.46
TCGA-CN-5358-10A-01D-1512-08_HNSC	-2.58	-2.69	-2.69	-2.92	-2.63	-2.71	-2.62	-2.61	-2.54	-4.56	0.00	-4.56	0.00	-4.56	0.00	-2.60	-2.56
TCGA-CN-5359-10A-01D-1434-08_HNSC	-2.56	0.00	-4.61	-2.67	-2.57	-2.61	-2.61	-2.49	-2.59	-3.25	0.00	0.00	0.00	0.00	-2.93	-4.13	-2.60
TCGA-CN-5360-10A-01D-1434-08_HNSC	-2.58	-2.71	-2.72	-2.93	-2.68	-2.70	-2.63	-2.56	-2.48	0.00	0.00	-4.57	0.00	0.00	0.00	-2.61	-2.55
TCGA-CN-5361-10A-01D-1434-08_HNSC	-2.66	-2.79	-2.78	-2.98	-2.58	-2.70	-2.71	-2.57	-2.57	0.00	-2.95	-2.73	0.00	0.00	0.00	-2.52	-2.59
TCGA-CN-5363-10A-01D-1434-08_HNSC	-2.56	0.00	0.00	-2.83	-2.48	-2.52	-2.56	-2.61	-2.55	0.00	0.00	-4.23	0.00	-4.53	-2.89	-4.53	-2.51
TCGA-CN-5364-10A-01D-1434-08_HNSC	-2.53	-4.30	0.00	-2.86	-2.55	-2.54	-2.66	-2.61	-2.60	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.58
TCGA-CN-5365-10A-01D-1434-08_HNSC	-2.60	-4.55	-4.08	-2.81	-2.57	-2.60	-2.59	-2.60	-3.95	-3.14	-2.74	0.00	-2.63	-2.56	0.00	-4.55	-2.51
TCGA-CN-5366-10A-01D-1434-08_HNSC	-2.57	-4.29	-4.59	-2.69	-2.59	-2.61	-2.63	-2.54	-2.72	-3.27	-2.87	-2.66	-4.59	-2.70	0.00	-2.73	-2.57
TCGA-CN-5367-10A-01D-1434-08_HNSC	-2.54	-4.22	0.00	-2.69	-2.54	-2.58	-2.59	-2.55	-2.47	0.00	-4.52	0.00	0.00	0.00	0.00	-2.57	-2.48
TCGA-CN-5369-10A-01D-1434-08_HNSC	-2.51	0.00	-4.25	-2.79	-2.51	-2.61	-2.57	-2.55	-2.59	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.49
TCGA-CN-5370-10A-01D-2013-08_HNSC	-2.53	-4.51	0.00	-2.72	-2.57	-2.59	-2.56	-2.46	-2.44	0.00	0.00	-4.51	0.00	0.00	-2.96	-2.75	-2.55
TCGA-CN-5373-10A-01D-1434-08_HNSC	-2.55	0.00	-4.56	-2.61	-2.55	-2.55	-2.63	-2.59	-2.55	0.00	0.00	0.00	0.00	0.00	-2.88	0.00	-2.57
TCGA-CN-5374-10A-01D-1434-08_HNSC	-2.58	-2.70	-2.69	-2.84	-2.69	-2.71	-2.63	-2.48	-2.53	0.00	0.00	0.00	0.00	-4.62	-3.02	-2.69	-2.55
TCGA-CN-6010-10A-01D-1683-08_HNSC	-2.48	-2.60	-2.61	-2.81	-2.60	-2.64	-2.46	-2.43	-2.42	0.00	-4.44	0.00	0.00	0.00	0.00	-2.54	-2.38
TCGA-CN-6011-10A-01D-1683-08_HNSC	-2.56	-2.66	-2.62	-2.87	-2.64	-2.64	-2.55	-2.48	-2.42	0.00	-4.45	-4.45	0.00	0.00	-3.07	-2.83	-2.42
TCGA-CN-6012-10A-01D-1683-08_HNSC	-2.51	-2.76	-2.74	-2.93	-2.49	-2.57	-2.58	-2.51	-2.49	0.00	-2.98	-2.74	0.00	-4.57	-3.21	-2.80	-2.49
TCGA-CN-6013-10A-01D-1683-08_HNSC	-2.48	0.00	-4.46	-2.73	-2.49	-2.51	-2.53	-2.41	-2.43	0.00	-4.46	0.00	-4.46	0.00	-3.06	-2.74	-2.41
TCGA-CN-6016-10A-01D-1683-08_HNSC	-2.57	-2.78	-2.70	-2.87	-2.50	-2.59	-2.66	-2.58	-2.73	-3.46	-2.84	-2.76	-2.81	-2.70	-3.11	0.00	-2.50
TCGA-CN-6017-10A-01D-1683-08_HNSC	-2.64	-2.75	-2.67	-2.90	-2.42	-2.54	-2.61	-2.61	-2.47	0.00	-2.97	-2.70	-4.54	-4.54	0.00	-2.59	-2.46
TCGA-CN-6018-10A-01D-1683-08_HNSC	-2.48	0.00	-4.45	-2.70	-2.43	-2.48	-2.53	-2.51	-2.45	-4.45	-4.45	-4.15	0.00	0.00	-3.09	-2.75	-2.40
TCGA-CN-6019-10A-01D-1683-08_HNSC	-2.42	-4.45	0.00	-2.61	-2.48	-2.50	-2.56	-2.49	-2.51	0.00	0.00	-4.45	0.00	0.00	0.00	-2.63	-2.38
TCGA-CN-6020-10A-01D-1683-08_HNSC	-2.54	-2.76	-2.64	-2.92	-2.55	-2.55	-2.59	-2.59	-2.46	0.00	-2.99	-2.74	0.00	-4.53	-3.08	-2.80	-2.49
TCGA-CN-6021-10A-01D-1683-08_HNSC	-2.43	-4.49	0.00	-2.69	-2.52	-2.48	-2.58	-2.53	-2.69	-3.23	-3.02	-2.74	0.00	-2.59	0.00	-2.83	-2.45
TCGA-CN-6022-10A-01D-1683-08_HNSC	-2.42	0.00	-4.57	-2.70	-2.55	-2.61	-2.61	-2.59	-2.77	-3.34	-2.92	0.00	-2.87	-2.65	0.00	-2.77	-2.46
TCGA-CN-6023-10A-01D-1683-08_HNSC	-2.54	-2.72	-2.75	-2.90	-2.41	-2.59	-2.56	-2.62	-2.56	0.00	-2.89	-2.72	0.00	0.00	-3.24	-2.80	-2.48
TCGA-CN-6024-10A-01D-1683-08_HNSC	-2.55	0.00	-4.21	-2.69	-2.50	-2.53	-2.55	-2.61	-2.83	-3.28	-2.95	0.00	-2.73	-2.75	0.00	-2.79	-2.42
TCGA-CN-6988-10A-01D-1912-08_HNSC	-2.42	-4.54	-4.54	-2.56	-2.51	-2.57	-2.53	-2.58	-2.50	0.00	0.00	-4.54	0.00	0.00	0.00	-2.58	-2.46
TCGA-CN-6989-10A-01D-1912-08_HNSC	-2.50	-2.70	-2.61	-2.81	-2.69	-2.63	-2.55	-2.47	-2.46	0.00	0.00	0.00	0.00	0.00	-3.10	-2.75	-2.42
TCGA-CN-6992-10A-01D-1912-08_HNSC	-2.36	0.00	0.00	-2.67	-2.47	-2.46	-2.49	-2.58	-2.51	0.00	0.00	0.00	0.00	-4.53	0.00	-2.55	-2.42
TCGA-CN-6994-10A-01D-1912-08_HNSC	-2.59	-2.78	-2.75	-2.93	-2.51	-2.58	-2.69	-2.68	-2.76	-3.60	-2.76	-2.67	0.00	-2.69	0.00	-2.82	-2.51
TCGA-CN-6995-10A-01D-2013-08_HNSC	-2.41	-2.71	-2.67	-2.82	-2.66	-2.60	-2.53	-2.53	-2.51	0.00	0.00	0.00	0.00	0.00	-2.99	-4.57	-2.42
TCGA-CN-6996-10A-01D-1912-08_HNSC	-2.46	-2.65	-2.60	-2.79	-2.56	-4.51	-2.62	-2.67	-2.67	0.00	-2.77	-2.62	-4.51	-2.67	0.00	-2.75	-2.39
TCGA-CN-6997-10A-01D-2013-08_HNSC	-2.44	-2.67	-2.65	-2.86	-2.66	-2.64	-2.54	-2.51	-2.45	0.00	0.00	0.00	-4.55	-4.55	0.00	-2.51	-2.45
TCGA-CN-6998-10A-01D-2013-08_HNSC	-2.60	-2.74	-2.70	-2.91	-2.49	-2.61	-2.61	-2.55	-2.57	0.00	-2.91	-2.75	0.00	-4.66	-3.20	-2.78	-2.50
TCGA-CN-A497-10A-01D-A24F-08_HNSC	-2.42	-2.70	-2.61	-2.85	-2.66	-2.68	-2.59	-2.42	-2.48	0.00	-4.46	0.00	-4.46	-3.98	-2.98	-2.72	-2.55
TCGA-CN-A498-10A-01D-A24F-08_HNSC	-2.59	-4.14	-4.14	-2.80	-2.60	-2.61	-2.61	-2.43	-2.51	0.00	0.00	-4.44	0.00	0.00	0.00	-2.39	-2.49
TCGA-CN-A499-10A-01D-A24F-08_HNSC	-2.63	-4.49	-4.49	-2.64	-2.61	-2.60	-2.61	-2.64	-2.79	-3.29	-2.81	-3.72	-2.78	-2.69	0.00	-2.75	-2.61
TCGA-CN-A49A-10A-01D-A24F-08_HNSC	-2.69	-2.85	-2.73	-3.04	-2.58	-2.66	-2.73	-2.78	-2.91	-3.43	-2.80	-2.73	-4.54	-2.74	0.00	-2.84	-2.63
TCGA-CN-A49B-10A-01D-A24F-08_HNSC	-2.43	0.00	0.00	-2.57	-2.50	-2.52	-2.57	-2.60	-2.53	0.00	0.00	0.00	-4.43	-4.43	-2.92	-3.95	-2.47
TCGA-CN-A49C-10B-01D-A24F-08_HNSC	-2.38	-3.83	-4.43	-2.73	-2.54	-2.54	-2.57	-2.50	-2.44	-4.43	-3.96	-4.43	-4.13	-3.83	0.00	-2.39	-2.49
TCGA-CN-A63U-10A-01D-A30H-08_HNSC	-2.49	-2.63	-2.61	-2.78	-2.61	-2.59	-2.50	-2.55	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.43
TCGA-CN-A63W-10A-01D-A30H-08_HNSC	-2.43	0.00	0.00	-2.60	-2.45	-2.43	-2.47	-2.46	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.32
TCGA-CN-A63Y-10A-01D-A30H-08_HNSC	-2.55	-2.75	-2.79	-2.94	-2.44	-2.57	-2.57	-2.65	0.00	-3.20	-2.65	-2.55	-2.85	-2.52	0.00	0.00	-2.49
TCGA-CN-A640-10A-01D-A30H-08_HNSC	-2.51	-2.66	-2.70	-2.82	-2.44	-2.54	-2.57	-2.53	-2.49	0.00	-2.98	-2.69	0.00	-4.69	-3.07	-2.81	-2.46
TCGA-CN-A641-10A-01D-A30H-08_HNSC	-2.43	0.00	0.00	-2.64	-2.44	-2.51	-2.51	-2.59	-2.58	-3.34	-2.98	0.00	-2.75	-2.63	0.00	-2.75	-2.40
TCGA-CN-A642-10A-01D-A30H-08_HNSC	-2.49	-2.73	-2.80	-2.93	-2.49	-2.55	-2.59	-2.63	0.00	-3.29	-2.59	-2.76	-2.65	-2.53	0.00	-4.73	-2.44
TCGA-CQ-5323-10A-01D-1683-08_HNSC	-2.54	-2.73	-2.71	-2.96	-2.47	-2.52	-2.64	-2.63	-2.50	0.00	-2.94	-2.77	0.00	-4.53	0.00	-2.64	-2.44
TCGA-CQ-5324-10A-01D-1683-08_HNSC	-2.55	-2.83	-2.82	-3.09	-2.51	-2.56	-2.63	-2.61	-2.79	-3.28	-2.73	-2.72	-2.87	-2.78	0.00	-2.87	-2.62
TCGA-CQ-5325-10A-01D-1683-08_HNSC	-2.49	-2.62	-2.58	-2.80	-2.60	-2.63	-2.49	-2.59	-2.40	0.00	0.00	0.00	0.00	0.00	-2.89	-4.14	-2.44
TCGA-CQ-5326-10A-01D-1870-08_HNSC	-2.47	0.00	-4.66	-2.75	-2.57	-2.53	-2.58	-2.60	-2.66	-3.30	-2.94	0.00	-2.80	-2.73	0.00	-2.77	-2.47
TCGA-CQ-5327-10A-01D-1683-08_HNSC	-2.50	-4.15	-4.15	-2.76	-2.45	-2.43	-2.50	-2.49	-2.51	0.00	0.00	0.00	0.00	0.00	-3.09	-2.70	-2.39
TCGA-CQ-5329-10A-01D-1683-08_HNSC	-2.35	-2.57	-2.51	-2.78	-2.49	0.00	-2.60	-2.64	-2.45	0.00	0.00	0.00	0.00	-2.53	0.00	-2.63	-2.38
TCGA-CQ-5330-10A-01D-1683-08_HNSC	-2.47	-2.72	-2.62	-2.84	-2.59	-2.63	-2.48	-2.51	-2.47	0.00	0.00	0.00	0.00	-4.43	0.00	-2.51	-2.40
TCGA-CQ-5331-10A-01D-1870-08_HNSC	-2.41	0.00	0.00	-2.58	-2.55	-2.61	-2.62	-2.54	-2.50	0.00	0.00	-4.59	0.00	-4.59	-3.07	-2.77	-2.45
TCGA-CQ-5332-10A-01D-1683-08_HNSC	-2.54	-2.72	-2.77	0.00	-2.49	-2.58	-2.64	-2.50	-2.51	0.00	-2.91	-2.67	-4.55	0.00	-3.14	-2.77	-2.45
TCGA-CQ-5333-10A-01D-2394-08_HNSC	-2.67	-2.80	-2.85	-3.03	-2.59	-2.69	-2.68	-2.66	-2.72	-3.48	-2.77	-2.76	-2.86	-2.74	0.00	-2.77	-2.61
TCGA-CQ-5334-10A-01D-1683-08_HNSC	-2.24	-3.80	-3.97	-2.73	-2.52	-2.46	-2.48	-2.66	-2.54	0.00	-4.28	-3.97	0.00	-4.28	0.00	-2.59	-2.25
TCGA-CQ-6218-10A-01D-1912-08_HNSC	-2.59	-2.70	-2.68	-2.84	-2.68	-2.76	-2.63	-2.62	-2.64	-3.43	-2.78	-4.07	-2.72	-2.68	0.00	-2.76	-2.53
TCGA-CQ-6219-10A-01D-1912-08_HNSC	-2.36	0.00	0.00	-2.67	-2.47	-2.46	-2.50	-2.47	-2.48	0.00	0.00	0.00	0.00	0.00	-3.27	-2.77	-2.37
TCGA-CQ-6220-10A-01D-1912-08_HNSC	-2.58	0.00	0.00	-2.64	-2.48	-2.58	-2.64	-2.53	-2.75	-3.34	-2.85	-4.57	-2.78	-2.70	0.00	-2.77	-2.58
TCGA-CQ-6221-10A-01D-2078-08_HNSC	-2.53	0.00	0.00	-2.64	-2.55	-2.59	-2.55	-2.53	-2.43	0.00	-4.14	0.00	0.00	-4.14	-3.12	-2.70	-2.47
TCGA-CQ-6222-10A-01D-1912-08_HNSC	-2.52	-2.67	-2.67	-2.82	-2.60	-2.66	-2.56	-2.49	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.51
TCGA-CQ-6223-10A-01D-1912-08_HNSC	-2.66	-2.76	-2.74	-2.94	-2.52	-2.68	-2.71	-2.69	-2.79	-3.32	-2.71	-2.74	-2.83	-2.73	0.00	-2.78	-2.61
TCGA-CQ-6224-10A-01D-1912-08_HNSC	-2.52	0.00	-4.50	-2.58	-2.53	-2.60	-2.60	-2.47	-2.44	0.00	0.00	0.00	-4.50	0.00	0.00	-2.43	-2.47
TCGA-CQ-6225-10A-01D-1912-08_HNSC	-2.56	0.00	-4.56	-2.59	-2.58	-2.62	-2.58	-2.69	-2.69	-3.28	-2.88	-2.72	0.00	-2.69	0.00	-2.81	-2.53
TCGA-CQ-6227-10A-01D-1912-08_HNSC	-2.56	0.00	-4.57	-2.63	-2.57	-2.60	-2.61	-2.66	-2.76	-3.22	-2.84	-2.74	0.00	-2.66	0.00	-2.76	-2.55
TCGA-CQ-6228-10A-01D-1912-08_HNSC	-2.46	-2.67	-2.69	-2.91	-2.71	-2.75	-2.57	-2.54	-2.64	-3.31	-2.81	-2.71	0.00	-2.72	-3.11	0.00	-2.52
TCGA-CQ-6229-10A-01D-1912-08_HNSC	-2.57	-2.60	-2.57	-4.55	-2.69	-2.73	-2.72	-2.68	0.00	-3.24	-2.55	-2.69	-2.62	-2.59	0.00	0.00	-2.48
TCGA-CQ-7063-10A-01D-2394-08_HNSC	-2.59	-4.52	0.00	-2.68	-2.58	-2.56	-2.64	-2.63	-2.67	-3.37	-2.88	0.00	-2.75	-2.69	0.00	-2.75	-2.56
TCGA-CQ-7064-10A-01D-2394-08_HNSC	-2.67	-2.83	-2.78	-2.92	-2.56	-2.72	-2.72	-2.71	-2.77	-3.33	-2.70	-2.81	-2.83	-2.75	0.00	-2.75	-2.66
TCGA-CQ-7065-10A-01D-2078-08_HNSC	-2.50	-2.73	-2.76	-2.80	-2.59	-2.71	-2.45	-2.60	-2.61	-3.28	-3.01	-4.43	-2.80	-2.75	0.00	-2.81	-2.39
TCGA-CQ-7067-10A-01D-2229-08_HNSC	-2.54	-2.73	-2.72	-2.90	-2.48	-2.56	-2.57	-2.66	-2.69	-3.41	-2.75	-2.67	-2.80	-2.69	0.00	-2.92	-2.48
TCGA-CQ-7068-10A-01D-2078-08_HNSC	-2.51	-2.74	-2.81	-2.89	-2.49	-2.63	-2.65	-2.69	-2.72	-3.33	-2.73	-2.76	-2.83	-2.77	0.00	-2.78	-2.60
TCGA-CQ-7069-10A-01D-2394-08_HNSC	-2.66	-2.75	-2.74	-2.95	-2.57	-2.71	-2.68	-2.69	-4.01	-3.17	-2.68	-2.69	-2.72	-2.62	0.00	-4.32	-2.63
TCGA-CQ-7071-10A-01D-A30H-08_HNSC	-2.44	0.00	0.00	-2.67	-2.47	-2.46	-2.48	-2.53	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.38

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CQ-7072-10A-01D-A30H-08_HNSC	-2.48	-2.61	-2.62	-2.92	-2.55	-2.59	-2.72	-2.69	-2.65	0.00	-2.78	-2.63	0.00	-2.60	0.00	-2.75	-2.36
TCGA-CQ-A4C6-10A-01D-A25E-08_HNSC	-2.51	0.00	0.00	-2.71	-2.47	-2.59	-2.60	-2.59	-4.04	-3.15	-2.69	-2.81	-2.66	-2.64	0.00	-4.51	-2.60
TCGA-CQ-A4C7-10A-01D-A25E-08_HNSC	-2.61	-2.62	-2.61	-4.20	-2.54	-2.62	-2.66	-2.59	-2.54	-4.20	-2.80	-2.64	0.00	0.00	-3.20	-2.73	-2.56
TCGA-CQ-A4C9-10A-01D-A25E-08_HNSC	-2.64	-2.77	-2.73	-2.91	-2.53	-2.68	-2.63	-2.71	-2.73	-3.36	-2.80	-2.66	-4.24	-2.71	0.00	-2.84	-2.59
TCGA-CQ-A4CA-10A-01D-A25E-08_HNSC	-2.61	-2.77	-2.79	-2.96	-2.55	-2.66	-2.70	-2.62	-2.83	-3.51	-2.76	-2.78	-2.84	-2.77	0.00	-2.79	-2.60
TCGA-CQ-A4CB-10A-01D-A25E-08_HNSC	-2.59	-3.72	-3.82	-2.75	-2.50	-2.58	-2.55	-2.50	-2.43	0.00	-4.42	-3.64	0.00	0.00	0.00	-2.42	-2.45
TCGA-CQ-A4CD-10A-01D-A25E-08_HNSC	-2.54	-2.66	-2.61	-2.88	-2.66	-2.66	-2.58	-2.47	-2.42	0.00	-4.41	-4.41	-4.41	-4.41	0.00	-2.39	-2.43
TCGA-CQ-A4CE-10A-01D-A25Y-08_HNSC	-2.64	-2.75	-2.80	-3.09	-2.57	-2.70	-2.71	-2.72	-2.71	-3.42	-2.76	-2.67	-4.53	-2.80	0.00	-2.98	-2.59
TCGA-CQ-A4CG-10A-01D-A25Y-08_HNSC	-2.53	-4.57	0.00	-2.66	-2.60	-2.64	-2.68	-2.68	-2.70	-3.37	-2.90	-2.76	0.00	-2.76	0.00	-2.72	-2.55
TCGA-CQ-A4CH-10A-01D-A25Y-08_HNSC	-2.54	-2.77	-2.65	-2.95	-2.46	-2.64	-2.64	-2.65	-2.54	0.00	-2.93	-2.76	-4.25	-4.25	-2.98	-4.25	-2.58
TCGA-CQ-A4CI-10A-01D-A25Y-08_HNSC	-2.58	-2.62	-2.62	-3.99	-2.71	-2.78	-2.67	-2.56	-2.73	-3.30	-2.73	-2.75	-2.80	-2.73	-3.02	-4.12	-2.59
TCGA-CR-5243-10A-01D-1512-08_HNSC	-2.53	-2.82	-2.73	-2.93	-2.75	-2.74	-2.58	-2.63	-2.69	-3.41	-2.93	0.00	-2.85	-2.76	0.00	-2.84	-2.59
TCGA-CR-5247-10A-01D-2013-08_HNSC	-2.47	0.00	-2.67	-2.81	-2.65	-2.64	-2.55	-2.38	-2.42	0.00	0.00	0.00	0.00	-4.20	-2.97	-2.64	-2.49
TCGA-CR-5248-10A-01D-2013-08_HNSC	-2.48	0.00	0.00	-2.55	-2.51	-2.52	-2.65	-2.64	-2.58	0.00	-4.50	0.00	0.00	0.00	0.00	-2.57	-2.48
TCGA-CR-5249-10A-01D-1512-08_HNSC	-2.62	-2.80	-2.73	-2.97	-2.51	-2.61	-2.66	-2.55	-2.51	0.00	-2.92	-2.74	0.00	-4.31	-3.18	-2.79	-2.64
TCGA-CR-5250-10A-01D-1512-08_HNSC	-2.54	-2.67	-2.72	-2.88	-2.47	-2.54	-2.54	-2.55	-2.51	0.00	-2.92	-2.75	0.00	0.00	-2.84	0.00	-2.45
TCGA-CR-6467-10A-01D-1870-08_HNSC	-2.53	-2.80	-2.78	-2.95	-2.55	-2.64	-2.64	-2.66	-2.66	0.00	-2.91	-2.76	-4.66	0.00	0.00	-2.68	-2.55
TCGA-CR-6470-10A-01D-1870-08_HNSC	-2.47	0.00	0.00	-2.82	-2.61	-2.64	-2.64	-2.58	-2.69	-3.56	-2.94	0.00	-2.82	-2.74	-3.15	0.00	-2.54
TCGA-CR-6471-10A-01D-1870-08_HNSC	-2.49	-2.78	-2.76	-2.94	-2.52	-2.66	-2.63	-2.67	-2.79	-3.55	-2.73	-2.77	-2.90	-2.73	0.00	-2.84	-2.45
TCGA-CR-6472-10A-01D-1870-08_HNSC	-2.57	0.00	-4.64	-2.76	-2.64	-2.70	-2.58	-2.53	-2.78	-3.22	-2.94	0.00	-2.86	-2.68	0.00	-2.82	-2.58
TCGA-CR-6473-10A-01D-1870-08_HNSC	-2.50	-2.81	-2.76	-3.01	-2.54	-2.67	-2.67	-2.71	-2.65	0.00	-2.96	-2.77	-4.65	-4.35	0.00	-2.73	-2.60
TCGA-CR-6474-10A-01D-1870-08_HNSC	-2.43	-2.69	-2.73	-2.89	-2.71	-2.73	-2.71	-2.80	-2.74	0.00	-2.90	0.00	-2.76	-2.73	0.00	-2.78	-2.47
TCGA-CR-6477-10A-01D-1870-08_HNSC	-2.58	-2.81	-2.74	-2.89	-2.73	-2.77	-2.56	-2.60	-2.50	-3.46	0.00	0.00	0.00	0.00	0.00	-2.66	-2.52
TCGA-CR-6478-10A-01D-1870-08_HNSC	-2.55	0.00	-4.62	-2.62	-2.59	-2.60	-2.68	-2.70	-2.75	-3.37	-2.96	0.00	-2.82	-2.72	0.00	-2.82	-2.53
TCGA-CR-6480-10A-01D-1870-08_HNSC	-2.48	0.00	0.00	-2.75	-2.59	-2.58	-2.57	-2.53	-2.47	0.00	-4.28	-4.28	0.00	0.00	0.00	-2.60	-2.48
TCGA-CR-6481-10A-01D-1870-08_HNSC	-2.48	-2.73	-2.69	-2.86	-2.72	-2.64	-2.57	-2.58	-2.52	0.00	-4.59	0.00	0.00	-4.29	-2.91	0.00	-2.46
TCGA-CR-6482-10A-01D-1870-08_HNSC	-2.52	0.00	-4.27	-2.71	-2.56	-2.59	-2.71	-2.73	-2.68	0.00	-2.84	-4.57	-2.72	-2.66	-3.08	-4.57	-2.48
TCGA-CR-6484-10A-01D-1870-08_HNSC	-2.55	0.00	-4.61	-2.61	-2.58	-2.57	-2.63	-2.56	-2.57	0.00	0.00	0.00	0.00	0.00	-3.03	-2.81	-2.53
TCGA-CR-6487-10A-01D-1870-08_HNSC	-2.52	0.00	0.00	-2.65	-2.56	-2.61	-2.61	-2.56	-2.55	0.00	0.00	0.00	0.00	-4.61	-3.14	-2.79	-2.50
TCGA-CR-6488-10A-01D-2078-08_HNSC	-2.60	-2.75	-2.73	-2.83	-2.45	-2.58	-2.59	-2.55	-2.49	0.00	-2.94	-2.70	0.00	-3.74	-3.16	-2.76	-2.51
TCGA-CR-6491-10A-01D-1870-08_HNSC	-2.56	0.00	-4.43	-2.82	-2.55	-2.64	-2.71	-2.57	-2.61	0.00	-2.98	-2.85	-4.73	0.00	-3.14	-2.83	-2.52
TCGA-CR-6492-10A-01D-2078-08_HNSC	-2.52	-2.60	-2.64	-2.80	-2.60	-2.68	-2.52	-2.49	-2.48	0.00	-4.38	0.00	0.00	0.00	-3.07	-2.81	-2.44
TCGA-CR-6493-10A-01D-1870-08_HNSC	-2.45	0.00	0.00	-2.77	-2.61	-2.65	-2.64	-2.66	-2.68	-3.25	-2.88	0.00	-2.77	-2.76	0.00	-2.76	-2.51
TCGA-CR-7364-10A-01D-2013-08_HNSC	-2.56	0.00	-4.61	-2.63	-2.62	-2.61	-2.61	-2.48	-2.52	0.00	0.00	0.00	0.00	-4.61	-3.07	-2.75	-2.54
TCGA-CR-7365-10A-01D-2013-08_HNSC	-2.55	0.00	0.00	-2.83	-2.57	-2.61	-2.64	-2.52	-2.56	0.00	0.00	0.00	0.00	0.00	-3.08	-2.70	-2.54
TCGA-CR-7367-10A-01D-2013-08_HNSC	-2.49	-2.50	-2.50	-4.50	0.00	-4.20	-2.52	-2.54	-2.52	0.00	0.00	-4.50	0.00	0.00	-2.85	0.00	-2.42
TCGA-CR-7368-10A-01D-2129-08_HNSC	-2.53	-4.46	0.00	-2.56	-2.50	-2.51	-2.54	-2.49	-2.55	0.00	0.00	-4.46	0.00	0.00	0.00	-2.42	-2.46
TCGA-CR-7369-10A-01D-2129-08_HNSC	-2.54	-2.78	-2.72	-2.89	-2.61	-2.71	-2.62	-2.59	-2.49	0.00	0.00	0.00	0.00	-4.50	0.00	-2.41	-2.54
TCGA-CR-7370-10A-01D-2129-08_HNSC	-2.44	-2.66	-2.65	-2.85	-2.63	-2.70	-2.64	-2.65	-3.92	-3.14	-2.67	-3.74	-2.65	-2.52	0.00	-4.22	-2.55
TCGA-CR-7371-10A-01D-2013-08_HNSC	-2.64	-4.35	-4.65	-2.73	-2.67	-2.67	-2.73	-2.58	-2.80	-3.33	-2.88	0.00	-2.81	-2.76	0.00	-2.78	-2.63
TCGA-CR-7372-10A-01D-2013-08_HNSC	-2.63	-2.67	-2.64	-4.66	-2.75	-2.80	-2.69	-2.72	-2.72	-3.45	-2.72	-2.80	-2.82	-2.73	0.00	-2.80	-2.61
TCGA-CR-7373-10A-01D-2013-08_HNSC	-2.58	-2.75	-2.70	-2.96	-2.70	-2.76	-2.77	-2.73	-2.77	0.00	-2.79	0.00	-2.77	-2.69	0.00	-2.76	-2.51
TCGA-CR-7374-10A-01D-2013-08_HNSC	-2.62	-2.78	-2.75	-2.95	-2.53	-2.66	-2.69	-2.62	-2.66	0.00	-2.85	-2.81	-4.34	0.00	0.00	-2.68	-2.65
TCGA-CR-7376-10A-01D-2129-08_HNSC	-2.46	-2.50	-2.47	-4.09	0.00	-4.09	-2.53	-2.39	-2.41	0.00	-4.39	0.00	-4.09	-3.69	-2.98	-2.65	-2.44
TCGA-CR-7377-10A-01D-2013-08_HNSC	-2.60	-2.79	-2.75	-2.94	-2.58	-2.67	-2.70	-2.55	-2.63	0.00	-2.88	-2.78	0.00	0.00	-3.20	-2.84	-2.65
TCGA-CR-7379-10A-01D-2013-08_HNSC	-2.59	-2.71	-2.73	-2.88	-2.71	-2.78	-2.67	-2.61	-2.71	-3.40	-2.89	0.00	-2.79	-2.75	-3.25	0.00	-2.59
TCGA-CR-7380-10A-01D-2013-08_HNSC	-2.43	0.00	-4.57	-2.61	-2.57	-2.62	-2.61	-2.60	-2.58	0.00	0.00	-4.57	0.00	-4.10	-3.08	-2.69	-2.54
TCGA-CR-7382-10A-01D-2129-08_HNSC	-2.50	-4.14	-4.14	-2.72	-2.48	-2.53	-2.53	-2.51	-2.44	-4.14	-4.14	-4.44	-4.14	0.00	-2.98	-2.74	-2.48
TCGA-CR-7383-10A-01D-2129-08_HNSC	-2.43	-3.39	-3.83	-2.55	-2.47	-2.53	-2.65	-2.72	-3.53	-3.15	-2.84	-2.60	-4.43	-2.58	0.00	-3.95	-2.46
TCGA-CR-7385-10A-01D-2013-08_HNSC	-2.53	-2.68	-2.69	-2.87	-2.72	-2.68	-2.61	-2.57	-2.52	0.00	-4.57	0.00	-4.57	0.00	0.00	-2.45	-2.47
TCGA-CR-7386-10A-01D-2013-08_HNSC	-2.56	0.00	0.00	-2.77	-2.58	-2.56	-2.61	-2.47	-2.52	0.00	-4.58	0.00	0.00	-4.58	0.00	-2.46	-2.52
TCGA-CR-7388-10A-01D-2013-08_HNSC	-2.70	-2.82	-2.79	-2.95	-2.63	-2.70	-2.75	-2.70	-2.85	-3.50	-2.79	-2.70	0.00	-2.77	0.00	-2.84	-2.65
TCGA-CR-7389-10A-01D-2013-08_HNSC	-2.54	-4.57	-4.27	-2.61	-2.39	-2.57	-2.60	-2.64	-2.56	0.00	0.00	-4.27	0.00	-3.96	-3.03	-4.57	-2.49
TCGA-CR-7390-10A-01D-2013-08_HNSC	-2.60	0.00	0.00	-2.68	-2.57	-2.61	-2.61	-2.49	-2.51	0.00	0.00	0.00	0.00	0.00	-3.14	-2.69	-2.58
TCGA-CR-7391-10A-01D-2013-08_HNSC	-2.60	0.00	-4.10	-2.74	-2.57	-2.58	-2.60	-2.50	-2.48	0.00	-4.58	0.00	-4.58	-4.28	0.00	-2.43	-2.54
TCGA-CR-7392-10A-01D-2013-08_HNSC	-2.52	0.00	-4.28	-2.82	-2.58	-2.59	-2.60	-2.62	-2.62	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.52
TCGA-CR-7393-10A-01D-2013-08_HNSC	-2.64	-4.16	-4.64	-2.86	-2.60	-2.62	-2.66	-2.63	-2.74	-3.36	-2.83	0.00	-2.77	-2.72	0.00	-2.76	-2.55
TCGA-CR-7394-10A-01D-2013-08_HNSC	-2.51	0.00	0.00	-2.81	-2.55	-2.56	-2.59	-2.50	-2.48	0.00	-4.53	0.00	0.00	-4.23	0.00	-2.42	-2.48
TCGA-CR-7395-10A-01D-2013-08_HNSC	-2.52	-2.71	-2.68	-2.82	-2.67	-2.65	-2.64	-2.52	-2.59	0.00	0.00	-4.57	0.00	0.00	-3.07	-2.75	-2.58
TCGA-CR-7397-10A-01D-2013-08_HNSC	-2.64	-2.87	-2.75	-2.98	-2.57	-2.72	-2.75	-2.59	-2.80	-3.50	-2.79	-2.69	0.00	-2.80	-3.20	0.00	-2.65
TCGA-CR-7398-10A-01D-2013-08_HNSC	-2.53	-4.60	-4.30	-2.72	-2.58	-2.66	-2.59	-2.59	-2.52	0.00	0.00	0.00	0.00	-4.30	0.00	-2.43	-2.55
TCGA-CR-7399-10A-01D-2013-08_HNSC	-2.55	-4.61	0.00	-2.65	-2.60	-2.60	-2.69	-2.55	-2.62	0.00	-4.61	-4.61	0.00	-4.61	0.00	-2.48	-2.60
TCGA-CR-7401-10A-01D-2013-08_HNSC	-2.49	-4.61	0.00	-2.69	-2.59	-2.60	-2.63	-2.55	-2.54	0.00	-4.61	0.00	0.00	0.00	-3.03	-2.74	-2.52
TCGA-CR-7402-10A-01D-2013-08_HNSC	-2.68	-2.82	-2.78	-2.97	-2.58	-2.74	-2.70	-2.60	-2.82	-3.32	-2.76	-2.81	-2.87	-2.80	-3.24	0.00	-2.66
TCGA-CR-7404-10A-01D-2129-08_HNSC	-2.54	0.00	-3.99	-2.80	-2.56	-2.54	-2.56	-2.46	-2.56	0.00	0.00	-4.47	0.00	-4.47	0.00	-2.42	-2.47
TCGA-CS-4938-10A-01D-1893-08_LGG	-2.53	0.00	0.00	-2.58	-2.57	-2.56	-2.59	-2.55	-2.50	0.00	-4.56	0.00	0.00	0.00	0.00	-2.61	-2.47
TCGA-CS-4941-10A-01D-1468-08_LGG	-2.66	-2.80	-2.74	-2.97	-2.53	-2.70	-2.72	-2.56	-2.62	0.00	-2.89	-2.75	-4.65	0.00	-3.10	-2.80	-2.66
TCGA-CS-4942-10A-01D-1468-08_LGG	-2.60	0.00	-4.65	-2.76	-2.63	-2.55	-2.73	-2.55	-2.72	-3.33	-2.99	-4.65	-2.83	-2.76	-3.13	-4.65	-2.57
TCGA-CS-4943-10A-01D-1468-08_LGG	-2.45	-4.42	-4.42	-2.70	-2.42	-2.57	-2.62	-2.67	-2.53	0.00	0.00	0.00	0.00	-2.67	0.00	-2.61	-2.51
TCGA-CS-4944-10A-01D-1468-08_LGG	-2.58	-2.69	-2.73	0.00	-2.62	-2.64	-2.74	-2.67	0.00	-3.29	-2.64	-2.69	-2.78	-2.68	0.00	0.00	-2.60
TCGA-CS-5390-10A-01D-1468-08_LGG	-2.52	0.00	0.00	-2.83	-2.56	-2.59	-2.60	-2.45	-2.50	0.00	-4.58	-4.58	0.00	-4.58	0.00	-2.43	-2.53
TCGA-CS-5393-10A-01D-1468-08_LGG	-2.68	-2.88	-2.88	-3.10	-2.53	-2.66	-2.68	-2.65	-2.88	-3.41	-2.74	-2.62	-4.39	-2.78	0.00	-2.84	-2.70
TCGA-CS-5394-10A-01D-1468-08_LGG	-2.62	-2.74	-2.73	0.00	-2.67	-2.70	-2.75	-2.65	-2.76	-3.48	-2.71	-2.71	-2.87	-2.78	0.00	-2.78	-2.60
TCGA-CS-5395-10A-01D-1468-08_LGG	-2.59	-2.82	-2.80	-3.01	-2.57	-2.69	-2.70	-2.53	-2.57	-3.47	-2.89	-2.80	0.00	-4.62	-3.22	-2.76	-2.61
TCGA-CS-5396-10A-01D-1468-08_LGG	-2.52	-2.72	-2.70	-2.88	-2.62	-2.66	-2.58	-2.57	-2.56	0.00	0.00	0.00	-4.24	-4.54	0.00	-2.55	-2.50
TCGA-CS-5397-10A-03D-1893-08_LGG	-2.32	0.00	0.00	-2.71	-2.52	-2.63	-2.56	-2.59	-2.54	0.00	-4.51	0.00	-4.51	-4.51	0.00	-2.52	-2.44
TCGA-CS-6186-10A-01D-2024-08_LGG	-2.56	-2.69	-2.66	-4.09	-2.61	-2.63	-2.62	-2.71	0.00	-3.22	-2.64	-2.64	-2.68	-2.57	0.00	0.00	-2.56
TCGA-CS-6188-10A-01D-1893-08_LGG	-2.47	0.00	-4.15	-2.74	-2.58	-2.66	-2.67	-2.54	-2.68	-3.29	-2.78	-4.63	-2.74	-2.71	-3.10	-4.63	-2.58
TCGA-CS-6290-10A-01D-1705-08_LGG	-2.47	0.00	-4.14	-2.68	-2.46	-2.49	-2.57	-2.52	-2.36	0.00	0.00	-4.44	0.00	-4.44	0.00	-2.48	-2.44
TCGA-CS-6665-10A-01D-1893-08_LGG	-2.52	-4.27	-4.57	-2.69	-2.55	-2.55	-2.61	-2.48	-2.51	0.00	0.00	0.00	0.00	-4.27	-3.08	-2.81	-2.48
TCGA-CS-6666-10A-01D-1893-08_LGG	-2.41	-2.71	-2.71	-2.80	-2.64	-2.70	-2.62	-2.56	-2.51	0.00	0.00	0.00	-4.57	-4.10	-2.92	0.00	-2.52
TCGA-CS-6667-10A-01D-2024-08_LGG	-2.61	-2.68	-2.64	0.00	-2.70	-2.74	-2.62	-2.50	-2.54	-3.35	-2.97	-2.76	0.00	-4.26	0.00	-2.52	-2.54
TCGA-CS-6668-10A-01D-1893-08_LGG	-2.51	-2.69	-2.65	-2.81	-2.63	-2.65	-2.56	-2.43	-2.47	0.00	0.00	0.00	0.00	0.00	-3.09	-2.66	-2.53
TCGA-CS-6669-10A-01D-1893-08_LGG	-2.52	-2.73	-2.67	-2.86	-2.63	-2.71	-2.55	-2.52	-2.47	0.00	0.00	0.00	-4.31	-4.14	0.00	-2.43	-2.48
TCGA-CS-6670-10A-01D-1893-08_LGG	-2.52	-2.79	-2.82	-2.93	-2.52	-2.65	-2.68	-2.64	-2.67	0.00	-2.85	-2.76	0.00	0.00	0.00	-2.50	-2.54
TCGA-CU-A0YO-10A-01D-A10S-08_BLCA	-2.64	-2.80	-2.84	-3.04	-2.58	-2.68	-2.72	-2.64	-2.78	-3.49	-2.84	-2.69	0.00	-2.77	0.00	-2.77	-2.60
TCGA-CU-A0YR-10A-01D-A10S-08_BLCA	-2.60	-2.70	-2.64	-4.32	-2.71	-2.69	-2.68	-2.57	-2.58	0.00	-2.89	-2.80	0.00	0.00	0.00	-2.60	-2.56
TCGA-CU-A3KJ-10A-01D-A21A-08_BLCA	-2.51	-2.80	-2.81	-2.83	-2.49	-2.51	-2.61	-2.69	-2.51	0.00	-3.14	-2.76	0.00	-4.52	0.00	-2.62	-2.41
TCGA-CU-A3QU-10B-01D-A22Z-08_BLCA	-2.43	0.00	0.00	-2.54	-2.48	-2.46	-2.49	-2.46	-2.43	0.00	0.00	0.00	0.00	0.00	-3.04	-2.69	-2.40
TCGA-CU-A3YL-10A-01D-A22Z-08_BLCA	-2.41	-2.66	-2.72	-2.76	-2.69	-2.62	-2.48	-2.55	-2.34	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.34
TCGA-CU-A5W6-10A-01D-A289-08_BLCA	-2.47	0.00	0.00	-2.55	-2.47	-2.51	-2.52	-2.49	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.42
TCGA-CU-A72E-10A-01D-A339-08_BLCA	-2.44	-2.63	-2.58	0.00	-2.67	-2.65	-2.61	-2.61	-2.75	-3.42	-2.71	-2.60	0.00	-2.68	-3.08	0.00	-2.50
TCGA-CV-5430-10A-01D-1870-08_HNSC	-2.51	0.00	-4.32	-2.59	-2.62	-2.62	-2.64	-2.66	-4.62	-3.23	-2.74	-4.62	-2.69	-2.57	0.00	0.00	-2.49
TCGA-CV-5432-10A-01D-1870-08_HNSC	-2.60	-2.75	-2.79	-2.97	-2.57	-2.68	-2.60	-2.59	-2.69	0.00	-2.91	-2.76	0.00	0.00	0.00	-2.57	-2.53
TCGA-CV-5434-10A-01D-1870-08_HNSC	-2.55	-2.62	-2.60	-4.34	-2.73	-2.73	-2.71	-2.78	-2.72	0.00	-2.71	-2.73	-2.87	-2.70	-3.02	0.00	-2.53
TCGA-CV-5435-10A-01D-1870-08_HNSC	-2.59	-2.70	-2.72	0.00	-2.68	-2.69	-2.67	-2.71	0.00	-3.28	-2.70	-2.54	-4.71	-2.65	0.00	0.00	-2.59

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CV-5436-10A-01D-1870-08_HNSC	-2.43	-2.79	0.00	-3.00	-2.50	-2.63	-2.62	-2.60	-2.71	-3.53	-2.98	0.00	-2.81	-2.70	-3.15	0.00	-2.54
TCGA-CV-5966-10A-01D-1870-08_HNSC	-2.47	-2.85	-2.75	-2.99	-2.54	-2.69	-2.66	-2.76	-2.83	-3.72	-2.79	-2.80	-2.85	-2.76	0.00	-2.83	-2.53
TCGA-CV-5970-10A-01D-1870-08_HNSC	-2.57	-2.81	-2.80	-2.99	-2.53	-2.61	-2.70	-2.61	-2.58	0.00	-2.99	-2.76	0.00	-4.66	-3.17	-2.87	-2.53
TCGA-CV-6933-10A-01D-1912-08_HNSC	-2.57	-2.72	-2.74	-2.98	-2.55	-2.63	-2.64	-2.47	-2.53	0.00	-2.85	-2.74	0.00	0.00	-3.06	-2.76	-2.52
TCGA-CV-6934-10A-01D-1912-08_HNSC	-2.55	0.00	-4.19	-2.73	-2.55	-2.58	-2.56	-2.48	-2.40	0.00	0.00	0.00	0.00	-4.49	0.00	-2.38	-2.49
TCGA-CV-6935-10A-01D-1912-08_HNSC	-2.61	-2.74	-2.72	-2.94	-2.51	-2.61	-2.65	-2.45	-2.50	0.00	-2.87	-2.72	0.00	-4.58	-3.18	-2.82	-2.56
TCGA-CV-6936-10A-01D-1912-08_HNSC	-2.55	-4.55	0.00	-2.82	-2.56	-2.58	-2.61	-2.50	-2.65	-3.20	-2.83	-4.55	-2.69	-2.68	-3.11	0.00	-2.50
TCGA-CV-6937-10A-01D-2013-08_HNSC	-2.55	0.00	0.00	-2.63	-2.61	-2.56	-2.57	-2.49	-2.53	0.00	0.00	0.00	0.00	0.00	-3.05	-2.68	-2.54
TCGA-CV-6938-10A-01D-1912-08_HNSC	-2.63	-2.79	-2.77	-2.98	-2.57	-2.70	-2.71	-2.61	-2.74	-3.30	-2.76	-2.80	-2.77	-2.74	0.00	-2.88	-2.58
TCGA-CV-6939-10A-01D-1912-08_HNSC	-2.55	0.00	-4.24	-2.73	-2.56	-2.59	-2.65	-2.66	-2.75	-3.39	-2.89	-4.54	-2.78	-2.72	0.00	-2.70	-2.56
TCGA-CV-6940-10A-01D-1912-08_HNSC	-2.62	-2.80	-2.77	-2.94	-2.55	-2.67	-2.70	-2.67	-2.72	-3.51	-2.71	-2.77	-2.79	-2.75	0.00	-2.85	-2.61
TCGA-CV-6941-10A-01D-1912-08_HNSC	-2.59	-2.71	-2.76	-2.89	-2.46	-2.61	-2.67	-2.51	-2.54	0.00	-2.90	-2.79	0.00	0.00	-3.13	-2.76	-2.59
TCGA-CV-6942-10A-01D-2013-08_HNSC	-2.60	0.00	0.00	-2.82	-2.62	-2.60	-2.59	-2.52	-2.69	-3.29	-2.82	0.00	-2.76	-2.69	-3.05	-4.57	-2.57
TCGA-CV-6943-10A-01D-1912-08_HNSC	-2.39	-4.50	0.00	-2.70	-2.56	-2.54	-2.59	-2.47	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.48
TCGA-CV-6945-10A-01D-1912-08_HNSC	-2.58	-2.60	-2.62	-4.56	-2.69	-2.72	-2.60	-2.66	-2.70	-3.36	-2.69	-2.64	-4.56	-2.64	0.00	-2.75	-2.51
TCGA-CV-6948-10A-01D-1912-08_HNSC	-2.50	0.00	-4.21	-2.71	-2.54	-2.57	-2.56	-2.45	-2.41	0.00	0.00	0.00	0.00	-4.51	0.00	-2.44	-2.49
TCGA-CV-6950-10A-01D-1912-08_HNSC	-2.55	-2.80	-2.77	-2.99	-2.52	-2.65	-2.66	-2.59	-2.74	-3.42	-2.77	-2.68	0.00	-2.72	0.00	-2.77	-2.59
TCGA-CV-6951-10A-01D-1912-08_HNSC	-2.50	0.00	-4.50	-2.70	-2.51	-2.55	-2.59	-2.45	-2.47	0.00	-4.50	0.00	-4.50	0.00	0.00	-2.40	-2.47
TCGA-CV-6952-10A-01D-1912-08_HNSC	-2.59	-2.80	-2.72	-2.93	-2.53	-2.63	-2.71	-2.55	-2.77	-3.38	-2.71	-2.65	0.00	-2.78	0.00	-2.81	-2.58
TCGA-CV-6953-10A-01D-1912-08_HNSC	-2.54	-2.67	-2.68	-2.82	-2.68	-2.63	-2.58	-2.51	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.38	-2.56
TCGA-CV-6954-10A-01D-1912-08_HNSC	-2.49	-4.51	0.00	-2.71	-2.52	-2.56	-2.58	-2.52	-2.53	0.00	-4.51	0.00	0.00	0.00	0.00	-2.38	-2.51
TCGA-CV-6955-10A-01D-2013-08_HNSC	-2.51	0.00	0.00	-2.77	-2.59	-2.57	-2.56	-2.38	-2.50	0.00	0.00	0.00	0.00	0.00	-3.00	-2.65	-2.51
TCGA-CV-6956-10A-01D-2013-08_HNSC	-2.54	0.00	0.00	-2.75	-2.50	-2.54	-2.57	-2.54	-2.55	0.00	0.00	0.00	0.00	0.00	-3.05	-2.68	-2.43
TCGA-CV-6959-10A-01D-1912-08_HNSC	-2.45	-4.47	-4.47	-2.53	-2.52	-2.52	-2.58	-2.60	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.45
TCGA-CV-6960-10A-01D-2013-08_HNSC	-2.52	-4.53	-4.53	-2.73	-2.57	-2.57	-2.59	-2.52	-2.49	0.00	0.00	0.00	0.00	-4.23	-2.97	-2.74	-2.54
TCGA-CV-6961-10A-01D-1912-08_HNSC	-2.52	-4.51	0.00	-2.57	-2.53	-2.54	-2.61	-2.56	-2.54	0.00	0.00	0.00	0.00	-4.51	-3.05	-2.69	-2.47
TCGA-CV-6962-10A-01D-1912-08_HNSC	-2.61	0.00	-2.72	-2.89	-2.46	-2.63	-2.63	-2.52	-2.51	0.00	-2.86	0.00	-2.74	0.00	-3.10	-2.76	-2.55
TCGA-CV-7089-10A-01D-2013-08_HNSC	-2.48	0.00	0.00	-2.70	-2.53	-2.58	-2.58	-2.55	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.44
TCGA-CV-7090-10A-01D-2013-08_HNSC	-2.47	-2.54	-2.50	-4.46	0.00	-4.46	-2.60	-2.70	-2.69	0.00	-2.72	-2.66	0.00	-2.58	0.00	-2.61	-2.45
TCGA-CV-7091-10A-01D-2013-08_HNSC	-2.68	0.00	-4.67	-2.71	-2.50	-2.68	-2.68	-2.71	-2.81	-3.30	-2.78	-2.81	-2.82	-2.81	0.00	-2.87	-2.68
TCGA-CV-7095-10A-01D-2013-08_HNSC	-2.52	-4.52	-4.52	-2.57	-2.51	-2.59	-2.58	-2.54	-2.54	0.00	0.00	0.00	-4.52	0.00	0.00	-2.46	-2.49
TCGA-CV-7097-10A-01D-2013-08_HNSC	-2.47	0.00	0.00	-2.72	-2.52	-2.53	-2.62	-2.54	-2.52	0.00	0.00	0.00	0.00	-4.61	0.00	-2.51	-2.42
TCGA-CV-7099-10A-01D-2013-08_HNSC	-2.56	-2.86	-2.82	-3.00	-2.53	-2.57	-2.64	-2.58	-2.82	-3.39	-2.79	-2.86	-2.86	-2.77	0.00	-2.95	-2.54
TCGA-CV-7100-10A-01D-2013-08_HNSC	-2.59	0.00	-4.31	-2.79	-2.58	-2.57	-2.62	-2.45	-2.54	0.00	0.00	0.00	-4.61	0.00	-3.13	-2.76	-2.53
TCGA-CV-7101-10A-01D-2013-08_HNSC	-2.70	-2.83	-2.82	-3.00	-2.57	-2.67	-2.73	-2.63	-2.85	-3.44	-2.78	-2.84	-2.87	-2.80	-3.20	-4.42	-2.64
TCGA-CV-7102-10A-01D-2013-08_HNSC	-2.56	0.00	-4.58	-2.81	-2.56	-2.62	-2.56	-2.54	-2.56	0.00	0.00	0.00	0.00	-4.58	-3.10	-2.74	-2.55
TCGA-CV-7103-10A-01D-2013-08_HNSC	-2.58	-2.68	-2.62	0.00	0.00	-4.28	-2.60	-2.53	-2.72	-3.43	-2.82	0.00	-2.69	-2.69	0.00	-2.77	-2.50
TCGA-CV-7104-10A-01D-2013-08_HNSC	-2.68	-2.78	-2.84	-3.00	-2.58	-2.70	-2.74	-2.64	-2.84	-3.50	-2.79	-2.84	-2.88	-2.78	0.00	-2.79	-2.62
TCGA-CV-7177-10A-01D-2013-08_HNSC	-2.58	-2.74	-2.69	-2.93	-2.50	-2.66	-2.77	-2.81	-4.31	-3.49	-2.68	-2.74	-2.73	-2.69	0.00	-4.61	-2.66
TCGA-CV-7178-10A-01D-2013-08_HNSC	-2.58	0.00	0.00	-2.78	-2.62	-2.58	-2.58	-2.53	-2.43	0.00	-4.57	-4.27	0.00	-4.57	-3.07	-2.73	-2.53
TCGA-CV-7180-10A-01D-2013-08_HNSC	-2.57	0.00	0.00	-2.66	-2.62	-2.66	-2.67	-2.55	-2.63	0.00	0.00	0.00	0.00	0.00	-3.03	-2.74	-2.56
TCGA-CV-7183-10A-01D-2013-08_HNSC	-2.42	0.00	0.00	-2.61	-2.58	-2.58	-2.59	-2.52	-2.62	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.45
TCGA-CV-7235-10A-01D-2013-08_HNSC	-2.57	-2.75	-2.75	-2.97	-2.55	-2.63	-2.57	-2.57	-2.57	0.00	-2.91	-2.72	0.00	-4.22	0.00	-2.68	-2.53
TCGA-CV-7236-10A-01D-2013-08_HNSC	-2.53	-4.60	-4.30	-2.74	-2.56	-2.53	-2.64	-2.54	-2.53	0.00	0.00	0.00	0.00	0.00	-3.06	-2.79	-2.52
TCGA-CV-7238-10A-01D-2013-08_HNSC	-2.46	0.00	-4.59	-2.63	-2.61	-2.59	-2.63	-2.51	-2.59	0.00	0.00	0.00	-4.59	0.00	-3.04	-2.70	-2.52
TCGA-CV-7242-10A-01D-2013-08_HNSC	-2.56	0.00	0.00	-2.61	-2.56	-2.62	-2.58	-2.50	-2.51	0.00	0.00	0.00	-4.58	0.00	0.00	-2.50	-2.54
TCGA-CV-7243-10A-01D-2013-08_HNSC	-2.61	-2.64	-2.73	-2.97	-2.70	-2.71	-2.63	-2.46	-2.59	0.00	0.00	0.00	0.00	0.00	-3.11	-2.74	-2.51
TCGA-CV-7245-10A-01D-2013-08_HNSC	-2.65	-2.70	-2.72	-2.92	-2.69	-2.72	-2.68	-2.67	-2.74	-3.36	-2.88	0.00	-2.75	-2.68	0.00	-2.79	-2.57
TCGA-CV-7247-10A-01D-2013-08_HNSC	-2.57	0.00	-4.59	-2.65	-2.60	-2.61	-2.67	-2.50	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.48	-2.56
TCGA-CV-7248-10A-01D-2013-08_HNSC	-2.60	-2.79	-2.76	-2.94	-2.65	-2.66	-2.69	-2.56	-2.62	0.00	-2.90	0.00	-2.81	-4.34	-3.06	-2.76	-2.58
TCGA-CV-7250-10A-01D-2013-08_HNSC	-2.49	0.00	-4.31	-2.79	-2.63	-2.56	-2.58	-2.54	-2.59	0.00	-4.61	0.00	0.00	-4.61	0.00	-2.48	-2.55
TCGA-CV-7252-10A-01D-2013-08_HNSC	-2.68	-2.81	-2.77	-3.01	-2.67	-2.76	-2.73	-2.64	-2.75	-3.43	-2.75	-2.85	-2.81	-2.81	0.00	-2.88	-2.65
TCGA-CV-7253-10A-01D-2013-08_HNSC	-2.62	-2.41	-2.56	-4.31	-2.69	-2.73	-2.65	-2.63	-2.60	0.00	-2.87	-2.74	0.00	-4.14	0.00	-2.73	-2.58
TCGA-CV-7254-10A-01D-2013-08_HNSC	-2.60	-4.63	-4.63	-2.69	-2.56	-2.65	-2.69	-2.70	-2.77	-3.31	-2.88	0.00	-2.74	-2.74	0.00	-2.81	-2.60
TCGA-CV-7255-10A-01D-2013-08_HNSC	-2.55	-2.71	-2.72	-2.90	-2.69	-2.72	-2.63	-2.47	-2.53	0.00	0.00	0.00	0.00	-4.57	-3.05	-2.78	-2.53
TCGA-CV-7261-10A-01D-2013-08_HNSC	-2.50	0.00	-4.10	-2.59	-2.56	-2.62	-2.60	-2.50	-2.57	0.00	0.00	0.00	0.00	-4.28	0.00	-2.66	-2.55
TCGA-CV-7263-10A-01D-2013-08_HNSC	-2.65	-2.81	-2.80	-2.97	-2.59	-2.71	-2.72	-2.75	-2.81	-3.43	-2.75	-2.83	-2.85	-2.78	0.00	-2.83	-2.63
TCGA-CV-7406-10A-01D-2078-08_HNSC	-2.56	-3.99	0.00	-2.60	-2.54	-2.56	-2.58	-2.66	-2.66	-3.32	-2.93	0.00	-2.73	-2.62	0.00	-2.75	-2.50
TCGA-CV-7407-10A-01D-2078-08_HNSC	-2.54	-4.46	0.00	-2.77	-2.54	-2.53	-2.64	-2.61	-2.67	-3.31	-2.86	0.00	-2.80	-2.66	0.00	-2.82	-2.48
TCGA-CV-7409-10A-01D-2229-08_HNSC	-2.50	0.00	-2.70	-2.81	-2.54	-2.55	-2.55	-2.66	-2.53	0.00	-2.87	0.00	-2.81	0.00	-3.18	-2.77	-2.40
TCGA-CV-7410-10A-01D-2078-08_HNSC	-2.36	-2.67	-2.67	-2.82	-2.65	-2.59	-2.56	-2.39	-2.40	-4.42	0.00	0.00	-4.12	-3.65	-2.96	-2.69	-2.46
TCGA-CV-7411-10A-01D-2078-08_HNSC	-2.54	0.00	0.00	-2.77	-2.54	-2.59	-2.61	-2.60	-2.70	-3.30	-2.87	0.00	-2.68	-2.59	0.00	-2.78	-2.47
TCGA-CV-7413-10A-01D-2078-08_HNSC	-2.58	0.00	-3.97	-2.58	-2.58	-2.59	-2.61	-2.51	-2.76	-3.34	-2.93	0.00	-2.73	-2.64	0.00	-2.73	-2.50
TCGA-CV-7414-10A-01D-2078-08_HNSC	-2.59	0.00	-4.49	-2.78	-2.58	-2.61	-2.58	-2.59	-2.75	-3.34	-2.86	0.00	-2.73	-2.65	0.00	-2.77	-2.53
TCGA-CV-7415-10A-01D-2078-08_HNSC	-2.50	-2.54	-2.49	-4.39	-4.09	-3.79	-2.54	-2.48	-2.64	-3.14	-2.90	-4.39	-2.72	-2.62	-3.09	-4.09	-2.46
TCGA-CV-7416-10A-01D-2078-08_HNSC	-2.60	-2.75	-2.74	-2.95	-2.48	-2.64	-2.66	-2.64	-2.77	-3.23	-2.76	-2.67	-4.23	-2.72	0.00	-2.80	-2.58
TCGA-CV-7418-10A-01D-2078-08_HNSC	-2.53	0.00	-2.69	-2.88	-2.46	-2.61	-2.57	-2.64	-2.55	0.00	-2.90	0.00	-2.76	-4.47	-3.09	-2.73	-2.51
TCGA-CV-7421-10A-01D-2078-08_HNSC	-2.52	0.00	0.00	-2.54	-2.52	-2.53	-2.58	-2.50	-2.52	0.00	0.00	-4.15	0.00	-4.45	-3.07	-2.80	-2.52
TCGA-CV-7422-10A-01D-2078-08_HNSC	-2.48	0.00	0.00	-2.71	-2.44	-2.53	-2.50	-2.56	-2.46	0.00	-4.42	0.00	-4.12	-3.95	0.00	-2.51	-2.40
TCGA-CV-7423-10A-01D-2078-08_HNSC	-2.52	0.00	0.00	-2.54	-2.50	-2.52	-2.56	-2.58	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.46
TCGA-CV-7424-10A-01D-2078-08_HNSC	-2.48	0.00	-4.47	-2.79	-2.57	-2.61	-2.58	-2.59	-2.60	-3.24	-2.99	0.00	-2.76	-2.68	-3.04	-4.47	-2.48
TCGA-CV-7425-10A-01D-2078-08_HNSC	-2.52	0.00	0.00	-2.57	-2.49	-2.52	-2.52	-2.45	-2.52	0.00	-4.39	0.00	0.00	-4.09	0.00	-2.38	-2.48
TCGA-CV-7427-10A-01D-2078-08_HNSC	-2.51	-2.71	-2.68	-2.77	-2.57	-2.66	-2.52	-2.45	-2.53	0.00	0.00	0.00	-4.08	-3.60	0.00	-2.42	-2.46
TCGA-CV-7429-10A-01D-2129-08_HNSC	-2.51	-4.17	0.00	-2.59	-2.50	-2.56	-2.55	-2.52	-2.44	0.00	0.00	0.00	0.00	0.00	-3.11	-2.70	-2.50
TCGA-CV-7430-10A-01D-2129-08_HNSC	-2.52	-4.17	-4.17	-2.58	-2.56	-2.57	-2.57	-2.50	-2.56	0.00	-4.47	0.00	-3.77	-4.17	0.00	-2.44	-2.49
TCGA-CV-7432-10A-01D-2129-08_HNSC	-2.68	-2.81	-2.81	-2.92	-2.47	-2.66	-2.72	-2.58	-2.61	-3.57	-2.84	-2.70	0.00	-4.31	0.00	-2.58	-2.61
TCGA-CV-7433-10A-01D-2129-08_HNSC	-2.49	-2.61	-2.68	-2.77	-2.60	-2.62	-2.52	-2.39	-2.44	0.00	0.00	0.00	0.00	0.00	-3.00	-2.66	-2.42
TCGA-CV-7434-10A-01D-2129-08_HNSC	-2.50	-2.59	-2.53	-4.22	-2.52	-2.54	-2.58	-2.62	-2.52	0.00	-2.74	-2.59	0.00	-4.69	-3.10	-2.84	-2.47
TCGA-CV-7435-10A-01D-2129-08_HNSC	-2.50	-2.64	-2.66	-3.85	-2.60	-2.62	-2.65	-2.70	-2.67	-3.32	-2.72	-2.66	-2.83	-2.71	0.00	-2.83	-2.60
TCGA-CV-7437-10A-01D-2129-08_HNSC	-2.59	-2.59	-2.70	-4.20	-2.65	-2.64	-2.60	-2.60	-3.51	-3.06	-2.68	0.00	-2.64	-2.57	0.00	-3.60	-2.53
TCGA-CV-7438-10A-01D-2129-08_HNSC	-2.57	-3.79	-3.89	-2.62	-2.53	-2.57	-2.57	-2.62	-2.71	-3.26	-2.85	-3.89	-2.77	-2.65	0.00	-2.74	-2.50
TCGA-CV-7440-10A-01D-2129-08_HNSC	-2.50	-4.45	0.00	-2.72	-2.50	-2.49	-2.61	-2.45	-2.46	0.00	-3.85	-3.61	0.00	-3.68	0.00	-2.45	-2.42
TCGA-CV-7446-10A-01D-2229-08_HNSC	-2.54	-2.77	-2.73	-2.94	-2.58	-2.78	-2.62	-2.64	-2.66	-3.21	-2.97	0.00	-2.74	-2.66	0.00	-2.71	-2.52
TCGA-CV-7568-10A-01D-2229-08_HNSC	-2.42	-2.74	-2.72	-2.73	-2.69	-2.64	-2.57	-2.57	-2.67	-3.25	-2.89	0.00	-2.85	-2.66	0.00	-2.74	-2.48
TCGA-CV-A45O-10A-01D-A24F-08_HNSC	-2.54	-2.60	-2.62	-2.85	-2.60	-2.65	-2.56	-2.59	-2.44	-4.43	-4.13	-4.13	0.00	-3.95	0.00	-2.51	-2.50
TCGA-CV-A45P-10A-01D-A24F-08_HNSC	-2.52	-2.60	-2.70	-2.85	-2.63	-2.60	-2.56	-2.59	-2.46	0.00	-4.41	0.00	-4.41	-4.41	0.00	-2.52	-2.47
TCGA-CV-A45Q-10A-01D-A24F-08_HNSC	-2.65	-2.76	-2.73	-3.01	-2.54	-2.68	-2.63	-2.57	-2.71	-3.30	-2.73	-2.78	-2.79	-2.72	0.00	-2.72	-2.59
TCGA-CV-A45R-10A-01D-A24F-08_HNSC	-2.45	0.00	0.00	-2.57	-2.47	-2.45	-2.49	-2.53	-2.45	0.00	0.00	0.00	0.00	0.00	-2.83	-4.64	-2.39
TCGA-CV-A45T-10A-01D-A24F-08_HNSC	-2.55	-4.03	-3.81	-2.61	-2.55	-2.55	-2.59	-2.56	-2.55	0.00	-4.03	-4.03	-4.50	-3.73	0.00	-2.60	-2.49
TCGA-CV-A45U-10A-01D-A24F-08_HNSC	-2.57	-2.73	-2.67	-2.86	-2.62	-2.67	-2.60	-2.60	-2.45	0.00	-4.53	0.00	-3.92	-3.92	0.00	-2.65	-2.49
TCGA-CV-A45V-10A-01D-A25E-08_HNSC	-2.57	0.00	0.00	-2.75	-2.61	-2.57	-2.59	-2.70	-2.69	-3.21	-2.96	-2.73	-3.79	-2.67	0.00	-2.75	-2.55
TCGA-CV-A45W-10A-01D-A25E-08_HNSC	-2.55	-2.70	-2.62	-2.81	-2.62	-2.68	-2.58	-2.49	-2.55	0.00	-4.17	0.00	-4.17	-4.17	-2.96	-2.69	-2.50
TCGA-CV-A45X-10A-01D-A25E-08_HNSC	-2.53	-4.46	-4.16	-2.65	-2.61	-2.57	-2.64	-2.52	-2.70	-3.31	-4.46	0.00	-2.71	-2.70	0.00	-2.69	-2.51
TCGA-CV-A45Y-10A-01D-A25E-08_HNSC	-2.57	0.00	0.00	-2.75	-2.57	-2.58	-2.64	-2.54	-2.67	-3.34	-2.90	0.00	-2.72	-2.67	-3.00	-4.01	-2.57
TCGA-CV-A45Z-10A-01D-A25E-08_HNSC	-2.55	0.00	0.00	-2.75	-2.54	-2.53	-2.60	-2.43	-2.40	0.00	0.00	0.00	-4.44	-4.44	-2.99	-2.66	-2.51
TCGA-CV-A460-10A-01D-A25E-08_HNSC	-2.56	-2.70	-2.70	-2.90	-2.68	-2.79	-2.62	-2.52	-2.69	-3.30	-2.79	0.00	-2.86	-2.71	0.00	-2.68	-2.53

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CV-A461-10A-01D-A25Y-08_HNSC	-2.60	-3.55	-4.03	-2.63	-2.55	-2.61	-2.59	-2.49	-2.58	0.00	-4.51	-4.03	-4.51	-3.81	0.00	-2.59	-2.50
TCGA-CV-A463-10A-01D-A25Y-08_HNSC	-2.64	-2.66	-2.61	-4.10	-2.66	-2.71	-2.65	-2.55	-2.54	0.00	-2.81	-3.88	-2.75	-4.28	-3.12	-2.73	-2.51
TCGA-CV-A464-10A-01D-A25Y-08_HNSC	-2.49	-2.73	-2.73	-2.95	-2.52	-2.66	-2.66	-2.65	-2.53	0.00	-2.92	-2.79	-4.59	-3.99	0.00	-2.66	-2.55
TCGA-CV-A465-10A-01D-A25Y-08_HNSC	-2.64	-4.60	0.00	-2.87	-2.61	-2.62	-2.64	-2.51	-2.71	-3.28	-2.89	0.00	-2.79	-2.69	0.00	-2.77	-2.59
TCGA-CV-A468-10A-01D-A25Y-08_HNSC	-2.63	-2.83	-2.75	-2.99	-2.53	-2.65	-2.68	-2.54	-2.55	0.00	-2.94	-2.79	-4.55	0.00	-3.12	-2.76	-2.64
TCGA-CV-A6JD-10A-01D-A31J-08_HNSC	-2.53	0.00	0.00	-2.58	-2.55	-2.57	-2.64	-2.67	-2.64	-3.50	-2.97	-4.50	-2.72	-2.71	0.00	-2.73	-2.49
TCGA-CV-A6JE-10A-01D-A31J-08_HNSC	-2.45	-2.68	-2.62	-2.83	-2.63	-2.58	-2.55	-2.51	-2.49	0.00	0.00	0.00	0.00	0.00	-3.05	-2.74	-2.40
TCGA-CV-A6JM-10A-01D-A31J-08_HNSC	-2.47	-2.70	-2.69	-2.82	-2.68	-2.62	-2.52	-2.60	-2.41	0.00	-4.44	0.00	0.00	0.00	0.00	-2.58	-2.50
TCGA-CV-A6JN-10A-01D-A31J-08_HNSC	-2.60	-2.67	-2.66	0.00	-2.63	-2.67	-2.70	-2.61	-2.72	-3.40	-2.74	-2.60	0.00	-2.79	-3.11	0.00	-2.61
TCGA-CV-A6JT-10A-01D-A31J-08_HNSC	-2.38	-2.65	-2.65	-2.78	-2.60	-2.69	-2.55	-2.52	-2.54	0.00	0.00	0.00	0.00	0.00	-3.01	-2.75	-2.47
TCGA-CV-A6JU-10A-01D-A31J-08_HNSC	-2.61	-2.79	-2.73	-2.93	-2.50	-2.60	-2.65	-2.70	-2.69	-3.39	-2.72	-2.78	-2.75	-2.68	0.00	-2.74	-2.54
TCGA-CV-A6JY-10A-01D-A31J-08_HNSC	-2.53	-2.78	-2.73	-2.94	-2.47	-2.61	-2.60	-2.68	-2.63	0.00	-3.01	-2.70	0.00	0.00	0.00	-2.61	-2.55
TCGA-CV-A6JZ-10A-01D-A31J-08_HNSC	-2.47	-2.69	-2.68	-2.88	-2.63	-2.65	-2.67	-2.74	-2.71	0.00	-2.82	0.00	-2.72	-2.59	0.00	-2.74	-2.50
TCGA-CV-A6K0-10A-01D-A31J-08_HNSC	-2.55	0.00	0.00	-2.65	-2.54	-2.54	-2.59	-2.47	-2.46	0.00	0.00	0.00	0.00	0.00	-3.00	-2.77	-2.46
TCGA-CV-A6K1-10A-01D-A31J-08_HNSC	-2.53	0.00	-4.48	-2.73	-2.56	-2.58	-2.58	-2.56	-2.64	-3.20	-2.78	0.00	-2.70	-2.61	-3.00	-4.48	-2.53
TCGA-CV-A6K2-10A-01D-A31J-08_HNSC	-2.50	0.00	0.00	-2.68	-2.51	-2.53	-2.57	-2.45	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.43
TCGA-CX-7082-10A-01D-2013-08_HNSC	-2.52	-4.58	0.00	-2.71	-2.42	-2.50	-2.51	-2.49	-2.42	0.00	0.00	0.00	0.00	-4.58	0.00	-2.47	-2.42
TCGA-CX-7085-10A-01D-2013-08_HNSC	-2.64	0.00	0.00	-2.77	-2.59	-2.63	-2.64	-2.56	-2.72	-3.33	-2.89	-4.58	-2.79	-2.67	-3.09	0.00	-2.56
TCGA-CX-7086-10D-01D-2078-08_HNSC	-2.50	-3.67	-3.67	-2.50	-2.45	-2.52	-2.53	-2.38	-2.49	0.00	0.00	0.00	-4.07	-3.90	0.00	-2.69	-2.52
TCGA-CX-7219-10A-01D-2013-08_HNSC	-2.48	-4.66	-4.18	-2.62	-2.42	-2.51	-2.57	-2.58	-2.53	0.00	0.00	0.00	0.00	-4.66	-3.04	0.00	-2.43
TCGA-CX-A4AQ-10A-01D-A25E-08_HNSC	-2.47	0.00	-4.12	-2.74	-2.50	-2.57	-2.57	-2.53	-2.46	0.00	-4.42	0.00	-4.12	-3.82	0.00	-2.56	-2.45
TCGA-D1-A0ZN-10A-01D-A122-09_UCEC	-2.94	0.00	-4.52	-3.00	-2.66	-2.66	-2.62	-2.59	-2.70	-3.48	-2.81	0.00	-2.77	-2.78	-3.02	0.00	-2.79
TCGA-D1-A0ZO-10A-01D-A122-09_UCEC	-2.84	0.00	0.00	-2.90	-2.56	-2.55	-2.53	-2.56	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.64
TCGA-D1-A0ZP-10A-01D-A10M-09_UCEC	-2.97	-2.81	-2.77	-3.23	-2.55	-2.77	-2.71	-2.86	-2.78	-3.42	-2.79	-2.83	-2.81	-2.81	0.00	-3.03	-2.80
TCGA-D1-A0ZQ-10A-01D-A122-09_UCEC	-2.97	-2.91	-2.90	-3.18	-2.60	-2.68	-2.68	-2.68	-2.85	-3.66	-2.76	-2.67	0.00	-2.85	-3.21	0.00	-2.83
TCGA-D1-A0ZR-10A-01D-A10M-09_UCEC	-3.05	-2.90	-2.89	-3.25	-2.64	-2.72	-2.68	-2.68	-2.87	-3.56	-2.77	-2.71	0.00	-2.87	0.00	-2.94	-2.81
TCGA-D1-A0ZS-10A-01D-A122-09_UCEC	-3.00	-2.90	-2.90	-3.26	-2.63	-2.75	-2.69	-2.77	-4.42	-3.42	-2.61	-2.71	-2.87	-2.78	0.00	0.00	-2.86
TCGA-D1-A0ZU-10A-01D-A10M-09_UCEC	-2.97	-2.83	-2.81	-3.15	-2.63	-2.71	-2.68	-2.76	-2.57	-4.96	-2.98	-2.84	-4.96	-4.96	0.00	-2.75	-2.77
TCGA-D1-A0ZV-10A-01D-A10M-09_UCEC	-3.01	-2.89	-2.90	-3.31	-2.63	-2.74	-2.69	-2.79	-2.89	-3.64	-2.81	-2.78	0.00	-2.93	0.00	-2.97	-2.91
TCGA-D1-A0ZZ-10A-01D-A10M-09_UCEC	-2.94	-2.85	-2.82	-3.27	-2.84	-2.86	-2.66	-2.65	-2.80	-3.50	-2.87	-4.89	-2.84	-2.82	-3.14	0.00	-2.88
TCGA-D1-A101-10A-01D-A10M-09_UCEC	-2.94	0.00	0.00	-2.82	-2.66	-2.69	-2.64	-2.75	-2.60	0.00	0.00	0.00	0.00	-4.87	0.00	-2.67	-2.80
TCGA-D1-A102-10A-01D-A10M-09_UCEC	-2.81	-2.59	-2.61	0.00	0.00	0.00	-2.56	-2.52	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.69
TCGA-D1-A103-10A-01D-A10M-09_UCEC	-3.10	-2.99	-3.00	-3.24	-2.72	-2.80	-2.74	-2.93	-5.07	-3.41	-2.67	-2.99	-2.82	-2.80	0.00	0.00	-2.91
TCGA-D1-A15V-10A-01D-A122-09_UCEC	-3.00	-2.93	-2.93	-3.21	-2.61	-2.76	-2.74	-2.71	-2.89	-3.56	-2.68	-2.93	-2.90	-2.90	0.00	-2.92	-2.88
TCGA-D1-A15W-10A-01D-A122-09_UCEC	-2.93	0.00	0.00	-2.94	-2.56	-2.65	-2.60	-2.68	-2.68	-3.45	-2.85	0.00	-2.77	-2.73	0.00	-2.90	-2.74
TCGA-D1-A15X-10A-01D-A122-09_UCEC	-2.89	0.00	0.00	-2.84	-2.66	-2.67	-2.62	-2.67	-2.80	-3.49	-2.84	-4.90	-2.80	-2.83	0.00	-2.84	-2.80
TCGA-D1-A15Z-10A-01D-A122-09_UCEC	-2.73	0.00	-4.76	-2.94	-2.54	-2.56	-2.52	-2.48	-2.42	0.00	0.00	0.00	-4.76	0.00	0.00	-2.60	-2.64
TCGA-D1-A160-10A-01D-A122-09_UCEC	-3.03	-4.50	-4.98	-2.84	-2.71	-2.69	-2.61	-2.67	-2.81	-3.46	-2.91	0.00	-2.80	-2.81	0.00	-2.92	-2.80
TCGA-D1-A161-10A-01D-A122-09_UCEC	-2.92	-2.85	-2.83	-3.20	-2.76	-2.80	-2.65	-2.68	-2.80	-3.52	-2.86	0.00	-2.84	-2.79	0.00	-2.82	-2.80
TCGA-D1-A163-10A-01D-A12J-09_UCEC	-2.80	0.00	-4.55	-2.94	-2.60	-2.67	-2.57	-2.59	-2.51	0.00	0.00	0.00	0.00	-4.86	0.00	-2.53	-2.70
TCGA-D1-A165-10A-01D-A12J-09_UCEC	-2.97	0.00	-4.90	-2.86	-2.62	-2.72	-2.60	-2.63	-2.82	-3.24	-2.91	0.00	-2.83	-2.82	0.00	-2.92	-2.82
TCGA-D1-A167-10A-01D-A12J-09_UCEC	-2.94	-2.73	-2.78	-3.16	-2.75	-2.72	-2.57	-2.64	-2.51	0.00	0.00	0.00	0.00	0.00	-3.13	-2.72	-2.76
TCGA-D1-A168-10A-01D-A12J-09_UCEC	-2.90	0.00	0.00	-2.86	-2.53	-2.59	-2.54	-2.69	-2.76	-3.30	-2.87	0.00	-2.71	-2.70	0.00	-2.84	-2.67
TCGA-D1-A169-10A-01D-A12J-09_UCEC	-3.01	-2.84	-2.81	0.00	-2.77	-2.74	-2.77	-2.67	-2.88	-3.61	-2.63	-2.62	0.00	-2.90	0.00	-2.88	-2.92
TCGA-D1-A16B-10A-01D-A12J-09_UCEC	-2.90	0.00	0.00	-3.00	-2.60	-2.58	-2.57	-2.59	-2.62	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.71
TCGA-D1-A16D-10A-01D-A12J-09_UCEC	-2.90	-4.93	0.00	-2.85	-2.60	-2.61	-2.61	-2.58	-2.61	0.00	0.00	-4.93	0.00	0.00	-3.09	-2.76	-2.70
TCGA-D1-A16E-10A-01D-A12J-09_UCEC	-2.83	0.00	0.00	-2.91	-2.72	-2.69	-2.68	-2.71	-2.84	-3.54	-2.90	0.00	-2.86	-2.84	0.00	-2.88	-2.84
TCGA-D1-A16F-10A-01D-A12J-09_UCEC	-2.88	0.00	-4.90	-2.98	-2.58	-2.66	-2.65	-2.53	-2.51	0.00	0.00	-4.90	0.00	-4.90	0.00	-2.48	-2.74
TCGA-D1-A16G-10A-01D-A12J-09_UCEC	-2.91	0.00	-4.75	-2.70	-2.57	-2.57	-2.54	-2.54	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.68
TCGA-D1-A16I-10A-01D-A12J-09_UCEC	-2.91	-2.85	-2.92	-3.15	-2.60	-2.68	-2.70	-2.76	-2.63	-4.89	-2.99	-2.82	0.00	0.00	0.00	-2.74	-2.84
TCGA-D1-A16J-10A-01D-A12J-09_UCEC	-3.02	-2.69	-2.65	0.00	-2.78	-2.79	-2.66	-2.72	-2.54	0.00	-2.80	-2.73	0.00	0.00	0.00	-2.68	-2.78
TCGA-D1-A16N-10A-01D-A12J-09_UCEC	-2.97	0.00	-4.97	-2.94	-2.52	-2.63	-2.62	-2.61	-2.75	-3.40	-2.86	0.00	-2.79	-2.75	0.00	-2.82	-2.78
TCGA-D1-A16O-10A-01D-A12J-09_UCEC	-2.96	0.00	-4.97	-3.17	-2.62	-2.66	-2.65	-2.81	0.00	-3.22	-2.66	-4.97	-2.66	-2.70	0.00	0.00	-2.81
TCGA-D1-A16Q-10A-01D-A12J-09_UCEC	-2.88	-2.82	-2.75	-3.13	-2.76	-2.75	-2.61	-2.51	-2.53	0.00	0.00	-4.86	0.00	0.00	-3.01	-2.76	-2.78
TCGA-D1-A16R-10A-01D-A12J-09_UCEC	-2.83	-5.00	-4.69	-2.89	-2.52	-2.53	-2.55	-2.58	-2.51	0.00	0.00	-5.00	0.00	-4.69	0.00	-2.51	-2.64
TCGA-D1-A16S-10A-01D-A12J-09_UCEC	-2.87	-4.84	-4.84	-3.08	-2.58	-2.63	-2.62	-2.56	-2.43	0.00	0.00	0.00	0.00	-4.84	0.00	-2.50	-2.73
TCGA-D1-A16V-10A-01D-A12J-09_UCEC	-2.92	-2.77	-2.75	-3.15	-2.78	-2.81	-2.63	-2.61	-2.62	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.79
TCGA-D1-A16X-10A-01D-A12J-09_UCEC	-2.87	-2.68	-2.69	-3.04	-2.70	-2.71	-2.55	-2.61	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.65	-2.73
TCGA-D1-A16Y-10A-01D-A12J-09_UCEC	-3.15	-2.90	-2.93	-3.20	-2.68	-2.80	-2.69	-2.82	-2.73	0.00	-3.14	-2.97	0.00	0.00	-3.41	-3.08	-2.89
TCGA-D1-A174-10A-01D-A12J-09_UCEC	-2.90	-2.71	-2.67	-3.03	-2.73	-2.78	-2.48	-2.59	-2.49	0.00	0.00	0.00	0.00	-4.82	-3.19	-2.82	-2.67
TCGA-D1-A175-10A-01D-A12J-09_UCEC	-2.90	-2.70	-2.69	-3.09	-2.74	-2.67	-2.47	-2.48	-2.44	0.00	-4.84	0.00	-4.84	-4.84	0.00	-2.57	-2.63
TCGA-D1-A176-10A-01D-A12J-09_UCEC	-3.06	-2.86	-2.69	-3.16	-2.91	-2.85	-2.60	-2.62	-2.82	-3.30	-2.67	0.00	-2.70	-2.85	0.00	-2.90	-2.85
TCGA-D1-A177-10A-01D-A12J-09_UCEC	-2.94	-2.74	-2.74	-3.02	-2.54	-2.62	-2.58	-2.63	-2.58	-4.01	-2.79	-2.76	-3.71	-3.47	0.00	-2.69	-2.70
TCGA-D1-A179-10A-01D-A12J-09_UCEC	-2.94	-2.80	-2.72	-3.59	-2.64	-2.72	-2.67	-2.68	-2.58	-3.89	-2.68	-2.64	-3.63	-3.73	0.00	-2.65	-2.86
TCGA-D1-A17A-10A-01D-A12J-09_UCEC	-2.79	0.00	-4.68	-2.73	-2.53	-2.52	-2.52	-2.71	-2.56	0.00	0.00	0.00	0.00	-2.60	0.00	-2.80	-2.70
TCGA-D1-A17B-10A-01D-A12J-09_UCEC	-2.96	-2.81	-2.79	-3.14	-2.67	-2.71	-2.55	-2.66	-2.57	-3.47	-2.94	-2.79	0.00	0.00	0.00	-2.83	-2.82
TCGA-D1-A17C-10A-01D-A12J-09_UCEC	-2.90	-2.80	-2.75	-3.09	-2.80	-2.83	-2.59	-2.70	-2.76	-3.39	-2.83	0.00	-2.79	-2.80	0.00	-2.87	-2.76
TCGA-D1-A17D-10A-01D-A12J-09_UCEC	-2.87	-2.68	-2.66	-3.01	-2.78	-2.71	-2.43	-2.50	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.65
TCGA-D1-A17F-10A-01D-A12J-09_UCEC	-3.04	0.00	0.00	-2.89	-2.65	-2.67	-2.64	-2.70	-2.82	-3.45	-2.84	0.00	-2.87	-2.82	0.00	-2.95	-2.80
TCGA-D1-A17H-10A-01D-A12J-09_UCEC	-2.93	-2.68	-2.70	-3.06	-2.71	-2.73	-2.43	-2.56	-2.50	0.00	0.00	0.00	0.00	0.00	-3.14	-2.89	-2.62
TCGA-D1-A17K-10A-01D-A12J-09_UCEC	-3.01	-2.78	-2.74	-3.12	-2.80	-2.80	-2.55	-2.71	-2.72	-3.40	-2.86	0.00	-2.77	-2.77	0.00	-2.84	-2.77
TCGA-D1-A17L-10A-01D-A12J-09_UCEC	-2.88	0.00	-4.86	-2.99	-2.54	-2.56	-2.57	-2.61	-2.57	0.00	0.00	0.00	0.00	0.00	-3.02	-2.74	-2.77
TCGA-D1-A17M-10A-01D-A12J-09_UCEC	-2.85	0.00	-4.89	-2.82	-2.48	-2.58	-2.58	-2.55	-2.50	0.00	0.00	0.00	0.00	0.00	-3.13	-2.81	-2.77
TCGA-D1-A17N-10A-01D-A12J-09_UCEC	-2.87	-4.88	0.00	-2.80	-2.55	-2.55	-2.55	-2.63	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.76
TCGA-D1-A17Q-10A-01D-A12J-09_UCEC	-2.96	0.00	0.00	-2.78	-2.61	-2.63	-2.59	-2.56	-2.53	0.00	0.00	0.00	0.00	-4.83	-3.18	-2.76	-2.73
TCGA-D1-A17R-10A-01D-A12J-09_UCEC	-2.86	0.00	-4.45	-2.82	-2.63	-2.58	-2.57	-2.56	-2.58	0.00	0.00	0.00	0.00	0.00	-3.09	-2.83	-2.67
TCGA-D1-A17S-10A-01D-A12J-09_UCEC	-2.90	0.00	0.00	-2.95	-2.61	-2.47	-2.57	-2.57	-2.73	-3.54	-2.76	0.00	-2.74	-2.77	0.00	-2.80	-2.70
TCGA-D1-A17T-10A-01D-A12J-09_UCEC	-2.93	-2.86	-2.84	-3.24	-2.53	-2.61	-2.54	-2.61	-2.63	0.00	-2.90	-2.73	0.00	-4.69	0.00	-2.57	-2.69
TCGA-D1-A17U-10A-01D-A12J-09_UCEC	-2.94	-2.95	-2.86	-3.25	-2.55	-2.66	-2.61	-2.71	-2.81	-3.61	-2.70	-2.78	-2.89	-2.89	0.00	-2.89	-2.81
TCGA-D1-A1NS-10A-01D-A14G-09_UCEC	-2.95	-2.77	-2.80	-3.35	-2.59	-2.63	-2.60	-2.50	-2.60	-3.59	-2.95	-2.84	-4.33	-4.15	-2.88	-4.63	-2.81
TCGA-D1-A1NU-10A-01D-A14G-09_UCEC	-2.87	-2.79	-2.83	-3.16	-2.91	-2.88	-2.56	-2.71	-2.60	0.00	0.00	0.00	0.00	0.00	-3.11	-2.96	-2.73
TCGA-D1-A1NX-10A-01D-A16D-09_UCEC	-2.95	0.00	0.00	-2.84	-2.62	-2.57	-2.53	-2.64	-2.57	0.00	0.00	0.00	0.00	0.00	-3.09	-2.81	-2.71
TCGA-D1-A1NY-10A-01D-A16D-09_UCEC	-2.86	-4.54	0.00	-3.18	-2.58	-2.59	-2.63	-2.63	-2.67	-3.54	-2.88	-4.54	-2.80	-2.79	0.00	-2.88	-2.70
TCGA-D1-A1NZ-10A-01D-A14G-09_UCEC	-2.77	-4.41	0.00	-2.96	-2.49	-2.54	-2.43	-2.51	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.54
TCGA-D1-A1O0-10A-01D-A17D-09_UCEC	-2.67	0.00	0.00	-3.00	-2.50	-2.50	-2.54	-2.49	-2.40	0.00	0.00	0.00	0.00	0.00	-2.97	-2.73	-2.55
TCGA-D1-A1O5-10A-01D-A14G-09_UCEC	-2.75	-2.66	-2.66	-3.30	-2.66	-2.67	-2.46	-2.44	-2.39	0.00	0.00	-4.08	0.00	0.00	0.00	-2.51	-2.52
TCGA-D1-A1O7-10A-01D-A14G-09_UCEC	-2.65	-4.38	-4.07	-2.94	-2.50	-2.51	-2.47	-2.40	-2.37	0.00	-4.38	-4.38	0.00	-4.38	-2.82	-2.72	-2.53
TCGA-D1-A1O8-10A-01D-A14G-09_UCEC	-2.87	0.00	-4.14	-3.18	-2.59	-2.60	-2.61	-2.63	-2.71	-3.49	-2.87	0.00	-2.82	-2.79	0.00	-2.83	-2.65
TCGA-D1-A2G0-10A-01D-A17D-09_UCEC	-2.77	0.00	-4.57	-3.13	-2.58	-2.59	-2.58	-2.46	-2.45	0.00	0.00	0.00	0.00	-4.27	-2.96	-2.77	-2.65
TCGA-D1-A2G5-10A-01D-A17D-09_UCEC	-2.69	0.00	-3.89	-3.06	-2.53	-2.51	-2.51	-2.51	-2.58	-3.49	-2.74	0.00	-2.71	-2.66	0.00	-2.71	-2.61
TCGA-D1-A2G6-10A-01D-A17D-09_UCEC	-2.86	-2.58	-2.57	0.00	-2.74	-2.71	-2.58	-2.55	-2.65	-3.47	-2.74	-2.57	0.00	-2.72	-2.93	0.00	-2.69
TCGA-D1-A2G7-10A-01D-A17W-09_UCEC	-2.69	-2.65	-2.68	-3.19	-2.65	-2.67	-2.47	-2.42	-2.46	0.00	0.00	0.00	-4.39	-4.39	-2.88	-2.75	-2.54
TCGA-D1-A3DA-10A-01D-A20S-09_UCEC	-2.66	-2.71	-2.76	-3.18	-2.69	-2.73	-2.51	-2.51	-2.39	0.00	0.00	0.00	-4.05	-3.92	-3.05	-2.71	-2.68
TCGA-D1-A3DG-10A-01D-A19Y-09_UCEC	-2.70	-4.53	-3.93	-2.78	-2.49	-2.71	-2.54	-2.59	-2.49	0.00	-4.53	0.00	0.00	-2.75	0.00	-2.82	-2.74
TCGA-D1-A3DH-10A-01D-A19Y-09_UCEC	-2.77	-2.63	-2.65	-3.10	-2.65	-2.65	-2.47	-2.75	-2.60	-3.53	-2.94	-4.48	-2.63	-2.65	0.00	-2.94	-2.61
TCGA-D1-A3JP-10B-01D-A22A-09_UCEC	-2.74	-2.80	-2.76	-3.27	-2.80	-2.76	-2.47	-2.49	-2.51	0.00	0.00	-4.23	0.00	-4.53	-2.96	-2.82	-2.65

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-D1-A3JQ-10B-01D-A22A-09_UCEC	-2.73	-4.23	0.00	-3.01	-2.56	-2.59	-2.51	-2.57	-2.42	-4.53	0.00	0.00	0.00	-4.23	-2.98	-2.85	-2.61
TCGA-D3-A1Q1-10A-01D-A198-08_SKCM	-2.52	0.00	0.00	-2.78	-2.54	-2.58	-2.64	-2.60	0.00	-3.17	-2.71	0.00	-2.65	-2.56	0.00	-4.55	-2.51
TCGA-D3-A1Q3-10A-01D-A198-08_SKCM	-2.49	0.00	0.00	-2.50	-2.48	-2.55	-2.54	-2.53	-2.48	0.00	0.00	0.00	0.00	-4.41	-2.87	0.00	-2.41
TCGA-D3-A1Q4-10A-01D-A198-08_SKCM	-2.45	0.00	0.00	-2.74	-2.53	-2.52	-2.56	-2.38	-2.42	0.00	0.00	0.00	0.00	0.00	-2.91	-2.68	-2.46
TCGA-D3-A1Q5-10A-01D-A198-08_SKCM	-2.33	0.00	0.00	-2.59	-2.50	-2.51	-2.53	-2.50	-2.50	0.00	0.00	0.00	0.00	0.00	-2.88	0.00	-2.40
TCGA-D3-A1Q6-10A-01D-A198-08_SKCM	-2.47	-2.76	-2.68	-2.82	-2.68	-2.67	-2.62	-2.56	-2.68	-3.51	-2.83	0.00	-2.76	-2.70	0.00	-2.70	-2.50
TCGA-D3-A1Q7-10A-01D-A19A-08_SKCM	-2.40	-2.48	-2.44	-4.38	0.00	0.00	-2.49	-2.50	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.48	-2.39
TCGA-D3-A1Q8-10A-01D-A19A-08_SKCM	-2.57	-2.76	-2.74	-2.93	-2.54	-2.68	-2.66	-2.65	-2.76	-3.45	-2.76	-2.65	0.00	-2.73	0.00	-2.80	-2.51
TCGA-D3-A1Q9-10A-01D-A19A-08_SKCM	-2.44	0.00	-4.41	-2.62	-2.47	-2.53	-2.51	-2.47	-2.41	0.00	0.00	0.00	0.00	-4.41	0.00	-2.41	-2.44
TCGA-D3-A1QA-10A-01D-A198-08_SKCM	-2.51	-2.68	-2.66	-2.81	-2.63	-2.69	-2.58	-2.59	-2.55	0.00	0.00	0.00	0.00	-4.22	0.00	-2.58	-2.50
TCGA-D3-A1QB-10A-01D-A19A-08_SKCM	-2.52	0.00	0.00	-2.62	-2.50	-2.62	-2.65	-2.62	0.00	-3.28	-2.66	0.00	-2.66	-2.57	0.00	-4.04	-2.49
TCGA-D3-A2J6-10A-01D-A19A-08_SKCM	-2.43	0.00	0.00	-2.63	-2.51	-2.63	-2.69	-2.60	0.00	-3.35	-2.79	0.00	-2.69	-2.46	0.00	0.00	-2.51
TCGA-D3-A2J7-10A-01D-A198-08_SKCM	-2.60	-2.82	-2.79	-2.95	-2.52	-2.66	-2.67	-2.57	-2.77	-3.41	-2.81	-2.85	-2.88	-2.74	-3.12	0.00	-2.59
TCGA-D3-A2J8-10A-01D-A198-08_SKCM	-2.53	-2.72	-2.71	-2.83	-2.65	-2.66	-2.54	-2.48	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.47
TCGA-D3-A2J9-10A-01D-A198-08_SKCM	-2.53	0.00	-4.07	-2.62	-2.56	-2.62	-2.67	-2.61	-2.66	-3.25	-2.93	0.00	-2.78	-2.75	0.00	-2.71	-2.50
TCGA-D3-A2JA-10A-01D-A198-08_SKCM	-2.40	-2.69	-2.66	-2.72	-2.59	-2.69	-2.55	-2.47	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.42
TCGA-D3-A2JB-10A-01D-A198-08_SKCM	-2.49	-2.70	-2.71	-2.89	-2.75	-2.70	-2.62	-2.50	-2.74	-3.19	-2.84	0.00	-2.79	-2.69	0.00	-2.74	-2.57
TCGA-D3-A2JC-10A-01D-A19A-08_SKCM	-2.53	0.00	-4.48	-2.61	-2.55	-2.60	-2.61	-2.37	-2.44	-4.48	0.00	-4.48	0.00	0.00	0.00	-2.37	-2.47
TCGA-D3-A2JD-10A-01D-A19A-08_SKCM	-2.57	-2.77	-2.76	-4.59	-2.50	-2.59	-2.61	-2.48	-2.55	0.00	-2.82	0.00	-2.84	-4.59	-3.11	-2.74	-2.56
TCGA-D3-A2JF-10A-01D-A198-08_SKCM	-2.46	-4.43	-4.43	-2.71	-2.51	-2.55	-2.54	-2.54	-2.53	0.00	0.00	0.00	0.00	0.00	-3.02	-2.71	-2.48
TCGA-D3-A2JG-10A-01D-A198-08_SKCM	-2.51	0.00	0.00	-2.76	-2.55	-2.54	-2.57	-2.49	-2.51	0.00	0.00	-4.49	0.00	0.00	-2.96	-2.66	-2.46
TCGA-D3-A2JH-10A-01D-A198-08_SKCM	-2.52	-2.68	-2.62	-2.80	-2.66	-2.62	-2.54	-2.51	-2.50	-4.46	0.00	0.00	0.00	0.00	-2.97	-2.68	-2.45
TCGA-D3-A2JK-10A-01D-A198-08_SKCM	-2.58	-2.74	-2.67	-2.88	-2.70	-2.73	-2.60	-2.60	-2.64	-3.56	-2.93	0.00	-2.78	-2.71	0.00	-2.78	-2.50
TCGA-D3-A2JL-10A-01D-A198-08_SKCM	-2.51	-2.60	-2.60	0.00	-2.68	-2.71	-2.57	-2.57	-2.64	-3.36	-2.72	-2.57	0.00	-2.73	0.00	-2.76	-2.48
TCGA-D3-A2JN-10A-01D-A198-08_SKCM	-2.57	-2.70	0.00	-2.87	-2.49	-2.62	-2.61	-2.51	-2.70	-3.42	-2.88	0.00	-2.82	-2.73	-3.05	0.00	-2.56
TCGA-D3-A2JO-10A-01D-A198-08_SKCM	-2.55	-2.61	-2.61	0.00	-2.71	-2.80	-2.65	-2.65	0.00	-3.23	-2.61	-2.60	-2.80	-2.61	0.00	-4.55	-2.52
TCGA-D3-A2JP-10A-01D-A19A-08_SKCM	-2.63	-2.76	-2.80	-2.92	-2.52	-2.63	-2.70	-2.53	-2.76	-3.32	-2.72	-2.83	-2.84	-2.72	-3.14	0.00	-2.55
TCGA-D3-A3BZ-10A-01D-A198-08_SKCM	-2.53	-2.77	-2.73	-2.97	-2.66	-2.71	-2.59	-2.59	-4.55	-3.22	-2.69	-4.55	-2.62	-2.55	0.00	-4.55	-2.49
TCGA-D3-A3C1-10A-01D-A198-08_SKCM	-2.56	-2.73	-2.71	-2.97	-2.50	-2.59	-2.65	-2.54	-2.64	0.00	-2.84	-2.75	0.00	-4.53	0.00	-2.47	-2.58
TCGA-D3-A3C3-10A-01D-A19A-08_SKCM	-2.45	-2.78	-2.80	-2.87	-2.51	-2.64	-2.65	-2.65	-2.75	-3.54	-2.78	-2.64	0.00	-2.79	0.00	-2.95	-2.46
TCGA-D3-A3C6-10A-01D-A198-08_SKCM	-2.50	0.00	0.00	-2.71	-2.51	-2.53	-2.55	-2.48	-2.43	0.00	0.00	0.00	0.00	-4.15	-3.06	-2.63	-2.41
TCGA-D3-A3C7-10A-01D-A198-08_SKCM	-2.40	-2.77	-2.69	-2.86	-2.79	-2.72	-2.59	-2.55	-2.66	-3.45	-2.87	0.00	-2.75	-2.61	-3.05	-4.45	-2.48
TCGA-D3-A3C8-10A-01D-A19A-08_SKCM	-2.37	-2.69	-2.74	-2.74	-2.69	-2.77	-2.50	-2.47	-2.44	0.00	-4.46	0.00	0.00	0.00	-3.23	-2.73	-2.42
TCGA-D3-A3CB-10A-01D-A198-08_SKCM	-2.43	0.00	-3.88	-2.46	-2.54	-2.57	-2.59	-2.54	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.40
TCGA-D3-A3CC-10A-01D-A19A-08_SKCM	-2.37	-2.46	-2.44	-4.42	-4.12	0.00	-2.52	-2.49	-2.37	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.36
TCGA-D3-A3CE-10A-01D-A19A-08_SKCM	-2.39	-2.53	-2.51	0.00	0.00	0.00	-2.54	-2.36	-2.40	0.00	0.00	-4.41	0.00	0.00	-2.87	-2.56	-2.39
TCGA-D3-A3CF-10A-01D-A198-08_SKCM	-2.45	-2.47	-2.46	-4.38	-4.38	-4.38	-2.54	-2.45	-2.43	0.00	0.00	0.00	0.00	-4.38	-2.98	-2.68	-2.44
TCGA-D3-A3ML-10A-01D-A21A-08_SKCM	-2.56	-2.76	-2.81	-2.96	-2.53	-2.62	-2.57	-2.54	-2.61	-3.50	-2.88	-2.82	-4.50	0.00	-2.97	-4.50	-2.55
TCGA-D3-A3MO-10A-01D-A21A-08_SKCM	-2.63	-2.80	-2.88	-2.83	-2.48	-2.62	-2.67	-2.64	-2.71	-3.36	-2.69	-2.65	0.00	-2.72	0.00	-2.72	-2.51
TCGA-D3-A3MR-10A-01D-A21A-08_SKCM	-2.52	-4.50	-4.20	-2.74	-2.52	-2.53	-2.54	-2.58	-2.56	0.00	0.00	0.00	0.00	-4.20	0.00	-2.38	-2.43
TCGA-D3-A3MU-10A-01D-A21A-08_SKCM	-2.66	-2.75	-2.74	-2.88	-2.48	-2.64	-2.60	-2.62	-2.53	0.00	-2.85	-2.78	-4.59	-4.11	-3.14	-2.77	-2.58
TCGA-D3-A3MV-10A-01D-A21A-08_SKCM	-2.58	0.00	0.00	-2.77	-2.61	-2.59	-2.62	-2.54	-2.70	-3.27	-2.90	0.00	-2.84	-2.64	0.00	-2.64	-2.52
TCGA-D3-A51E-10A-01D-A25O-08_SKCM	-2.49	0.00	0.00	-2.68	-2.48	-2.49	-2.48	-2.49	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.42
TCGA-D3-A51F-10A-01D-A25O-08_SKCM	-2.45	-2.61	-2.54	-2.80	-2.52	-2.59	-2.49	-2.54	-2.45	0.00	0.00	0.00	0.00	-3.99	0.00	-2.54	-2.35
TCGA-D3-A51G-10A-01D-A25O-08_SKCM	-2.60	0.00	0.00	-2.83	-2.55	-2.57	-2.57	-2.50	-2.73	-3.32	-2.86	0.00	-2.77	-2.67	0.00	-2.67	-2.47
TCGA-D3-A51H-10A-01D-A25O-08_SKCM	-2.49	0.00	0.00	-2.86	-2.51	-2.60	-2.54	-2.53	-2.77	-3.33	-2.75	-2.79	-2.79	-2.68	0.00	-2.82	-2.56
TCGA-D3-A51J-10A-01D-A25O-08_SKCM	-2.36	-2.70	-2.68	-2.81	-2.59	-2.68	-2.53	-2.57	-2.47	0.00	0.00	0.00	0.00	-4.07	-2.82	0.00	-2.47
TCGA-D3-A51K-10A-01D-A25O-08_SKCM	-2.43	0.00	0.00	-2.72	-2.47	-2.52	-2.51	-2.45	-2.37	0.00	0.00	0.00	0.00	0.00	-2.99	-2.68	-2.39
TCGA-D3-A51N-10A-01D-A25O-08_SKCM	-2.50	0.00	0.00	-2.94	-2.47	-2.52	-2.52	-2.46	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.46
TCGA-D3-A51R-10A-01D-A25O-08_SKCM	-2.51	-2.88	-2.75	-2.95	-2.46	-2.54	-2.61	-2.58	-2.73	-3.34	-2.73	-2.70	-2.83	-2.61	0.00	-2.82	-2.47
TCGA-D3-A51T-10A-01D-A25O-08_SKCM	-2.47	-2.62	-2.63	-2.86	-2.57	-2.60	-2.49	-2.41	-2.43	0.00	0.00	0.00	0.00	-4.35	0.00	-2.41	-2.43
TCGA-D3-A5GL-10A-01D-A27N-08_SKCM	-2.51	0.00	0.00	-2.74	-2.51	-2.53	-2.55	-2.49	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.47
TCGA-D3-A5GN-10A-01D-A27N-08_SKCM	-2.63	-2.81	-2.78	-2.91	-2.56	-2.66	-2.61	-2.52	-2.57	-3.30	-2.88	-2.78	0.00	-4.57	-3.21	-2.85	-2.57
TCGA-D3-A5GO-10A-01D-A27N-08_SKCM	-2.62	-2.79	-2.74	-2.86	-2.69	-2.72	-2.67	-2.50	-2.66	-3.25	-2.89	0.00	-2.73	-2.72	-3.05	0.00	-2.54
TCGA-D3-A5GR-10A-01D-A27N-08_SKCM	-2.48	-2.69	-2.63	-2.79	-2.63	-2.60	-2.55	-2.47	-2.66	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.48
TCGA-D3-A5GS-10A-01D-A27N-08_SKCM	-2.52	0.00	0.00	-2.70	-2.53	-2.51	-2.57	-2.46	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.50
TCGA-D3-A5GT-10A-01D-A30X-08_SKCM	-2.71	-2.81	-2.79	-2.95	-2.57	-2.68	-2.72	-2.73	-2.67	0.00	-3.04	-2.80	0.00	0.00	0.00	-2.62	-2.68
TCGA-D3-A5GU-10A-01D-A27N-08_SKCM	-2.49	0.00	-4.46	-2.52	-2.54	-2.54	-2.58	-2.44	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.45
TCGA-D5-5537-10A-01D-1924-10_COAD	-2.55	0.00	0.00	-2.59	-2.66	-2.61	-2.40	-2.55	-2.60	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.36
TCGA-D5-5538-10A-02D-1650-10_COAD	-2.56	0.00	0.00	-2.73	-2.46	-2.49	-2.45	-2.58	-2.59	-3.51	-2.95	0.00	-2.75	-2.70	-3.31	0.00	-2.41
TCGA-D5-6529-10A-01D-1771-10_COAD	-2.54	-2.95	-2.99	-2.75	-2.64	-3.01	-2.48	-2.54	-2.40	0.00	0.00	0.00	0.00	0.00	-3.39	-2.84	-2.51
TCGA-D5-6531-10A-01D-1719-10_COAD	-2.47	-2.87	-2.83	-2.95	-2.61	-2.51	-2.41	-2.61	-2.65	-3.49	-2.92	-2.89	-2.92	-2.71	0.00	-2.77	-2.36
TCGA-D5-6532-10A-01D-1719-10_COAD	-2.46	-2.32	-2.34	0.00	0.00	0.00	-2.26	-2.51	-2.29	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.23
TCGA-D5-6533-10A-01D-1719-10_COAD	-2.50	0.00	-4.53	-2.65	-2.38	-2.43	-2.30	-2.45	-2.21	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.33
TCGA-D5-6534-10A-01D-1924-10_COAD	-2.54	-2.84	-2.91	-2.85	-2.53	-2.55	-2.46	-2.64	-2.79	-3.64	-2.88	-2.60	0.00	-2.80	0.00	-2.95	-2.53
TCGA-D5-6535-10A-01D-1719-10_COAD	-2.52	0.00	0.00	-2.71	-2.41	-2.44	-2.33	-2.49	-2.29	0.00	0.00	0.00	0.00	0.00	-3.06	-2.81	-2.37
TCGA-D5-6536-10A-01D-1719-10_COAD	-2.49	0.00	0.00	-2.58	-2.40	-2.40	-2.29	-2.40	-2.26	0.00	0.00	0.00	0.00	-4.55	0.00	-2.49	-2.31
TCGA-D5-6538-10A-01D-1719-10_COAD	-2.43	-2.56	-2.62	-2.82	-2.68	-2.62	-2.31	-2.52	-2.30	0.00	0.00	0.00	0.00	-4.06	0.00	-2.58	-2.29
TCGA-D5-6539-10A-01D-1719-10_COAD	-2.47	-3.97	-4.45	-2.64	-2.44	-2.49	-2.39	-2.56	-2.69	-3.34	-2.83	-4.45	-2.83	-2.81	0.00	-3.03	-2.35
TCGA-D5-6540-10A-01D-1719-10_COAD	-2.38	0.00	-4.14	-2.78	-2.44	-2.40	-2.32	-2.46	-2.31	0.00	0.00	0.00	0.00	-4.44	0.00	-2.65	-2.28
TCGA-D5-6541-10A-01D-1719-10_COAD	-2.44	-4.55	0.00	-2.59	-2.45	-2.43	-2.32	-2.38	-2.32	0.00	0.00	-4.55	0.00	0.00	-3.04	-2.85	-2.41
TCGA-D5-6898-10A-01D-1924-10_COAD	-2.56	0.00	0.00	-2.62	-2.67	-2.53	-2.45	-2.56	-2.46	0.00	0.00	0.00	0.00	0.00	-2.93	-2.87	-2.38
TCGA-D5-6920-10A-01D-1924-10_COAD	-2.52	0.00	0.00	-2.56	-2.46	-2.52	-2.42	-2.52	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.35
TCGA-D5-6922-10A-01D-1924-10_COAD	-2.59	0.00	0.00	-2.70	-2.60	-2.57	-2.46	-2.65	-2.66	-3.30	-3.16	0.00	-2.90	-2.89	0.00	-2.94	-2.50
TCGA-D5-6924-10A-01D-1924-10_COAD	-2.58	-2.97	0.00	-2.88	-2.62	-2.57	-2.63	-2.72	-2.69	-3.27	-2.86	0.00	-2.97	-2.92	0.00	-2.81	-2.47
TCGA-D5-6926-10A-01D-1924-10_COAD	-2.63	0.00	0.00	-2.59	-2.55	-2.76	-2.39	-2.47	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.70	-2.42
TCGA-D5-6927-10A-01D-1924-10_COAD	-2.53	0.00	0.00	-2.64	-2.59	-2.64	-2.43	-2.57	-2.47	0.00	0.00	0.00	0.00	-4.28	0.00	-2.77	-2.48
TCGA-D5-6928-10A-01D-1924-10_COAD	-2.56	-2.57	-2.64	0.00	-2.98	-2.91	-2.64	-2.65	-2.72	-3.41	-2.63	-2.89	-2.86	-2.74	0.00	-3.05	-2.52
TCGA-D5-6929-10A-01D-1924-10_COAD	-2.66	-2.82	-2.92	-2.94	-2.64	-2.65	-2.49	-2.82	-2.85	-3.24	-2.78	-2.87	0.00	-2.87	0.00	-2.96	-2.56
TCGA-D5-6930-10A-01D-1924-10_COAD	-2.61	0.00	0.00	-2.71	-2.58	-2.66	-2.59	-2.63	-2.50	0.00	0.00	0.00	0.00	0.00	-3.43	-3.08	-2.47
TCGA-D5-6931-10A-01D-1924-10_COAD	-2.72	-2.81	-2.65	0.00	-2.63	-2.69	-2.58	-2.85	-2.83	-3.20	-2.79	-2.66	0.00	-2.90	0.00	0.00	-2.62
TCGA-D5-6932-10A-01D-1924-10_COAD	-2.46	-2.90	-2.79	-3.01	-2.83	-2.90	-2.50	-2.59	-2.40	0.00	0.00	-4.15	0.00	-4.15	0.00	-2.53	-2.38
TCGA-D5-7000-10A-01D-1924-10_COAD	-2.64	-2.87	-2.90	-2.96	-2.85	-2.82	-2.46	-2.70	0.00	-3.02	-2.99	0.00	-2.67	-2.44	0.00	0.00	-2.44
TCGA-D6-6515-10A-01D-1870-08_HNSC	-2.59	-2.70	-2.68	-4.67	-2.63	-2.61	-2.71	-2.62	-2.56	-4.67	-2.72	-2.64	0.00	-4.67	-3.27	-2.82	-2.58
TCGA-D6-6516-10A-01D-1870-08_HNSC	-2.48	0.00	0.00	-2.62	-2.52	-2.57	-2.59	-2.57	-2.54	0.00	0.00	-4.58	0.00	-4.58	0.00	-2.47	-2.47
TCGA-D6-6517-10A-01D-1870-08_HNSC	-2.51	0.00	-4.58	-2.61	-2.55	-2.55	-2.56	-2.65	-2.56	0.00	0.00	0.00	0.00	-4.58	-3.16	-2.81	-2.43
TCGA-D6-6823-10A-01D-1912-08_HNSC	-2.45	0.00	0.00	-2.58	-2.50	-2.54	-2.52	-2.49	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.40
TCGA-D6-6824-10A-01D-1912-08_HNSC	-2.43	0.00	-4.53	-2.59	-2.46	-2.49	-2.56	-2.52	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.40
TCGA-D6-6825-10A-01D-1912-08_HNSC	-2.45	-2.71	-2.68	-2.88	-2.68	-2.64	-2.49	-2.54	-2.46	0.00	-4.54	0.00	0.00	0.00	0.00	-2.47	-2.42
TCGA-D6-6826-10A-01D-1912-08_HNSC	-2.52	0.00	0.00	-2.73	-2.52	-2.58	-2.57	-2.53	-2.59	-3.45	-2.94	0.00	-2.82	-2.70	0.00	-2.84	-2.53
TCGA-D6-6827-10A-01D-1912-08_HNSC	-2.40	0.00	-4.55	-2.68	-2.49	-2.48	-2.47	-2.43	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.38
TCGA-D6-8568-10A-01D-2394-08_HNSC	-2.47	-2.71	-2.74	-2.76	-2.38	-2.69	-2.73	-2.72	0.00	-3.26	-2.64	-2.67	-2.81	-2.46	0.00	0.00	-2.52
TCGA-D6-8569-10A-01D-2394-08_HNSC	-2.53	-2.64	-2.66	-2.77	-2.63	-2.69	-2.57	-2.43	-2.57	0.00	0.00	0.00	0.00	-4.47	0.00	-2.38	-2.55
TCGA-D6-A4Z9-10A-01D-A25E-08_HNSC	-2.53	-3.76	-3.98	-2.58	-2.54	-2.53	-2.53	-2.56	-2.49	0.00	-4.16	0.00	-3.98	-3.68	0.00	-2.58	-2.54
TCGA-D6-A4ZB-10A-01D-A25E-08_HNSC	-2.59	-4.03	-4.51	-2.62	-2.59	-2.63	-2.67	-2.54	-2.63	-3.33	-2.84	-4.03	-2.82	-2.70	-3.03	-3.91	-2.57
TCGA-D6-A6EK-10A-01D-A31J-08_HNSC	-2.54	0.00	0.00	-2.79	-2.54	-2.58	-2.58	-2.50	-2.67	-3.39	-2.91	-2.71	0.00	-2.66	-3.04	-4.51	-2.49

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-D6-A6EM-10A-01D-A31J-08_HNSC	-2.55	-2.79	0.00	-2.85	-2.47	-2.58	-2.61	-2.61	-2.70	-3.40	-2.88	0.00	-2.72	-2.68	0.00	-2.76	-2.51
TCGA-D6-A6EN-10A-01D-A31J-08_HNSC	-2.45	-2.51	-2.44	-4.35	-4.35	-4.05	-2.47	-2.42	-2.45	0.00	0.00	-4.35	0.00	0.00	-2.99	-2.64	-2.38
TCGA-D6-A6EO-10A-01D-A31J-08_HNSC	-2.51	-2.67	-2.60	-2.89	-2.61	-2.65	-2.67	-2.76	-2.68	0.00	-2.85	0.00	-2.80	-2.66	0.00	-2.67	-2.47
TCGA-D6-A6EP-10A-01D-A31J-08_HNSC	-2.56	0.00	0.00	-2.70	-2.54	-2.56	-2.61	-2.58	-2.65	-3.35	-2.87	0.00	-2.74	-2.64	-3.06	-4.49	-2.55
TCGA-D6-A6EQ-10A-01D-A31J-08_HNSC	-2.52	-2.68	-2.63	-2.79	-2.63	-2.64	-2.54	-2.43	-2.43	0.00	0.00	0.00	0.00	0.00	-3.01	-2.67	-2.51
TCGA-D6-A6ES-10A-01D-A31J-08_HNSC	-2.57	0.00	0.00	-2.80	-2.55	-2.61	-2.61	-2.62	0.00	-3.20	-2.74	-2.70	-2.75	-2.55	0.00	-4.50	-2.52
TCGA-D7-5577-10A-01D-1600-08_STAD	-2.51	-4.63	0.00	-2.79	-2.51	-2.55	-2.58	-2.47	-2.47	0.00	0.00	-4.32	0.00	-4.63	0.00	-2.45	-2.49
TCGA-D7-5578-10A-01D-1600-08_STAD	-2.58	-2.78	-2.76	-3.01	-2.50	-2.65	-2.68	-2.71	-2.55	0.00	-2.90	-2.73	0.00	-4.67	0.00	-2.66	-2.58
TCGA-D7-5579-10A-01D-1600-08_STAD	-2.51	-2.66	-2.79	0.00	-2.63	-2.68	-2.67	-2.54	-2.71	-3.25	-2.97	0.00	-2.81	-2.68	-3.23	0.00	-2.54
TCGA-D7-6518-10A-01D-1800-08_STAD	-2.52	-4.27	-4.09	-2.79	-2.59	-2.60	-2.58	-2.54	-2.67	-3.42	-2.90	-4.57	-2.78	-2.69	-3.04	0.00	-2.55
TCGA-D7-6519-10A-01D-1800-08_STAD	-2.65	-2.69	-2.67	-4.32	-2.64	-2.67	-2.61	-2.64	0.00	-3.21	-2.62	-2.61	-2.71	-2.67	0.00	-4.62	-2.56
TCGA-D7-6520-10A-01D-1800-08_STAD	-2.57	0.00	-4.28	-2.62	-2.54	-2.59	-2.58	-2.60	-2.67	-3.35	-2.91	0.00	-2.74	-2.62	0.00	-2.87	-2.53
TCGA-D7-6521-10A-01D-1800-08_STAD	-2.50	0.00	0.00	-2.74	-2.61	-2.60	-2.68	-2.65	-2.71	-3.38	-2.86	0.00	-2.70	-2.66	0.00	-2.75	-2.56
TCGA-D7-6522-10A-01D-1800-08_STAD	-2.53	0.00	-4.52	-2.53	-2.47	-2.54	-2.52	-2.60	-2.45	0.00	0.00	-4.22	-4.52	-4.52	0.00	-2.55	-2.50
TCGA-D7-6524-10A-01D-1800-08_STAD	-2.53	-4.52	-4.52	-2.57	-2.54	-2.57	-2.54	-2.44	-2.46	0.00	-4.52	0.00	0.00	0.00	0.00	-2.44	-2.55
TCGA-D7-6525-10A-01D-1800-08_STAD	-2.54	0.00	0.00	-2.60	-2.54	-2.54	-2.50	-2.45	-2.45	0.00	-4.52	-4.52	0.00	-4.22	-3.06	-2.69	-2.44
TCGA-D7-6526-10A-01D-1800-08_STAD	-2.61	-2.77	-2.75	-2.93	-2.48	-2.61	-2.62	-2.49	-2.55	0.00	-2.94	-2.73	0.00	-4.62	-3.12	-2.76	-2.56
TCGA-D7-6527-10A-01D-1800-08_STAD	-2.51	-4.52	-4.22	-2.75	-2.54	-2.55	-2.59	-2.57	-2.44	0.00	-4.52	-4.52	0.00	-4.22	0.00	-2.53	-2.49
TCGA-D7-6528-10A-01D-1800-08_STAD	-2.53	0.00	-4.56	-2.68	-2.56	-2.55	-2.64	-2.64	-2.64	-3.30	-2.83	0.00	-2.75	-2.68	0.00	-2.67	-2.52
TCGA-D7-6815-10A-01D-1882-08_STAD	-2.39	-4.54	0.00	-2.70	-2.53	-2.42	-2.48	-2.60	-2.57	0.00	0.00	-4.54	0.00	0.00	0.00	-2.56	-2.45
TCGA-D7-6817-10A-01D-1882-08_STAD	-2.59	-2.82	-2.76	-2.93	-2.52	-2.65	-2.70	-2.67	-2.81	-3.39	-2.78	-2.78	-2.85	-2.78	0.00	-2.84	-2.55
TCGA-D7-6818-10A-01D-1882-08_STAD	-2.53	0.00	0.00	-2.64	-2.59	-2.61	-2.59	-2.66	-2.49	0.00	0.00	0.00	0.00	-4.32	0.00	-2.62	-2.47
TCGA-D7-6820-10A-01D-1882-08_STAD	-2.54	0.00	-4.29	-2.63	-2.54	-2.58	-2.59	-2.54	-2.49	0.00	0.00	-4.59	0.00	-4.59	0.00	-2.40	-2.47
TCGA-D7-6822-10A-01D-1882-08_STAD	-2.61	0.00	-4.64	-2.86	-2.55	-2.68	-2.65	-2.60	-2.69	-3.36	-2.87	0.00	-2.78	-2.70	-3.16	0.00	-2.52
TCGA-D7-8570-10A-01D-2341-08_STAD	-2.48	0.00	-4.55	-2.64	-2.55	-2.54	-2.51	-2.59	-2.47	0.00	0.00	0.00	0.00	0.00	-3.01	-2.69	-2.45
TCGA-D7-8572-10A-01D-2341-08_STAD	-2.61	-2.76	-2.74	-2.92	-2.47	-2.63	-2.63	-2.62	-2.57	0.00	-2.94	-2.76	0.00	-4.32	-2.97	0.00	-2.56
TCGA-D7-8573-10A-01D-2341-08_STAD	-2.58	-2.78	-2.75	-2.95	-2.53	-2.61	-2.59	-2.65	0.00	-3.24	-2.65	-2.67	-2.82	-2.60	0.00	0.00	-2.49
TCGA-D7-8574-10A-01D-2341-08_STAD	-2.55	0.00	-4.55	-2.55	-2.53	-2.49	-2.50	-2.51	-2.43	0.00	0.00	-4.55	0.00	0.00	0.00	-2.58	-2.50
TCGA-D7-8575-10A-01D-2341-08_STAD	-2.56	0.00	0.00	-2.85	-2.53	-2.68	-2.62	-2.53	-2.77	-3.18	-2.79	-2.79	-2.77	-2.77	-3.17	0.00	-2.55
TCGA-D7-8576-10A-01D-2341-08_STAD	-2.43	-3.21	-3.19	-2.67	-2.45	-2.58	-2.54	-2.62	-2.50	0.00	-3.34	-3.24	0.00	-2.58	0.00	-2.60	-2.50
TCGA-D7-8578-10A-01D-2341-08_STAD	-2.61	-2.77	-2.74	-2.96	-2.49	-2.59	-2.66	-2.55	-2.53	0.00	-2.93	-2.73	0.00	0.00	0.00	-2.50	-2.57
TCGA-D7-8579-10A-01D-2341-08_STAD	-2.52	-2.70	-2.70	-2.87	-2.66	-2.62	-2.59	-2.50	-2.60	0.00	0.00	0.00	0.00	-4.54	0.00	-2.44	-2.46
TCGA-D7-A4YT-10A-01D-A25E-08_STAD	-2.56	-3.94	-4.54	-2.73	-2.57	-2.60	-2.60	-2.60	-2.67	-3.29	-2.89	-4.54	-2.73	-2.68	0.00	-2.71	-2.50
TCGA-D7-A4YU-10A-01D-A25E-08_STAD	-2.49	-2.71	-2.63	-2.88	-2.67	-2.65	-2.63	-2.69	-2.54	0.00	-2.82	0.00	-2.72	-2.63	0.00	-2.66	-2.47
TCGA-D7-A4YV-10A-01D-A25E-08_STAD	-2.53	0.00	-4.48	-2.71	-2.51	-2.54	-2.52	-2.45	-2.46	0.00	0.00	-4.48	-4.48	-4.48	0.00	-2.39	-2.46
TCGA-D7-A4YX-10A-01D-A25E-08_STAD	-2.73	-2.65	-2.63	0.00	-2.74	-2.74	-2.68	-2.59	-2.54	0.00	-2.89	-2.77	0.00	0.00	-3.07	-2.78	-2.58
TCGA-D7-A4YY-10A-01D-A25E-08_STAD	-2.57	-2.73	-2.69	-2.87	-2.71	-2.73	-2.64	-2.54	-2.62	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.56
TCGA-D7-A4Z0-10A-01D-A25E-08_STAD	-2.41	0.00	-4.49	-2.56	-2.55	-2.54	-2.62	-2.40	-2.48	0.00	0.00	0.00	-4.49	-4.01	-2.97	-2.67	-2.46
TCGA-D7-A6ET-10A-01D-A32N-08_STAD	-2.59	0.00	0.00	-2.65	-2.56	-2.57	-2.57	-2.50	-2.59	0.00	0.00	0.00	0.00	-4.60	-3.07	-2.78	-2.57
TCGA-D7-A6EV-10A-01D-A31J-08_STAD	-2.55	-2.67	-2.60	-2.91	-2.59	-2.64	-2.58	-2.45	-2.46	0.00	0.00	0.00	0.00	-4.46	-3.08	-2.68	-2.49
TCGA-D7-A6EX-10A-01D-A31J-08_STAD	-2.42	0.00	0.00	-2.73	-2.53	-2.54	-2.57	-2.48	-2.56	0.00	0.00	0.00	0.00	-4.44	0.00	-2.58	-2.50
TCGA-D7-A6EY-10A-01D-A31J-08_STAD	-2.61	-2.71	-4.22	-2.84	-2.48	-2.64	-2.63	-2.53	-2.73	-3.30	-2.91	0.00	-2.71	-2.71	0.00	-2.78	-2.59
TCGA-D7-A6EZ-10A-01D-A31J-08_STAD	-2.64	-2.78	-2.75	-2.91	-2.55	-2.65	-2.73	-2.71	-2.80	-3.29	-2.74	-2.75	-2.80	-2.71	0.00	-2.87	-2.64
TCGA-D7-A6F0-10A-01D-A31J-08_STAD	-2.61	-2.76	-2.74	-2.92	-2.48	-2.63	-2.67	-2.70	-2.70	-3.37	-2.78	-2.80	-2.79	-2.74	0.00	-2.87	-2.61
TCGA-D7-A6F2-10A-01D-A31J-08_STAD	-2.62	-2.63	-2.63	0.00	-2.64	-2.70	-2.59	-2.57	-2.67	-3.37	-2.74	-2.66	-4.51	-2.66	-3.05	0.00	-2.55
TCGA-D7-A747-10A-21D-A33W-08_STAD	-2.60	-2.80	-2.75	-2.92	-2.49	-2.62	-2.67	-2.67	-2.75	-3.54	-2.69	-2.74	-2.81	-2.79	0.00	-2.75	-2.55
TCGA-D7-A748-10A-21D-A32N-08_STAD	-2.61	-4.37	-4.20	-2.87	-2.70	-2.66	-2.63	-2.59	-2.80	-3.53	-2.89	0.00	-2.80	-2.74	0.00	-2.82	-2.61
TCGA-D7-A74A-10A-21D-A32N-08_STAD	-2.68	-2.68	-2.70	0.00	-2.68	-2.65	-2.70	-2.73	-2.66	0.00	-2.77	-2.68	-4.68	-4.68	-3.10	0.00	-2.58
TCGA-D7-A74B-10A-01D-A33W-08_STAD	-2.66	-2.75	-2.76	-2.91	-2.60	-2.67	-2.65	-2.51	-2.61	-3.41	-2.94	-2.80	0.00	0.00	-3.20	-2.83	-2.58
TCGA-D8-A13Y-10A-01D-A110-09_BRCA	-2.91	-2.70	-2.74	-3.05	-2.67	-2.66	-2.50	-2.63	-2.75	-3.34	-2.80	0.00	-2.74	-2.77	0.00	-2.82	-2.70
TCGA-D8-A13Z-10A-01D-A110-09_BRCA	-2.72	-2.63	-2.60	-2.89	-3.23	-2.68	-2.34	-2.37	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.68	-2.57
TCGA-D8-A140-10A-01D-A110-09_BRCA	-2.99	-2.88	-2.84	-3.26	-2.62	-2.68	-2.67	-2.77	-2.83	-3.45	-2.74	-2.66	0.00	-2.86	0.00	-2.90	-2.79
TCGA-D8-A141-10A-01D-A110-09_BRCA	-2.86	0.00	0.00	-2.92	-2.61	-2.59	-2.51	-2.54	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.67
TCGA-D8-A142-10A-01D-A110-09_BRCA	-2.83	0.00	0.00	-2.89	-2.67	-2.69	-2.66	-2.66	-2.65	0.00	0.00	0.00	0.00	0.00	-3.23	-2.93	-2.83
TCGA-D8-A143-10A-01D-A110-09_BRCA	-3.06	-2.73	-2.71	-3.20	-2.78	-2.90	-2.58	-2.78	-2.75	-3.36	-2.93	0.00	-2.79	-2.75	0.00	-2.97	-2.68
TCGA-D8-A145-10A-01D-A110-09_BRCA	-2.84	0.00	0.00	-2.92	-2.56	-2.65	-2.52	-2.58	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.71	-2.78
TCGA-D8-A146-10A-01D-A110-09_BRCA	-2.86	-2.64	-2.69	-3.09	-2.88	-2.77	-2.51	-2.71	-2.58	0.00	0.00	0.00	0.00	0.00	0.00	-2.69	-2.60
TCGA-D8-A147-10A-01D-A110-09_BRCA	-2.92	-4.76	-4.76	-2.80	-2.49	-2.62	-2.58	-2.59	-2.73	-3.44	-2.75	0.00	-2.77	-2.73	0.00	-2.74	-2.73
TCGA-D8-A1J8-10A-01D-A13O-09_BRCA	-2.90	0.00	-4.64	-2.73	-2.54	-2.56	-2.47	-2.53	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.62
TCGA-D8-A1J9-10A-01D-A13O-09_BRCA	-2.98	0.00	-4.54	-2.92	-2.58	-2.58	-2.58	-2.59	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.67
TCGA-D8-A1JB-10A-01D-A13O-09_BRCA	-2.85	-2.70	-2.75	-3.11	-2.81	-2.75	-2.52	-2.60	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.63	-2.60
TCGA-D8-A1JC-10A-01D-A13O-09_BRCA	-2.93	0.00	0.00	-2.92	-2.55	-2.59	-2.57	-2.61	-2.58	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.72
TCGA-D8-A1JD-10A-01D-A13O-09_BRCA	-2.90	0.00	0.00	-2.88	-2.64	-2.66	-2.66	-2.57	-2.60	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.77
TCGA-D8-A1JE-10A-01D-A188-09_BRCA	-2.92	-2.48	-2.51	0.00	-2.92	-2.80	-2.48	-2.60	-2.71	-3.21	-2.71	-2.51	0.00	-2.78	0.00	-2.98	-2.65
TCGA-D8-A1JF-10A-01D-A17G-09_BRCA	-3.00	-2.70	-2.70	-4.76	-2.89	-2.86	-2.72	-2.67	-2.87	-3.43	-2.82	-2.73	0.00	-2.82	0.00	-2.92	-2.84
TCGA-D8-A1JG-10A-01D-A13O-09_BRCA	-3.03	-2.77	-2.83	-3.18	-2.64	-2.64	-2.56	-2.57	-2.64	-3.42	-3.03	-2.88	0.00	-4.30	-3.14	-3.00	-2.73
TCGA-D8-A1JH-10A-01D-A13O-09_BRCA	-2.89	-2.79	-2.80	-3.04	-2.71	-2.85	-2.55	-2.53	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.69
TCGA-D8-A1JI-10A-01D-A13O-09_BRCA	-3.00	-2.70	-2.73	0.00	-2.71	-2.71	-2.71	-2.70	-2.84	-3.50	-2.74	-2.63	0.00	-2.84	-3.17	0.00	-2.85
TCGA-D8-A1JJ-10A-01D-A14K-09_BRCA	-3.03	-2.81	-2.80	-3.19	-2.56	-2.72	-2.68	-2.68	-2.68	0.00	-2.90	-2.76	0.00	0.00	-3.16	-2.82	-2.82
TCGA-D8-A1JK-10A-01D-A13O-09_BRCA	-3.24	-2.88	-2.84	-3.22	-2.66	-2.68	-2.63	-2.73	-2.96	-3.46	-2.82	-2.72	0.00	-2.93	0.00	-3.07	-2.83
TCGA-D8-A1JL-10A-01D-A188-09_BRCA	-2.88	0.00	0.00	-2.97	-2.67	-2.66	-2.69	-2.55	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.77
TCGA-D8-A1JM-10A-01D-A188-09_BRCA	-2.96	-4.70	0.00	-2.82	-2.63	-2.66	-2.61	-2.67	-2.56	0.00	0.00	-4.70	0.00	0.00	0.00	-2.67	-2.69
TCGA-D8-A1JN-10A-01D-A13O-09_BRCA	-3.01	0.00	0.00	-2.82	-2.53	-2.58	-2.56	-2.66	-2.56	0.00	0.00	0.00	0.00	0.00	-3.19	-2.81	-2.70
TCGA-D8-A1JP-10A-01D-A13O-09_BRCA	-3.02	-4.79	0.00	-2.84	-2.68	-2.72	-2.69	-2.76	-2.90	-3.41	-2.89	0.00	-2.86	-2.87	0.00	-2.93	-2.78
TCGA-D8-A1JS-10A-01D-A13O-09_BRCA	-2.93	0.00	0.00	-2.82	-2.62	-2.60	-2.58	-2.58	-2.60	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.72
TCGA-D8-A1JT-10A-01D-A13O-09_BRCA	-2.98	0.00	-4.50	-2.87	-2.58	-2.54	-2.48	-2.56	-2.52	-4.50	0.00	0.00	0.00	-4.50	-3.22	-2.98	-2.73
TCGA-D8-A1JU-10A-01D-A188-09_BRCA	-3.20	-2.75	-2.81	0.00	-3.14	-3.03	-2.75	-2.79	-2.93	-3.62	-2.82	-3.06	-3.27	-3.00	-3.57	-4.52	-2.88
TCGA-D8-A1X5-10A-01D-A14G-09_BRCA	-2.88	-4.38	0.00	-2.72	-2.56	-2.47	-2.45	-2.62	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.64
TCGA-D8-A1X6-10A-01D-A14K-09_BRCA	-2.98	-2.77	-2.83	-3.13	-2.54	-2.59	-2.64	-2.80	-2.73	-3.25	-2.70	-2.77	-2.80	-2.77	0.00	-2.90	-2.77
TCGA-D8-A1X7-10A-01D-A14K-09_BRCA	-2.70	0.00	-4.35	-2.71	-2.49	-2.81	-2.58	-2.77	-2.65	0.00	0.00	0.00	0.00	-2.63	0.00	-2.74	-2.61
TCGA-D8-A1X9-10A-01D-A17G-09_BRCA	-3.04	-2.80	-2.83	-3.20	-2.63	-2.69	-2.59	-2.85	-2.66	0.00	-3.04	-2.92	0.00	-4.26	-3.14	-3.16	-2.73
TCGA-D8-A1XA-10A-01D-A14G-09_BRCA	-2.95	0.00	0.00	-3.05	-2.62	-2.62	-2.65	-2.65	-2.80	-3.49	-2.83	0.00	-2.79	-2.81	-3.07	0.00	-2.74
TCGA-D8-A1XB-10A-01D-A14G-09_BRCA	-2.87	0.00	0.00	-2.79	-2.59	-2.60	-2.55	-2.55	-2.56	-4.58	0.00	0.00	0.00	0.00	0.00	-2.50	-2.70
TCGA-D8-A1XC-10A-01D-A14G-09_BRCA	-2.80	0.00	0.00	-2.87	-2.57	-2.54	-2.51	-2.63	-2.39	0.00	0.00	0.00	0.00	0.00	-3.32	-2.90	-2.72
TCGA-D8-A1XF-10A-01D-A14G-09_BRCA	-2.74	0.00	0.00	-2.80	-2.58	-2.69	-2.55	-2.61	-2.52	0.00	-4.54	0.00	-4.54	0.00	-3.26	-2.99	-2.78
TCGA-D8-A1XG-10A-01D-A14G-09_BRCA	-2.90	-2.92	-2.88	-3.22	-2.63	-2.73	-2.67	-2.78	-2.69	0.00	-3.03	-2.83	0.00	-4.69	-3.09	-2.90	-2.77
TCGA-D8-A1XK-10A-01D-A14K-09_BRCA	-2.98	-2.57	-2.62	0.00	-2.73	-2.70	-2.72	-2.92	-2.76	0.00	-2.64	-2.54	0.00	-2.72	-3.10	0.00	-2.69
TCGA-D8-A1XL-10A-01D-A14K-09_BRCA	-3.00	0.00	-4.47	-2.98	-2.64	-2.65	-2.58	-2.77	-2.80	-3.36	-2.85	0.00	-2.75	-2.75	0.00	-2.81	-2.80
TCGA-D8-A1XM-10A-01D-A14K-09_BRCA	-3.07	0.00	0.00	-2.92	-2.59	-2.66	-2.62	-2.69	-2.78	-3.41	-2.93	0.00	-2.74	-2.72	0.00	-2.83	-2.76
TCGA-D8-A1XO-10A-01D-A14K-09_BRCA	-2.95	-2.62	-2.61	0.00	-2.80	-2.72	-2.72	-2.88	-2.81	0.00	-2.57	-2.76	-2.70	-2.71	0.00	-2.80	-2.74
TCGA-D8-A1XQ-10A-01D-A14K-09_BRCA	-3.02	0.00	0.00	-2.78	-2.60	-2.59	-2.57	-2.64	-2.59	-4.75	0.00	0.00	0.00	0.00	0.00	-2.53	-2.71
TCGA-D8-A1XR-10A-01D-A14K-09_BRCA	-3.07	-2.78	-2.82	-3.09	-2.53	-2.72	-2.65	-2.78	-2.62	0.00	-2.96	-2.81	-4.84	0.00	0.00	-2.66	-2.86
TCGA-D8-A1XS-10A-01D-A14K-09_BRCA	-2.98	-4.11	-4.11	-2.76	-2.54	-2.55	-2.43	-2.56	-2.51	0.00	0.00	0.00	0.00	0.00	-2.91	-4.41	-2.64
TCGA-D8-A1XT-10A-01D-A14K-09_BRCA	-2.85	-2.57	-2.50	0.00	0.00	0.00	-2.55	-2.51	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.67
TCGA-D8-A1XU-10A-01D-A14K-09_BRCA	-2.90	-4.65	0.00	-2.96	-2.61	-2.55	-2.55	-2.57	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.72
TCGA-D8-A1XV-10A-01D-A14K-09_BRCA	-3.04	-2.86	-2.85	-3.18	-2.60	-2.70	-2.76	-2.78	-2.87	-3.49	-2.66	-2.82	-2.85	-2.84	0.00	-2.87	-2.87

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-D8-A1XW-10A-01D-A14K-09_BRCA	-2.86	-2.57	-2.56	0.00	0.00	0.00	-2.53	-2.63	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.69
TCGA-D8-A1XY-10A-01D-A14K-09_BRCA	-2.86	-4.18	-4.35	-2.75	-2.53	-2.57	-2.52	-2.55	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.74
TCGA-D8-A1XZ-10A-01D-A14K-09_BRCA	-2.93	-2.80	-2.85	-3.13	-2.57	-2.70	-2.66	-2.61	-2.61	0.00	-2.88	-2.80	0.00	0.00	-3.09	-2.86	-2.87
TCGA-D8-A1Y0-10A-01D-A14K-09_BRCA	-2.89	-2.75	-2.78	-3.13	-2.79	-2.81	-2.59	-2.62	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.71	-2.67
TCGA-D8-A1Y1-10A-01D-A14K-09_BRCA	-2.94	-2.61	-2.75	-3.13	-2.63	-2.72	-2.47	-2.55	-2.47	0.00	0.00	-4.43	-4.43	0.00	0.00	-2.55	-2.63
TCGA-D8-A1Y2-10A-01D-A159-09_BRCA	-2.94	0.00	-4.55	-2.97	-2.79	-2.61	-2.58	-2.64	-2.68	0.00	0.00	-4.55	0.00	0.00	0.00	-3.32	-2.73
TCGA-D8-A1Y3-10A-01D-A159-09_BRCA	-3.01	-2.67	-2.74	-2.98	-2.76	-2.74	-2.57	-2.59	-2.67	0.00	0.00	-4.60	0.00	0.00	-3.07	-2.90	-2.71
TCGA-D8-A27E-10A-01D-A16D-09_BRCA	-3.10	-2.99	-2.86	-3.13	-2.62	-2.80	-2.64	-2.70	-2.68	-3.48	-3.13	-2.90	0.00	0.00	0.00	-2.81	-2.86
TCGA-D8-A27F-10A-01D-A16D-09_BRCA	-3.09	0.00	0.00	-3.03	-2.55	-2.67	-2.58	-2.78	-2.83	-3.28	-2.87	0.00	-2.84	-2.76	0.00	-2.98	-2.76
TCGA-D8-A27G-10A-01D-A16D-09_BRCA	-2.90	-2.87	-2.90	-3.07	-2.57	-2.78	-2.67	-2.70	-2.75	-3.48	-2.81	-2.91	-2.91	-2.96	0.00	-2.99	-2.84
TCGA-D8-A27H-10A-01D-A16D-09_BRCA	-2.83	-2.75	-2.72	-3.05	-2.74	-2.76	-2.58	-2.55	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.70
TCGA-D8-A27I-10A-02D-A16D-09_BRCA	-2.97	-2.87	-2.95	-3.05	-2.53	-2.64	-2.54	-2.65	-2.59	0.00	-2.97	-2.86	0.00	0.00	0.00	-2.65	-2.74
TCGA-D8-A27K-10A-01D-A16D-09_BRCA	-2.87	-4.64	0.00	-2.75	-2.58	-2.60	-2.53	-2.53	-2.58	0.00	0.00	-4.64	-4.64	0.00	0.00	-2.55	-2.69
TCGA-D8-A27L-10A-01D-A16D-09_BRCA	-2.95	-2.83	-2.73	-3.21	-2.81	-2.84	-2.63	-2.68	-2.84	-3.38	-2.75	0.00	-2.77	-2.85	0.00	-2.89	-2.82
TCGA-D8-A27M-10A-01D-A16D-09_BRCA	-2.97	0.00	0.00	-2.73	-2.61	-2.64	-2.54	-2.70	-2.79	-3.32	-2.91	-2.77	0.00	-2.78	0.00	-2.91	-2.70
TCGA-D8-A27N-10A-01D-A16D-09_BRCA	-3.01	-2.63	-2.65	0.00	-2.84	-2.92	-2.56	-2.76	-2.87	-3.35	-2.80	-2.63	0.00	-2.96	-3.24	0.00	-2.77
TCGA-D8-A27P-10A-01D-A16D-09_BRCA	-2.82	0.00	0.00	-2.88	-2.48	-2.72	-2.64	-2.75	-2.64	0.00	0.00	0.00	0.00	-2.61	0.00	-2.72	-2.80
TCGA-D8-A27R-10A-01D-A16D-09_BRCA	-2.88	-4.61	0.00	-2.79	-2.65	-2.63	-2.54	-2.65	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.63	-2.74
TCGA-D8-A27T-10A-01D-A16D-09_BRCA	-2.94	-2.76	-2.74	-3.17	-2.86	-2.85	-2.52	-2.77	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.68	-2.74
TCGA-D8-A27V-10A-01D-A17D-09_BRCA	-2.94	-2.68	-2.86	-3.11	-2.73	-2.77	-2.52	-2.74	-2.57	0.00	0.00	0.00	0.00	0.00	-3.11	-3.14	-2.64
TCGA-D8-A27W-10A-01D-A16D-09_BRCA	-2.87	0.00	-4.58	-2.80	-2.53	-2.57	-2.46	-2.65	-2.54	0.00	-4.58	0.00	0.00	0.00	0.00	-2.60	-2.72
TCGA-D8-A3Z5-10A-01D-A243-09_BRCA	-2.80	-2.61	-2.67	-3.10	-2.65	-2.63	-2.44	-2.48	-2.30	-4.05	-4.05	-4.35	0.00	-4.35	0.00	-2.43	-2.51
TCGA-D8-A3Z6-10A-01D-A23C-09_BRCA	-2.74	-2.68	-2.81	-3.30	-2.68	-2.73	-2.42	-2.57	-2.48	0.00	-4.41	0.00	-4.41	-4.11	0.00	-2.53	-2.55
TCGA-D8-A4Z1-10A-01D-A25Q-09_BRCA	-2.67	0.00	-3.94	-2.99	-2.54	-2.49	-2.50	-2.53	-2.37	0.00	-4.42	0.00	0.00	0.00	0.00	-2.59	-2.54
TCGA-D9-A148-10A-01D-A19A-08_SKCM	-2.43	0.00	-4.46	-2.58	-2.49	-2.50	-2.53	-2.56	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.40
TCGA-D9-A149-10A-01D-A198-08_SKCM	-2.44	0.00	0.00	-2.69	-2.54	-2.60	-2.50	-2.56	-2.50	0.00	0.00	0.00	0.00	-4.15	-2.89	-2.66	-2.36
TCGA-D9-A1JW-10A-01D-A19A-08_SKCM	-2.42	-2.69	-2.67	-2.76	-2.67	-2.60	-2.52	-2.52	-2.44	0.00	0.00	-4.12	0.00	-4.42	0.00	-2.40	-2.40
TCGA-D9-A1JX-10A-01D-A19A-08_SKCM	-2.45	-2.77	-2.64	-2.77	-2.63	-2.67	-2.49	-2.57	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.33
TCGA-D9-A1X3-10A-01D-A199-08_SKCM	-2.54	-4.20	0.00	-2.74	-2.51	-2.67	-2.65	-2.53	-2.69	-3.39	-2.86	0.00	-2.77	-2.63	0.00	-2.71	-2.48
TCGA-D9-A3Z1-10A-01D-A23B-08_SKCM	-2.58	-2.66	-2.75	-2.89	-2.73	-2.67	-2.60	-2.52	-2.73	-3.34	-2.91	-4.55	-2.76	-2.72	0.00	-2.73	-2.55
TCGA-D9-A3Z3-10A-01D-A23B-08_SKCM	-2.42	-4.19	-4.19	-2.63	-2.53	-2.60	-2.59	-2.45	-2.49	0.00	-3.80	-3.89	-3.89	-4.02	0.00	-2.43	-2.51
TCGA-D9-A3Z4-10A-01D-A23B-08_SKCM	-2.68	-2.78	-2.79	-2.99	-2.55	-2.75	-2.72	-2.60	-2.78	-3.37	-2.75	-2.78	-2.83	-2.75	0.00	-2.78	-2.62
TCGA-D9-A4Z2-10A-01D-A24R-08_SKCM	-2.62	-2.63	-2.59	-3.64	-2.67	-2.69	-2.58	-2.52	-2.54	0.00	-2.92	-2.71	-4.48	-3.78	0.00	-2.76	-2.52
TCGA-D9-A4Z3-10A-01D-A25O-08_SKCM	-2.45	0.00	0.00	-2.70	-2.48	-2.52	-2.56	-2.38	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.42
TCGA-D9-A4Z5-10A-01D-A25O-08_SKCM	-2.58	-2.71	-2.71	-2.91	-2.51	-2.60	-2.58	-2.63	-2.70	-3.48	-2.77	-2.59	0.00	-2.68	0.00	-2.81	-2.51
TCGA-D9-A4Z6-10A-01D-A25O-08_SKCM	-2.48	-2.66	-2.58	-2.78	-2.58	-2.67	-2.50	-2.57	-2.43	0.00	0.00	0.00	0.00	0.00	-2.83	0.00	-2.43
TCGA-D9-A6E9-10A-01D-A30X-08_SKCM	-2.59	-2.75	-2.66	-2.86	-2.73	-2.73	-2.67	-2.66	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.71	-2.55
TCGA-D9-A6EA-10A-01D-A30X-08_SKCM	-2.71	-2.81	-2.82	-3.07	-2.50	-2.69	-2.74	-2.65	-2.63	0.00	-3.03	-2.80	0.00	0.00	-3.18	-2.87	-2.62
TCGA-D9-A6EC-10A-01D-A30X-08_SKCM	-2.62	-2.78	-2.77	-2.88	-2.76	-2.81	-2.67	-2.56	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.73	-2.57
TCGA-D9-A6EG-10A-01D-A32N-08_SKCM	-2.56	-2.75	-2.68	-2.92	-2.49	-2.69	-2.73	-2.82	-2.68	0.00	-2.88	-2.73	0.00	-2.72	-3.09	0.00	-2.65
TCGA-DA-A1HV-10A-01D-A198-08_SKCM	-2.32	0.00	0.00	-2.57	-2.51	-2.55	-2.54	-2.44	-2.47	0.00	0.00	0.00	0.00	0.00	-3.06	-2.65	-2.39
TCGA-DA-A1HW-10A-01D-A19A-08_SKCM	-2.45	-2.62	-2.62	0.00	-2.58	-2.61	-2.54	-2.46	-2.45	0.00	-4.44	0.00	0.00	0.00	0.00	-2.42	-2.43
TCGA-DA-A1HY-10A-01D-A19A-08_SKCM	-2.42	0.00	0.00	-2.60	-2.54	-2.47	-2.61	-2.54	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.48	-2.40
TCGA-DA-A1I0-10B-01D-A20D-08_SKCM	-2.54	-2.77	-2.78	-2.90	-2.48	-2.56	-2.67	-2.59	-2.54	0.00	-2.90	-2.70	0.00	-4.54	-3.09	-2.71	-2.45
TCGA-DA-A1I1-10A-01D-A198-08_SKCM	-2.50	-2.56	-2.56	0.00	0.00	0.00	-2.58	-2.52	-2.65	-3.26	-2.93	0.00	-2.71	-2.62	0.00	-2.75	-2.45
TCGA-DA-A1I2-10A-01D-A19A-08_SKCM	-2.55	-2.93	-2.74	-2.89	-2.61	-2.61	-2.64	-2.64	-2.86	-3.42	-2.77	-2.68	0.00	-2.77	0.00	-2.99	-2.50
TCGA-DA-A1I4-10A-01D-A198-08_SKCM	-2.39	-2.69	-2.69	-2.79	-2.60	-2.71	-2.69	-2.67	-2.69	0.00	-2.92	-4.50	-2.81	-2.66	0.00	-2.63	-2.46
TCGA-DA-A1I5-10A-01D-A199-08_SKCM	-2.39	-2.73	-2.77	-2.86	-2.48	-2.60	-2.58	-2.58	-2.59	0.00	-2.98	-2.74	0.00	0.00	0.00	-2.52	-2.47
TCGA-DA-A1I7-10A-01D-A199-08_SKCM	-2.41	0.00	0.00	-2.63	-2.52	-2.58	-2.60	-2.60	0.00	-3.13	-2.79	-4.55	-2.59	-2.52	0.00	0.00	-2.38
TCGA-DA-A1I8-10A-01D-A199-08_SKCM	-2.56	0.00	0.00	-2.65	-2.47	-2.48	-2.59	-2.52	-2.52	-3.43	-3.26	-2.91	0.00	0.00	0.00	-2.66	-2.46
TCGA-DA-A1IA-10A-01D-A198-08_SKCM	-2.48	0.00	-4.46	-2.59	-2.52	-2.65	-2.50	-2.51	-2.52	0.00	-4.46	0.00	0.00	-4.16	-3.05	-2.78	-2.40
TCGA-DA-A1IB-10A-01D-A198-08_SKCM	-2.43	-2.71	-2.63	-2.86	-2.67	-2.71	-2.55	-2.56	-2.52	0.00	-2.85	-2.85	0.00	0.00	-2.95	0.00	-2.42
TCGA-DA-A1IC-10A-01D-A199-08_SKCM	-2.47	-2.83	-2.74	-2.87	-2.72	-2.69	-2.59	-2.55	-2.69	-3.23	-2.96	-4.57	-2.95	-2.72	-3.14	0.00	-2.43
TCGA-DA-A3F2-10A-01D-A20D-08_SKCM	-2.54	0.00	0.00	-2.76	-2.51	-2.52	-2.58	-2.54	-2.64	-3.35	-2.88	-4.50	-2.80	-2.63	0.00	-2.77	-2.43
TCGA-DA-A3F3-10A-01D-A20D-08_SKCM	-2.55	-4.53	-4.53	-2.58	-2.57	-2.57	-2.60	-2.63	-2.71	-3.16	-2.83	0.00	-2.84	-2.66	0.00	-2.73	-2.50
TCGA-DA-A3F5-10A-01D-A20D-08_SKCM	-2.45	-2.73	-2.73	-2.87	-2.64	-2.64	-2.57	-2.61	-2.63	-3.21	-2.84	0.00	-2.79	-2.65	0.00	-2.74	-2.49
TCGA-DA-A3F8-10A-01D-A20D-08_SKCM	-2.51	0.00	0.00	-2.54	-2.52	-2.56	-2.56	-2.52	-2.43	0.00	0.00	-4.46	0.00	0.00	0.00	-2.57	-2.43
TCGA-DB-5270-10A-01D-1468-08_LGG	-2.51	-2.71	-2.70	-2.93	-2.70	-2.72	-2.61	-2.45	-2.57	0.00	0.00	0.00	0.00	0.00	-3.02	-2.67	-2.55
TCGA-DB-5273-10A-01D-1468-08_LGG	-2.53	0.00	0.00	-2.91	-2.57	-2.60	-2.62	-2.50	-2.50	-4.59	0.00	0.00	0.00	0.00	-3.01	-2.69	-2.55
TCGA-DB-5274-10A-01D-1468-08_LGG	-2.44	0.00	0.00	-2.68	-2.55	-2.60	-2.68	-2.61	-2.49	0.00	-4.61	0.00	-4.61	-4.61	0.00	-2.55	-2.56
TCGA-DB-5275-10A-01D-1468-08_LGG	-2.61	0.00	0.00	-2.72	-2.62	-2.63	-2.68	-2.70	-2.71	-3.41	-2.95	-4.64	-2.81	-2.76	0.00	-2.76	-2.54
TCGA-DB-5276-10A-01D-1468-08_LGG	-2.55	-2.70	-2.72	-2.90	-2.72	-2.70	-2.61	-2.52	-2.55	0.00	0.00	0.00	0.00	0.00	-3.04	-2.66	-2.55
TCGA-DB-5277-10A-01D-1468-08_LGG	-2.56	-2.78	-2.79	-2.96	-2.51	-2.59	-2.62	-2.62	-2.60	0.00	-3.04	-2.81	0.00	0.00	-2.89	-4.59	-2.60
TCGA-DB-5278-10A-01D-1468-08_LGG	-2.60	0.00	0.00	-2.89	-2.64	-2.59	-2.67	-2.60	-2.74	-3.31	-2.90	0.00	-2.84	-2.73	0.00	-2.74	-2.59
TCGA-DB-5279-10A-01D-1468-08_LGG	-2.42	0.00	0.00	-2.81	-2.61	-2.59	-2.65	-2.49	-2.49	-4.58	0.00	-4.58	0.00	-4.58	0.00	-2.44	-2.56
TCGA-DB-5280-10A-01D-1468-08_LGG	-2.56	0.00	0.00	-2.67	-2.51	-2.55	-2.59	-2.61	-2.62	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.52
TCGA-DB-5281-10A-01D-1468-08_LGG	-2.59	-2.82	-2.77	-2.96	-2.57	-2.64	-2.66	-2.68	-2.68	0.00	-2.89	-2.75	0.00	0.00	0.00	-2.68	-2.51
TCGA-DB-A4X9-10A-01D-A26K-08_LGG	-2.39	-4.56	-4.56	-2.61	-2.45	-2.45	-2.48	-2.52	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.34
TCGA-DB-A4XA-10A-01D-A26K-08_LGG	-2.53	-2.73	-2.71	-2.77	-2.56	-2.58	-2.48	-2.45	-2.46	-4.45	0.00	0.00	-4.45	-3.67	-2.90	-4.15	-2.43
TCGA-DB-A4XB-10A-01D-A26K-08_LGG	-2.58	-2.74	-2.76	-2.89	-2.48	-2.58	-2.58	-2.64	-2.75	-3.40	-2.76	-2.75	-2.83	-2.66	0.00	-2.75	-2.53
TCGA-DB-A4XC-10A-01D-A26K-08_LGG	-2.54	-2.60	-2.61	-3.90	-2.60	-2.70	-2.54	-2.53	-2.65	-3.11	-2.71	-2.60	0.00	-2.67	0.00	-2.87	-2.49
TCGA-DB-A4XD-10A-01D-A27N-08_LGG	-2.47	0.00	0.00	-2.56	-2.51	-2.51	-2.53	-2.58	-2.42	0.00	0.00	0.00	0.00	-4.56	0.00	-2.58	-2.44
TCGA-DB-A4XE-10A-01D-A27N-08_LGG	-2.44	0.00	0.00	-2.69	-2.47	-2.52	-2.49	-2.43	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.37	-2.41
TCGA-DB-A4XF-10A-01D-A27N-08_LGG	-2.41	-2.67	-2.68	-2.78	-2.64	-2.62	-2.51	-2.52	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.37
TCGA-DB-A4XG-10A-01D-A27N-08_LGG	-2.47	-2.59	-2.63	-2.80	-2.69	-2.63	-2.55	-2.43	-2.44	0.00	0.00	0.00	0.00	0.00	-3.05	-2.69	-2.39
TCGA-DB-A4XH-10A-01D-A27N-08_LGG	-2.50	-2.73	-2.65	-2.85	-2.59	-2.65	-2.54	-2.50	-2.44	-4.53	0.00	0.00	0.00	0.00	0.00	-2.36	-2.38
TCGA-DB-A64L-10A-01D-A29Q-08_LGG	-2.56	-2.86	-2.76	-2.93	-2.48	-2.55	-2.67	-2.50	-2.76	-3.41	-2.74	-2.72	-2.86	-2.73	-3.08	0.00	-2.49
TCGA-DB-A64O-10A-01D-A29Q-08_LGG	-2.50	0.00	0.00	-2.60	-2.54	-2.58	-2.59	-2.47	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.38	-2.38
TCGA-DB-A64P-10A-01D-A29Q-08_LGG	-2.52	-2.73	-2.64	-2.86	-2.64	-2.63	-2.55	-2.51	-2.45	0.00	-4.54	0.00	-4.54	0.00	0.00	-2.36	-2.41
TCGA-DB-A64Q-10A-01D-A29Q-08_LGG	-2.49	0.00	0.00	-2.83	-2.49	-2.52	-2.58	-2.56	-2.48	0.00	0.00	0.00	0.00	-4.58	0.00	-2.43	-2.45
TCGA-DB-A64R-10A-01D-A29Q-08_LGG	-2.37	0.00	0.00	-2.63	-2.52	-2.50	-2.56	-2.53	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.40
TCGA-DB-A64S-10A-01D-A29Q-08_LGG	-2.36	0.00	0.00	-2.59	-2.50	-2.51	-2.58	-2.48	-2.48	0.00	0.00	0.00	0.00	0.00	-3.00	-2.76	-2.43
TCGA-DB-A64U-10A-01D-A29Q-08_LGG	-2.48	-2.72	-2.64	-2.90	-2.63	-2.66	-2.55	-2.55	-2.70	-3.33	-2.89	0.00	-2.75	-2.63	0.00	-2.71	-2.48
TCGA-DB-A64V-10A-01D-A29Q-08_LGG	-2.48	-2.66	-2.67	-2.84	-2.62	-2.67	-2.52	-2.46	-2.43	0.00	0.00	0.00	0.00	0.00	-2.94	-2.68	-2.43
TCGA-DB-A64W-10A-01D-A29Q-08_LGG	-2.49	0.00	0.00	-2.67	-2.51	-2.49	-2.53	-2.50	-2.41	0.00	0.00	0.00	0.00	-4.28	0.00	-2.53	-2.38
TCGA-DB-A64X-10A-01D-A29Q-08_LGG	-2.51	-2.72	-2.76	-2.86	-2.45	-2.55	-2.61	-2.65	-2.51	0.00	-2.92	-2.76	0.00	0.00	0.00	-2.57	-2.43
TCGA-DB-A75K-10A-01D-A329-08_LGG	-2.50	0.00	0.00	-2.54	-2.50	-2.52	-2.52	-2.49	-2.48	0.00	0.00	0.00	0.00	-4.40	0.00	-2.41	-2.40
TCGA-DB-A75L-10A-01D-A329-08_LGG	-2.48	0.00	-4.39	-2.58	-2.49	-2.50	-2.42	-2.42	-2.40	0.00	0.00	0.00	0.00	0.00	-3.03	-2.66	-2.40
TCGA-DB-A75M-10A-01D-A329-08_LGG	-2.48	-2.63	-2.60	-2.73	-2.54	-2.60	-2.49	-2.46	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.42
TCGA-DB-A75O-10A-01D-A329-08_LGG	-2.46	-2.74	-2.74	-2.93	-2.46	-2.57	-2.61	-2.61	-2.63	-3.20	-2.80	-2.63	0.00	-2.71	-3.20	0.00	-2.54
TCGA-DB-A75P-10A-01D-A329-08_LGG	-2.52	-2.76	-2.67	-2.85	-2.65	-2.66	-2.43	-2.59	0.00	-3.11	-2.72	0.00	-2.56	-2.45	0.00	0.00	-2.48
TCGA-DC-4745-10A-01D-1733-10_READ	-2.60	-4.40	-4.40	-2.70	-2.49	-2.53	-2.41	-2.56	-2.38	0.00	0.00	0.00	0.00	-4.10	0.00	-2.55	-2.41
TCGA-DC-4749-10A-01D-1733-10_READ	-2.60	0.00	-4.19	-2.86	-2.52	-2.61	-2.47	-2.54	-2.69	-3.53	-3.00	0.00	-3.00	-2.67	-3.34	0.00	-2.38
TCGA-DC-5337-10A-01D-1657-10_READ	-2.62	-2.80	-2.72	-2.99	-2.73	-2.76	-2.47	-2.81	-2.63	-3.32	-3.18	0.00	-2.84	-2.81	0.00	-3.20	-2.48
TCGA-DC-5869-10A-01D-1657-10_READ	-2.54	-2.71	-2.72	-3.07	-2.56	-2.53	-2.43	-2.74	-2.68	-3.46	-2.93	-2.87	-2.75	-2.71	0.00	-3.20	-2.46
TCGA-DC-6154-10A-01D-1924-10_READ	-2.64	0.00	0.00	-2.66	-2.58	-2.33	-2.29	-2.63	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.36

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DC-6155-10A-01D-1657-10_READ	-2.60	0.00	0.00	-2.70	-2.44	-2.53	-2.43	-2.64	-3.95	-3.30	-2.85	-2.85	-2.75	-2.50	0.00	0.00	-2.48
TCGA-DC-6157-10A-01D-1657-10_READ	-2.64	-2.44	-2.43	0.00	-2.61	-2.75	-2.38	-2.77	-2.35	0.00	-3.10	-2.82	0.00	0.00	0.00	-2.70	-2.34
TCGA-DC-6158-10A-01D-1657-10_READ	-2.62	-2.79	-2.69	-3.06	-2.59	-2.58	-2.41	-2.81	-2.39	0.00	-3.22	-2.84	0.00	-4.22	0.00	-2.94	-2.40
TCGA-DC-6681-10A-01D-1826-10_READ	-2.59	0.00	0.00	-2.70	-2.57	-2.65	-2.49	-2.68	-2.68	-3.36	-2.90	0.00	-2.96	-2.87	0.00	-2.87	-2.42
TCGA-DC-6682-10A-01D-1826-10_READ	-2.61	-3.00	-2.92	-3.09	-2.78	-2.65	-2.60	-2.69	-2.56	0.00	-3.03	-3.05	0.00	0.00	0.00	-2.74	-2.55
TCGA-DC-6683-10A-01D-1826-10_READ	-2.70	0.00	0.00	-2.78	-2.64	-2.60	-2.55	-2.65	-2.82	-3.37	-3.19	0.00	-2.75	-2.99	0.00	-2.80	-2.55
TCGA-DD-A113-10A-01D-A12Z-10_LIHC	-2.57	-2.67	-2.75	-3.04	-2.42	-2.53	-2.46	-2.60	-2.37	0.00	-3.01	-2.77	0.00	0.00	-3.14	-2.96	-2.47
TCGA-DD-A114-10A-01D-A12Z-10_LIHC	-2.47	0.00	0.00	-2.67	-2.36	-2.43	-2.43	-2.53	-2.33	0.00	0.00	0.00	0.00	0.00	0.00	-2.81	-2.53
TCGA-DD-A115-10A-01D-A12Z-10_LIHC	-2.49	0.00	0.00	-2.61	-2.38	-2.45	-2.39	-2.64	-2.37	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.44
TCGA-DD-A116-10A-01D-A12Z-10_LIHC	-2.38	0.00	0.00	-2.72	-2.39	-2.45	-2.43	-2.54	-2.41	0.00	0.00	0.00	0.00	0.00	-3.04	-2.88	-2.32
TCGA-DD-A119-10A-01D-A12Z-10_LIHC	-2.51	-2.61	-2.65	-2.98	-2.63	-2.68	-2.39	-2.61	-2.31	0.00	0.00	0.00	0.00	0.00	-3.24	-2.80	-2.39
TCGA-DD-A11A-10A-01D-A12Z-10_LIHC	-2.57	0.00	0.00	-3.07	-2.46	-2.53	-2.34	-2.56	-2.44	-3.32	-3.13	-2.84	0.00	-4.27	-3.13	0.00	-2.43
TCGA-DD-A11B-10A-01D-A12Z-10_LIHC	-2.46	-2.38	-2.40	0.00	0.00	-4.39	-2.57	-2.78	0.00	-3.34	-2.48	-2.65	-2.61	-2.38	0.00	0.00	-2.41
TCGA-DD-A1EA-10A-01D-A12Z-10_LIHC	-2.40	-2.68	-2.52	-2.90	-2.57	-2.59	-2.31	-2.63	-2.37	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.35
TCGA-DD-A1EB-10A-01D-A12Z-10_LIHC	-2.50	0.00	0.00	-2.78	-2.47	-2.47	-2.43	-2.67	-2.68	-3.03	-3.01	0.00	-2.93	-2.71	0.00	-3.13	-2.38
TCGA-DD-A1ED-10A-01D-A152-10_LIHC	-2.62	-2.80	-2.87	-3.02	-2.69	-2.71	-2.60	-2.63	-2.81	-3.32	-2.87	-2.67	0.00	-2.91	0.00	-2.92	-2.55
TCGA-DD-A1EE-10A-01D-A12Z-10_LIHC	-2.40	0.00	0.00	-2.71	-2.42	-2.55	-2.31	-2.55	-2.32	0.00	-3.84	0.00	0.00	0.00	-3.24	-2.96	-2.31
TCGA-DD-A1EF-10A-01D-A12Z-10_LIHC	-2.46	-2.62	-2.64	-2.94	-2.62	-2.69	-2.36	-2.62	-2.32	0.00	0.00	0.00	0.00	0.00	0.00	-2.68	-2.36
TCGA-DD-A1EG-10A-01D-A20W-10_LIHC	-2.47	-2.43	-2.46	0.00	-2.51	-2.42	-2.32	-2.43	-2.61	-3.26	-2.53	-2.41	-2.65	-2.65	-3.05	0.00	-2.39
TCGA-DD-A1EH-10A-01D-A12Z-10_LIHC	-2.43	-2.38	-2.37	0.00	-2.76	-2.66	-2.61	-2.78	0.00	-3.10	-2.48	-2.57	-2.71	-2.48	0.00	0.00	-2.32
TCGA-DD-A1EJ-10A-01D-A152-10_LIHC	-2.41	-3.68	-3.48	-3.68	-3.43	-3.38	-2.94	-2.19	-2.77	0.00	0.00	0.00	0.00	0.00	0.00	-2.48	-2.88
TCGA-DD-A1EK-10A-01D-A20W-10_LIHC	-2.42	-4.32	0.00	-2.66	-2.35	-2.26	-2.29	-2.28	-2.22	0.00	0.00	0.00	0.00	0.00	-3.04	-2.75	-2.35
TCGA-DD-A1EL-10A-01D-A152-10_LIHC	-2.68	-2.82	-2.77	-2.98	-2.52	-2.63	-2.52	-2.64	-2.54	0.00	-3.03	-2.85	0.00	-4.53	-3.12	-2.90	-2.55
TCGA-DD-A4NF-10A-01D-A27I-10_LIHC	-2.50	-2.54	-2.55	-2.74	-2.40	-2.39	-2.35	-2.41	-2.41	-4.42	-2.72	0.00	-2.62	-4.42	0.00	-2.51	-2.58
TCGA-DD-A4NG-10A-01D-A27I-10_LIHC	-2.53	0.00	-4.39	-2.73	-2.46	-2.38	-2.49	-2.52	-2.60	-3.48	-2.91	0.00	-2.64	-2.55	0.00	-2.55	-2.42
TCGA-DD-A4NH-10A-01D-A27I-10_LIHC	-2.42	-2.62	-2.68	-2.78	-2.36	-2.30	-2.32	-2.40	-2.38	0.00	-3.26	-2.59	0.00	0.00	-2.70	0.00	-2.43
TCGA-DD-A4NI-10A-01D-A27I-10_LIHC	-2.34	-4.26	-4.26	-2.44	-2.41	-2.27	-2.32	-2.41	-2.24	0.00	0.00	-3.96	0.00	0.00	-2.82	-2.49	-2.36
TCGA-DD-A4NJ-10A-01D-A27I-10_LIHC	-2.37	-2.49	-2.46	-2.70	-2.62	-2.32	-2.26	-2.37	-2.24	0.00	0.00	0.00	0.00	0.00	0.00	-2.31	-2.32
TCGA-DD-A4NK-10A-01D-A28X-10_LIHC	-2.33	-2.50	-2.52	-2.88	-2.50	-2.46	-2.25	-2.22	-2.33	0.00	0.00	-4.28	0.00	0.00	0.00	-2.21	-2.41
TCGA-DD-A4NN-10A-01D-A28X-10_LIHC	-2.46	-4.28	-4.28	-2.63	-2.44	-2.36	-2.33	-2.33	-2.62	-3.68	-2.67	0.00	-2.53	-2.43	0.00	-2.51	-2.44
TCGA-DD-A4NO-10A-01D-A28X-10_LIHC	-2.50	-2.54	-2.66	-2.89	-2.34	-2.34	-2.34	-2.51	-2.54	-3.97	-2.53	-2.43	0.00	-2.60	0.00	-2.74	-2.51
TCGA-DD-A4NP-10A-01D-A28X-10_LIHC	-2.39	-3.86	-4.16	-2.59	-2.39	-2.25	-2.30	-2.39	-2.72	-3.47	-2.67	-2.51	0.00	-2.50	0.00	-2.62	-2.43
TCGA-DD-A4NQ-10A-01D-A28X-10_LIHC	-2.29	-2.32	-2.28	0.00	-2.54	-2.46	-2.30	-2.29	-2.40	0.00	-2.57	-2.46	0.00	0.00	-2.80	-2.46	-2.46
TCGA-DD-A4NR-10A-01D-A30V-10_LIHC	-2.49	-2.84	-2.41	-2.98	-2.76	-2.57	-2.24	-2.37	-2.76	-3.17	-2.80	0.00	-2.53	-2.63	0.00	-2.80	-2.41
TCGA-DD-A4NS-10A-01D-A30V-10_LIHC	-2.41	-2.44	-2.70	-2.77	-2.63	-2.59	-2.41	-2.58	-2.44	0.00	-2.77	0.00	-2.77	-2.59	0.00	-2.63	-2.37
TCGA-DD-A4NV-10A-01D-A30V-10_LIHC	-2.51	-2.60	-2.50	0.00	-2.66	-2.60	-2.26	-2.33	-2.37	0.00	0.00	0.00	0.00	0.00	-2.93	-2.63	-2.34
TCGA-DE-A0XZ-10A-01D-A17V-08_THCA	-2.56	-2.75	-2.75	-2.87	-2.74	-2.79	-2.73	-2.54	-2.72	-3.39	-2.88	-2.74	0.00	-2.68	-3.17	0.00	-2.54
TCGA-DE-A0Y2-10A-01D-A10S-08_THCA	-2.62	-2.70	-2.72	-2.91	-2.70	-2.69	-2.61	-2.54	-2.49	0.00	0.00	0.00	0.00	-4.27	-3.04	-2.65	-2.58
TCGA-DE-A0Y3-10A-01D-A10S-08_THCA	-2.57	-2.70	-2.72	-2.90	-2.64	-2.67	-2.62	-2.58	-2.53	0.00	0.00	0.00	0.00	0.00	-2.95	-4.55	-2.54
TCGA-DE-A2OL-10A-01D-A18F-08_THCA	-2.56	-2.61	-2.58	-4.52	-2.67	-2.71	-2.57	-2.67	-2.53	0.00	-2.80	-2.68	0.00	0.00	-2.98	0.00	-2.48
TCGA-DE-A3KN-10A-01D-A20C-08_THCA	-2.55	0.00	0.00	-2.51	-2.51	-2.54	-2.56	-2.62	-2.52	0.00	0.00	-4.50	0.00	-4.50	-2.89	-4.50	-2.44
TCGA-DE-A4M8-10A-01D-A25A-08_THCA	-2.60	0.00	0.00	-2.82	-2.58	-2.60	-2.63	-2.47	-2.60	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.57
TCGA-DE-A4M9-10A-01D-A25A-08_THCA	-2.56	0.00	0.00	-2.68	-2.54	-2.54	-2.58	-2.54	-2.53	0.00	0.00	0.00	0.00	0.00	-3.05	-2.79	-2.51
TCGA-DE-A4MA-10A-01D-A25A-08_THCA	-2.58	-4.43	-4.13	-2.66	-2.59	-2.62	-2.64	-2.50	-2.68	-3.47	-2.90	-4.13	-2.72	-2.79	0.00	-2.73	-2.46
TCGA-DE-A4MB-10A-01D-A25A-08_THCA	-2.48	-2.73	-2.70	-2.89	-2.39	-2.54	-2.51	-2.57	-2.44	0.00	-3.01	-2.68	0.00	0.00	-3.10	-2.82	-2.44
TCGA-DE-A4MC-10A-01D-A25A-08_THCA	-2.41	-2.80	-2.71	-2.65	-2.51	-2.50	-2.48	-2.50	-2.45	-3.91	-3.66	0.00	-3.43	-2.96	-3.12	-2.81	-2.36
TCGA-DF-A2KN-10A-01D-A17W-09_UCEC	-2.77	0.00	-4.19	-3.00	-2.50	-2.58	-2.52	-2.44	-2.36	0.00	0.00	-4.49	-4.19	0.00	0.00	-2.42	-2.57
TCGA-DF-A2KR-10A-01D-A17W-09_UCEC	-2.70	-4.08	-4.38	-2.87	-2.54	-2.58	-2.49	-2.47	-2.36	0.00	0.00	0.00	0.00	0.00	-2.86	-2.73	-2.63
TCGA-DF-A2KS-10A-01D-A18P-09_UCEC	-2.89	-2.82	-2.83	-3.32	-2.52	-2.62	-2.63	-2.63	-2.59	0.00	-2.91	-2.78	-4.64	0.00	-3.05	-2.81	-2.77
TCGA-DF-A2KU-10A-01D-A17W-09_UCEC	-2.81	-2.72	-2.66	-3.27	-2.66	-2.61	-2.40	-2.59	-2.39	0.00	-4.35	0.00	0.00	0.00	-3.03	-2.70	-2.55
TCGA-DF-A2KV-10A-01D-A17W-09_UCEC	-2.82	0.00	0.00	-3.03	-2.58	-2.60	-2.51	-2.66	-2.67	-3.48	-2.91	0.00	-2.74	-2.69	0.00	-2.75	-2.65
TCGA-DF-A2KY-10A-01D-A20S-09_UCEC	-2.86	-2.71	-2.84	-3.35	-2.75	-2.83	-2.51	-2.54	-2.72	-3.35	-2.88	-2.69	-4.49	-2.71	0.00	-2.84	-2.64
TCGA-DF-A2KZ-10A-01D-A20S-09_UCEC	-2.86	-2.65	-2.70	-3.32	-2.71	-2.61	-2.46	-2.56	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.63
TCGA-DF-A2L0-10A-01D-A17W-09_UCEC	-2.76	-4.00	0.00	-2.88	-2.40	-2.62	-2.50	-2.63	-2.51	0.00	0.00	0.00	0.00	-2.56	0.00	-2.68	-2.65
TCGA-DG-A2KH-10A-01D-A22X-09_CESC	-2.89	-2.72	-2.77	-3.42	-2.55	-2.63	-2.59	-2.56	-2.70	-3.34	-2.68	-2.66	0.00	-2.72	0.00	-2.85	-2.66
TCGA-DG-A2KJ-10A-01D-A18J-09_CESC	-2.84	-2.71	-2.75	-3.08	-2.60	-2.69	-2.48	-2.49	-2.46	0.00	-4.12	-4.42	0.00	-4.42	-2.89	-2.73	-2.59
TCGA-DG-A2KK-10A-01D-A17W-09_CESC	-2.79	0.00	-4.60	-2.95	-2.57	-2.53	-2.55	-2.59	-2.60	-3.56	-2.86	0.00	-2.73	-2.69	0.00	-2.78	-2.67
TCGA-DG-A2KL-10A-01D-A17W-09_CESC	-2.89	0.00	0.00	-3.10	-2.49	-2.55	-2.52	-2.60	-3.80	-3.39	-2.54	-2.80	-2.64	-2.64	0.00	-4.64	-2.75
TCGA-DG-A2KM-10A-01D-A17W-09_CESC	-2.76	0.00	0.00	-3.06	-2.52	-2.52	-2.45	-2.50	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.53
TCGA-DH-5140-10A-01D-1468-08_LGG	-2.46	-2.76	-2.71	-2.94	-2.70	-2.74	-2.65	-2.60	-2.54	0.00	-4.64	0.00	0.00	0.00	0.00	-2.63	-2.51
TCGA-DH-5141-10A-01D-1468-08_LGG	-2.63	-4.69	-4.69	-2.83	-2.63	-2.64	-2.59	-2.50	-2.77	-3.33	-2.90	0.00	-2.80	-2.72	-3.08	-4.69	-2.50
TCGA-DH-5142-10A-01D-1468-08_LGG	-2.59	-2.65	-2.67	-4.62	-2.68	-2.69	-2.68	-2.55	-2.64	0.00	-2.92	-2.70	0.00	-4.62	-3.07	-2.82	-2.57
TCGA-DH-5143-10A-01D-1468-08_LGG	-2.51	-2.78	-2.75	-3.03	-2.52	-2.63	-2.72	-2.57	-2.57	0.00	-2.92	0.00	-4.68	-4.68	-3.09	-2.73	-2.57
TCGA-DH-5144-10A-01D-1468-08_LGG	-2.57	0.00	0.00	-2.82	-2.64	-2.60	-2.62	-2.51	-2.59	0.00	-4.65	-4.65	-4.65	-4.17	-3.00	-2.72	-2.58
TCGA-DH-A669-10A-01D-A31J-08_LGG	-2.53	0.00	0.00	-2.75	-2.53	-2.54	-2.57	-2.47	-2.58	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.48
TCGA-DH-A66B-10A-01D-A29Q-08_LGG	-2.47	0.00	0.00	-2.81	-2.49	-2.48	-2.53	-2.50	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.42
TCGA-DH-A66D-10A-01D-A31J-08_LGG	-2.56	0.00	-4.50	-2.73	-2.46	-2.57	-2.62	-2.63	0.00	-3.08	-2.65	0.00	-2.59	-2.55	0.00	0.00	-2.52
TCGA-DH-A66F-10A-01D-A29Q-08_LGG	-2.57	0.00	-4.64	-2.63	-2.54	-2.51	-2.59	-2.51	-2.64	-3.41	-2.91	0.00	-2.71	-2.73	0.00	-2.71	-2.51
TCGA-DH-A66G-10A-01D-A31J-08_LGG	-2.57	0.00	0.00	-2.55	-2.56	-2.56	-2.54	-2.42	-2.58	0.00	0.00	0.00	0.00	0.00	0.00	-2.40	-2.49
TCGA-DI-A0WH-10B-01D-A12J-09_UCEC	-2.80	0.00	0.00	-2.81	-2.58	-2.58	-2.58	-2.58	-2.58	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.69
TCGA-DI-A1BU-10A-01D-A135-09_UCEC	-2.77	-2.88	-2.88	-3.38	-2.49	-2.57	-2.62	-2.60	-2.51	0.00	-2.92	-2.85	0.00	-4.38	-3.08	-2.92	-2.70
TCGA-DI-A1BY-10A-01D-A135-09_UCEC	-2.83	-2.70	-2.83	-3.44	-2.76	-2.78	-2.53	-2.65	-2.68	-3.40	-2.82	-4.52	-2.75	-2.76	0.00	-2.78	-2.66
TCGA-DI-A1C3-10A-01D-A135-09_UCEC	-2.77	-3.99	-4.16	-3.16	-2.56	-2.48	-2.51	-2.57	-2.38	0.00	0.00	0.00	-4.46	-4.46	0.00	-2.55	-2.60
TCGA-DI-A2QT-10A-01D-A19Y-09_UCEC	-2.72	-2.57	-2.63	-3.10	-2.58	-2.58	-2.44	-2.61	-2.39	0.00	0.00	-4.43	0.00	-4.43	-2.78	-4.43	-2.50
TCGA-DJ-A13L-10A-01D-A21Z-08_THCA	-2.55	-2.74	-2.71	-2.84	-2.69	-2.67	-2.63	-2.64	-2.66	-3.21	-2.80	0.00	-2.72	-2.64	0.00	-2.75	-2.51
TCGA-DJ-A13M-10A-01D-A10S-08_THCA	-2.63	-2.75	-2.83	-3.04	-2.56	-2.69	-2.72	-2.68	-2.75	-3.44	-2.81	-2.77	-2.85	-2.82	0.00	-2.78	-2.59
TCGA-DJ-A13O-10A-01D-A10S-08_THCA	-2.57	-2.75	-2.77	-3.00	-2.67	-2.72	-2.63	-2.58	-2.71	-3.38	-2.98	0.00	-2.79	-2.68	0.00	-2.79	-2.54
TCGA-DJ-A13P-10A-01D-A10S-08_THCA	-2.43	-2.69	-2.68	-2.95	-2.64	-2.74	-2.65	-2.50	-2.55	0.00	0.00	0.00	0.00	-4.59	-3.03	-2.68	-2.50
TCGA-DJ-A13R-10A-01D-A10S-08_THCA	-2.50	-2.84	-2.80	-2.96	-2.53	-2.62	-2.68	-2.62	-2.66	0.00	-2.92	-2.75	0.00	-4.63	0.00	-2.49	-2.58
TCGA-DJ-A13S-10A-01D-A10S-08_THCA	-2.58	0.00	0.00	-2.66	-2.54	-2.52	-2.67	-2.47	-2.45	0.00	0.00	-4.56	0.00	-4.26	-3.03	-2.67	-2.48
TCGA-DJ-A13T-10A-01D-A10S-08_THCA	-2.63	-2.77	-2.74	-2.94	-2.72	-2.76	-2.69	-2.53	-2.73	-3.45	-2.88	0.00	-2.81	-2.73	0.00	-2.76	-2.55
TCGA-DJ-A13U-10A-01D-A10S-08_THCA	-2.63	-2.78	-2.72	-2.98	-2.73	-2.77	-2.61	-2.55	-2.70	-3.25	-2.94	0.00	-2.78	-2.70	-3.11	0.00	-2.53
TCGA-DJ-A13V-10A-01D-A10S-08_THCA	-2.45	0.00	-4.56	-2.62	-2.53	-2.51	-2.59	-2.46	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.45
TCGA-DJ-A13W-10A-01D-A10S-08_THCA	-2.60	-2.80	-2.78	-2.98	-2.54	-2.64	-2.63	-2.68	-2.64	0.00	-2.93	-2.74	0.00	0.00	0.00	-2.64	-2.58
TCGA-DJ-A13X-10A-01D-A10S-08_THCA	-2.59	-2.64	-2.67	-4.66	-2.73	-2.71	-2.64	-2.58	-2.72	-3.43	-2.78	-2.72	-2.86	-2.71	-3.12	0.00	-2.56
TCGA-DJ-A1QD-10A-01D-A14W-08_THCA	-2.48	-2.61	-2.64	-2.79	-2.61	-2.60	-2.70	-2.68	0.00	-3.24	-2.60	0.00	-2.55	-2.50	0.00	0.00	-2.44
TCGA-DJ-A1QE-10A-01D-A14W-08_THCA	-2.48	-2.74	-2.67	-2.90	-2.62	-2.65	-2.52	-2.58	-2.65	-3.23	-2.90	0.00	-2.70	-2.62	0.00	-2.72	-2.40
TCGA-DJ-A1QF-10A-01D-A14W-08_THCA	-2.61	-2.65	-2.56	0.00	-2.81	-2.78	-2.52	-2.56	-2.71	-3.23	-2.71	-2.77	-2.63	-2.73	-3.13	0.00	-2.46
TCGA-DJ-A1QG-10A-01D-A14W-08_THCA	-2.55	-2.53	-2.54	-4.18	-2.63	-2.66	-2.66	-2.71	-2.63	0.00	-2.63	-2.67	-2.73	-2.57	0.00	-2.75	-2.42
TCGA-DJ-A1QH-10A-01D-A14W-08_THCA	-2.50	-4.45	-3.98	-2.65	-2.45	-2.43	-2.43	-2.55	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.31
TCGA-DJ-A1QI-10A-01D-A14W-08_THCA	-2.47	-2.54	-2.41	0.00	0.00	0.00	-2.47	-2.50	-2.57	-3.18	-2.90	0.00	-2.78	-2.54	-3.14	0.00	-2.33
TCGA-DJ-A1QL-10A-01D-A14W-08_THCA	-2.46	-2.80	-2.76	-2.97	-2.49	-2.61	-2.58	-2.65	-2.70	-3.22	-2.71	-2.63	0.00	-2.70	-3.19	-4.57	-2.44
TCGA-DJ-A1QM-10A-01D-A14W-08_THCA	-2.46	0.00	0.00	-2.60	-2.47	-2.50	-2.52	-2.61	-2.78	-3.23	-2.94	0.00	-2.78	-2.75	0.00	-2.82	-2.42
TCGA-DJ-A1QN-10A-01D-A14W-08_THCA	-2.59	-2.75	-2.71	-2.96	-2.53	-2.60	-2.62	-2.69	-2.70	-3.44	-2.75	-2.74	-2.76	-2.74	0.00	-2.83	-2.49
TCGA-DJ-A1QO-10A-01D-A14W-08_THCA	-2.52	0.00	-4.48	-2.72	-2.47	-2.50	-2.50	-2.55	-2.44	0.00	0.00	0.00	0.00	-4.18	-3.10	-2.79	-2.42
TCGA-DJ-A1QQ-10A-01D-A14W-08_THCA	-2.55	-2.81	-2.76	-2.93	-2.48	-2.56	-2.58	-2.55	-2.56	0.00	-3.01	-2.64	0.00	-4.57	0.00	-2.71	-2.41

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DJ-A2PN-10A-01D-A19M-08_THCA	-2.42	0.00	-4.55	-2.72	-2.48	-2.50	-2.57	-2.50	-2.41	0.00	0.00	-4.55	0.00	0.00	-3.09	-2.70	-2.38
TCGA-DJ-A2PO-10A-01D-A19M-08_THCA	-2.48	-4.25	-4.08	-2.66	-2.45	-2.44	-2.44	-2.49	-2.44	0.00	-4.55	-4.55	0.00	0.00	0.00	-2.52	-2.37
TCGA-DJ-A2PP-10A-01D-A19M-08_THCA	-2.51	-2.74	-2.74	-2.85	-2.64	-2.74	-2.56	-2.54	-2.65	-3.33	-2.80	0.00	-2.77	-2.62	-3.05	-4.28	-2.42
TCGA-DJ-A2PQ-10A-01D-A18F-08_THCA	-2.63	-2.80	-2.79	-2.92	-2.53	-2.65	-2.67	-2.57	-2.80	-3.40	-2.75	-2.62	-4.61	-2.74	0.00	-2.83	-2.59
TCGA-DJ-A2PR-10A-01D-A19M-08_THCA	-2.49	-2.66	-2.67	-2.74	-2.58	-2.62	-2.61	-2.76	-2.55	0.00	-2.76	0.00	-2.76	-2.66	0.00	-2.72	-2.34
TCGA-DJ-A2PS-10A-01D-A18F-08_THCA	-2.53	-2.72	-2.70	-2.80	-2.64	-2.63	-2.65	-2.71	-2.64	0.00	-2.82	0.00	-2.73	-2.64	-3.03	0.00	-2.50
TCGA-DJ-A2PT-10A-01D-A18F-08_THCA	-2.59	0.00	-4.27	-2.62	-2.58	-2.57	-2.62	-2.53	-2.72	-3.31	-2.84	-4.27	-2.77	-2.66	0.00	-2.78	-2.47
TCGA-DJ-A2PU-10A-01D-A19M-08_THCA	-2.50	-2.76	-2.62	-2.82	-2.64	-2.68	-2.57	-2.47	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.45
TCGA-DJ-A2PV-10A-01D-A19M-08_THCA	-2.46	-4.04	0.00	-2.63	-2.43	-2.44	-2.47	-2.54	-2.46	0.00	-4.52	-4.52	-4.22	-4.04	0.00	-2.53	-2.35
TCGA-DJ-A2PW-10A-01D-A19M-08_THCA	-2.49	-4.23	-4.05	-2.50	-2.44	-2.43	-2.52	-2.56	-2.46	0.00	0.00	0.00	-4.53	-4.53	0.00	-2.55	-2.30
TCGA-DJ-A2PX-10A-01D-A18F-08_THCA	-2.52	0.00	-4.52	-2.71	-2.49	-2.56	-2.53	-2.47	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.42
TCGA-DJ-A2PY-10A-01D-A18F-08_THCA	-2.47	0.00	0.00	-2.55	-2.50	-2.49	-2.53	-2.59	-2.42	0.00	-4.49	0.00	0.00	-4.49	0.00	-2.53	-2.48
TCGA-DJ-A2PZ-10A-01D-A18F-08_THCA	-2.55	0.00	0.00	-2.72	-2.49	-2.53	-2.59	-2.52	-2.67	-3.28	-2.98	0.00	-2.77	-2.67	0.00	-2.71	-2.51
TCGA-DJ-A2Q0-10A-01D-A202-08_THCA	-2.46	-2.63	-2.63	-2.84	-2.66	-2.61	-2.57	-2.59	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.49
TCGA-DJ-A2Q1-10A-01D-A19M-08_THCA	-2.57	-2.83	-2.75	-2.88	-2.43	-2.58	-2.53	-2.56	-2.49	0.00	-3.01	-2.69	0.00	0.00	0.00	-2.56	-2.44
TCGA-DJ-A2Q2-10A-01D-A19M-08_THCA	-2.52	-2.74	-2.67	-2.81	-2.49	-2.52	-2.51	-2.69	-2.52	0.00	-3.05	-2.72	0.00	0.00	-3.32	-2.91	-2.38
TCGA-DJ-A2Q3-10A-01D-A18F-08_THCA	-2.42	-2.72	-2.71	-2.61	-2.51	-2.56	-2.55	-2.60	-2.47	0.00	-4.56	0.00	0.00	0.00	0.00	-2.61	-2.45
TCGA-DJ-A2Q4-10A-01D-A18F-08_THCA	-2.56	-2.75	-2.74	-2.87	-2.67	-2.67	-2.58	-2.62	-2.62	-3.43	-2.80	0.00	-2.77	-2.68	0.00	-2.68	-2.52
TCGA-DJ-A2Q5-10A-01D-A18F-08_THCA	-2.53	0.00	0.00	-2.75	-2.55	-2.57	-2.55	-2.47	-2.56	0.00	0.00	0.00	0.00	0.00	-3.01	-2.75	-2.51
TCGA-DJ-A2Q6-10A-01D-A18F-08_THCA	-2.39	0.00	0.00	-2.57	-2.52	-2.59	-2.59	-2.43	-2.49	0.00	0.00	0.00	-4.52	0.00	-3.06	-2.76	-2.47
TCGA-DJ-A2Q7-10A-01D-A18F-08_THCA	-2.47	0.00	-3.85	-2.56	-2.53	-2.55	-2.64	-2.62	-2.68	-3.37	-2.90	0.00	-2.77	-2.71	0.00	-2.69	-2.54
TCGA-DJ-A2Q8-10A-01D-A18F-08_THCA	-2.44	-2.67	-2.68	-2.76	-2.59	-2.65	-2.52	-2.48	-2.57	0.00	0.00	0.00	0.00	0.00	-3.00	-2.67	-2.44
TCGA-DJ-A2Q9-10A-01D-A18F-08_THCA	-2.59	0.00	0.00	-2.67	-2.57	-2.61	-2.63	-2.58	-2.67	-3.47	-2.93	0.00	-2.75	-2.72	-3.02	0.00	-2.53
TCGA-DJ-A2QA-10A-01D-A18F-08_THCA	-2.43	0.00	0.00	-2.68	-2.50	-2.50	-2.53	-2.61	-2.46	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.43
TCGA-DJ-A2QB-10A-01D-A19M-08_THCA	-2.50	-2.67	-2.67	-2.80	-2.66	-2.62	-2.50	-2.49	-2.40	0.00	0.00	0.00	0.00	0.00	-2.99	-2.71	-2.42
TCGA-DJ-A2QC-10A-01D-A18F-08_THCA	-2.48	-2.68	-2.64	-2.77	-2.63	-2.64	-2.54	-2.55	-2.42	0.00	0.00	0.00	0.00	-4.17	0.00	-2.53	-2.42
TCGA-DJ-A3UK-10A-01D-A22D-08_THCA	-2.59	-2.61	-2.60	-4.55	-2.64	-2.71	-2.57	-2.53	-2.67	-3.18	-2.70	-2.63	0.00	-2.69	-3.20	0.00	-2.55
TCGA-DJ-A3UM-10A-01D-A22D-08_THCA	-2.49	0.00	0.00	-2.69	-2.55	-2.53	-2.53	-2.53	-2.50	0.00	0.00	0.00	0.00	0.00	-2.98	-2.67	-2.45
TCGA-DJ-A3UN-10A-01D-A22D-08_THCA	-2.56	0.00	0.00	-2.76	-2.53	-2.52	-2.63	-2.56	-2.64	-3.31	-2.87	0.00	-2.77	-2.68	-3.09	0.00	-2.53
TCGA-DJ-A3UO-10A-01D-A22D-08_THCA	-2.40	-2.55	-2.63	-2.69	-2.49	-4.36	-2.58	-2.63	-2.56	0.00	-4.36	-4.36	0.00	-2.50	0.00	-2.57	-2.42
TCGA-DJ-A3UP-10A-01D-A22D-08_THCA	-2.58	0.00	-4.54	-2.82	-2.54	-2.62	-2.58	-2.56	-4.54	-3.04	-2.72	0.00	-2.67	-2.54	0.00	0.00	-2.51
TCGA-DJ-A3UQ-10A-01D-A22D-08_THCA	-2.48	-3.84	0.00	-2.66	-2.52	-2.42	-2.50	-2.53	-2.48	0.00	0.00	0.00	0.00	-4.45	-2.98	-2.65	-2.41
TCGA-DJ-A3UR-10A-01D-A22D-08_THCA	-2.54	0.00	-4.24	-2.64	-2.57	-2.61	-2.60	-2.54	-2.64	-3.29	-2.80	0.00	-2.75	-2.64	-3.03	0.00	-2.51
TCGA-DJ-A3US-10A-01D-A22D-08_THCA	-2.54	0.00	0.00	-2.78	-2.54	-2.59	-2.66	-2.57	-2.69	-3.44	-3.04	0.00	-2.80	-2.67	-3.05	0.00	-2.50
TCGA-DJ-A3UT-10A-01D-A22D-08_THCA	-2.53	-4.51	0.00	-2.63	-2.61	-2.55	-2.69	-2.66	-2.68	-3.28	-2.94	0.00	-2.74	-2.72	0.00	-2.77	-2.50
TCGA-DJ-A3UU-10A-01D-A22D-08_THCA	-2.53	-2.70	-2.74	-2.90	-2.67	-2.73	-2.58	-2.70	-2.67	-3.28	-2.82	-2.69	0.00	-2.64	0.00	-2.73	-2.47
TCGA-DJ-A3UV-10A-01D-A22D-08_THCA	-2.50	0.00	0.00	-2.71	-2.47	-2.53	-2.50	-2.56	-2.52	0.00	0.00	-4.14	0.00	0.00	-3.01	-2.63	-2.48
TCGA-DJ-A3UW-10A-01D-A22D-08_THCA	-2.54	-2.72	-2.70	-2.81	-2.67	-2.70	-2.61	-2.61	-2.63	-3.42	-2.86	-2.67	0.00	-2.67	-3.07	0.00	-2.50
TCGA-DJ-A3UX-10A-01D-A22D-08_THCA	-2.45	-4.54	-4.24	-2.75	-2.53	-2.59	-2.63	-2.55	-2.65	-3.28	-2.81	-2.70	0.00	-2.60	0.00	-2.67	-2.48
TCGA-DJ-A3UY-10A-01D-A22D-08_THCA	-2.50	0.00	0.00	-2.62	-2.49	-2.45	-2.51	-2.58	-2.50	0.00	0.00	-4.44	0.00	-4.44	-2.88	-4.44	-2.39
TCGA-DJ-A3UZ-10A-01D-A22Z-08_THCA	-2.58	0.00	-4.26	-2.77	-2.51	-2.58	-2.58	-2.62	-2.57	-4.56	-4.26	-4.56	0.00	-4.26	-3.14	-2.76	-2.43
TCGA-DJ-A3V0-10A-01D-A22Z-08_THCA	-2.55	-2.70	-2.78	-2.89	-2.47	-2.52	-2.48	-2.65	-2.64	-3.41	-2.70	-2.68	-2.79	-2.64	0.00	-2.92	-2.46
TCGA-DJ-A3V2-10A-01D-A22Z-08_THCA	-2.50	-2.64	-2.72	-2.94	-2.64	-2.66	-2.54	-2.56	-2.67	-3.54	-2.80	0.00	-2.64	-2.63	0.00	-2.70	-2.47
TCGA-DJ-A3V3-10A-01D-A22Z-08_THCA	-2.54	-2.60	-2.68	0.00	-2.57	-2.57	-2.63	-2.57	-2.66	-3.34	-2.65	-2.69	-2.75	-2.64	-3.06	0.00	-2.52
TCGA-DJ-A3V4-10A-01D-A22Z-08_THCA	-2.54	-2.70	-2.67	-2.86	-2.69	-2.64	-2.56	-2.57	-2.52	0.00	0.00	-4.55	0.00	0.00	0.00	-2.45	-2.42
TCGA-DJ-A3V5-10A-01D-A22Z-08_THCA	-2.59	-2.70	-2.68	-2.91	-2.51	-2.58	-2.60	-2.68	-2.73	-3.23	-2.73	-2.72	-2.76	-2.70	0.00	-2.85	-2.50
TCGA-DJ-A3V6-10A-01D-A22Z-08_THCA	-2.44	0.00	0.00	-2.63	-2.42	-2.43	-2.46	-2.56	-2.41	0.00	0.00	0.00	0.00	0.00	-2.80	0.00	-2.34
TCGA-DJ-A3V7-10A-01D-A23K-08_THCA	-2.56	-2.68	-2.70	-2.85	-2.63	-2.68	-2.62	-2.55	-2.47	0.00	0.00	-4.50	0.00	-4.50	0.00	-2.59	-2.50
TCGA-DJ-A3V8-10A-01D-A23K-08_THCA	-2.60	-3.76	-3.64	-2.65	-2.56	-2.64	-2.66	-2.53	-2.68	-3.31	-2.92	-4.54	-2.75	-2.73	-3.08	-3.94	-2.59
TCGA-DJ-A3V9-10A-01D-A23K-08_THCA	-2.52	-3.93	-4.15	-2.89	-2.71	-2.66	-2.70	-2.49	-2.58	-4.15	-3.85	-4.63	-3.93	-4.03	-3.11	-2.79	-2.59
TCGA-DJ-A3VA-10A-01D-A23K-08_THCA	-2.64	-2.82	-2.80	-2.97	-2.58	-2.71	-2.73	-2.65	-2.76	-3.33	-2.78	-2.76	-2.77	-2.78	0.00	-2.75	-2.68
TCGA-DJ-A3VB-10A-01D-A23K-08_THCA	-2.59	0.00	-4.19	-2.72	-2.57	-2.62	-2.40	-2.61	-2.53	0.00	0.00	-4.49	0.00	-4.49	0.00	-2.38	-2.54
TCGA-DJ-A3VD-10A-01D-A23K-08_THCA	-2.57	-2.87	-2.73	-2.92	-2.39	-2.49	-2.52	-2.54	-2.68	-3.22	-2.71	-2.49	0.00	-2.78	-3.25	0.00	-2.46
TCGA-DJ-A3VE-10A-01D-A23K-08_THCA	-2.65	-2.70	-2.73	-2.91	-2.70	-2.71	-2.63	-2.63	-2.72	-3.19	-2.83	-4.55	-2.76	-2.70	0.00	-2.74	-2.63
TCGA-DJ-A3VF-10A-01D-A23K-08_THCA	-2.58	-2.69	-2.69	-2.83	-2.64	-2.68	-2.61	-2.45	-2.53	0.00	-4.03	-3.91	-4.03	-3.73	0.00	-2.44	-2.53
TCGA-DJ-A3VG-10A-01D-A23K-08_THCA	-2.65	-2.78	-2.73	-2.94	-2.54	-2.68	-2.67	-2.53	-2.59	0.00	-2.93	-2.74	-4.62	0.00	-3.06	-2.75	-2.59
TCGA-DJ-A3VI-10A-01D-A23K-08_THCA	-2.58	-2.69	-2.70	-2.85	-2.59	-2.65	-2.65	-2.72	-2.66	-4.50	-2.81	-3.60	-2.71	-2.66	-3.07	-4.20	-2.55
TCGA-DJ-A3VJ-10A-01D-A23K-08_THCA	-2.52	-2.58	-2.57	-4.20	-3.59	-3.80	-2.49	-2.55	-2.54	-4.50	-4.50	-3.54	-4.02	-3.80	0.00	-2.57	-2.47
TCGA-DJ-A3VK-10A-01D-A23K-08_THCA	-2.63	-2.64	-2.67	-3.78	-2.59	-2.64	-2.66	-2.67	-2.60	0.00	-2.74	-2.65	0.00	-4.25	0.00	-2.68	-2.59
TCGA-DJ-A3VL-10A-01D-A23K-08_THCA	-2.56	-2.79	-2.78	-2.97	-2.57	-2.71	-2.68	-2.60	-2.71	-3.38	-2.77	-2.80	-2.80	-2.77	-3.26	-4.58	-2.62
TCGA-DJ-A3VM-10A-01D-A23K-08_THCA	-2.59	-3.91	-3.74	-2.61	-2.54	-2.61	-2.61	-2.67	-2.49	0.00	0.00	-4.52	0.00	-4.52	0.00	-2.59	-2.52
TCGA-DJ-A4UL-10A-01D-A25A-08_THCA	-2.69	-2.76	-2.74	-2.97	-2.55	-2.68	-2.63	-2.66	-2.66	0.00	-2.89	-2.83	-4.13	-4.43	0.00	-2.51	-2.61
TCGA-DJ-A4UP-10A-01D-A25A-08_THCA	-2.54	-2.62	-2.64	-2.78	-2.64	-2.69	-2.70	-2.74	-2.64	0.00	-2.83	0.00	-2.65	-2.67	0.00	-2.73	-2.47
TCGA-DJ-A4UQ-10A-01D-A25A-08_THCA	-2.32	0.00	-4.60	-2.56	-2.44	-2.43	-2.43	-2.55	-2.36	0.00	0.00	0.00	0.00	0.00	-2.91	0.00	-2.32
TCGA-DJ-A4UR-10A-01D-A25A-08_THCA	-2.51	-2.75	-2.75	-2.87	-2.47	-2.52	-2.57	-2.65	-2.41	0.00	-2.99	-2.68	0.00	-4.72	0.00	-2.48	-2.46
TCGA-DJ-A4UT-10A-01D-A25A-08_THCA	-2.64	-2.76	-2.75	-2.96	-2.55	-2.61	-2.63	-2.65	-2.73	-3.48	-2.76	-2.81	-2.82	-2.82	0.00	-2.74	-2.60
TCGA-DJ-A4UW-10A-01D-A25A-08_THCA	-2.60	-4.37	-4.37	-2.73	-2.44	-2.54	-2.58	-2.59	-2.53	0.00	0.00	0.00	0.00	0.00	-2.88	-3.77	-2.51
TCGA-DJ-A4V0-10A-01D-A25A-08_THCA	-2.52	-4.39	-3.79	-2.73	-2.55	-2.56	-2.58	-2.56	-2.52	0.00	-3.79	-4.39	0.00	0.00	-2.93	-3.91	-2.53
TCGA-DJ-A4V2-10A-01D-A25A-08_THCA	-2.52	0.00	0.00	-2.76	-2.56	-2.57	-2.62	-2.53	-2.48	0.00	0.00	0.00	0.00	0.00	-3.05	-2.67	-2.50
TCGA-DJ-A4V4-10A-01D-A25A-08_THCA	-2.64	-2.72	-2.78	-2.93	-2.50	-2.63	-2.64	-2.50	-2.54	-4.44	-2.98	-2.80	-4.44	-3.97	-3.05	-2.82	-2.59
TCGA-DJ-A4V5-10A-01D-A25A-08_THCA	-2.57	-2.74	-2.67	-2.99	-2.74	-2.75	-2.68	-2.62	-2.75	-3.30	-2.92	-4.15	-2.70	-2.72	0.00	-2.75	-2.60
TCGA-DK-A1A3-10A-01D-A13W-08_BLCA	-2.38	-2.63	-2.67	-2.78	-2.53	-2.63	-2.71	-2.73	-2.70	0.00	-2.97	-4.67	-2.73	-2.59	0.00	-2.79	-2.32
TCGA-DK-A1A5-10A-01D-A13W-08_BLCA	-2.40	0.00	0.00	-2.67	-2.41	-2.44	-2.48	-2.50	-2.35	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.33
TCGA-DK-A1A6-10A-01D-A13W-08_BLCA	-2.48	-2.67	-2.66	-2.86	-2.59	-2.63	-2.48	-2.50	-2.41	0.00	-4.63	0.00	0.00	-4.33	-2.97	0.00	-2.32
TCGA-DK-A1A7-10A-01D-A13W-08_BLCA	-2.51	-2.70	-2.73	-2.86	-2.36	-2.51	-2.53	-2.56	-2.46	0.00	-3.22	-2.64	0.00	-4.25	-3.10	-2.83	-2.38
TCGA-DK-A1AA-10A-01D-A13W-08_BLCA	-2.44	-2.72	-2.70	-2.70	-2.57	-2.66	-2.45	-2.63	-2.39	0.00	-4.65	0.00	0.00	-4.65	-2.88	0.00	-2.37
TCGA-DK-A1AB-10A-01D-A13W-08_BLCA	-2.52	-2.86	-2.82	-2.93	-2.41	-2.50	-2.50	-2.60	-2.59	-3.55	-2.85	-2.58	0.00	0.00	0.00	-2.69	-2.51
TCGA-DK-A1AC-10A-01D-A13W-08_BLCA	-2.59	-2.63	-2.52	0.00	-2.50	-2.75	-2.49	-2.63	-2.46	0.00	-2.98	-2.76	-4.61	-4.61	-3.29	-2.78	-2.31
TCGA-DK-A1AD-10A-01D-A13W-08_BLCA	-2.53	-4.73	-4.73	-2.56	-2.41	-2.50	-2.49	-2.61	-2.52	-4.42	-4.73	-4.73	-4.73	-4.73	0.00	-2.51	-2.35
TCGA-DK-A1AE-10A-01D-A13W-08_BLCA	-2.57	-2.68	-4.19	-2.76	-2.35	-2.51	-2.51	-2.60	-2.67	-3.46	-3.14	-4.67	-2.79	-2.60	0.00	-2.74	-2.37
TCGA-DK-A1AF-10A-01D-A13W-08_BLCA	-2.41	-2.45	-2.43	-4.43	-4.43	-4.13	0.00	-4.43	-4.13	0.00	-2.53	0.00	-2.48	-2.18	0.00	-4.43	-2.16
TCGA-DK-A1AG-10A-01D-A13W-08_BLCA	-2.58	-3.43	-3.43	-2.60	-2.49	-2.55	-2.56	-2.53	-2.44	-4.51	-3.81	-3.47	0.00	-4.03	0.00	-2.52	-2.44
TCGA-DK-A2HX-10A-01D-A18F-08_BLCA	-2.51	0.00	0.00	-2.56	-2.58	-2.55	-2.55	-2.49	-2.51	0.00	-4.47	0.00	0.00	-4.16	0.00	-2.55	-2.47
TCGA-DK-A2I1-10A-01D-A17V-08_BLCA	-2.42	-2.75	-2.69	-2.84	-2.62	-2.74	-2.55	-2.53	-2.48	0.00	0.00	0.00	-4.29	-4.11	-3.23	-2.84	-2.37
TCGA-DK-A2I2-10A-01D-A17V-08_BLCA	-2.49	-2.73	-2.70	-2.80	-2.63	-2.65	-2.52	-2.54	-2.56	0.00	0.00	-4.58	0.00	0.00	-3.22	-2.76	-2.41
TCGA-DK-A2I4-10A-01D-A21A-08_BLCA	-2.41	-2.93	-2.74	-2.86	-2.52	-2.64	-2.63	-2.57	-2.74	-3.43	-2.72	-2.58	0.00	-2.75	-3.09	0.00	-2.54
TCGA-DK-A2I6-10A-01D-A18F-08_BLCA	-2.42	0.00	-4.14	-2.56	-2.50	-2.58	-2.52	-2.49	-2.44	0.00	-4.44	0.00	0.00	0.00	-3.03	-2.72	-2.46
TCGA-DK-A3IK-10A-01D-A21A-08_BLCA	-2.50	-4.43	-4.43	-2.62	-2.48	-2.45	-2.51	-2.71	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.34	-2.39
TCGA-DK-A3IL-10A-01D-A20D-08_BLCA	-2.52	-2.69	-2.72	-2.79	-2.65	-2.64	-2.64	-2.70	-2.61	0.00	-2.82	-2.66	0.00	-2.66	0.00	-2.65	-2.48
TCGA-DK-A3IM-10A-01D-A20D-08_BLCA	-2.49	0.00	0.00	-2.58	-2.55	-2.53	-2.62	-2.58	-2.49	0.00	0.00	0.00	0.00	0.00	-3.04	-2.69	-2.41
TCGA-DK-A3IN-10A-01D-A20D-08_BLCA	-2.65	-2.80	-2.77	-2.84	-2.50	-2.65	-2.65	-2.71	-2.76	-3.32	-2.73	-2.78	-2.89	-2.73	0.00	-2.78	-2.59
TCGA-DK-A3IQ-10A-01D-A20D-08_BLCA	-2.55	-2.86	-2.83	-2.82	-2.51	-2.57	-2.63	-2.72	-2.79	-3.23	-2.79	-2.81	-2.92	-2.70	0.00	-2.84	-2.47
TCGA-DK-A3IS-10A-01D-A21A-08_BLCA	-2.46	-2.64	-2.69	-2.77	-2.59	-2.65	-2.55	-2.60	-2.43	0.00	0.00	0.00	0.00	0.00	-3.00	-2.55	-2.46
TCGA-DK-A3IT-10A-01D-A20D-08_BLCA	-2.57	-4.50	-4.50	-2.58	-2.50	-2.55	-2.53	-2.47	-2.40	0.00	0.00	0.00	0.00	-4.50	-2.95	-2.64	-2.45
TCGA-DK-A3IU-10A-01D-A20D-08_BLCA	-2.51	-4.48	0.00	-2.74	-2.55	-2.51	-2.57	-2.48	-2.39	0.00	0.00	0.00	0.00	0.00	-3.09	-2.65	-2.40
TCGA-DK-A3IV-10A-01D-A21A-08_BLCA	-2.47	0.00	-4.56	-2.81	-2.61	-2.63	-2.65	-2.48	-2.70	-3.36	-2.82	0.00	-2.73	-2.70	0.00	-2.69	-2.54

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DK-A3WW-10A-01D-A23K-08_BLCA	-2.64	-2.80	-2.83	-2.99	-2.61	-2.72	-2.71	-2.57	-2.76	-3.31	-2.76	-2.83	-2.84	-2.80	0.00	-2.89	-2.63
TCGA-DK-A3WX-10A-01D-A22Z-08_BLCA	-2.45	0.00	0.00	-2.59	-2.50	-2.45	-2.50	-2.53	-2.75	-3.34	-2.91	0.00	-2.75	-2.66	0.00	-2.76	-2.41
TCGA-DK-A3WY-10A-01D-A22Z-08_BLCA	-2.53	-2.74	-2.63	-2.89	-2.69	-2.72	-2.52	-2.50	-2.67	-3.35	-2.92	0.00	-2.75	-2.65	-3.02	0.00	-2.43
TCGA-DK-A3X1-10A-01D-A22Z-08_BLCA	-2.50	-2.68	-2.61	-2.84	-2.66	-2.66	-2.54	-2.55	-2.64	-3.33	-2.92	0.00	-2.73	-2.69	0.00	-2.75	-2.43
TCGA-DK-A3X2-10A-01D-A22Z-08_BLCA	-2.54	-2.78	-2.72	-2.90	-2.46	-2.55	-2.59	-2.59	-2.54	-3.70	-2.97	-2.71	0.00	0.00	-3.07	-2.75	-2.47
TCGA-DK-A6AV-10A-01D-A30H-08_BLCA	-2.43	0.00	-4.30	-2.51	-2.44	-2.45	-2.48	-2.49	-2.45	0.00	0.00	0.00	0.00	-4.30	-3.08	-2.78	-2.36
TCGA-DK-A6AW-10A-01D-A30H-08_BLCA	-2.51	-2.73	-2.74	-2.86	-2.50	-2.55	-2.61	-2.62	-4.45	-3.25	-2.65	-2.61	-2.79	-2.52	0.00	0.00	-2.42
TCGA-DK-A6B0-10A-01D-A31J-08_BLCA	-2.50	-2.67	-2.65	-2.80	-2.67	-2.65	-2.58	-2.55	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.44
TCGA-DK-A6B1-10A-01D-A30H-08_BLCA	-2.41	0.00	0.00	-2.84	-2.45	-2.45	-2.47	-2.47	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.34
TCGA-DK-A6B2-10A-01D-A30H-08_BLCA	-2.56	-2.52	-2.57	0.00	-2.53	-2.58	-2.56	-2.63	-2.69	-3.30	-2.59	-2.59	-2.84	-2.68	0.00	-2.75	-2.47
TCGA-DK-A6B5-10A-01D-A31J-08_BLCA	-2.59	-2.79	-2.73	-2.89	-2.50	-2.64	-2.71	-2.69	-2.78	-3.46	-2.75	-2.76	-2.83	-2.73	0.00	-2.80	-2.56
TCGA-DK-A6B6-10A-01D-A30H-08_BLCA	-2.54	-2.79	-2.71	-2.95	-2.50	-2.54	-2.57	-2.64	-2.74	-3.48	-2.73	-2.74	-2.77	-2.68	0.00	-2.82	-2.44
TCGA-DM-A0X9-10A-01D-A152-10_COAD	-2.60	0.00	0.00	-2.78	-2.64	-2.52	-2.46	-2.59	-2.49	0.00	0.00	0.00	0.00	-4.31	0.00	-2.70	-2.42
TCGA-DM-A0XD-10A-01D-A152-10_COAD	-2.64	-2.93	-2.82	-3.00	-2.65	-2.66	-2.61	-2.64	-2.54	0.00	-3.06	-2.88	0.00	0.00	0.00	-2.65	-2.55
TCGA-DM-A0XF-10A-01D-A152-10_COAD	-2.54	-2.81	-2.80	-2.98	-2.98	-3.04	-2.51	-2.80	0.00	-3.04	-3.07	0.00	-2.62	-2.60	0.00	0.00	-2.55
TCGA-DM-A1D0-10A-01D-A152-10_COAD	-2.53	-2.72	-2.75	-2.82	-2.71	-2.75	-2.64	-2.89	-2.66	0.00	-2.84	0.00	-2.77	-2.70	0.00	-2.84	-2.44
TCGA-DM-A1D4-10A-01D-A152-10_COAD	-2.66	0.00	0.00	-2.62	-2.62	-2.70	-2.51	-2.58	-2.72	-3.46	-2.97	0.00	-2.77	-2.77	0.00	-3.02	-2.52
TCGA-DM-A1D6-10A-01D-A152-10_COAD	-2.54	0.00	0.00	-2.71	-2.58	-2.58	-2.51	-2.58	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.63	-2.41
TCGA-DM-A1D7-10A-01D-A152-10_COAD	-2.63	0.00	0.00	-2.72	-2.67	-2.48	-2.48	-2.67	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.53
TCGA-DM-A1D8-10A-01D-A152-10_COAD	-2.73	-2.98	-2.91	-2.92	-2.58	-2.69	-2.58	-2.54	-2.68	-3.42	-3.09	-2.78	0.00	0.00	-3.39	-2.98	-2.68
TCGA-DM-A1D9-10A-01D-A152-10_COAD	-2.54	0.00	0.00	-2.65	-2.64	-2.60	-2.64	-2.62	-2.71	-3.27	-3.13	0.00	-2.96	-2.87	-3.21	0.00	-2.51
TCGA-DM-A1DA-10A-01D-A152-10_COAD	-2.57	0.00	-4.37	-2.78	-2.61	-2.58	-2.58	-2.59	-2.51	0.00	0.00	0.00	0.00	0.00	-2.92	0.00	-2.54
TCGA-DM-A1DB-10A-01D-A152-10_COAD	-2.54	0.00	0.00	-2.67	-2.55	-2.65	-2.49	-2.51	-2.40	0.00	0.00	0.00	0.00	0.00	-3.20	-2.94	-2.47
TCGA-DM-A1HA-10A-01D-A152-10_COAD	-2.46	0.00	0.00	-2.44	-2.76	-2.59	-2.49	-2.70	-2.46	0.00	0.00	0.00	0.00	0.00	-3.03	0.00	-2.49
TCGA-DM-A285-10A-01D-A16V-10_COAD	-2.52	-2.61	-2.59	0.00	0.00	0.00	-2.35	-2.56	-2.44	0.00	0.00	0.00	0.00	0.00	-2.79	0.00	-2.29
TCGA-DM-A28C-10A-01D-A16V-10_COAD	-2.47	-2.77	-2.94	-2.91	-2.81	-2.81	-2.47	-2.68	-2.41	0.00	0.00	0.00	0.00	0.00	-3.20	-2.82	-2.43
TCGA-DM-A28E-10A-01D-A16V-10_COAD	-2.55	-2.86	-2.76	-2.96	-2.69	-2.58	-2.54	-2.55	-2.38	0.00	-2.99	-2.86	0.00	0.00	-3.18	-2.77	-2.35
TCGA-DM-A28F-10A-01D-A16V-10_COAD	-2.58	0.00	-3.74	-2.56	-2.54	-2.60	-2.40	-2.50	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.63	-2.40
TCGA-DM-A28G-10A-01D-A16V-10_COAD	-2.50	-2.53	-2.60	0.00	-2.88	-2.90	-2.57	-2.64	-2.57	0.00	-3.14	-2.86	0.00	0.00	-3.11	-2.95	-2.39
TCGA-DM-A28H-10A-01D-A16V-10_COAD	-2.54	0.00	0.00	-2.84	-2.60	-2.63	-2.65	-2.62	-2.67	-3.30	-2.95	-4.20	-3.25	-2.97	-3.20	0.00	-2.57
TCGA-DM-A28K-10A-01D-A16V-10_COAD	-2.49	-2.76	-2.71	-2.98	-2.71	-2.69	-2.48	-2.53	-2.59	-4.12	0.00	0.00	0.00	0.00	0.00	-2.57	-2.44
TCGA-DO-A1JZ-10A-01D-A13W-08_THCA	-2.51	-2.74	-2.67	-2.93	-2.47	-2.56	-2.57	-2.60	-2.76	-3.39	-2.83	-2.74	-2.88	-2.72	-3.18	0.00	-2.46
TCGA-DO-A1K0-10A-01D-A13W-08_THCA	-2.43	0.00	0.00	-2.70	-2.40	-2.44	-2.50	-2.51	-2.41	0.00	0.00	-4.65	-4.65	-4.35	-3.19	-2.75	-2.36
TCGA-DO-A2HM-10B-01D-A22D-08_THCA	-2.62	-2.80	-2.75	-2.97	-2.51	-2.61	-2.68	-2.58	-2.70	-3.35	-2.75	-2.74	-2.81	-2.74	-3.09	0.00	-2.56
TCGA-DQ-5624-10A-01D-1870-08_HNSC	-2.56	0.00	-4.10	-2.62	-2.57	-2.58	-2.59	-2.62	-2.60	0.00	0.00	0.00	-4.57	0.00	-3.10	-2.82	-2.50
TCGA-DQ-5625-10A-01D-1870-08_HNSC	-2.50	0.00	-4.58	-2.68	-2.52	-2.57	-2.56	-2.60	-2.59	-4.58	0.00	0.00	0.00	-4.28	0.00	-2.57	-2.46
TCGA-DQ-5629-10A-01D-1870-08_HNSC	-2.56	0.00	0.00	-2.79	-2.52	-2.56	-2.57	-2.63	-2.48	0.00	-4.63	0.00	0.00	-4.63	0.00	-2.61	-2.49
TCGA-DQ-5630-10A-01D-1870-08_HNSC	-2.59	-2.80	-2.79	-3.00	-2.59	-2.69	-2.66	-2.58	-2.80	-3.43	-2.76	-2.79	-2.88	-2.80	0.00	-2.86	-2.62
TCGA-DQ-5631-10A-01D-1870-08_HNSC	-2.46	-4.65	0.00	-2.74	-2.61	-2.58	-2.66	-2.62	-2.70	-3.25	-2.88	0.00	-2.77	-2.67	-3.07	-4.65	-2.53
TCGA-DQ-7588-10B-01D-2078-08_HNSC	-2.47	-2.66	-2.67	-2.83	-2.65	-2.62	-2.51	-2.46	-2.53	0.00	-4.40	-4.40	-4.40	-4.40	-3.02	-2.68	-2.43
TCGA-DQ-7589-10C-01D-2229-08_HNSC	-2.61	0.00	0.00	-2.65	-2.40	-2.53	-2.55	-2.48	-2.50	-3.48	-2.96	-2.77	0.00	-4.63	0.00	-2.59	-2.52
TCGA-DQ-7590-10D-01D-2229-08_HNSC	-2.40	0.00	-4.51	-2.54	-2.50	-2.50	-2.47	-2.52	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.40
TCGA-DQ-7591-10A-01D-2078-08_HNSC	-2.56	0.00	0.00	-2.63	-2.58	-2.60	-2.61	-2.65	-3.61	-3.05	-2.72	0.00	-2.67	-2.59	0.00	-4.45	-2.46
TCGA-DQ-7592-10A-01D-2078-08_HNSC	-2.57	-2.71	-2.68	-2.85	-2.62	-2.63	-2.54	-2.50	-2.57	0.00	0.00	-4.43	0.00	0.00	0.00	-2.37	-2.51
TCGA-DQ-7593-10D-01D-2229-08_HNSC	-2.56	-2.77	-2.68	-2.85	-2.45	-2.55	-2.57	-2.61	-2.50	0.00	-2.95	-2.66	0.00	0.00	0.00	-2.61	-2.47
TCGA-DQ-7594-10D-01D-2229-08_HNSC	-2.54	-2.73	-2.69	-2.91	-2.49	-2.55	-2.65	-2.70	-2.76	-3.33	-2.75	-2.60	0.00	-2.69	0.00	-2.81	-2.50
TCGA-DQ-7595-10D-01D-2229-08_HNSC	-2.53	0.00	0.00	-2.70	-2.45	-2.52	-2.51	-2.47	-2.37	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.43
TCGA-DQ-7596-10D-01D-2229-08_HNSC	-2.46	0.00	0.00	-2.63	-2.43	-2.46	-2.47	-2.57	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.42
TCGA-DR-A0ZL-10A-01D-A10S-08_CESC	-2.58	0.00	-4.52	-2.81	-2.54	-2.54	-2.58	-2.56	-2.48	0.00	0.00	0.00	0.00	-4.52	-2.83	-4.52	-2.53
TCGA-DR-A0ZM-10A-01D-A10S-08_CESC	-2.51	0.00	0.00	-2.78	-2.51	-2.57	-2.57	-2.62	-2.55	0.00	0.00	0.00	-4.53	-4.53	0.00	-2.54	-2.46
TCGA-DS-A0VK-10A-01D-A10S-08_CESC	-2.54	-2.70	-2.71	-2.93	-2.67	-2.69	-2.60	-2.45	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.38	-2.50
TCGA-DS-A0VL-10A-01D-A10S-08_CESC	-2.56	-4.54	-4.06	-2.76	-2.51	-2.59	-2.64	-2.49	-2.52	-4.54	0.00	-4.54	-3.69	-3.64	0.00	-2.37	-2.49
TCGA-DS-A0VM-10A-01D-A10S-08_CESC	-2.56	-4.56	-4.56	-2.64	-2.57	-2.56	-2.64	-2.51	-2.54	0.00	-4.56	0.00	0.00	-4.26	-3.09	-2.74	-2.57
TCGA-DS-A0VN-10A-01D-A10S-08_CESC	-2.59	-2.73	-2.73	-4.26	-2.67	-2.68	-2.74	-2.67	0.00	-3.36	-2.70	-2.68	-2.70	-2.58	0.00	-4.57	-2.56
TCGA-DS-A1OA-10A-01D-A16Y-08_CESC	-2.61	0.00	0.00	-2.61	-2.61	-2.60	-2.59	-2.45	-2.49	0.00	0.00	-4.53	0.00	-4.22	-3.03	-2.76	-2.57
TCGA-DS-A1OB-10A-01D-A14W-08_CESC	-2.48	0.00	0.00	-2.67	-2.51	-2.56	-2.56	-2.53	-2.56	0.00	0.00	0.00	-4.48	0.00	0.00	-2.50	-2.44
TCGA-DS-A1OC-10A-01D-A14W-08_CESC	-2.50	-3.52	-3.52	-2.68	-2.50	-2.53	-2.53	-2.53	-2.48	0.00	-4.47	-3.99	0.00	0.00	0.00	-3.36	-2.45
TCGA-DS-A1OD-10A-01D-A14W-08_CESC	-2.55	0.00	0.00	-2.55	-2.50	-2.57	-2.59	-2.57	-2.58	0.00	-4.51	0.00	0.00	0.00	-2.99	-2.67	-2.46
TCGA-DS-A3LQ-10A-01D-A21Q-09_CESC	-2.80	0.00	0.00	-2.88	-2.40	-2.45	-2.47	-2.52	-2.41	0.00	0.00	0.00	0.00	-4.45	-2.87	-2.83	-2.53
TCGA-DS-A5RQ-10A-01D-A28E-09_CESC	-2.78	-2.63	-2.73	-3.24	-2.77	-2.70	-2.33	-2.47	-2.34	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.56
TCGA-DT-5265-10A-01D-1826-10_READ	-2.46	-2.82	-2.87	-2.69	-2.69	-2.76	-2.37	-2.62	-2.39	0.00	0.00	0.00	0.00	0.00	-3.14	-2.79	-2.38
TCGA-DU-5847-10A-01D-1705-08_LGG	-2.54	-2.58	-2.58	0.00	-2.71	-2.72	-2.60	-2.67	-2.63	-3.27	-2.85	-2.59	0.00	-2.70	0.00	-2.80	-2.44
TCGA-DU-5849-10A-01D-1705-08_LGG	-2.53	-2.64	-2.71	-2.89	-2.45	-2.55	-2.59	-2.59	-2.54	0.00	-2.93	-2.75	0.00	-4.48	-2.95	-4.48	-2.52
TCGA-DU-5851-10A-01D-1893-08_LGG	-2.51	0.00	-4.55	-2.71	-2.54	-2.54	-2.51	-2.44	-2.45	0.00	0.00	-4.55	-4.55	0.00	0.00	-2.40	-2.48
TCGA-DU-5852-10A-01D-1705-08_LGG	-2.46	0.00	0.00	-2.72	-2.43	-2.42	-2.53	-2.50	-2.36	0.00	0.00	0.00	0.00	-4.12	-3.08	-2.73	-2.37
TCGA-DU-5853-10A-01D-1893-08_LGG	-2.45	-4.56	0.00	-2.71	-2.55	-2.60	-2.60	-2.52	-2.48	0.00	-4.56	0.00	0.00	-3.96	-3.07	-2.67	-2.52
TCGA-DU-5854-10A-01D-1705-08_LGG	-2.46	-4.43	-4.13	-2.74	-2.51	-2.46	-2.49	-2.57	-2.43	0.00	0.00	0.00	-4.43	0.00	-2.87	-4.43	-2.41
TCGA-DU-5855-10A-01D-1705-08_LGG	-2.57	-2.60	-2.58	-4.24	-2.57	-2.61	-2.61	-2.65	-2.72	-3.36	-2.70	-2.54	-4.54	-2.70	-3.24	0.00	-2.50
TCGA-DU-5870-10A-01D-1705-08_LGG	-2.39	0.00	-4.14	-2.65	-2.49	-2.51	-2.48	-2.52	-2.39	0.00	0.00	0.00	-4.14	-4.44	-3.14	-2.82	-2.43
TCGA-DU-5871-10A-01D-1705-08_LGG	-2.51	-2.60	-2.55	-4.49	-2.63	-2.69	-2.63	-2.66	-4.19	-3.13	-2.61	-2.67	-2.62	-2.58	0.00	0.00	-2.48
TCGA-DU-5872-10A-01D-1705-08_LGG	-2.49	-2.70	-2.65	-2.90	-2.61	-2.66	-2.57	-2.49	-2.60	-3.21	-2.89	0.00	-2.82	-2.60	-3.12	0.00	-2.45
TCGA-DU-5874-10A-01D-1705-08_LGG	-2.39	-4.33	0.00	-2.49	-2.43	-2.52	-2.55	-2.75	-2.53	0.00	0.00	0.00	-4.33	-2.48	0.00	-2.63	-2.46
TCGA-DU-6392-10A-01D-1705-08_LGG	-2.60	-2.69	-2.71	-2.92	-2.46	-2.57	-2.58	-2.55	-2.59	0.00	-3.04	-2.66	0.00	-4.23	-3.18	-2.87	-2.50
TCGA-DU-6393-10A-01D-1705-08_LGG	-2.47	-2.71	-2.65	-2.84	-2.63	-2.63	-2.56	-2.52	-2.36	0.00	0.00	0.00	-4.44	-4.44	-3.12	-2.70	-2.38
TCGA-DU-6394-10A-01D-1705-08_LGG	-2.46	-2.64	-2.62	-2.82	-2.56	-2.65	-2.50	-2.55	-2.44	0.00	0.00	-4.46	0.00	-4.46	0.00	-2.55	-2.41
TCGA-DU-6395-10A-01D-1705-08_LGG	-2.54	-2.61	-2.62	0.00	-2.57	-2.56	-2.64	-2.57	-2.87	-3.39	-2.75	-2.53	0.00	-2.72	0.00	-2.83	-2.56
TCGA-DU-6396-10A-01D-1705-08_LGG	-2.50	-4.20	0.00	-2.73	-2.57	-2.49	-2.56	-2.61	-2.71	-3.38	-3.07	-4.20	-2.82	-2.62	0.00	-2.84	-2.48
TCGA-DU-6397-10A-01D-1705-08_LGG	-2.51	-2.61	-2.55	-4.48	-2.63	-2.65	-2.58	-2.59	-2.61	-3.40	-2.74	-2.70	-2.75	-2.67	0.00	-2.74	-2.49
TCGA-DU-6399-10A-01D-1705-08_LGG	-2.50	0.00	-4.17	-2.73	-2.54	-2.52	-2.57	-2.49	-2.62	-3.33	-2.92	-2.68	0.00	-2.63	-3.09	0.00	-2.46
TCGA-DU-6400-10A-01D-1705-08_LGG	-2.43	0.00	0.00	-2.55	-2.50	-2.53	-2.53	-2.56	-2.43	0.00	0.00	-4.13	0.00	-4.13	0.00	-2.60	-2.44
TCGA-DU-6401-10A-01D-1705-08_LGG	-2.57	-2.76	-2.68	-2.95	-2.47	-2.57	-2.61	-2.58	-2.73	-3.21	-2.82	-2.82	-2.77	-2.65	-3.26	0.00	-2.54
TCGA-DU-6402-10A-01D-1705-08_LGG	-2.40	-2.66	-2.63	-2.88	-2.60	-2.61	-2.57	-2.56	-2.45	0.00	0.00	-4.12	-4.42	-4.42	-2.91	0.00	-2.39
TCGA-DU-6403-10A-01D-1705-08_LGG	-2.52	-2.76	-2.71	-2.90	-2.53	-2.60	-2.57	-2.59	-2.53	0.00	-3.00	-2.68	0.00	0.00	-3.20	-2.95	-2.47
TCGA-DU-6404-10A-01D-1705-08_LGG	-2.55	0.00	-4.49	-2.64	-2.49	-2.57	-2.57	-2.57	-2.67	-3.28	-3.01	0.00	-2.79	-2.65	0.00	-2.74	-2.45
TCGA-DU-6405-10A-01D-1705-08_LGG	-2.43	-2.68	-2.69	-2.85	-2.64	-2.68	-2.56	-2.51	-2.68	-3.26	-2.96	-2.68	0.00	-2.64	0.00	-2.76	-2.42
TCGA-DU-6406-10A-01D-1705-08_LGG	-2.40	0.00	-3.99	-2.74	-2.54	-2.56	-2.58	-2.56	-2.88	-3.22	-2.87	0.00	-2.78	-2.69	0.00	-2.82	-2.40
TCGA-DU-6407-10A-01D-1705-08_LGG	-2.46	-2.66	-2.59	-2.91	-2.66	-2.71	-2.55	-2.47	-2.42	0.00	0.00	0.00	0.00	-4.13	-2.92	-2.71	-2.43
TCGA-DU-6408-10A-01D-1705-08_LGG	-2.45	0.00	0.00	-2.71	-2.46	-2.50	-2.53	-2.51	-2.54	0.00	-4.43	-4.43	0.00	0.00	0.00	-2.41	-2.39
TCGA-DU-6410-10A-01D-1893-08_LGG	-2.57	-2.88	-2.80	-2.94	-2.52	-2.62	-2.66	-2.63	-4.41	-3.12	-2.69	-2.53	-4.72	-2.69	0.00	0.00	-2.62
TCGA-DU-6542-10A-01D-1893-08_LGG	-2.56	-2.71	-2.74	-2.90	-2.70	-2.71	-2.65	-2.55	-2.69	-3.39	-2.83	0.00	-2.79	-2.68	-3.10	0.00	-2.59
TCGA-DU-7006-10A-01D-2024-08_LGG	-2.55	-4.01	-4.19	-2.73	-2.54	-2.55	-2.58	-2.60	-2.67	-3.41	-2.98	0.00	-2.80	-2.64	0.00	-2.71	-2.49
TCGA-DU-7007-10A-01D-2024-08_LGG	-2.61	-2.78	-2.78	-2.94	-2.53	-2.64	-2.66	-2.66	-2.71	-3.58	-2.75	-2.59	0.00	-2.74	0.00	-2.78	-2.57
TCGA-DU-7008-10A-01D-2024-08_LGG	-2.53	-2.68	-2.62	-2.80	-2.66	-2.62	-2.64	-2.82	-2.68	0.00	-2.81	-4.46	-2.67	-2.60	0.00	-2.69	-2.47
TCGA-DU-7009-10A-01D-2024-08_LGG	-2.62	-2.82	-2.75	-2.93	-2.52	-2.62	-2.62	-2.52	-2.76	-3.26	-2.80	-2.73	-2.91	-2.76	-3.37	-4.30	-2.59
TCGA-DU-7010-10A-01D-2024-08_LGG	-2.35	-4.42	-4.12	-2.72	-2.49	-2.54	-2.46	-2.45	-2.43	0.00	0.00	0.00	0.00	0.00	-2.90	-2.70	-2.43
TCGA-DU-7011-10A-01D-2024-08_LGG	-2.49	-2.66	-2.63	-2.81	-2.63	-2.62	-2.53	-2.58	-2.45	0.00	-4.43	0.00	-4.43	-3.95	0.00	-2.54	-2.46

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DU-7012-10A-01D-2024-08_LGG	-2.53	0.00	0.00	-2.61	-2.38	-2.51	-2.55	-2.58	-2.48	0.00	0.00	0.00	-4.44	-3.84	-2.92	-4.14	-2.44
TCGA-DU-7013-10A-01D-2024-08_LGG	-2.53	-2.70	-2.66	-2.86	-2.60	-2.61	-2.58	-2.49	-2.48	0.00	-3.83	-3.57	0.00	-3.93	0.00	-2.45	-2.50
TCGA-DU-7014-10A-01D-2024-08_LGG	-2.49	-4.44	-3.66	-2.53	-2.49	-2.54	-2.48	-2.42	-2.42	-4.44	-3.66	-3.96	-3.96	-4.44	-3.10	-2.69	-2.46
TCGA-DU-7015-10B-01D-2024-08_LGG	-2.52	-4.09	-4.57	-2.81	-2.49	-2.65	-2.62	-2.52	-2.65	-3.29	-2.86	-2.81	0.00	-4.57	-3.01	-3.97	-2.57
TCGA-DU-7018-10A-01D-2024-08_LGG	-2.53	-2.68	-2.60	-2.84	-2.60	-2.65	-2.52	-2.54	-2.51	0.00	-4.45	-4.45	0.00	0.00	-3.09	-2.66	-2.48
TCGA-DU-7019-10A-01D-2024-08_LGG	-2.48	-2.70	-2.63	-2.80	-2.65	-2.63	-2.57	-2.47	-2.45	0.00	0.00	0.00	-4.42	0.00	-3.08	-2.58	-2.45
TCGA-DU-7290-10A-01D-2024-08_LGG	-2.44	0.00	-4.14	-2.74	-2.54	-2.57	-2.50	-2.45	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.40	-2.43
TCGA-DU-7292-10A-01D-2024-08_LGG	-2.52	-2.60	-2.59	-4.03	-2.61	-2.67	-2.59	-2.58	-2.62	0.00	-2.85	-2.67	0.00	-4.21	0.00	-2.61	-2.50
TCGA-DU-7294-10A-01D-2024-08_LGG	-2.49	0.00	0.00	-2.55	-2.46	-2.48	-2.53	-2.46	-2.55	0.00	-3.95	0.00	-3.83	-3.83	0.00	-2.39	-2.46
TCGA-DU-7298-10A-01D-2024-08_LGG	-2.58	-2.72	-2.67	-2.95	-2.44	-2.62	-2.61	-2.51	-2.51	0.00	-2.95	-2.76	0.00	0.00	0.00	-2.53	-2.57
TCGA-DU-7299-10A-01D-2024-08_LGG	-2.54	0.00	0.00	-2.76	-2.51	-2.55	-2.56	-2.62	-2.66	-3.41	-2.81	0.00	-2.78	-2.70	0.00	-2.72	-2.51
TCGA-DU-7300-10A-01D-2086-08_LGG	-2.48	-2.72	-2.64	-2.77	-2.59	-2.65	-2.51	-2.55	-2.44	0.00	0.00	-4.39	0.00	-4.09	0.00	-2.49	-2.43
TCGA-DU-7301-10A-01D-2086-08_LGG	-2.49	0.00	-4.45	-2.58	-2.49	-2.52	-2.53	-2.47	-2.45	0.00	0.00	-4.45	0.00	0.00	0.00	-2.37	-2.46
TCGA-DU-7302-10A-01D-2086-08_LGG	-2.51	-2.64	-2.70	-2.75	-2.61	-2.57	-2.55	-2.48	-2.50	0.00	-4.45	0.00	0.00	0.00	-3.04	-2.64	-2.45
TCGA-DU-7304-10A-01D-2086-08_LGG	-2.56	0.00	-4.50	-2.63	-2.55	-2.57	-2.58	-2.65	-4.19	-3.13	-2.69	-2.76	-2.80	-2.54	0.00	0.00	-2.51
TCGA-DU-7306-10A-01D-2086-08_LGG	-2.42	0.00	-4.45	-2.52	-2.50	-2.51	-2.58	-2.54	-2.46	0.00	0.00	0.00	0.00	-4.45	0.00	-2.38	-2.47
TCGA-DU-7309-10A-01D-2086-08_LGG	-2.40	-2.48	-2.48	0.00	-4.09	-3.79	-2.41	-2.38	-2.43	0.00	-4.40	-4.40	0.00	-4.40	-2.92	-2.58	-2.37
TCGA-DU-8158-10A-01D-2253-08_LGG	-2.61	0.00	-4.56	-2.59	-2.60	-2.56	-2.62	-2.64	-2.66	-3.26	-2.92	0.00	-2.81	-2.65	0.00	-2.66	-2.48
TCGA-DU-8161-10A-01D-2253-08_LGG	-2.53	-2.69	-2.72	-2.88	-2.68	-2.71	-2.61	-2.54	-2.66	-3.26	-2.79	0.00	-2.79	-2.67	0.00	-2.70	-2.50
TCGA-DU-8162-10A-01D-2253-08_LGG	-2.53	0.00	0.00	-2.81	-2.66	-2.66	-2.68	-2.72	-2.65	0.00	0.00	0.00	0.00	-4.68	0.00	-2.59	-2.54
TCGA-DU-8163-10A-01D-2253-08_LGG	-2.53	-2.76	-2.86	-2.92	-2.48	-2.59	-2.67	-2.67	-2.70	-3.33	-2.70	-2.61	0.00	-2.71	0.00	-2.72	-2.62
TCGA-DU-8164-10A-01D-2253-08_LGG	-2.55	0.00	-4.20	-2.76	-2.52	-2.55	-2.56	-2.56	-2.61	-3.55	-2.90	-2.71	0.00	-2.65	0.00	-2.73	-2.50
TCGA-DU-8165-10A-01D-2253-08_LGG	-2.40	0.00	0.00	-2.69	-2.46	-2.56	-2.56	-2.57	-2.68	-3.28	-2.90	0.00	-2.85	-2.69	0.00	-2.64	-2.46
TCGA-DU-8166-10A-01D-2253-08_LGG	-2.53	-4.16	-4.46	-2.65	-2.49	-2.52	-2.62	-2.58	-2.51	0.00	0.00	0.00	0.00	-4.16	-2.87	0.00	-2.46
TCGA-DU-8167-10A-01D-2253-08_LGG	-2.61	-2.74	-2.78	-2.83	-2.43	-2.59	-2.65	-2.54	-2.59	0.00	-2.92	-2.70	-4.55	-4.55	-3.02	-2.67	-2.58
TCGA-DU-8168-10A-01D-2253-08_LGG	-2.57	-2.73	-2.71	-2.85	-2.65	-2.69	-2.54	-2.68	-2.66	-3.31	-2.87	0.00	-2.78	-2.66	0.00	-2.67	-2.48
TCGA-DU-A5TP-10A-01D-A289-08_LGG	-2.48	-2.65	-2.64	-2.87	-2.61	-2.64	-2.50	-2.55	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.40
TCGA-DU-A5TR-10A-01D-A289-08_LGG	-2.50	0.00	-4.60	-2.70	-2.53	-2.59	-2.48	-2.53	-2.66	-3.28	-2.95	0.00	-2.76	-2.67	0.00	-2.73	-2.46
TCGA-DU-A5TS-10A-01D-A289-08_LGG	-2.49	0.00	-4.57	-2.59	-2.52	-2.45	-2.57	-2.47	-2.53	0.00	0.00	0.00	0.00	-4.57	-2.93	-2.78	-2.44
TCGA-DU-A5TT-10A-01D-A289-08_LGG	-2.51	0.00	0.00	-2.77	-2.57	-2.50	-2.57	-2.63	-4.29	-3.19	-2.67	0.00	-2.58	-2.49	0.00	0.00	-2.46
TCGA-DU-A5TU-10A-01D-A289-08_LGG	-2.58	-2.82	-2.74	-2.98	-2.54	-2.62	-2.58	-2.68	-2.70	-3.37	-2.73	-2.75	-2.80	-2.80	0.00	-2.81	-2.52
TCGA-DU-A5TW-10A-01D-A289-08_LGG	-2.52	-2.78	-2.76	-2.97	-2.53	-2.72	-2.41	-2.54	-2.49	0.00	-2.89	0.00	-2.76	-4.60	0.00	-2.49	-2.49
TCGA-DU-A5TY-10A-01D-A289-08_LGG	-2.57	-2.65	-2.61	0.00	-2.66	-2.74	-2.59	-2.59	-2.70	-3.26	-2.74	-2.74	-2.85	-2.65	0.00	-2.72	-2.52
TCGA-DU-A6S2-10A-01D-A329-08_LGG	-2.49	0.00	-4.08	-2.74	-2.42	-2.54	-2.54	-2.49	-2.40	0.00	0.00	0.00	0.00	0.00	-2.99	-2.70	-2.41
TCGA-DU-A6S3-10A-01D-A329-08_LGG	-2.55	0.00	0.00	-2.63	-2.53	-2.57	-2.55	-2.49	-2.60	-3.49	-2.93	0.00	-2.75	-2.61	-3.22	0.00	-2.47
TCGA-DU-A6S6-10A-01D-A329-08_LGG	-2.49	-2.51	-2.50	0.00	0.00	-4.39	-2.49	-2.54	-2.60	-3.39	-2.88	0.00	-2.70	-2.58	0.00	-2.83	-2.39
TCGA-DU-A6S7-10A-01D-A329-08_LGG	-2.49	0.00	0.00	-2.55	-2.49	-2.53	-2.53	-2.43	-2.40	0.00	0.00	0.00	0.00	0.00	-3.20	-2.69	-2.44
TCGA-DU-A6S8-10A-01D-A329-08_LGG	-2.55	-2.71	-2.65	0.00	-2.63	-2.71	-2.57	-2.63	0.00	-3.21	-2.61	-2.51	-2.82	-2.54	0.00	0.00	-2.51
TCGA-DU-A76L-10A-01D-A329-08_LGG	-2.58	-2.77	-2.82	-2.96	-2.47	-2.58	-2.61	-2.56	-2.76	-3.35	-2.76	-2.63	0.00	-2.64	0.00	-2.82	-2.53
TCGA-DU-A76O-10A-01D-A329-08_LGG	-2.44	-2.52	-2.50	0.00	-4.18	-4.18	-2.51	-2.52	-2.53	0.00	0.00	-4.18	0.00	-4.48	-2.91	0.00	-2.36
TCGA-DU-A76R-10A-01D-A329-08_LGG	-2.46	-2.60	-2.59	-2.81	-2.59	-2.56	-2.50	-2.46	-2.43	0.00	0.00	0.00	0.00	0.00	-2.93	-2.72	-2.47
TCGA-DV-5565-10A-01D-1535-10_KIRC	-2.93	0.00	0.00	-2.68	-2.59	-2.61	-2.56	-2.62	0.00	-3.06	-2.86	0.00	-2.70	-2.75	0.00	0.00	-2.71
TCGA-DV-5566-10A-01D-1535-10_KIRC	-2.99	0.00	0.00	-2.72	-2.65	-2.64	-2.57	-2.76	-2.78	-3.17	-2.98	0.00	-2.77	-2.83	0.00	-3.01	-2.69
TCGA-DV-5568-10A-01D-1535-10_KIRC	-2.97	-2.66	-2.74	-3.10	-2.82	-2.78	-2.61	-2.68	-2.76	-3.03	-2.89	0.00	-2.74	-2.80	-3.54	0.00	-2.75
TCGA-DV-5569-10A-01D-1535-10_KIRC	-2.94	0.00	-4.55	-2.83	-2.60	-2.60	-2.37	-2.57	-2.70	-3.21	-2.88	0.00	-2.66	-2.68	-3.40	0.00	-2.64
TCGA-DV-5573-10A-01D-1535-10_KIRC	-2.81	0.00	0.00	-2.73	-2.54	-2.55	-2.49	-2.52	-2.49	0.00	0.00	0.00	0.00	0.00	-3.27	-2.82	-2.56
TCGA-DV-5574-10A-01D-1535-10_KIRC	-2.79	0.00	0.00	-2.79	-2.55	-2.51	-2.47	-2.49	-2.48	0.00	0.00	0.00	0.00	0.00	-3.16	-2.80	-2.56
TCGA-DV-5575-10A-01D-1535-10_KIRC	-2.79	-2.47	-2.55	-2.88	-2.65	-2.61	-2.48	-2.54	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.63
TCGA-DV-5576-10A-01D-1535-10_KIRC	-2.75	0.00	-4.47	-2.83	-2.47	-2.50	-2.42	-2.53	-2.48	0.00	0.00	0.00	0.00	0.00	-3.29	-2.81	-2.47
TCGA-DV-A4VX-10A-01D-A25V-10_KIRC	-2.39	0.00	-3.91	-2.65	-2.38	-2.27	-2.32	-2.25	-2.29	0.00	0.00	0.00	0.00	0.00	-2.75	-2.52	-2.36
TCGA-DV-A4VZ-10A-01D-A25V-10_KIRC	-2.44	0.00	-2.65	0.00	-2.59	-2.32	-2.36	-2.42	-2.28	0.00	-2.83	0.00	-2.56	0.00	-2.95	-2.68	-2.36
TCGA-DV-A4W0-10A-01D-A25V-10_KIRC	-2.44	-2.53	-2.62	-2.81	-2.28	-2.35	-2.32	-2.42	-2.33	0.00	-2.78	-3.77	-2.60	0.00	-2.89	-2.55	-2.47
TCGA-DW-5560-10A-01D-1589-08_KIRP	-2.56	-4.50	-4.03	-2.90	-2.53	-2.59	-2.60	-2.55	-2.52	0.00	-4.20	-4.20	-4.50	-4.50	-3.04	-2.70	-2.51
TCGA-DW-5561-10A-01D-1589-08_KIRP	-2.48	-4.23	-4.53	-2.73	-2.51	-2.53	-2.53	-2.56	-2.49	0.00	0.00	0.00	0.00	-4.53	0.00	-2.54	-2.45
TCGA-DW-7834-10A-01D-2136-08_KIRP	-2.48	-2.71	-2.67	-2.88	-2.63	-2.58	-2.55	-2.48	-2.54	0.00	-4.02	0.00	-4.19	-3.65	-2.98	-2.70	-2.47
TCGA-DW-7836-10A-01D-2136-08_KIRP	-2.48	-4.51	0.00	-2.69	-2.51	-2.56	-2.50	-2.48	-2.43	0.00	0.00	-4.51	0.00	0.00	0.00	-2.39	-2.39
TCGA-DW-7837-10A-01D-2136-08_KIRP	-2.52	-4.22	-4.04	-2.59	-2.47	-2.57	-2.56	-2.57	-2.57	0.00	-4.52	-3.92	0.00	-4.22	-2.93	-2.70	-2.49
TCGA-DW-7838-10A-01D-2136-08_KIRP	-2.58	-4.53	0.00	-2.61	-2.51	-2.59	-2.56	-2.46	-2.47	-4.53	0.00	-4.23	-4.23	-4.05	0.00	-2.41	-2.50
TCGA-DW-7839-10A-01D-2136-08_KIRP	-2.55	-4.24	-3.94	-2.78	-2.58	-2.56	-2.56	-2.43	-2.57	0.00	0.00	0.00	0.00	0.00	0.00	-2.37	-2.52
TCGA-DW-7840-10A-01D-2136-08_KIRP	-2.62	-2.79	-2.64	-4.55	-2.62	-2.63	-2.63	-2.65	-2.58	0.00	-2.71	-2.71	-2.82	-4.07	-2.91	-4.25	-2.54
TCGA-DW-7841-10A-01D-2136-08_KIRP	-2.55	-2.75	-2.77	-2.88	-2.48	-2.59	-2.64	-2.56	-2.54	0.00	-2.91	-2.73	0.00	0.00	-3.10	-2.76	-2.53
TCGA-DW-7842-10A-01D-2136-08_KIRP	-2.58	-4.06	-4.53	-2.81	-2.51	-2.63	-2.63	-2.64	-2.72	-3.39	-2.89	0.00	-2.71	-2.66	0.00	-2.68	-2.51
TCGA-DW-7963-10C-01D-A28G-10_KIRP	-2.45	-2.48	-2.63	-2.95	-2.43	-2.32	-2.31	-2.45	-2.38	0.00	-2.80	-2.60	0.00	0.00	-2.80	0.00	-2.41
TCGA-DX-A1KU-10A-01D-A24N-09_SARC	-2.74	-2.64	-2.73	-3.13	-2.65	-2.71	-2.45	-2.52	-2.42	-4.15	0.00	-4.45	-4.45	0.00	0.00	-2.57	-2.62
TCGA-DX-A1KW-10A-01D-A24N-09_SARC	-2.70	-4.30	0.00	-3.03	-2.49	-2.45	-2.46	-2.51	-2.46	-4.30	0.00	-3.83	0.00	-3.60	-3.07	-2.91	-2.52
TCGA-DX-A1KX-10A-01D-A24N-09_SARC	-2.84	-4.48	0.00	-3.07	-2.59	-2.61	-2.51	-2.57	-2.73	-3.44	-2.89	0.00	-2.78	-2.64	-2.96	-4.48	-2.70
TCGA-DX-A1KY-10A-01D-A24N-09_SARC	-2.83	-3.46	-3.69	-2.98	-2.51	-2.52	-2.50	-2.39	-2.39	0.00	0.00	-3.94	-4.06	-4.54	0.00	-2.52	-2.59
TCGA-DX-A1KZ-10A-01D-A24N-09_SARC	-2.82	-2.78	-2.84	-3.26	-2.54	-2.56	-2.56	-2.64	-2.55	0.00	-2.88	-2.83	-3.89	-4.01	0.00	-2.65	-2.63
TCGA-DX-A1L0-10A-01D-A24N-09_SARC	-2.74	-4.00	-3.78	-3.00	-2.50	-2.49	-2.52	-2.56	-2.39	0.00	0.00	-4.48	0.00	0.00	0.00	-2.45	-2.53
TCGA-DX-A1L1-10A-01D-A24N-09_SARC	-2.86	-2.68	-2.80	-3.32	-2.80	-2.70	-2.46	-2.58	-2.59	-3.29	-2.99	-4.46	-2.81	-2.65	-2.92	-4.16	-2.57
TCGA-DX-A1L2-10A-01D-A24N-09_SARC	-2.84	-2.66	-2.75	-3.27	-2.68	-2.63	-2.48	-2.45	-2.37	0.00	0.00	-4.12	-3.94	0.00	0.00	-2.48	-2.53
TCGA-DX-A1L3-10A-01D-A24N-09_SARC	-2.85	0.00	0.00	-3.03	-2.54	-2.56	-2.53	-2.49	-2.68	-3.45	-2.78	0.00	-2.92	-2.72	0.00	-2.88	-2.64
TCGA-DX-A1L4-10A-01D-A26G-09_SARC	-2.85	-3.82	-3.94	-3.12	-2.62	-2.57	-2.47	-2.54	-2.72	-3.21	-3.00	0.00	-2.91	-2.82	0.00	-2.90	-2.68
TCGA-DX-A23R-10A-01D-A26G-09_SARC	-2.74	-2.70	-2.79	-3.16	-2.74	-2.72	-2.72	-2.75	-2.64	-4.48	-2.89	0.00	-2.85	-2.71	0.00	-2.89	-2.58
TCGA-DX-A23T-10A-01D-A26G-09_SARC	-2.88	-2.75	-2.79	-3.41	-2.73	-2.81	-2.46	-2.54	-2.71	-3.58	-3.00	0.00	-2.79	-2.68	0.00	-2.78	-2.63
TCGA-DX-A23U-10A-01D-A26G-09_SARC	-2.86	-2.54	-2.63	-3.95	-3.43	-3.83	-2.50	-2.52	-2.66	-3.39	-2.83	0.00	-2.71	-2.77	-2.97	-3.83	-2.64
TCGA-DX-A23V-10A-01D-A29N-09_SARC	-2.82	-2.79	-2.86	-3.33	-2.57	-2.60	-2.58	-2.58	-2.50	0.00	-2.98	-3.03	-4.47	-4.47	0.00	-2.61	-2.69
TCGA-DX-A23Y-10A-01D-A27P-09_SARC	-2.78	-2.76	-2.74	-3.39	-2.80	-2.80	-2.56	-2.49	-2.77	-3.36	-2.85	0.00	-2.78	-2.71	0.00	-2.82	-2.57
TCGA-DX-A240-10A-01D-A27P-09_SARC	-2.81	-4.44	0.00	-2.90	-2.53	-2.51	-2.54	-2.58	-2.60	-3.29	-2.88	-4.14	-2.67	-2.72	0.00	-2.81	-2.60
TCGA-DX-A2IZ-10A-01D-A21Q-09_SARC	-2.73	-2.63	-2.69	-3.05	-2.76	-2.54	-2.42	-2.48	-2.31	-4.43	0.00	-4.43	0.00	0.00	-2.88	-2.61	-2.56
TCGA-DX-A2J0-10A-01D-A21Q-09_SARC	-2.71	0.00	-4.37	-3.04	-2.44	-2.42	-2.47	-2.41	-2.33	-4.06	-4.37	-4.37	-4.37	0.00	0.00	-2.40	-2.50
TCGA-DX-A2J1-10A-01D-A21Q-09_SARC	-2.74	-4.51	0.00	-3.04	-2.51	-2.45	-2.48	-2.50	-2.45	0.00	0.00	-3.90	-4.20	0.00	-2.86	-2.70	-2.55
TCGA-DX-A2J4-10A-01D-A21Q-09_SARC	-2.85	-2.76	-2.88	-3.40	-2.60	-2.55	-2.62	-2.61	-2.72	-3.49	-2.68	-2.82	-2.80	-2.73	0.00	-2.87	-2.73
TCGA-DX-A3LS-10A-01D-A21Q-09_SARC	-2.79	0.00	0.00	-3.01	-2.50	-2.61	-2.51	-2.49	-2.59	-3.36	-2.93	-4.50	-2.79	-2.84	0.00	-2.80	-2.69
TCGA-DX-A3LT-10A-01D-A21Q-09_SARC	-2.71	-2.58	-2.73	-3.12	-2.65	-2.57	-2.45	-2.48	-2.41	0.00	0.00	0.00	0.00	0.00	-2.89	-2.70	-2.55
TCGA-DX-A3LU-10A-01D-A21Q-09_SARC	-2.80	-2.72	-2.76	-3.10	-2.64	-2.69	-2.53	-2.76	-2.62	0.00	-2.68	0.00	-2.67	-2.63	0.00	-2.71	-2.55
TCGA-DX-A3LW-10A-01D-A21Q-09_SARC	-2.74	-2.44	-2.46	0.00	0.00	0.00	-2.43	-2.37	-2.33	0.00	0.00	0.00	-4.13	-4.43	0.00	-2.42	-2.52
TCGA-DX-A3LY-10B-01D-A27P-09_SARC	-2.81	-2.52	-2.55	0.00	-2.83	-2.72	-2.58	-2.56	-2.69	-3.35	-2.64	-2.58	0.00	-2.73	0.00	-2.87	-2.67
TCGA-DX-A3M1-10A-01D-A22A-09_SARC	-2.80	0.00	0.00	-3.07	-2.61	-2.56	-2.37	-2.59	-3.81	-3.26	-2.68	0.00	-2.63	-2.59	0.00	-4.59	-2.67
TCGA-DX-A3M2-10A-01D-A22A-09_SARC	-2.76	0.00	0.00	-2.93	-2.51	-2.53	-2.46	-2.53	-2.37	-4.46	0.00	0.00	-4.46	0.00	0.00	-2.42	-2.55
TCGA-DX-A3U5-10A-01D-A22A-09_SARC	-2.85	-2.76	-2.80	-3.32	-2.70	-2.65	-2.51	-2.56	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.56
TCGA-DX-A3U6-10A-01D-A29N-09_SARC	-2.68	-2.70	-2.73	-3.33	-2.73	-2.80	-2.49	-2.58	-2.35	0.00	-4.44	0.00	0.00	0.00	0.00	-2.54	-2.56
TCGA-DX-A3U7-10A-01D-A29N-09_SARC	-2.76	-3.93	-4.41	-3.13	-2.58	-2.61	-2.57	-2.61	-2.62	-3.37	-2.93	0.00	-2.67	-2.72	0.00	-2.84	-2.65
TCGA-DX-A3U8-10A-01D-A29N-09_SARC	-2.86	-4.44	-4.14	-3.14	-2.53	-2.58	-2.49	-2.52	-2.39	0.00	0.00	0.00	-4.44	0.00	0.00	-2.46	-2.63
TCGA-DX-A3U9-10A-01D-A307-09_SARC	-2.97	-2.86	-2.84	-3.26	-2.76	-2.81	-2.53	-2.62	-2.67	-3.33	-2.90	0.00	-2.80	-2.74	-3.09	0.00	-2.60
TCGA-DX-A3UA-10A-01D-A307-09_SARC	-2.98	-2.70	-2.78	-3.24	-2.78	-2.79	-2.52	-2.54	-2.65	-3.37	-2.96	0.00	-2.74	-2.69	0.00	-2.71	-2.59

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DX-A3UB-10A-01D-A307-09_SARC	-2.81	0.00	0.00	-3.07	-2.39	-2.47	-2.46	-2.51	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.33	-2.50
TCGA-DX-A3UC-10A-01D-A307-09_SARC	-3.09	-2.48	-2.58	0.00	-2.72	-2.77	-2.52	-2.47	-2.41	0.00	-2.95	-2.72	0.00	0.00	-3.00	-2.84	-2.55
TCGA-DX-A3UD-10A-01D-A307-09_SARC	-2.78	-2.60	-2.67	-3.23	-2.69	-2.69	-2.51	-2.42	-2.42	0.00	0.00	0.00	0.00	0.00	-2.90	-2.73	-2.56
TCGA-DX-A3UE-10A-01D-A307-09_SARC	-2.82	-2.65	-2.66	-3.26	-2.69	-2.69	-2.66	-2.85	-2.54	0.00	-3.00	-2.81	0.00	-2.56	0.00	-2.66	-2.46
TCGA-DX-A3UF-10A-01D-A307-09_SARC	-2.92	0.00	0.00	-2.92	-2.55	-2.56	-2.48	-2.56	-2.32	0.00	0.00	0.00	0.00	0.00	-2.87	-2.79	-2.67
TCGA-DX-A48J-10A-01D-A307-09_SARC	-2.96	-2.74	-2.73	0.00	-2.55	-2.66	-2.62	-2.67	-2.73	-3.60	-2.72	-2.86	-2.75	-2.79	-3.11	0.00	-2.73
TCGA-DX-A48K-10A-01D-A307-09_SARC	-2.83	0.00	0.00	-3.00	-2.49	-2.53	-2.43	-2.49	-2.32	0.00	0.00	0.00	0.00	0.00	-2.80	-2.77	-2.51
TCGA-DX-A48L-10A-01D-A307-09_SARC	-2.91	0.00	0.00	-3.06	-2.45	-2.61	-2.55	-2.64	0.00	-3.14	-2.82	0.00	-2.61	-2.51	0.00	0.00	-2.60
TCGA-DX-A48O-10A-01D-A307-09_SARC	-2.88	-2.70	-2.78	-3.13	-2.51	-2.64	-2.59	-2.62	-2.52	0.00	-2.93	-2.75	0.00	0.00	-2.97	-2.85	-2.67
TCGA-DX-A48P-10A-01D-A307-09_SARC	-2.88	-2.60	-2.65	0.00	-2.66	-2.57	-2.60	-2.62	-2.68	-3.45	-2.62	-2.66	-2.79	-2.77	0.00	-2.90	-2.65
TCGA-DX-A48R-10A-01D-A307-09_SARC	-2.95	-2.81	-2.83	-3.34	-2.56	-2.66	-2.62	-2.56	-2.50	0.00	-2.94	-2.86	0.00	0.00	-3.00	-2.88	-2.75
TCGA-DX-A48U-10A-01D-A307-09_SARC	-2.77	-2.65	-2.71	-3.10	-2.74	-2.67	-2.47	-2.51	-2.45	0.00	0.00	-4.56	0.00	0.00	-2.86	-2.74	-2.61
TCGA-DX-A48V-10A-01D-A307-09_SARC	-2.81	-2.75	-2.74	-3.23	-2.72	-2.73	-2.55	-2.52	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.67
TCGA-DX-A6B7-10A-01D-A307-09_SARC	-2.91	-2.55	-2.65	0.00	-2.65	-2.74	-2.52	-2.57	-2.49	0.00	-2.94	-2.80	0.00	0.00	0.00	-2.58	-2.60
TCGA-DX-A6B8-10A-01D-A307-09_SARC	-2.91	-2.78	-2.85	-3.26	-2.53	-2.65	-2.63	-2.62	-2.61	0.00	-2.93	-2.88	0.00	0.00	0.00	-2.56	-2.69
TCGA-DX-A6BA-10A-01D-A307-09_SARC	-2.80	0.00	0.00	-2.84	-2.53	-2.57	-2.57	-2.57	-2.48	0.00	0.00	-4.65	-4.65	0.00	0.00	-2.56	-2.69
TCGA-DX-A6BF-10A-01D-A307-09_SARC	-2.84	0.00	-4.65	-2.98	-2.58	-2.59	-2.54	-2.42	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.63
TCGA-DX-A6BG-10A-01D-A307-09_SARC	-2.83	0.00	0.00	-2.97	-2.58	-2.58	-2.51	-2.51	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.48	-2.67
TCGA-DX-A6BH-10A-01D-A307-09_SARC	-2.96	-2.80	-2.89	-3.39	-2.58	-2.69	-2.59	-2.51	-2.52	-3.43	-2.89	-2.82	0.00	0.00	-3.02	-2.90	-2.73
TCGA-DX-A6BK-10A-01D-A307-09_SARC	-2.91	-2.78	-2.83	-3.37	-2.54	-2.65	-2.68	-2.68	-2.50	0.00	-2.98	-2.81	0.00	0.00	0.00	-2.69	-2.77
TCGA-DY-A0XA-10A-01D-A152-10_READ	-2.62	-3.00	-2.97	-2.95	-2.64	-2.62	-2.60	-2.70	-2.82	-3.38	-2.79	-2.83	-2.92	-2.90	0.00	-2.86	-2.58
TCGA-DY-A1DC-10A-01D-A152-10_READ	-2.68	-2.83	-2.79	-3.13	-2.60	-2.68	-2.58	-2.61	-2.74	-3.37	-2.69	-2.62	0.00	-2.89	0.00	-2.98	-2.61
TCGA-DY-A1DD-10A-01D-A152-10_READ	-2.57	-2.71	-2.69	-2.88	-2.71	-2.80	-2.65	-2.90	0.00	-3.25	-2.63	0.00	-2.56	-2.51	0.00	0.00	-2.44
TCGA-DY-A1DF-10A-01D-A152-10_READ	-2.54	-2.89	-2.86	-3.06	-2.60	-2.62	-2.56	-2.59	-2.52	0.00	-3.06	-2.83	0.00	0.00	0.00	-2.52	-2.51
TCGA-DY-A1DG-10A-01D-A152-10_READ	-2.68	-2.66	-2.69	-4.35	-2.99	-2.92	-2.45	-2.60	-2.88	-3.27	-2.72	-2.60	0.00	-2.74	0.00	-2.91	-2.53
TCGA-DY-A1H8-10A-01D-A152-10_READ	-2.61	-2.87	-2.96	-2.89	-3.15	-3.04	-2.48	-2.55	-2.93	-3.41	-3.01	0.00	-2.98	-2.79	0.00	-2.96	-2.52
TCGA-DZ-6133-10A-01D-1962-08_KIRP	-2.56	-4.34	-4.64	-2.75	-2.56	-2.60	-2.59	-2.53	-2.55	0.00	0.00	0.00	0.00	0.00	-3.06	-2.71	-2.49
TCGA-DZ-6134-10A-01D-1962-08_KIRP	-2.55	-4.65	-4.18	-2.56	-2.56	-2.61	-2.61	-2.59	-2.66	0.00	0.00	0.00	-4.65	-4.65	0.00	-2.62	-2.54
TCGA-DZ-6135-10A-01D-1962-08_KIRP	-2.61	-2.80	-2.74	-2.99	-2.73	-2.78	-2.67	-2.62	-2.74	-3.36	-2.87	0.00	-2.82	-2.76	0.00	-2.77	-2.53
TCGA-E1-5302-10A-01D-1468-08_LGG	-2.61	-2.80	-2.83	-3.03	-2.52	-2.65	-2.70	-2.59	-2.61	0.00	-3.00	-2.74	0.00	0.00	-3.07	-2.75	-2.64
TCGA-E1-5303-10A-01D-1468-08_LGG	-2.60	-4.77	-4.47	-2.98	-2.53	-2.68	-2.67	-2.53	-2.82	-3.26	-2.83	-2.89	-2.86	-2.85	0.00	-2.83	-2.66
TCGA-E1-5304-10A-01D-1468-08_LGG	-2.63	-4.69	-4.69	-2.94	-2.59	-2.65	-2.70	-2.66	-2.80	-3.29	-2.93	0.00	-2.83	-2.73	0.00	-2.82	-2.57
TCGA-E1-5305-10A-01D-1893-08_LGG	-2.43	-4.58	-4.28	-2.71	-2.59	-2.58	-2.62	-2.48	-2.46	0.00	0.00	0.00	0.00	0.00	-3.12	-2.73	-2.47
TCGA-E1-5307-10A-01D-1893-08_LGG	-2.54	-2.62	-2.71	-4.63	-2.62	-2.74	-2.66	-2.48	-2.66	-3.40	-2.91	0.00	-2.77	-2.74	-3.16	0.00	-2.41
TCGA-E1-5311-10A-01D-1468-08_LGG	-2.53	-4.34	-4.16	-2.80	-2.57	-2.63	-2.67	-2.48	-2.49	0.00	0.00	-4.16	0.00	-4.16	0.00	-2.43	-2.54
TCGA-E1-5318-10A-01D-1468-08_LGG	-2.62	-4.69	-4.69	-2.72	-2.58	-2.63	-2.71	-2.67	-2.74	-3.41	-2.90	-4.69	-2.82	-2.74	0.00	-2.82	-2.57
TCGA-E1-5319-10A-01D-1893-08_LGG	-2.48	0.00	0.00	-2.56	-2.56	-2.52	-2.53	-2.48	-2.58	0.00	0.00	0.00	0.00	-4.58	0.00	-2.38	-2.46
TCGA-E1-5322-10A-01D-1468-08_LGG	-2.61	-4.21	-4.38	-2.88	-2.65	-2.55	-2.66	-2.58	-2.77	-3.38	-2.88	0.00	-2.85	-2.77	0.00	-2.71	-2.51
TCGA-E2-A105-10A-01D-A10M-09_BRCA	-3.01	0.00	0.00	-2.92	-2.54	-2.57	-2.54	-2.72	-2.47	0.00	0.00	0.00	0.00	0.00	-3.27	-2.93	-2.67
TCGA-E2-A107-10A-01D-A10M-09_BRCA	-2.95	0.00	0.00	-2.77	-2.47	-2.52	-2.42	-2.62	-2.50	0.00	0.00	0.00	0.00	-4.87	0.00	-2.53	-2.58
TCGA-E2-A108-10A-01D-A10M-09_BRCA	-2.85	0.00	0.00	-2.91	-2.55	-2.57	-2.53	-2.54	-2.49	0.00	0.00	-4.77	0.00	0.00	0.00	-2.59	-2.72
TCGA-E2-A109-10A-01D-A10M-09_BRCA	-2.74	-2.64	-2.60	-2.97	-2.56	-2.64	-2.44	-2.47	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.35	-2.62
TCGA-E2-A10A-10A-01D-A110-09_BRCA	-2.84	-4.38	-4.56	-2.71	-2.41	-2.55	-2.50	-2.52	-2.52	0.00	0.00	0.00	-4.86	-4.86	0.00	-2.81	-2.82
TCGA-E2-A10B-10A-01D-A10M-09_BRCA	-2.99	0.00	-4.84	-2.81	-2.53	-2.51	-2.43	-2.64	-2.47	-4.84	0.00	0.00	0.00	0.00	-3.23	-2.82	-2.68
TCGA-E2-A10C-10A-01D-A10M-09_BRCA	-2.90	0.00	0.00	-2.75	-2.54	-2.59	-2.53	-2.68	-2.52	0.00	0.00	0.00	0.00	-4.43	0.00	-2.60	-2.70
TCGA-E2-A10F-10A-01D-A10M-09_BRCA	-3.06	-2.66	-2.63	0.00	-2.72	-2.71	-2.61	-2.96	-2.84	-3.39	-2.84	-2.61	-4.84	-2.83	-3.37	0.00	-2.85
TCGA-E2-A14N-10A-01D-A135-09_BRCA	-2.98	0.00	-5.11	-2.99	-2.63	-2.67	-2.65	-2.71	-2.82	-3.52	-2.92	0.00	-2.87	-2.85	0.00	-2.86	-2.80
TCGA-E2-A14O-10A-01D-A110-09_BRCA	-2.84	-4.64	0.00	-2.70	-2.49	-2.53	-2.54	-2.48	-2.53	0.00	0.00	0.00	0.00	0.00	-2.93	-2.67	-2.72
TCGA-E2-A14P-10A-01D-A12B-09_BRCA	-2.99	0.00	-4.54	-2.85	-2.63	-2.69	-2.59	-2.67	-2.84	-3.52	-2.96	0.00	-2.84	-2.87	-3.14	0.00	-2.85
TCGA-E2-A14Q-10A-01D-A12B-09_BRCA	-2.87	0.00	-4.53	-2.86	-2.52	-2.53	-2.50	-2.56	-2.45	0.00	0.00	0.00	0.00	-4.53	0.00	-2.59	-2.71
TCGA-E2-A14R-10A-01D-A110-09_BRCA	-2.93	0.00	-4.90	-2.92	-2.61	-2.56	-2.59	-2.65	-2.72	-3.41	-2.89	0.00	-2.75	-2.79	0.00	-2.94	-2.69
TCGA-E2-A14S-10A-01D-A12B-09_BRCA	-3.01	-2.85	-2.85	-3.17	-2.63	-2.73	-2.70	-2.73	-2.71	0.00	-2.92	-2.89	0.00	-5.01	0.00	-2.72	-2.83
TCGA-E2-A14T-10A-01D-A110-09_BRCA	-2.93	0.00	0.00	-2.87	-2.62	-2.66	-2.60	-2.64	-2.76	-3.48	-2.82	0.00	-2.78	-2.82	0.00	-2.79	-2.71
TCGA-E2-A14U-10A-01D-A22A-09_BRCA	-2.80	-2.57	-2.64	-4.02	-2.88	-2.79	-2.53	-2.63	-2.70	-3.59	-2.68	-2.90	-2.83	-2.73	-3.11	0.00	-2.66
TCGA-E2-A14V-10A-01D-A12B-09_BRCA	-2.98	-2.83	-2.80	-3.21	-2.52	-2.65	-2.64	-2.62	-2.55	0.00	-2.93	-2.86	0.00	0.00	0.00	-2.61	-2.79
TCGA-E2-A14W-10A-01D-A12B-09_BRCA	-2.88	0.00	-4.69	-2.93	-2.59	-2.60	-2.59	-2.63	-2.56	0.00	0.00	0.00	0.00	-4.99	-2.96	-2.86	-2.70
TCGA-E2-A14X-10A-01D-A110-09_BRCA	-2.92	-2.85	-2.87	-4.56	-2.83	-2.88	-2.79	-2.84	-2.81	-5.04	-2.69	0.00	-2.69	-2.85	-3.16	-5.04	-2.83
TCGA-E2-A14Y-10A-01D-A12B-09_BRCA	-2.90	-2.87	-2.91	-3.24	-2.56	-2.65	-2.64	-2.60	-2.62	0.00	-2.94	-2.78	0.00	0.00	0.00	-2.64	-2.76
TCGA-E2-A14Z-10A-01D-A110-09_BRCA	-2.99	-2.72	-2.74	-3.13	-2.54	-2.68	-2.62	-2.79	-2.52	0.00	-3.02	-2.76	-4.74	0.00	0.00	-2.69	-2.73
TCGA-E2-A150-10A-01D-A12B-09_BRCA	-2.98	0.00	-5.00	-2.84	-2.65	-2.70	-2.64	-2.63	-2.84	-3.39	-2.85	0.00	-2.79	-2.80	-3.11	0.00	-2.77
TCGA-E2-A152-10A-01D-A12B-09_BRCA	-2.90	-2.81	-2.79	-3.08	-2.67	-2.69	-2.66	-2.73	-4.55	-3.32	-2.58	-2.66	-2.78	-2.65	0.00	0.00	-2.73
TCGA-E2-A153-10A-01D-A12B-09_BRCA	-2.87	-2.77	-2.80	-3.15	-2.68	-2.79	-2.57	-2.56	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.73
TCGA-E2-A154-10A-01D-A110-09_BRCA	-2.84	0.00	0.00	-2.88	-2.57	-2.56	-2.54	-2.55	-2.50	0.00	0.00	0.00	0.00	0.00	-3.00	-2.74	-2.67
TCGA-E2-A155-10A-01D-A12B-09_BRCA	-2.82	-2.57	-2.53	0.00	0.00	0.00	-2.52	-2.52	-2.51	0.00	0.00	-4.78	0.00	0.00	-2.86	0.00	-2.62
TCGA-E2-A156-10A-01D-A12B-09_BRCA	-3.01	-2.88	-2.86	-3.18	-2.60	-2.65	-2.71	-2.67	-2.85	-3.65	-2.73	-2.84	-2.87	-2.86	0.00	-2.98	-2.80
TCGA-E2-A158-10A-01D-A12B-09_BRCA	-2.88	-2.80	-2.82	-3.17	-2.76	-2.73	-2.56	-2.53	-2.61	0.00	0.00	0.00	0.00	0.00	-3.09	-2.84	-2.76
TCGA-E2-A159-10A-01D-A110-09_BRCA	-3.02	-2.95	-2.94	-3.27	-2.69	-2.74	-2.62	-2.64	-2.71	-3.79	-2.98	-2.89	0.00	0.00	-3.11	0.00	-2.88
TCGA-E2-A15A-10A-01D-A12B-09_BRCA	-2.95	0.00	0.00	-2.95	-2.61	-2.58	-2.54	-2.49	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.63	-2.71
TCGA-E2-A15C-10A-01D-A12B-09_BRCA	-2.85	0.00	-4.61	-2.82	-2.61	-2.67	-2.69	-2.59	-2.82	-3.59	-2.79	0.00	-2.79	-2.80	-3.16	0.00	-2.81
TCGA-E2-A15D-10A-01D-A110-09_BRCA	-2.86	0.00	0.00	-3.08	-2.62	-2.59	-2.60	-2.53	-2.53	0.00	0.00	0.00	-5.00	-5.00	-3.11	-2.80	-2.69
TCGA-E2-A15E-10A-01D-A12B-09_BRCA	-2.91	-2.79	-2.80	-3.15	-2.51	-2.66	-2.65	-2.63	-2.57	0.00	-2.80	-2.79	-4.88	-4.88	-3.09	-2.87	-2.82
TCGA-E2-A15F-10A-01D-A110-09_BRCA	-2.98	-2.75	-2.72	-3.16	-2.81	-2.75	-2.60	-2.66	-2.71	-3.40	-2.90	-4.82	-2.75	-2.75	0.00	-2.81	-2.75
TCGA-E2-A15G-10A-01D-A12B-09_BRCA	-2.92	0.00	-4.35	-3.00	-2.58	-2.59	-2.59	-2.67	-2.60	0.00	0.00	0.00	0.00	-4.95	0.00	-2.62	-2.74
TCGA-E2-A15H-10A-01D-A12B-09_BRCA	-2.94	0.00	-4.91	-2.83	-2.53	-2.58	-2.60	-2.58	-2.49	0.00	0.00	0.00	0.00	0.00	-3.13	-2.81	-2.73
TCGA-E2-A15I-10A-01D-A135-09_BRCA	-2.91	0.00	-5.04	-2.91	-2.64	-2.67	-2.61	-2.66	-2.84	-3.59	-2.84	0.00	-2.84	-2.83	0.00	-2.86	-2.75
TCGA-E2-A15J-10A-01D-A12Q-09_BRCA	-2.84	-2.71	-2.65	-2.99	-2.83	-2.72	-2.53	-2.63	-2.60	0.00	0.00	0.00	0.00	0.00	0.00	-2.75	-2.70
TCGA-E2-A15K-10A-01D-A12Q-09_BRCA	-2.98	0.00	0.00	-2.89	-2.68	-2.63	-2.60	-2.65	-2.80	-3.48	-2.95	0.00	-2.81	-2.80	-3.13	0.00	-2.85
TCGA-E2-A15L-10A-01D-A12B-09_BRCA	-2.92	-2.74	-2.78	-3.12	-2.75	-2.73	-2.57	-2.52	-2.49	0.00	0.00	0.00	0.00	-4.96	-3.11	-2.73	-2.72
TCGA-E2-A15M-10A-01D-A12B-09_BRCA	-2.93	0.00	-4.94	-3.11	-2.56	-2.56	-2.55	-2.55	-2.50	0.00	0.00	0.00	0.00	-4.64	0.00	-2.45	-2.71
TCGA-E2-A15O-10A-01D-A110-09_BRCA	-2.82	-2.50	-2.48	0.00	-4.72	-4.72	-2.60	-2.70	-2.62	0.00	-2.68	0.00	-2.64	-2.59	0.00	-2.72	-2.61
TCGA-E2-A15P-10A-01D-A110-09_BRCA	-2.77	-2.74	-2.76	-3.09	-2.52	-2.69	-2.61	-2.63	-2.65	0.00	-2.82	-2.80	0.00	0.00	-3.05	-2.89	-2.83
TCGA-E2-A15R-10A-01D-A110-09_BRCA	-2.86	-4.86	-4.56	-3.03	-2.57	-2.63	-2.58	-2.53	-2.76	-3.44	-2.76	-4.26	-2.77	-2.73	0.00	-2.74	-2.74
TCGA-E2-A15S-10A-01D-A110-09_BRCA	-2.93	-2.90	-2.91	-3.25	-2.91	-2.89	-2.70	-2.73	-2.84	-3.55	-2.88	0.00	-2.83	-2.89	0.00	-2.92	-2.92
TCGA-E2-A15T-10A-01D-A110-09_BRCA	-2.88	-2.83	-2.81	-3.21	-2.80	-2.83	-2.59	-2.56	-2.61	0.00	0.00	-4.97	0.00	-4.97	-3.11	-2.82	-2.76
TCGA-E2-A1AZ-10A-01D-A12Q-09_BRCA	-2.81	0.00	-4.34	-2.96	-2.62	-2.61	-2.60	-2.53	-2.61	0.00	-4.82	-4.82	0.00	-4.82	0.00	-2.59	-2.78
TCGA-E2-A1B0-10A-01D-A12Q-09_BRCA	-2.92	-2.84	-2.87	-3.23	-2.79	-2.82	-2.75	-2.76	-2.83	-3.57	-2.79	0.00	-2.83	-2.85	0.00	-2.85	-2.80
TCGA-E2-A1B1-10A-01D-A12Q-09_BRCA	-2.96	-2.90	-2.88	-3.10	-2.61	-2.78	-2.76	-2.76	-2.84	-3.57	-2.80	-2.77	0.00	-2.84	0.00	-2.93	-2.88
TCGA-E2-A1B4-10A-01D-A12Q-09_BRCA	-2.85	0.00	0.00	-2.82	-2.58	-2.57	-2.62	-2.59	-2.60	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.75
TCGA-E2-A1B5-10A-01D-A12Q-09_BRCA	-2.88	0.00	0.00	-2.76	-2.60	-2.66	-2.59	-2.71	-2.62	0.00	0.00	0.00	0.00	0.00	0.00	-2.65	-2.71
TCGA-E2-A1B6-10A-01D-A12Q-09_BRCA	-3.08	-2.86	-2.86	-3.21	-2.54	-2.65	-2.63	-2.67	-2.60	0.00	-3.03	-2.80	0.00	-4.97	-3.23	-2.99	-2.78
TCGA-E2-A1BC-10A-01D-A12Q-09_BRCA	-3.03	-2.83	-2.80	0.00	-2.76	-2.76	-2.74	-2.72	-2.93	-3.59	-2.74	-2.66	0.00	-2.90	0.00	-2.95	-2.86
TCGA-E2-A1BD-10A-01D-A12Q-09_BRCA	-2.89	0.00	-4.54	-2.79	-2.59	-2.55	-2.52	-2.59	-2.58	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.71
TCGA-E2-A1IE-10A-01D-A13O-09_BRCA	-2.99	0.00	-2.70	-3.06	-2.72	-2.70	-2.61	-2.61	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.76
TCGA-E2-A1IF-10A-01D-A142-09_BRCA	-3.05	-2.85	-2.94	-3.21	-2.71	-2.78	-2.65	-2.70	-2.69	0.00	-3.09	-2.96	0.00	0.00	-3.24	-2.97	-2.79
TCGA-E2-A1IG-10A-01D-A142-09_BRCA	-2.91	0.00	0.00	-2.84	-2.58	-2.61	-2.59	-2.66	-2.79	-3.51	-2.92	-2.78	0.00	-2.76	0.00	-2.77	-2.75
TCGA-E2-A1IH-10A-01D-A13O-09_BRCA	-2.98	-2.76	-2.72	-3.12	-2.79	-2.79	-2.62	-2.61	-2.58	0.00	0.00	0.00	0.00	0.00	-3.12	-2.78	-2.76

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-E2-A1II-10A-01D-A142-09_BRCA	-2.98	-2.75	-2.79	-4.30	-2.94	-3.10	-2.74	-2.69	-2.67	0.00	-3.11	-2.97	0.00	0.00	-3.21	-3.06	-2.83
TCGA-E2-A1IJ-10A-01D-A142-09_BRCA	-3.03	0.00	0.00	-2.93	-2.67	-2.71	-2.68	-2.71	-2.87	-3.34	-2.98	0.00	-2.88	-2.86	0.00	-3.04	-2.82
TCGA-E2-A1IK-10A-01D-A142-09_BRCA	-3.01	-2.77	-2.82	-3.12	-2.61	-2.68	-2.64	-2.67	-2.56	0.00	-2.94	-2.80	0.00	0.00	0.00	-2.63	-2.79
TCGA-E2-A1IL-10A-01D-A14G-09_BRCA	-3.16	-2.89	-2.89	-3.22	-2.83	-2.87	-2.73	-2.78	-2.84	-3.48	-2.88	0.00	-2.89	-2.84	0.00	-3.00	-2.80
TCGA-E2-A1IN-10A-01D-A188-09_BRCA	-3.07	-2.72	-2.73	0.00	-2.74	-2.72	-2.72	-2.83	-4.77	-3.37	-2.67	-2.60	0.00	-2.73	0.00	0.00	-2.86
TCGA-E2-A1IO-10A-01D-A142-09_BRCA	-2.91	-2.74	-2.77	-3.23	-2.73	-2.81	-2.55	-2.63	-2.67	-4.51	0.00	0.00	0.00	-4.51	-3.08	-2.88	-2.67
TCGA-E2-A1L6-10A-01D-A13O-09_BRCA	-3.07	-4.13	-4.13	-2.91	-2.58	-2.57	-2.48	-2.61	-2.57	0.00	-4.43	0.00	0.00	0.00	-3.39	-2.84	-2.60
TCGA-E2-A1L7-10A-01D-A142-09_BRCA	-2.95	0.00	0.00	-2.84	-2.67	-2.62	-2.62	-2.74	-2.83	-3.32	-2.85	0.00	-2.89	-2.80	0.00	-2.86	-2.72
TCGA-E2-A1L8-10A-01D-A13O-09_BRCA	-3.00	0.00	0.00	-2.95	-2.61	-2.64	-2.60	-2.69	-2.63	0.00	0.00	0.00	-4.35	-4.65	-2.96	0.00	-2.72
TCGA-E2-A1L9-10A-01D-A188-09_BRCA	-3.07	-2.90	-2.96	-3.28	-2.69	-2.72	-2.74	-2.80	-2.86	-3.54	-2.78	-2.73	0.00	-2.92	0.00	-2.90	-2.84
TCGA-E2-A1LA-10A-01D-A142-09_BRCA	-2.90	0.00	0.00	-2.87	-2.62	-2.63	-2.58	-2.63	-2.58	0.00	0.00	0.00	0.00	0.00	-3.17	-2.88	-2.76
TCGA-E2-A2P5-10B-01D-A19Y-09_BRCA	-2.89	0.00	0.00	-2.94	-2.55	-2.56	-2.62	-2.58	-2.64	-3.30	-2.96	0.00	-2.83	-2.76	0.00	-2.84	-2.59
TCGA-E2-A2P6-10B-01D-A19Y-09_BRCA	-2.90	-3.91	-4.09	-3.07	-2.49	-2.66	-2.56	-2.65	-2.66	-3.49	-2.93	-3.91	-2.75	-2.79	0.00	-2.78	-2.64
TCGA-E2-A3DX-10A-01D-A20S-09_BRCA	-2.98	-3.49	-3.61	-3.07	-2.63	-2.56	-2.55	-2.59	-3.35	-3.35	-2.71	-4.09	-2.62	-2.69	0.00	-3.49	-2.59
TCGA-E2-A56Z-10A-01D-A29N-09_BRCA	-2.84	-2.82	-2.79	-3.32	-2.54	-2.61	-2.60	-2.58	-2.65	0.00	-3.01	-2.93	0.00	-4.64	-3.03	-2.89	-2.72
TCGA-E2-A570-10A-01D-A29N-09_BRCA	-2.80	-2.74	-2.77	-3.22	-2.73	-2.53	-2.56	-2.43	-2.46	-4.56	0.00	-4.56	-4.26	-4.56	-2.89	-2.81	-2.67
TCGA-E2-A572-10B-01D-A31U-09_BRCA	-2.86	-2.56	-2.42	0.00	0.00	0.00	-2.33	-2.31	-2.22	0.00	0.00	0.00	0.00	0.00	-2.82	-2.66	-2.38
TCGA-E2-A573-10A-01D-A29N-09_BRCA	-2.84	-4.09	-4.09	-2.99	-2.49	-2.36	-2.45	-2.48	-2.46	0.00	0.00	0.00	0.00	0.00	-2.84	-2.67	-2.61
TCGA-E2-A574-10A-01D-A29N-09_BRCA	-2.70	-4.16	0.00	-3.12	-2.48	-2.51	-2.54	-2.58	-2.44	0.00	0.00	0.00	-4.46	-4.46	-2.90	-2.77	-2.60
TCGA-E2-A576-10B-01D-A31U-09_BRCA	-2.77	0.00	0.00	-2.97	-2.44	-2.46	-2.45	-2.44	-2.35	0.00	0.00	0.00	0.00	0.00	-2.72	0.00	-2.71
TCGA-E3-A3DY-10A-01D-A20C-08_THCA	-2.47	0.00	0.00	-2.57	-2.52	-2.56	-2.57	-2.58	-2.44	0.00	0.00	-4.49	0.00	-4.49	0.00	-2.41	-2.44
TCGA-E3-A3DZ-10A-01D-A20C-08_THCA	-2.40	-2.60	-2.58	-2.74	-2.50	-2.52	-2.55	-2.64	-2.62	0.00	0.00	0.00	-4.45	0.00	0.00	-2.58	-2.46
TCGA-E3-A3E0-10A-01D-A20C-08_THCA	-2.60	-2.73	-2.71	-2.90	-2.69	-2.73	-2.59	-2.57	-2.69	-3.22	-2.87	-4.30	-2.82	-2.68	-3.08	0.00	-2.48
TCGA-E3-A3E1-10A-01D-A20C-08_THCA	-2.48	-2.75	-2.70	-2.85	-2.68	-2.67	-2.44	-2.60	-2.68	-3.37	-2.94	-4.57	-2.80	-2.68	-3.04	-4.57	-2.45
TCGA-E3-A3E2-10A-01D-A20C-08_THCA	-2.57	0.00	0.00	-2.75	-2.57	-2.58	-2.62	-2.69	-2.67	-3.33	-2.91	0.00	-2.80	-2.67	0.00	-2.74	-2.52
TCGA-E3-A3E3-10A-01D-A20C-08_THCA	-2.58	-4.53	0.00	-2.73	-2.54	-2.57	-2.60	-2.54	-2.69	-3.15	-2.83	0.00	-2.77	-2.66	0.00	-2.68	-2.51
TCGA-E3-A3E5-10A-01D-A20C-08_THCA	-2.53	-2.65	-2.62	-4.21	-2.70	-2.70	-2.60	-2.59	-2.53	0.00	-2.88	-2.70	0.00	0.00	-3.04	-2.73	-2.47
TCGA-E5-A2PC-10B-01D-A202-08_BLCA	-2.51	-4.43	-4.43	-2.56	-2.55	-2.57	-2.61	-2.54	-2.50	-4.43	-4.13	0.00	0.00	-3.95	0.00	-2.47	-2.48
TCGA-E5-A4TZ-10B-01D-A31J-08_BLCA	-2.47	0.00	0.00	-2.82	-2.57	-2.59	-2.66	-2.61	-2.70	-3.38	-2.91	0.00	-2.79	-2.71	-3.11	0.00	-2.50
TCGA-E5-A4U1-10B-01D-A31J-08_BLCA	-2.54	-2.68	-2.62	-2.83	-2.63	-2.64	-2.55	-2.62	-2.45	0.00	0.00	-4.53	0.00	0.00	0.00	-2.58	-2.43
TCGA-E6-A1LX-10A-01D-A14G-09_UCEC	-2.82	-4.10	0.00	-2.92	-2.50	-2.48	-2.43	-2.51	-2.37	0.00	0.00	-4.10	0.00	-4.40	-2.98	-2.75	-2.57
TCGA-E6-A1LZ-10A-01D-A142-09_UCEC	-3.08	0.00	0.00	-3.15	-2.66	-2.61	-2.62	-2.74	-2.87	-3.46	-2.74	-2.86	-2.96	-2.88	-3.21	0.00	-2.75
TCGA-E6-A1M0-10A-01D-A142-09_UCEC	-2.82	-2.65	-2.81	-3.21	-2.69	-2.73	-2.49	-2.45	-2.39	-4.51	-4.21	0.00	-4.21	-4.51	-2.94	-2.80	-2.57
TCGA-E6-A2P8-10B-01D-A19Y-09_UCEC	-2.91	-2.80	-2.80	-3.24	-2.47	-2.52	-2.50	-2.64	-2.46	0.00	-2.85	-2.77	0.00	0.00	-2.98	-2.83	-2.62
TCGA-E6-A2P9-10B-01D-A19Y-09_UCEC	-2.85	-3.72	-4.42	-2.95	-2.51	-2.43	-2.49	-2.51	-2.43	0.00	-4.42	0.00	-4.12	-4.42	0.00	-2.57	-2.63
TCGA-E7-A3X6-10A-01D-A22Z-08_BLCA	-2.46	-4.58	-4.11	-2.59	-2.43	-2.45	-2.51	-2.55	-2.49	-4.58	-4.11	-4.58	0.00	-4.28	0.00	-2.54	-2.38
TCGA-E7-A3Y1-10A-01D-A22Z-08_BLCA	-2.51	0.00	-4.67	-2.57	-2.50	-2.53	-2.58	-2.59	0.00	-3.22	-2.73	0.00	-2.62	-2.50	0.00	0.00	-2.44
TCGA-E7-A4IJ-10A-01D-A26K-08_BLCA	-2.55	-2.71	-2.83	-2.97	-2.46	-2.53	-2.56	-2.45	-2.56	-3.45	-2.89	-2.79	-3.89	-4.19	-2.99	-4.19	-2.53
TCGA-E7-A4XJ-10A-01D-A26K-08_BLCA	-2.47	0.00	0.00	-2.63	-2.49	-2.41	-2.51	-2.51	-2.48	0.00	0.00	0.00	0.00	0.00	-2.83	-4.40	-2.37
TCGA-E7-A519-10A-01D-A26K-08_BLCA	-2.44	0.00	-4.40	-2.57	-2.46	-2.49	-2.55	-2.51	-2.40	0.00	-4.40	0.00	-4.40	-3.92	0.00	-2.51	-2.39
TCGA-E7-A541-10A-01D-A26K-08_BLCA	-2.53	0.00	0.00	-2.72	-2.49	-2.54	-2.59	-2.64	-2.57	-3.37	-2.82	0.00	-2.67	-2.65	0.00	-2.73	-2.41
TCGA-E7-A5KE-10A-01D-A289-08_BLCA	-2.51	-4.57	0.00	-2.81	-2.52	-2.74	-2.50	-2.46	-2.63	-3.29	-2.91	0.00	-2.84	-2.68	-3.14	0.00	-2.48
TCGA-E7-A5KF-10A-01D-A289-08_BLCA	-2.52	0.00	0.00	-2.65	-2.58	-2.56	-2.60	-2.56	-2.79	-3.30	-2.84	0.00	-2.81	-2.68	0.00	-2.66	-2.49
TCGA-E7-A677-10A-01D-A30H-08_BLCA	-2.47	0.00	-4.70	-2.65	-2.50	-2.50	-2.48	-2.47	-2.64	-3.30	-2.92	0.00	-2.78	-2.59	-3.12	0.00	-2.42
TCGA-E7-A678-10A-01D-A30H-08_BLCA	-2.48	0.00	0.00	-2.68	-2.46	-2.46	-2.48	-2.50	-2.35	0.00	0.00	0.00	0.00	-4.66	-3.02	-2.66	-2.41
TCGA-E7-A6ME-10B-01D-A329-08_BLCA	-2.40	-4.48	-4.48	-2.71	-2.49	-2.51	-2.46	-2.56	-2.45	0.00	0.00	0.00	0.00	0.00	-3.09	-2.82	-2.41
TCGA-E7-A6MF-10B-01D-A329-08_BLCA	-2.56	0.00	-4.49	-2.69	-2.45	-2.55	-2.56	-2.67	-2.63	-3.31	-2.98	0.00	-2.80	-2.68	0.00	-2.92	-2.45
TCGA-E7-A7DU-10A-01D-A329-08_BLCA	-2.41	-2.68	-2.63	-2.81	-2.65	-2.58	-2.49	-2.51	-2.40	0.00	0.00	0.00	0.00	0.00	-3.13	-2.77	-2.38
TCGA-E7-A7DV-10A-01D-A339-08_BLCA	-2.56	-2.51	-2.49	0.00	0.00	0.00	-2.54	-2.60	-2.61	-3.29	-2.84	0.00	-2.65	-2.61	0.00	-2.73	-2.46
TCGA-E8-A242-10A-01D-A16O-08_THCA	-2.61	-2.78	-2.76	-2.96	-2.52	-2.66	-2.65	-2.55	-2.65	0.00	-2.90	-2.75	0.00	-4.67	-3.12	-2.77	-2.60
TCGA-E8-A2EA-10A-01D-A17V-08_THCA	-2.49	-2.69	-4.56	-2.84	-2.60	-2.64	-2.66	-2.73	-2.64	0.00	-2.82	0.00	-2.69	-2.62	0.00	-2.71	-2.46
TCGA-E8-A2JQ-10A-01D-A19M-08_THCA	-2.53	-3.67	-3.97	-2.58	-2.48	-2.49	-2.59	-2.49	-2.41	0.00	0.00	0.00	0.00	-4.44	0.00	-2.42	-2.47
TCGA-E8-A3X7-10A-01D-A22Z-08_THCA	-2.61	-2.59	-2.61	0.00	-2.58	-2.64	-2.60	-2.58	-2.53	0.00	-2.74	-2.59	0.00	0.00	-3.07	-2.81	-2.52
TCGA-E8-A413-10A-01D-A23K-08_THCA	-2.53	-2.59	-2.55	-4.52	-4.52	-3.82	-2.57	-2.62	-3.82	-3.12	-2.68	0.00	-2.63	-2.56	0.00	0.00	-2.52
TCGA-E8-A414-10A-01D-A23K-08_THCA	-2.61	-4.58	0.00	-2.83	-2.67	-2.63	-2.69	-2.50	-2.75	-3.30	-2.84	-2.74	-3.97	-2.71	-3.16	0.00	-2.56
TCGA-E8-A415-10A-01D-A23K-08_THCA	-2.53	-3.71	-3.44	-2.79	-2.56	-2.57	-2.63	-2.49	-2.46	0.00	-4.18	-3.78	0.00	-4.01	-2.98	-2.67	-2.51
TCGA-E8-A416-10A-01D-A23K-08_THCA	-2.57	-4.04	-3.92	-2.74	-2.64	-2.66	-2.63	-2.50	-2.57	-4.52	-3.74	-4.04	-3.92	-4.22	-3.07	-2.80	-2.54
TCGA-E8-A417-10A-01D-A23K-08_THCA	-2.45	-3.81	-4.21	-2.56	-2.52	-2.62	-2.60	-2.64	-2.48	0.00	-4.21	-4.21	-4.03	-3.81	0.00	-2.46	-2.56
TCGA-E8-A418-10A-01D-A23K-08_THCA	-2.55	-2.76	-2.77	-2.67	-2.64	-2.76	-2.61	-2.46	-2.63	0.00	0.00	0.00	0.00	0.00	-3.11	-2.78	-2.62
TCGA-E8-A419-10A-01D-A23K-08_THCA	-2.62	-3.82	-3.56	-2.69	-2.61	-2.61	-2.65	-2.66	-2.69	-3.34	-2.85	-3.60	-2.75	-2.67	0.00	-2.78	-2.56
TCGA-E8-A432-10A-01D-A23K-08_THCA	-2.40	-2.74	-2.70	-2.76	-2.61	-2.64	-2.48	-2.49	-2.58	-3.32	-2.91	0.00	-2.75	-2.63	-3.08	0.00	-2.38
TCGA-E8-A433-10A-01D-A23K-08_THCA	-2.61	-2.72	-2.68	-2.89	-2.71	-2.72	-2.64	-2.61	-2.68	-3.20	-2.84	0.00	-2.73	-2.67	0.00	-2.75	-2.58
TCGA-E8-A434-10A-01D-A23K-08_THCA	-2.55	-2.66	-2.67	-2.88	-2.66	-2.63	-2.61	-2.51	-2.60	-4.56	0.00	-4.56	-3.71	-3.78	-3.03	-2.72	-2.51
TCGA-E8-A436-10A-01D-A23U-08_THCA	-2.46	-2.48	-2.45	-3.52	-3.34	-3.82	-2.61	-2.64	-3.45	-3.18	-2.58	0.00	-2.49	-2.42	0.00	-4.29	-2.39
TCGA-E8-A437-10A-01D-A23U-08_THCA	-2.63	-2.81	-2.89	-2.97	-2.56	-2.60	-2.67	-2.42	-2.53	0.00	-2.88	-2.75	0.00	-4.48	-3.06	-2.71	-2.56
TCGA-E8-A438-10B-01D-A23U-08_THCA	-2.66	-2.88	-2.86	-3.02	-2.62	-2.71	-2.70	-2.63	-2.79	-3.48	-2.62	-2.82	-2.85	-2.73	0.00	-2.71	-2.63
TCGA-E8-A44K-10A-01D-A23U-08_THCA	-2.61	-2.76	-2.79	-2.91	-2.71	-2.70	-2.67	-2.54	-2.60	0.00	-4.50	-4.50	0.00	0.00	-3.00	-2.76	-2.58
TCGA-E8-A44M-10A-01D-A23U-08_THCA	-2.43	0.00	-4.39	-2.75	-2.54	-2.53	-2.50	-2.48	-2.48	0.00	-3.79	0.00	-4.39	-4.09	-2.96	-2.65	-2.47
TCGA-E9-A1N3-10A-01D-A159-09_BRCA	-2.74	-2.69	-2.72	-3.02	-2.76	-2.67	-2.45	-2.55	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.59
TCGA-E9-A1N4-10A-01D-A14K-09_BRCA	-2.86	-2.79	-4.53	-3.12	-2.54	-2.62	-2.63	-2.60	-2.57	-4.83	0.00	0.00	-4.53	0.00	-3.10	-2.84	-2.78
TCGA-E9-A1N5-10A-01D-A14G-09_BRCA	-2.87	-2.94	-2.87	-3.19	-2.85	-2.79	-2.54	-2.64	-2.81	-3.42	-2.96	-3.72	-2.94	-2.71	0.00	-3.02	-2.80
TCGA-E9-A1N8-10A-01D-A142-09_BRCA	-2.77	0.00	0.00	-2.94	-2.57	-2.79	-2.66	-2.84	-2.81	0.00	0.00	0.00	0.00	-2.72	0.00	-2.86	-2.78
TCGA-E9-A1N9-10A-01D-A14G-09_BRCA	-3.04	-2.85	-2.84	-3.24	-2.62	-2.73	-2.70	-2.78	0.00	-3.37	-2.58	-2.87	-2.70	-2.63	0.00	0.00	-2.79
TCGA-E9-A1NA-10A-01D-A142-09_BRCA	-3.03	-2.81	-2.97	-3.16	-2.67	-2.86	-2.77	-2.83	-4.53	-3.75	-2.75	-2.81	-2.89	-2.66	0.00	-4.53	-3.08
TCGA-E9-A1NC-10A-01D-A159-09_BRCA	-2.82	0.00	-4.45	-2.82	-2.51	-2.51	-2.50	-2.58	-2.46	0.00	0.00	0.00	0.00	0.00	-3.20	-2.79	-2.57
TCGA-E9-A1NE-10A-01D-A14K-09_BRCA	-2.98	-2.72	-2.67	-4.79	-2.78	-2.76	-2.67	-2.66	-2.76	-3.43	-2.62	-2.80	-2.79	-2.80	-3.13	0.00	-2.83
TCGA-E9-A1NF-10A-01D-A14G-09_BRCA	-3.00	-2.74	-2.76	-3.08	-2.88	-2.83	-2.60	-2.80	-2.57	0.00	0.00	0.00	0.00	-4.71	0.00	-2.70	-2.77
TCGA-E9-A1NG-10A-01D-A14K-09_BRCA	-2.84	-4.51	0.00	-2.93	-2.56	-2.55	-2.52	-2.59	-2.55	0.00	-4.51	0.00	0.00	0.00	-3.08	-2.86	-2.68
TCGA-E9-A1NI-10A-01D-A17G-09_BRCA	-2.95	-2.76	0.00	-3.05	-2.77	-2.77	-2.73	-2.84	-2.79	0.00	-2.90	0.00	-2.76	-2.70	-3.07	0.00	-2.65
TCGA-E9-A1QZ-10A-01D-A167-09_BRCA	-2.89	-2.75	-2.80	-2.99	-2.76	-2.81	-2.53	-2.66	-2.59	0.00	0.00	0.00	0.00	0.00	-3.15	-2.88	-2.66
TCGA-E9-A1R0-10A-01D-A16D-09_BRCA	-3.05	-2.75	-2.76	-3.19	-2.81	-2.78	-2.71	-2.59	-2.86	-3.50	-2.88	0.00	-2.77	-2.81	0.00	-2.94	-2.77
TCGA-E9-A1R2-10A-01D-A14G-09_BRCA	-3.01	-2.77	-2.73	-3.07	-2.75	-2.75	-2.57	-2.63	-2.82	-3.34	-2.96	-2.79	0.00	-2.75	0.00	-2.86	-2.72
TCGA-E9-A1R3-10A-01D-A14K-09_BRCA	-3.03	-2.55	-2.54	0.00	-2.74	-2.77	-2.50	-2.67	-2.53	0.00	-2.93	-2.74	0.00	0.00	-3.19	-2.86	-2.66
TCGA-E9-A1R4-10A-01D-A14G-09_BRCA	-2.87	0.00	0.00	-3.00	-2.63	-2.69	-2.66	-2.71	-2.75	-3.49	-2.91	-2.80	0.00	-2.81	-3.03	0.00	-2.76
TCGA-E9-A1R5-10A-01D-A14K-09_BRCA	-2.97	0.00	-4.84	-3.13	-2.57	-2.62	-2.68	-2.67	-4.37	-3.46	-2.67	0.00	-2.64	-2.71	0.00	-4.84	-2.78
TCGA-E9-A1R6-10A-01D-A14G-09_BRCA	-2.82	0.00	0.00	-2.91	-2.57	-2.61	-2.53	-2.51	-2.56	0.00	0.00	0.00	0.00	0.00	-3.04	-2.73	-2.68
TCGA-E9-A1R7-10A-01D-A14K-09_BRCA	-2.89	-2.73	-2.75	-3.14	-2.95	-2.80	-2.60	-2.73	-2.56	0.00	-4.44	0.00	0.00	0.00	-3.21	-2.86	-2.62
TCGA-E9-A1RA-10A-01D-A14G-09_BRCA	-2.90	0.00	0.00	-2.86	-2.59	-2.57	-2.58	-2.62	-2.65	0.00	0.00	0.00	0.00	0.00	-3.23	-3.00	-2.68
TCGA-E9-A1RB-10A-01D-A159-09_BRCA	-3.01	-2.60	-2.62	0.00	-2.84	-2.78	-2.61	-2.68	-2.80	-3.44	-2.73	-2.68	0.00	-2.74	-3.11	0.00	-2.78
TCGA-E9-A1RC-10A-01D-A159-09_BRCA	-2.99	-2.75	-2.77	-3.15	-2.61	-2.66	-2.67	-2.77	-2.83	-3.51	-2.78	-2.65	0.00	-2.78	0.00	-2.91	-2.82
TCGA-E9-A1RD-10A-01D-A159-09_BRCA	-2.88	0.00	0.00	-2.75	-2.61	-2.63	-2.55	-2.52	-2.54	0.00	0.00	0.00	0.00	-4.60	0.00	-2.49	-2.74
TCGA-E9-A1RE-10A-01D-A159-09_BRCA	-2.78	-2.76	-2.78	-3.01	-3.01	-2.80	-2.44	-2.60	-2.58	0.00	0.00	0.00	-4.40	0.00	0.00	-3.23	-2.60
TCGA-E9-A1RF-10A-01D-A159-09_BRCA	-2.91	-2.71	-2.63	0.00	-2.83	-2.83	-2.64	-2.62	-2.61	0.00	-2.90	-2.77	0.00	0.00	-3.19	-2.96	-2.78
TCGA-E9-A1RG-10A-01D-A14G-09_BRCA	-2.86	-2.75	-2.71	-3.05	-2.97	-2.79	-2.52	-2.64	-2.58	0.00	0.00	0.00	0.00	0.00	-2.83	0.00	-2.74
TCGA-E9-A1RH-10A-01D-A167-09_BRCA	-2.84	0.00	-4.53	-2.88	-2.53	-2.55	-2.56	-2.58	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.68
TCGA-E9-A1RI-10A-01D-A167-09_BRCA	-2.90	-2.46	-2.50	0.00	0.00	-4.44	-2.49	-2.54	-2.48	-4.44	-4.44	-4.44	0.00	0.00	-3.12	-2.75	-2.61

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-E9-A226-10A-01D-A159-09_BRCA	-2.93	-2.90	-2.88	-3.22	-2.67	-2.75	-2.77	-2.71	-2.84	-3.61	-2.75	-2.90	-2.95	-2.90	0.00	-3.08	-2.94
TCGA-E9-A227-10A-01D-A159-09_BRCA	-3.02	-2.58	-2.65	0.00	-2.69	-2.61	-2.66	-2.79	-2.91	-3.26	-2.63	-2.67	-2.77	-2.77	0.00	-3.00	-2.74
TCGA-E9-A228-10A-01D-A159-09_BRCA	-2.82	0.00	0.00	-2.93	-2.81	-2.56	-2.59	-2.62	-2.77	-3.33	-3.05	0.00	-2.86	-2.77	0.00	-3.17	-2.62
TCGA-E9-A229-10B-01D-A159-09_BRCA	-2.94	-2.65	-2.63	0.00	-2.76	-2.79	-2.63	-2.67	-2.58	0.00	-2.88	-2.83	0.00	0.00	-3.16	-2.78	-2.79
TCGA-E9-A22A-10A-01D-A159-09_BRCA	-2.73	0.00	0.00	-2.70	-2.66	-2.63	-2.39	-2.44	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.93	-2.75
TCGA-E9-A22B-10A-01D-A159-09_BRCA	-2.98	-2.78	-2.84	-3.09	-2.78	-2.84	-2.66	-2.75	-4.37	-3.37	-2.72	-2.83	-2.88	-2.67	0.00	-4.67	-2.86
TCGA-E9-A22D-10A-01D-A159-09_BRCA	-2.85	-2.72	-2.76	-3.01	-2.67	-2.68	-2.56	-2.66	-2.62	0.00	0.00	0.00	-4.59	-4.59	0.00	-2.60	-2.73
TCGA-E9-A22E-10A-01D-A159-09_BRCA	-2.60	0.00	-3.93	-2.74	-2.46	-2.70	-2.74	-2.96	-2.69	0.00	-4.24	0.00	0.00	-2.66	0.00	-2.77	-2.80
TCGA-E9-A22G-10A-01D-A159-09_BRCA	-2.92	0.00	0.00	-2.76	-2.52	-2.64	-2.47	-2.54	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.67	-2.65
TCGA-E9-A22H-10A-01D-A17G-09_BRCA	-2.95	0.00	0.00	-2.69	-2.61	-2.48	-2.40	-2.56	-2.55	-4.23	0.00	0.00	0.00	0.00	-3.23	-3.08	-2.58
TCGA-E9-A243-10A-01D-A17G-09_BRCA	-2.91	0.00	0.00	-2.79	-2.60	-2.61	-2.60	-2.62	-2.54	0.00	0.00	0.00	0.00	0.00	-3.14	-2.84	-2.68
TCGA-E9-A244-10A-01D-A167-09_BRCA	-3.12	0.00	0.00	-3.00	-2.62	-2.71	-2.61	-2.65	-2.97	-3.49	-2.84	-2.91	-3.09	-3.01	0.00	-3.10	-2.80
TCGA-E9-A245-10A-01D-A16D-09_BRCA	-3.05	0.00	0.00	-2.94	-2.63	-2.56	-2.57	-2.68	-2.77	-3.51	-2.95	0.00	-2.77	-2.84	0.00	-3.02	-2.69
TCGA-E9-A247-10A-01D-A167-09_BRCA	-2.97	-2.76	-2.79	0.00	-3.13	-3.13	-2.65	-2.77	-3.09	-3.67	-2.83	-2.99	-2.92	-2.92	0.00	-3.05	-2.84
TCGA-E9-A248-10A-01D-A167-09_BRCA	-2.81	-2.80	-2.87	-3.33	-2.90	-2.73	-2.47	-2.60	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.65	-2.54
TCGA-E9-A249-10A-01D-A167-09_BRCA	-2.89	-3.75	-3.55	-2.94	-2.68	-2.60	-2.56	-2.62	-2.63	-4.45	0.00	-4.45	0.00	-4.45	0.00	-2.60	-2.71
TCGA-E9-A24A-10A-01D-A167-09_BRCA	-3.00	0.00	0.00	-2.72	-2.58	-2.59	-2.57	-2.60	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.76
TCGA-E9-A295-10A-01D-A16D-09_BRCA	-2.91	-2.84	-2.88	-3.17	-2.59	-2.69	-2.64	-2.69	-2.62	0.00	-2.92	-2.81	0.00	0.00	-3.17	-3.04	-2.72
TCGA-E9-A2JS-10A-01D-A17W-09_BRCA	-2.75	-2.51	-2.53	0.00	0.00	0.00	-2.53	-2.53	-2.53	0.00	0.00	0.00	-4.51	0.00	-3.04	-2.68	-2.68
TCGA-E9-A2JT-10A-01D-A18P-09_BRCA	-2.88	-2.66	-2.68	-2.98	-2.83	-2.80	-2.46	-2.63	-2.41	-4.50	0.00	0.00	-4.50	0.00	-3.20	-2.83	-2.56
TCGA-E9-A3HO-10A-02D-A20S-09_BRCA	-2.86	-2.44	-2.46	-3.81	-3.51	-3.34	-2.49	-2.52	-2.38	-4.29	-3.99	-3.69	-3.99	-3.99	0.00	-2.77	-2.50
TCGA-E9-A3Q9-10A-01D-A21Q-09_BRCA	-2.83	-2.59	-2.60	-4.34	-2.77	-2.76	-2.59	-2.55	-2.71	-3.36	-2.71	-2.64	-4.04	-2.73	0.00	-2.86	-2.69
TCGA-E9-A3QA-10A-01D-A22A-09_BRCA	-2.81	-2.75	-2.76	0.00	-2.72	-2.72	-2.53	-2.48	-2.44	0.00	0.00	0.00	0.00	0.00	-2.88	-2.79	-2.58
TCGA-E9-A3X8-10B-01D-A22X-09_BRCA	-2.91	-2.55	-2.92	-4.54	-2.65	-2.66	-2.65	-2.57	-2.55	0.00	-2.73	-2.66	-4.54	-4.54	0.00	-2.61	-2.66
TCGA-E9-A54X-10A-01D-A25Q-09_BRCA	-2.78	-2.59	-2.78	-3.14	-2.63	-2.72	-2.46	-2.48	-2.36	0.00	-4.04	0.00	-4.34	-4.34	0.00	-2.52	-2.49
TCGA-E9-A54Y-10A-01D-A25Q-09_BRCA	-2.96	-2.62	-2.65	-4.61	-2.86	-2.78	-2.61	-2.58	-2.70	-3.47	-2.66	-2.70	-4.31	-2.80	0.00	-2.80	-2.68
TCGA-E9-A5FK-10A-01D-A27P-09_BRCA	-2.80	-2.79	-2.75	-3.27	-2.53	-2.66	-2.58	-2.61	-2.57	0.00	-2.84	-2.78	0.00	-4.50	-2.84	-4.50	-2.68
TCGA-E9-A5FL-10A-01D-A27P-09_BRCA	-2.78	-2.75	-2.69	-3.24	-2.67	-2.70	-2.53	-2.60	-2.38	0.00	-4.24	0.00	0.00	0.00	0.00	-2.57	-2.66
TCGA-E9-A5UO-10A-01D-A28E-09_BRCA	-2.75	-2.56	-2.57	-3.19	-2.68	-2.60	-2.46	-2.47	-2.31	0.00	-4.47	0.00	0.00	-4.47	0.00	-2.42	-2.54
TCGA-E9-A5UP-10A-01D-A28E-09_BRCA	-2.85	-4.63	0.00	-2.99	-2.58	-2.68	-2.54	-2.64	-2.51	-3.68	-2.90	-2.78	0.00	-2.82	0.00	-2.80	-2.70
TCGA-E9-A6HE-10A-01D-A31U-09_BRCA	-2.82	-2.65	-2.67	-3.19	-2.67	-2.63	-2.45	-2.53	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.51
TCGA-EA-A1QS-10A-01D-A22X-09_CESC	-2.65	0.00	-3.98	-2.89	-2.43	-2.57	-2.62	-2.55	-2.48	0.00	0.00	-4.46	0.00	-2.58	0.00	-2.65	-2.64
TCGA-EA-A1QT-10A-01D-A14W-08_CESC	-2.56	0.00	-4.52	-2.70	-2.46	-2.55	-2.52	-2.62	-2.59	-3.44	-3.02	0.00	-2.74	-2.70	0.00	-2.88	-2.49
TCGA-EA-A3HQ-10A-01D-A20U-09_CESC	-2.74	-2.67	-2.72	-3.25	-2.72	-2.68	-2.57	-2.46	-2.51	0.00	-4.53	-4.53	0.00	0.00	0.00	-2.44	-2.64
TCGA-EA-A3HR-10A-01D-A20U-09_CESC	-2.69	-4.04	-3.82	-2.86	-2.55	-2.57	-2.47	-2.48	-2.43	0.00	-4.22	-4.22	0.00	-4.52	-2.91	-2.72	-2.67
TCGA-EA-A3HS-10B-01D-A20U-09_CESC	-2.85	-2.57	-2.57	0.00	-2.77	-2.74	-2.57	-2.51	-2.64	-3.80	-2.75	-2.63	0.00	-2.77	0.00	-2.80	-2.71
TCGA-EA-A3HT-10A-01D-A21Q-09_CESC	-2.87	-2.78	-2.83	-3.32	-2.55	-2.60	-2.58	-2.53	-2.73	-3.46	-2.68	-2.81	-2.86	-2.76	0.00	-2.82	-2.69
TCGA-EA-A3HU-10B-01D-A20U-09_CESC	-2.79	-2.53	-2.56	0.00	-2.74	-2.70	-2.54	-2.49	-2.43	-4.59	-2.82	-4.59	0.00	-4.29	-2.92	-2.82	-2.66
TCGA-EA-A3QD-10A-01D-A22X-09_CESC	-2.86	-2.73	-2.77	-3.22	-2.50	-2.56	-2.50	-2.60	-2.71	-3.50	-2.65	-2.56	0.00	-2.75	0.00	-2.82	-2.66
TCGA-EA-A3QE-10A-01D-A21Q-09_CESC	-2.79	-2.70	-2.73	-3.13	-2.58	-2.67	-2.38	-2.51	-2.38	0.00	0.00	-3.69	0.00	-4.17	0.00	-2.49	-2.53
TCGA-EA-A3Y4-10A-01D-A243-09_CESC	-2.76	-4.51	-4.21	-2.85	-2.53	-2.56	-2.48	-2.56	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.63
TCGA-EA-A410-10A-01D-A243-09_CESC	-2.74	-4.11	-4.41	-3.00	-2.44	-2.52	-2.46	-2.48	-2.40	0.00	0.00	-4.41	0.00	0.00	0.00	-2.38	-2.53
TCGA-EA-A411-10A-01D-A243-09_CESC	-2.71	-2.43	-2.47	-4.39	-3.78	-4.08	-2.38	-2.37	-2.27	0.00	0.00	0.00	-4.39	0.00	0.00	-2.40	-2.50
TCGA-EA-A439-10A-01D-A243-09_CESC	-2.84	-4.21	-3.74	-3.05	-2.52	-2.54	-2.52	-2.55	-2.57	-3.52	-2.85	0.00	-2.75	-2.71	0.00	-2.86	-2.67
TCGA-EA-A43B-10A-01D-A243-09_CESC	-2.73	-2.69	-2.76	-3.34	-2.67	-2.71	-2.51	-2.62	-2.66	-3.53	-2.81	0.00	-2.65	-2.70	0.00	-2.75	-2.58
TCGA-EA-A44S-10A-01D-A26G-09_CESC	-2.71	-2.52	-2.53	-3.88	-3.25	-3.37	-2.51	-2.50	-2.50	-4.48	-4.48	-3.52	-4.48	-4.00	0.00	-2.55	-2.62
TCGA-EA-A4BA-10A-01D-A26G-09_CESC	-2.85	-2.78	-2.78	-3.26	-2.58	-2.67	-2.59	-2.64	-2.55	-4.60	-2.92	-2.86	-3.91	-3.83	0.00	-2.70	-2.69
TCGA-EA-A50E-10A-01D-A26G-09_CESC	-2.80	-3.73	-3.83	-3.11	-2.58	-2.59	-2.56	-2.54	-2.47	-4.13	-3.65	-3.95	-4.13	-3.73	-2.92	-3.73	-2.60
TCGA-EA-A556-10A-01D-A26G-09_CESC	-2.79	-3.55	-3.65	-3.05	-2.58	-2.60	-2.58	-2.66	-2.50	-4.55	-3.71	-3.95	-4.25	-3.95	0.00	-2.67	-2.68
TCGA-EA-A5FO-10A-01D-A28E-09_CESC	-2.71	0.00	-4.42	-3.14	-2.50	-2.45	-2.47	-2.45	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.35	-2.49
TCGA-EA-A5O9-10A-01D-A28E-09_CESC	-2.67	-2.66	-2.69	-3.47	-2.65	-2.73	-2.47	-2.56	-2.58	-3.47	-2.81	0.00	-2.70	-2.71	-2.96	0.00	-2.52
TCGA-EA-A5ZD-10A-01D-A28E-09_CESC	-2.74	-4.44	0.00	-3.03	-2.47	-2.49	-2.44	-2.55	-2.37	0.00	0.00	0.00	0.00	0.00	-2.69	0.00	-2.55
TCGA-EA-A5ZE-10A-01D-A28E-09_CESC	-2.76	0.00	0.00	-2.96	-2.47	-2.44	-2.38	-2.52	-2.41	0.00	0.00	0.00	0.00	0.00	-2.66	-4.43	-2.58
TCGA-EA-A5ZF-10A-01D-A28E-09_CESC	-2.73	-4.57	0.00	-2.94	-2.48	-2.71	-2.45	-2.52	-2.66	-3.42	-2.80	-2.66	0.00	-2.72	-2.93	0.00	-2.53
TCGA-EB-A1NK-10A-01D-A198-08_SKCM	-2.26	-2.71	-2.62	-2.81	-2.75	-2.76	-2.45	-2.37	-2.42	0.00	0.00	0.00	0.00	0.00	-3.14	-2.73	-2.33
TCGA-EB-A24C-10A-01D-A199-08_SKCM	-2.48	-2.50	-2.62	0.00	-2.69	-2.71	-2.54	-2.44	-2.47	0.00	-2.90	-2.77	0.00	0.00	-3.23	-2.70	-2.39
TCGA-EB-A24D-10A-01D-A199-08_SKCM	-2.51	-2.58	-2.63	0.00	-2.55	-2.64	-2.57	-2.65	-2.57	0.00	-2.80	-2.60	0.00	0.00	-3.08	-2.80	-2.43
TCGA-EB-A299-10A-01D-A199-08_SKCM	-2.41	-2.67	-2.74	-2.76	-2.62	-2.69	-2.48	-2.42	-2.40	0.00	0.00	0.00	-4.39	0.00	0.00	-2.50	-2.39
TCGA-EB-A3HV-10B-01D-A21A-08_SKCM	-2.49	-2.64	-2.66	-2.74	-2.59	-2.59	-2.57	-2.58	-2.46	-4.44	-4.44	0.00	0.00	-4.44	0.00	-2.54	-2.45
TCGA-EB-A3XB-10B-01D-A23B-08_SKCM	-2.62	0.00	-4.05	-2.85	-2.44	-2.62	-2.65	-2.62	-2.68	-3.23	-2.85	-2.71	-3.83	-2.66	0.00	-2.76	-2.56
TCGA-EB-A3XC-10A-01D-A23B-08_SKCM	-2.67	-2.76	-2.77	-2.92	-2.53	-2.63	-2.68	-2.50	-2.59	0.00	-2.90	-2.70	-4.35	0.00	-3.13	-2.78	-2.61
TCGA-EB-A3XD-10A-01D-A23B-08_SKCM	-2.54	-2.54	-2.55	-4.09	-3.79	-3.92	-2.52	-2.42	-2.53	0.00	0.00	-4.39	0.00	0.00	-3.01	-2.62	-2.46
TCGA-EB-A3XE-10A-01D-A23B-08_SKCM	-2.50	0.00	0.00	-2.70	-2.56	-2.56	-2.57	-2.55	-2.46	0.00	-3.76	-3.62	0.00	-3.76	0.00	-2.57	-2.51
TCGA-EB-A3XF-10A-01D-A23B-08_SKCM	-2.62	0.00	-4.05	-2.59	-2.61	-2.60	-2.61	-2.59	-2.75	-3.25	-3.00	-2.76	-4.53	-2.66	0.00	-2.78	-2.56
TCGA-EB-A3Y6-10A-01D-A23B-08_SKCM	-2.60	-2.70	-2.69	-2.87	-2.47	-2.68	-2.69	-2.66	-2.66	-4.25	-2.78	-2.66	0.00	-2.67	-3.04	-3.86	-2.62
TCGA-EB-A3Y7-10A-01D-A23B-08_SKCM	-2.51	-2.66	-2.63	-2.83	-2.56	-2.62	-2.56	-2.58	-2.44	0.00	-3.98	-3.68	0.00	-3.55	0.00	-2.58	-2.51
TCGA-EB-A41A-10A-01D-A24R-08_SKCM	-2.63	-2.60	-2.57	-4.17	-2.60	-2.62	-2.64	-2.59	-2.50	0.00	-2.65	-2.63	-4.17	-3.99	0.00	-2.53	-2.55
TCGA-EB-A41B-10A-01D-A24R-08_SKCM	-2.64	-2.77	-2.77	-2.95	-2.55	-2.65	-2.66	-2.55	-2.73	-3.47	-2.69	-2.68	-4.55	-2.70	-3.10	-4.55	-2.58
TCGA-EB-A42Y-10A-01D-A24R-08_SKCM	-2.42	-2.67	-2.68	-2.92	-2.65	-2.70	-2.65	-2.54	-2.51	0.00	0.00	0.00	0.00	-4.51	-3.02	-2.72	-2.55
TCGA-EB-A42Z-10A-01D-A24R-08_SKCM	-2.66	-2.77	-2.74	-2.93	-2.54	-2.62	-2.67	-2.67	-2.57	0.00	-2.84	-2.76	-4.57	0.00	0.00	-2.71	-2.61
TCGA-EB-A430-10A-01D-A24R-08_SKCM	-2.55	-2.68	-2.61	-2.81	-2.61	-2.66	-2.59	-2.68	-2.59	0.00	-4.48	0.00	0.00	0.00	0.00	-2.61	-2.54
TCGA-EB-A431-10A-01D-A25O-08_SKCM	-2.44	-2.64	-2.69	-2.81	-2.55	-2.69	-2.51	-2.46	-2.54	0.00	0.00	0.00	0.00	-4.31	0.00	-2.40	-2.40
TCGA-EB-A44N-10A-01D-A25O-08_SKCM	-2.46	-2.61	-2.58	-2.86	-2.57	-2.61	-2.52	-2.52	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.45
TCGA-EB-A44O-10A-01D-A25O-08_SKCM	-2.62	-2.74	-2.73	-2.87	-2.55	-2.58	-2.62	-2.62	-2.51	0.00	-2.94	-2.66	0.00	0.00	0.00	-2.63	-2.49
TCGA-EB-A44P-10A-01D-A25O-08_SKCM	-2.50	-2.78	-2.66	-2.85	-2.72	-2.72	-2.53	-2.54	-2.63	-3.38	-2.85	0.00	-2.74	-2.67	0.00	-2.72	-2.45
TCGA-EB-A44Q-10A-01D-A25O-08_SKCM	-2.48	0.00	0.00	-2.70	-2.48	-2.50	-2.49	-2.51	-2.48	0.00	0.00	0.00	0.00	0.00	-2.89	0.00	-2.44
TCGA-EB-A44R-10A-01D-A25O-08_SKCM	-2.56	-2.86	-2.79	-2.92	-2.47	-2.58	-2.59	-2.54	-2.67	-3.37	-2.61	-2.83	-2.80	-2.75	-3.05	0.00	-2.54
TCGA-EB-A4IQ-10A-01D-A25O-08_SKCM	-2.46	0.00	0.00	-2.70	-2.47	-2.48	-2.50	-2.47	-2.49	0.00	0.00	0.00	0.00	0.00	-3.10	-2.74	-2.43
TCGA-EB-A4IS-10A-01D-A25O-08_SKCM	-2.42	-2.49	-2.46	0.00	0.00	0.00	-2.49	-2.42	-2.42	0.00	0.00	0.00	0.00	0.00	-2.95	-2.63	-2.41
TCGA-EB-A4OY-10A-01D-A25O-08_SKCM	-2.54	-2.84	-2.69	-2.88	-2.49	-2.52	-2.57	-2.54	-2.55	0.00	-2.82	-2.68	0.00	0.00	0.00	-2.61	-2.48
TCGA-EB-A4OZ-10A-01D-A25O-08_SKCM	-2.58	-2.57	-2.55	0.00	-2.66	-2.76	-2.57	-2.58	-2.70	-3.25	-2.65	-2.71	-2.77	-2.59	-3.04	0.00	-2.44
TCGA-EB-A4P0-10A-01D-A25O-08_SKCM	-2.51	-2.61	-2.57	0.00	-2.65	-2.64	-2.59	-2.49	-2.45	0.00	-2.89	-2.64	0.00	0.00	-3.18	-2.85	-2.49
TCGA-EB-A4XL-10A-01D-A27N-08_SKCM	-2.53	0.00	-4.45	-2.58	-2.51	-2.55	-2.52	-2.47	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.44	-2.47
TCGA-EB-A51B-10A-01D-A27N-08_SKCM	-2.62	-2.80	-2.71	-2.91	-2.53	-2.67	-2.67	-2.62	-2.76	-3.41	-2.77	-2.66	0.00	-2.73	0.00	-2.82	-2.65
TCGA-EB-A550-10A-01D-A27N-08_SKCM	-2.52	-2.64	-2.63	-2.83	-2.58	-2.63	-2.53	-2.43	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.36	-2.47
TCGA-EB-A551-10A-01D-A27N-08_SKCM	-2.53	0.00	-4.46	-2.61	-2.58	-2.58	-2.59	-2.61	-2.78	-3.46	-2.84	-2.70	0.00	-2.70	0.00	-2.78	-2.53
TCGA-EB-A553-10A-01D-A27N-08_SKCM	-2.60	-2.60	-2.62	0.00	-2.69	-2.73	-2.66	-2.53	-2.66	-3.22	-2.71	-2.63	0.00	-2.67	-3.07	0.00	-2.54
TCGA-EB-A57M-10A-01D-A30X-08_SKCM	-2.56	0.00	0.00	-2.81	-2.57	-2.60	-2.61	-2.61	-2.60	0.00	0.00	0.00	0.00	0.00	-3.11	-2.95	-2.53
TCGA-EB-A5FP-10A-01D-A27N-08_SKCM	-2.61	-2.72	-2.69	-2.90	-2.68	-2.66	-2.61	-2.57	-2.74	-3.34	-2.82	-4.54	-2.76	-2.67	0.00	-2.76	-2.56
TCGA-EB-A5KH-10A-01D-A27N-08_SKCM	-2.56	0.00	0.00	-2.83	-2.57	-2.57	-2.58	-2.60	-2.63	-3.33	-2.87	0.00	-2.70	-2.69	0.00	-2.77	-2.53
TCGA-EB-A5SE-10A-01D-A30X-08_SKCM	-2.62	-4.58	-4.58	-2.86	-2.64	-2.65	-2.66	-2.62	-2.64	0.00	0.00	0.00	-4.58	0.00	0.00	-2.54	-2.57
TCGA-EB-A5SF-10A-01D-A30X-08_SKCM	-2.59	0.00	0.00	-2.78	-2.61	-2.55	-2.61	-2.63	-2.56	0.00	0.00	0.00	0.00	-4.50	0.00	-2.65	-2.55
TCGA-EB-A5SG-10A-01D-A30X-08_SKCM	-2.64	-2.84	-2.75	-2.98	-2.70	-2.83	-2.67	-2.77	-2.75	-3.50	-2.94	0.00	-2.89	-2.72	0.00	-2.83	-2.57
TCGA-EB-A5SH-10A-01D-A30X-08_SKCM	-2.46	0.00	0.00	-2.67	-2.59	-2.65	-2.62	-2.67	-2.52	0.00	0.00	0.00	0.00	-4.52	0.00	-2.56	-2.50
TCGA-EB-A5UL-10A-01D-A30X-08_SKCM	-2.48	-2.60	-2.61	-2.78	-2.60	0.00	0.00	-4.44	0.00	0.00	-2.82	0.00	-2.65	-2.43	0.00	0.00	-2.53
TCGA-EB-A5UM-10A-01D-A30X-08_SKCM	-2.60	-2.81	-2.82	-3.03	-2.68	-2.72	-2.63	-2.60	-2.56	0.00	0.00	0.00	0.00	0.00	-3.18	-2.77	-2.57

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EB-A5UN-10A-01D-A30X-08_SKCM	-2.58	0.00	0.00	-2.84	-2.62	-2.62	-2.65	-2.73	-2.73	-3.46	-3.22	0.00	-2.83	-2.74	0.00	-2.89	-2.58
TCGA-EB-A5VU-10A-01D-A32N-08_SKCM	-2.56	0.00	-4.63	-2.60	-2.63	-2.60	-2.66	-2.69	-2.58	0.00	0.00	-4.63	0.00	-4.33	0.00	-2.65	-2.55
TCGA-EB-A5VV-10A-01D-A32N-08_SKCM	-2.63	-2.86	-2.86	-3.10	-2.65	-2.79	-2.70	-2.62	-2.83	-3.34	-2.80	-2.85	-2.90	-2.77	-3.18	0.00	-2.67
TCGA-EB-A6L9-10A-01D-A32N-08_SKCM	-2.64	0.00	0.00	-2.81	-2.66	-2.67	-2.63	-2.66	-2.74	-3.38	-2.92	-4.66	-2.81	-2.74	-3.16	0.00	-2.56
TCGA-EB-A6QY-10B-01D-A32N-08_SKCM	-2.73	-2.87	-2.84	-3.05	-2.61	-2.76	-2.78	-2.65	-2.82	-3.53	-2.84	-2.88	-2.91	-2.84	-3.23	0.00	-2.68
TCGA-EB-A6QZ-10B-01D-A32N-08_SKCM	-2.60	0.00	-4.62	-2.68	-2.57	-2.63	-2.65	-2.56	-2.63	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.52
TCGA-EB-A6R0-10B-01D-A32N-08_SKCM	-2.63	-2.80	-2.77	-2.97	-2.57	-2.72	-2.69	-2.62	-2.58	0.00	-2.95	-2.80	0.00	0.00	-3.21	-2.78	-2.61
TCGA-EC-A1NJ-10A-01D-A14G-09_UCEC	-2.88	-2.83	-2.90	-3.37	-2.56	-2.60	-2.56	-2.72	-2.55	0.00	-2.85	-2.77	-4.54	0.00	-2.90	0.00	-2.72
TCGA-EC-A1QX-10A-01D-A16D-09_UCEC	-2.67	-2.74	-2.68	-3.08	-2.73	-2.62	-2.46	-2.56	-2.43	0.00	0.00	0.00	0.00	-4.38	0.00	-2.46	-2.52
TCGA-EC-A24G-10A-01D-A16D-09_UCEC	-2.90	-2.88	-2.83	-3.41	-2.60	-2.66	-2.63	-2.65	-2.79	-3.46	-2.76	-2.71	-4.67	-2.74	-3.09	0.00	-2.78
TCGA-ED-A459-10A-01D-A25V-10_LIHC	-2.38	-2.42	-2.47	-2.68	-2.53	-2.38	-2.34	-2.30	-2.28	0.00	0.00	0.00	0.00	0.00	-2.81	-2.47	-2.40
TCGA-ED-A4XI-10A-01D-A25V-10_LIHC	-2.34	-2.42	-2.43	-2.77	-2.62	-2.41	-2.24	-2.34	-2.27	0.00	0.00	0.00	0.00	0.00	-2.66	-4.30	-2.32
TCGA-ED-A5KG-10A-01D-A27I-10_LIHC	-2.35	0.00	0.00	-2.55	-2.38	-2.27	-2.26	-2.40	-2.29	0.00	0.00	0.00	0.00	0.00	-2.87	-2.47	-2.35
TCGA-ED-A627-10B-01D-A30V-10_LIHC	-2.40	-2.62	-2.71	-2.79	-2.79	-2.58	-2.32	-2.37	-2.54	-3.51	-2.88	0.00	-2.79	-2.51	0.00	-2.93	-2.39
TCGA-ED-A66X-10A-01D-A30V-10_LIHC	-2.32	-4.06	0.00	-2.55	-2.43	-2.45	-2.39	-2.43	-2.35	0.00	0.00	0.00	-3.76	0.00	0.00	-2.35	-2.40
TCGA-ED-A66Y-10A-01D-A30V-10_LIHC	-2.63	-2.58	-2.80	-2.78	-2.45	-2.46	-2.33	-2.63	-2.41	0.00	-2.87	-2.70	0.00	0.00	-2.80	0.00	-2.46
TCGA-EE-A17X-10A-01D-A199-08_SKCM	-2.38	-2.80	-2.65	-2.70	-2.60	-2.69	-2.54	-2.55	-2.40	0.00	0.00	0.00	0.00	-4.51	-3.00	0.00	-2.36
TCGA-EE-A17Y-10B-01D-A198-08_SKCM	-2.36	0.00	0.00	-2.58	-2.44	-2.56	-2.53	-2.54	-2.43	0.00	0.00	0.00	0.00	-4.46	-2.93	0.00	-2.41
TCGA-EE-A17Z-10A-01D-A198-08_SKCM	-2.44	-3.06	-2.92	-2.85	-2.57	-2.62	-2.65	-2.77	-2.54	0.00	-3.01	-2.93	0.00	0.00	0.00	-2.68	-2.42
TCGA-EE-A180-10B-01D-A21A-08_SKCM	-2.52	-2.72	-2.65	-2.80	-2.60	-2.67	-2.53	-2.48	-2.44	-4.48	0.00	0.00	0.00	0.00	-3.05	-2.63	-2.44
TCGA-EE-A181-10A-01D-A198-08_SKCM	-2.40	-4.51	0.00	-2.68	-2.48	-2.53	-2.55	-2.44	-2.39	0.00	0.00	0.00	0.00	-4.51	0.00	-2.47	-2.38
TCGA-EE-A182-10A-01D-A198-08_SKCM	-2.47	-2.72	-2.71	-2.79	-2.65	-2.67	-2.53	-2.55	-2.66	-3.47	-2.86	0.00	-2.86	-2.68	0.00	-2.77	-2.45
TCGA-EE-A183-10A-01D-A198-08_SKCM	-2.52	0.00	-4.50	-2.60	-2.57	-2.58	-2.59	-2.62	-2.75	-3.32	-2.87	0.00	-2.75	-2.65	0.00	-2.76	-2.57
TCGA-EE-A184-10B-01D-A198-08_SKCM	-2.41	0.00	0.00	-2.62	-2.50	-2.58	-2.58	-2.54	-2.55	0.00	-4.55	0.00	-4.55	-4.55	0.00	-2.55	-2.43
TCGA-EE-A185-10A-01D-A198-08_SKCM	-2.36	-2.78	-2.71	-2.79	-2.60	-2.62	-2.47	-2.48	-2.44	0.00	0.00	0.00	0.00	0.00	-2.93	0.00	-2.33
TCGA-EE-A20B-10A-01D-A198-08_SKCM	-2.46	-2.82	-2.71	-2.93	-2.50	-2.59	-2.62	-2.48	-2.51	0.00	-2.91	-2.86	0.00	0.00	-3.10	-2.77	-2.43
TCGA-EE-A20C-10A-01D-A198-08_SKCM	-2.45	-4.52	-4.52	-2.60	-2.48	-2.52	-2.54	-2.51	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.50
TCGA-EE-A20F-10A-01D-A198-08_SKCM	-2.50	-4.09	-4.27	-2.73	-2.51	-2.55	-2.57	-2.47	-2.47	0.00	0.00	0.00	0.00	-4.57	-3.08	-2.75	-2.42
TCGA-EE-A20H-10A-01D-A199-08_SKCM	-2.42	-2.82	-2.72	-2.88	-2.62	-2.56	-2.64	-2.71	-2.54	0.00	-3.20	-2.87	0.00	0.00	-3.22	-3.02	-2.44
TCGA-EE-A20I-10A-01D-A198-08_SKCM	-2.41	-2.78	-2.72	-2.76	-2.72	-2.73	-2.50	-2.50	-2.49	0.00	0.00	0.00	0.00	0.00	-3.14	-2.80	-2.37
TCGA-EE-A29A-10A-01D-A198-08_SKCM	-2.52	-2.73	-2.77	-2.88	-2.55	-2.59	-2.64	-2.57	-2.51	0.00	-2.99	-2.80	0.00	-4.29	0.00	-2.57	-2.52
TCGA-EE-A29B-10A-01D-A199-08_SKCM	-2.40	0.00	0.00	-2.56	-2.53	-2.51	-2.53	-2.50	-2.52	0.00	0.00	0.00	0.00	-4.51	0.00	-2.43	-2.41
TCGA-EE-A29C-10A-01D-A199-08_SKCM	-2.59	-4.66	0.00	-2.80	-2.66	-2.67	-2.65	-2.68	-2.84	-3.29	-2.88	-2.81	-4.05	-2.76	0.00	-2.74	-2.53
TCGA-EE-A29D-10A-01D-A199-08_SKCM	-2.49	-2.82	-2.68	-2.84	-2.66	-2.77	-2.58	-2.50	-2.68	-3.53	-2.90	0.00	-2.82	-2.67	-3.17	-4.27	-2.36
TCGA-EE-A29E-10A-01D-A199-08_SKCM	-2.52	0.00	-4.24	-2.78	-2.53	-2.60	-2.59	-2.58	-2.69	-3.43	-3.01	0.00	-2.78	-2.73	0.00	-2.74	-2.46
TCGA-EE-A29G-10A-01D-A198-08_SKCM	-2.42	0.00	-4.51	-2.59	-2.48	-2.43	-2.54	-2.47	-2.48	0.00	0.00	0.00	0.00	-4.51	0.00	-2.49	-2.40
TCGA-EE-A29H-10A-01D-A199-08_SKCM	-2.52	-2.82	-2.77	-2.84	-2.69	-2.84	-2.59	-2.55	-2.70	-3.41	-2.98	0.00	-2.93	-2.71	0.00	-2.82	-2.43
TCGA-EE-A29L-10A-01D-A198-08_SKCM	-2.45	0.00	0.00	-2.59	-2.47	-2.56	-2.50	-2.54	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.41
TCGA-EE-A29M-10A-01D-A198-08_SKCM	-2.39	0.00	-4.53	-2.69	-2.50	-2.52	-2.59	-2.47	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.38
TCGA-EE-A29N-10A-01D-A199-08_SKCM	-2.42	-4.53	0.00	-2.48	-2.49	-2.53	-2.49	-2.54	-2.57	0.00	0.00	0.00	0.00	-4.53	0.00	-2.55	-2.36
TCGA-EE-A29P-10A-01D-A199-08_SKCM	-2.41	-2.73	-2.71	-2.83	-2.68	-2.74	-2.54	-2.45	-2.38	0.00	0.00	-4.18	0.00	0.00	-3.12	-2.71	-2.35
TCGA-EE-A29Q-10A-01D-A199-08_SKCM	-2.51	-2.62	-2.59	0.00	-2.66	-2.79	-2.59	-2.56	-2.69	-3.27	-2.77	-2.73	-2.85	-2.67	0.00	-2.78	-2.43
TCGA-EE-A29R-10A-01D-A199-08_SKCM	-2.45	0.00	0.00	-2.61	-2.52	-2.53	-2.50	-2.49	-2.43	0.00	0.00	-4.21	-4.51	0.00	0.00	-2.54	-2.40
TCGA-EE-A29S-10A-01D-A199-08_SKCM	-2.43	0.00	0.00	-2.58	-2.47	-2.49	-2.51	-2.49	-2.44	0.00	0.00	0.00	-4.45	-4.15	-3.24	-2.81	-2.32
TCGA-EE-A29T-10A-01D-A199-08_SKCM	-2.46	-2.73	-2.74	-2.88	-2.67	-2.68	-2.64	-2.54	-2.47	0.00	0.00	0.00	-4.58	0.00	0.00	-2.47	-2.49
TCGA-EE-A29V-10A-01D-A199-08_SKCM	-2.53	-2.71	-2.72	-2.82	-2.73	-2.76	-2.59	-2.63	-2.83	-3.42	-2.97	0.00	-3.03	-2.73	0.00	-2.97	-2.43
TCGA-EE-A29W-10A-01D-A198-08_SKCM	-2.43	0.00	0.00	-2.56	-2.46	-2.66	-2.56	-2.55	-2.73	-3.63	-2.99	0.00	-2.88	-2.68	0.00	-2.78	-2.46
TCGA-EE-A29X-10A-01D-A198-08_SKCM	-2.43	-2.83	-2.74	-2.85	-2.51	-2.67	-2.66	-2.63	-2.81	-3.30	-2.70	-2.85	-2.88	-2.72	0.00	-2.87	-2.48
TCGA-EE-A2A0-10A-01D-A198-08_SKCM	-2.37	0.00	0.00	-2.52	-2.48	-2.50	-2.53	-2.49	-2.43	0.00	0.00	0.00	0.00	0.00	-3.07	-2.82	-2.37
TCGA-EE-A2A1-10A-01D-A199-08_SKCM	-2.47	-4.44	0.00	-2.56	-2.43	-2.59	-2.58	-2.57	-2.68	-3.30	-2.94	0.00	-2.84	-2.59	0.00	-2.69	-2.45
TCGA-EE-A2A2-10A-01D-A198-08_SKCM	-2.53	-2.65	-2.61	0.00	-2.77	-2.78	-2.54	-2.46	-2.74	-3.22	-2.79	-2.83	-2.81	-2.73	0.00	-2.83	-2.49
TCGA-EE-A2A5-10A-01D-A199-08_SKCM	-2.36	-4.50	0.00	-2.58	-2.46	-2.52	-2.55	-2.41	-2.42	0.00	0.00	-4.50	0.00	-4.50	0.00	-2.48	-2.38
TCGA-EE-A2A6-10A-01D-A199-08_SKCM	-2.27	0.00	0.00	-2.71	-2.53	-2.50	-2.52	-2.44	-2.58	0.00	0.00	0.00	0.00	-4.49	0.00	-2.44	-2.40
TCGA-EE-A2GB-10A-01D-A199-08_SKCM	-2.41	0.00	0.00	-2.51	-2.46	-2.48	-2.56	-2.51	-2.48	0.00	0.00	0.00	0.00	-4.46	0.00	-2.57	-2.28
TCGA-EE-A2GC-10A-01D-A199-08_SKCM	-2.56	-2.79	-2.82	-2.93	-2.79	-2.76	-2.63	-2.60	-2.72	-3.42	-2.87	0.00	-2.80	-2.71	0.00	-2.76	-2.60
TCGA-EE-A2GD-10A-01D-A198-08_SKCM	-2.44	0.00	0.00	-2.53	-2.46	-2.60	-2.53	-2.51	-2.48	0.00	0.00	0.00	0.00	-4.02	0.00	-2.46	-2.43
TCGA-EE-A2GE-10A-01D-A198-08_SKCM	-2.44	0.00	-4.48	-2.55	-2.46	-2.49	-2.57	-2.58	-2.46	0.00	0.00	0.00	0.00	0.00	-2.94	0.00	-2.43
TCGA-EE-A2GH-10A-01D-A198-08_SKCM	-2.52	-2.62	-2.65	-2.82	-2.58	-2.66	-2.51	-2.60	-2.54	0.00	-4.12	0.00	0.00	-4.42	0.00	-2.58	-2.45
TCGA-EE-A2GI-10A-01D-A198-08_SKCM	-2.34	-2.48	-2.46	-4.45	0.00	0.00	-2.46	-2.49	-2.49	0.00	-4.45	0.00	0.00	-4.45	-2.85	0.00	-2.40
TCGA-EE-A2GJ-10A-01D-A198-08_SKCM	-2.42	-4.43	0.00	-2.61	-2.54	-2.53	-2.57	-2.54	-2.94	-3.32	-3.00	-4.43	-2.93	-2.76	0.00	-2.90	-2.36
TCGA-EE-A2GK-10A-01D-A198-08_SKCM	-2.48	0.00	-4.53	-2.74	-2.53	-2.53	-2.59	-2.46	-2.72	-3.27	-2.88	0.00	-2.77	-2.68	0.00	-2.69	-2.43
TCGA-EE-A2GL-10A-01D-A198-08_SKCM	-2.57	-2.86	-2.82	-2.93	-2.54	-2.66	-2.58	-2.47	-2.61	-3.42	-3.07	-2.76	0.00	0.00	-3.20	-2.85	-2.50
TCGA-EE-A2GM-10A-01D-A198-08_SKCM	-2.37	-4.49	0.00	-2.55	-2.49	-2.50	-2.53	-2.57	-2.47	0.00	0.00	0.00	0.00	-3.59	-3.15	-2.77	-2.38
TCGA-EE-A2GN-10A-01D-A198-08_SKCM	-2.42	-2.80	-2.78	-2.90	-2.52	-2.61	-2.64	-2.56	-2.54	0.00	-3.07	-2.92	0.00	0.00	-3.21	-2.86	-2.43
TCGA-EE-A2GO-10A-01D-A198-08_SKCM	-2.48	-2.78	-2.71	-2.72	-2.63	-2.70	-2.50	-2.57	-2.69	-3.51	-2.97	0.00	-2.88	-2.62	-3.12	-4.16	-2.37
TCGA-EE-A2GP-10A-01D-A199-08_SKCM	-2.43	0.00	0.00	-2.80	-2.62	-2.60	-2.58	-2.39	-2.63	-3.36	-2.93	0.00	-2.95	-2.73	-3.14	0.00	-2.53
TCGA-EE-A2GR-10A-01D-A199-08_SKCM	-2.53	-2.90	-2.84	-2.87	-2.54	-2.66	-2.71	-2.56	-2.89	-3.25	-2.94	-2.92	-3.12	-2.87	0.00	-2.95	-2.45
TCGA-EE-A2GS-10A-01D-A199-08_SKCM	-2.45	0.00	0.00	-2.78	-2.59	-2.57	-2.58	-2.57	-2.47	0.00	0.00	0.00	-4.34	-4.04	0.00	-2.58	-2.41
TCGA-EE-A2GT-10A-01D-A199-08_SKCM	-2.64	-4.61	-4.31	-2.79	-2.62	-2.69	-2.67	-2.63	-2.70	-3.35	-2.84	-4.61	-2.87	-2.72	0.00	-2.81	-2.55
TCGA-EE-A2GU-10A-01D-A198-08_SKCM	-2.46	-2.74	-2.64	-2.81	-2.66	-2.71	-2.61	-2.56	-2.51	0.00	-4.18	0.00	0.00	-4.48	-3.05	-2.65	-2.46
TCGA-EE-A2M5-10A-01D-A199-08_SKCM	-2.56	-2.86	-2.82	-2.83	-2.61	-2.61	-2.66	-2.68	-2.78	-3.54	-2.94	-2.65	0.00	-2.67	0.00	-2.92	-2.43
TCGA-EE-A2M6-10A-01D-A199-08_SKCM	-2.50	0.00	0.00	-2.53	-2.55	-2.49	-2.52	-2.53	-2.53	0.00	0.00	0.00	0.00	-4.39	0.00	-2.58	-2.33
TCGA-EE-A2M7-10A-01D-A199-08_SKCM	-2.43	0.00	0.00	-2.57	-2.42	-2.52	-2.53	-2.46	-2.55	0.00	0.00	0.00	0.00	-4.52	0.00	-2.44	-2.38
TCGA-EE-A2M8-10A-01D-A198-08_SKCM	-2.49	-2.77	-2.75	-2.90	-2.47	-2.59	-2.57	-2.62	-2.85	-3.59	-2.74	-2.82	-2.89	-2.69	0.00	-2.78	-2.47
TCGA-EE-A2MC-10A-01D-A199-08_SKCM	-2.40	0.00	0.00	-2.69	-2.54	-2.53	-2.55	-2.51	-2.55	0.00	0.00	0.00	0.00	0.00	-3.28	-2.89	-2.35
TCGA-EE-A2MD-10A-01D-A199-08_SKCM	-2.55	-2.79	-2.69	-2.84	-2.59	-2.72	-2.58	-2.54	-4.01	-3.12	-2.65	0.00	-2.58	-2.53	0.00	0.00	-2.44
TCGA-EE-A2ME-10A-01D-A199-08_SKCM	-2.52	0.00	0.00	-2.74	-2.53	-2.57	-2.63	-2.56	-2.65	-3.27	-2.96	0.00	-2.79	-2.67	0.00	-2.77	-2.44
TCGA-EE-A2MF-10B-01D-A21A-08_SKCM	-2.31	0.00	0.00	-2.65	-2.44	-2.46	-2.53	-2.58	-2.40	0.00	0.00	0.00	0.00	-4.41	0.00	-2.52	-2.39
TCGA-EE-A2MG-10A-01D-A199-08_SKCM	-2.39	-2.66	-2.69	-2.85	-2.67	-2.67	-2.50	-2.54	-2.48	0.00	0.00	0.00	0.00	-4.49	0.00	-2.52	-2.38
TCGA-EE-A2MH-10A-01D-A199-08_SKCM	-2.50	0.00	0.00	-2.52	-2.50	-2.55	-2.64	-2.66	-2.59	0.00	-4.31	0.00	0.00	0.00	-3.27	-2.93	-2.38
TCGA-EE-A2MI-10A-01D-A199-08_SKCM	-2.38	0.00	0.00	-2.50	-2.48	-2.46	-2.50	-2.56	-2.52	0.00	0.00	0.00	0.00	-4.42	0.00	-2.52	-2.39
TCGA-EE-A2MJ-10A-01D-A199-08_SKCM	-2.43	0.00	-4.39	-2.49	-2.48	-2.47	-2.50	-2.50	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.34
TCGA-EE-A2MK-10A-01D-A198-08_SKCM	-2.58	-2.80	-2.86	-2.86	-2.58	-2.72	-2.61	-2.70	-3.13	-3.55	-2.90	-2.62	-4.45	-2.87	0.00	-2.88	-2.47
TCGA-EE-A2ML-10A-01D-A199-08_SKCM	-2.35	-3.03	-2.84	-2.84	-2.83	-2.86	-2.56	-2.62	-2.48	0.00	0.00	0.00	-4.26	-4.26	-3.05	-2.78	-2.38
TCGA-EE-A2MM-10A-01D-A198-08_SKCM	-2.46	0.00	0.00	-2.72	-2.49	-2.58	-2.58	-2.53	-2.73	-3.45	-2.98	0.00	-2.83	-2.67	-3.24	0.00	-2.39
TCGA-EE-A2MN-10A-01D-A199-08_SKCM	-2.42	0.00	-4.38	-2.63	-2.40	-2.51	-2.51	-2.49	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.48	-2.35
TCGA-EE-A2MP-10A-01D-A199-08_SKCM	-2.52	-2.81	-2.72	-2.90	-2.49	-2.51	-2.64	-2.48	-2.48	0.00	-2.83	-2.72	0.00	0.00	-3.22	-2.79	-2.44
TCGA-EE-A2MQ-10A-01D-A199-08_SKCM	-2.46	0.00	0.00	-2.52	-2.53	-2.49	-2.50	-2.48	-2.46	0.00	0.00	0.00	0.00	-4.22	-2.99	-2.69	-2.36
TCGA-EE-A2MR-10A-01D-A198-08_SKCM	-2.47	-4.51	0.00	-2.64	-2.47	-2.57	-2.47	-2.52	-2.49	0.00	0.00	-4.51	0.00	-4.51	0.00	-2.51	-2.37
TCGA-EE-A2MS-10A-01D-A199-08_SKCM	-2.55	-2.61	-2.58	0.00	-2.56	-2.68	-2.62	-2.52	-2.72	-3.66	-2.66	-2.60	0.00	-2.76	-3.07	0.00	-2.52
TCGA-EE-A2MT-10A-01D-A199-08_SKCM	-2.32	-4.45	-4.15	-2.67	-2.57	-2.56	-2.55	-2.62	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.37
TCGA-EE-A2MU-10A-01D-A198-08_SKCM	-2.48	0.00	0.00	-2.55	-2.50	-2.55	-2.57	-2.53	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.41
TCGA-EE-A3AA-10A-01D-A198-08_SKCM	-2.48	0.00	-4.63	-2.73	-2.50	-2.62	-2.58	-2.55	-2.78	-3.43	-2.97	0.00	-2.91	-2.71	0.00	-2.71	-2.47
TCGA-EE-A3AB-10A-01D-A198-08_SKCM	-2.47	0.00	0.00	-2.67	-2.48	-2.57	-2.55	-2.54	-2.47	0.00	-4.52	0.00	0.00	0.00	0.00	-2.47	-2.37
TCGA-EE-A3AC-10A-01D-A198-08_SKCM	-2.48	0.00	0.00	-2.72	-2.47	-2.58	-2.54	-2.52	-2.77	-3.25	-2.94	0.00	-2.84	-2.74	0.00	-2.83	-2.42
TCGA-EE-A3AD-10A-01D-A198-08_SKCM	-2.39	-4.21	-4.51	-2.64	-2.48	-2.55	-2.56	-2.43	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.36

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EE-A3AE-10A-01D-A198-08_SKCM	-2.47	0.00	0.00	-2.58	-2.55	-2.56	-2.58	-2.47	-2.48	0.00	0.00	-4.53	0.00	0.00	-3.04	-2.66	-2.42
TCGA-EE-A3AF-10A-01D-A198-08_SKCM	-2.35	0.00	0.00	-2.74	-2.54	-2.55	-2.57	-2.52	-2.47	0.00	0.00	-4.46	0.00	-4.46	-2.93	-2.65	-2.48
TCGA-EE-A3AG-10A-01D-A198-08_SKCM	-2.45	-2.78	-2.85	-2.87	-2.56	-2.66	-2.65	-2.55	0.00	-3.17	-2.65	-2.82	-2.76	-2.62	0.00	0.00	-2.58
TCGA-EE-A3AH-10A-01D-A198-08_SKCM	-2.37	-2.55	-2.52	-4.42	-2.75	-2.72	-2.58	-2.59	-2.48	0.00	-3.19	-2.71	0.00	0.00	0.00	-2.53	-2.45
TCGA-EE-A3J3-10A-01D-A20D-08_SKCM	-2.67	-2.75	-2.77	-2.93	-2.50	-2.68	-2.64	-2.63	-2.69	-3.30	-2.72	-2.75	-2.76	-2.68	0.00	-2.78	-2.57
TCGA-EE-A3J4-10A-01D-A20D-08_SKCM	-2.48	-4.47	-4.47	-2.57	-2.55	-2.56	-2.57	-2.48	-2.40	0.00	0.00	0.00	0.00	-4.47	-3.02	-2.69	-2.45
TCGA-EE-A3J5-10A-01D-A20D-08_SKCM	-2.57	0.00	0.00	-2.60	-2.58	-2.56	-2.58	-2.44	-2.59	-3.39	0.00	-4.51	0.00	0.00	0.00	-2.44	-2.53
TCGA-EE-A3J7-10A-01D-A20D-08_SKCM	-2.36	0.00	0.00	-2.66	-2.47	-2.54	-2.52	-2.48	-2.49	0.00	0.00	0.00	0.00	-4.48	-2.98	-2.65	-2.40
TCGA-EE-A3J8-10A-01D-A20D-08_SKCM	-2.59	-2.71	-2.76	-2.84	-2.47	-2.62	-2.65	-2.64	-2.59	0.00	-2.85	-2.71	0.00	-4.55	-2.99	-2.75	-2.53
TCGA-EE-A3JA-10A-01D-A20D-08_SKCM	-2.42	0.00	0.00	-2.49	-2.44	-2.49	-2.51	-2.52	-2.43	-4.43	0.00	0.00	0.00	-4.43	0.00	-2.37	-2.46
TCGA-EE-A3JB-10A-01D-A21A-08_SKCM	-2.54	-4.54	0.00	-2.71	-2.53	-2.51	-2.57	-2.51	-2.48	-4.54	0.00	0.00	0.00	-4.54	0.00	-2.52	-2.48
TCGA-EE-A3JD-10A-01D-A20D-08_SKCM	-2.37	-4.45	0.00	-2.68	-2.42	-2.62	-2.50	-2.56	-2.37	0.00	0.00	0.00	0.00	-4.45	-2.96	-2.68	-2.42
TCGA-EE-A3JE-10A-01D-A20D-08_SKCM	-2.46	0.00	0.00	-2.68	-2.46	-2.51	-2.54	-2.47	-2.53	0.00	0.00	-4.43	0.00	-4.43	0.00	-2.40	-2.44
TCGA-EE-A3JH-10A-01D-A21A-08_SKCM	-2.55	0.00	0.00	-2.78	-2.55	-2.61	-2.59	-2.66	-2.67	-3.31	-2.88	0.00	-2.83	-2.67	0.00	-2.75	-2.52
TCGA-EE-A3JI-10A-01D-A21A-08_SKCM	-2.63	-2.78	-2.81	-2.98	-2.53	-2.64	-2.60	-2.56	-2.58	-3.29	-2.97	-2.78	0.00	0.00	-3.18	-2.78	-2.49
TCGA-EF-5830-10A-01D-1657-10_READ	-2.45	0.00	0.00	-2.71	-2.35	-2.46	-2.30	-2.56	-2.29	0.00	0.00	0.00	0.00	0.00	0.00	-2.69	-2.41
TCGA-EI-6506-10A-01D-1733-10_READ	-2.59	-2.80	-2.76	0.00	-2.73	-2.74	-2.51	-2.69	-2.61	-3.50	-2.97	0.00	-2.82	-2.83	-3.50	0.00	-2.37
TCGA-EI-6507-10A-01D-1733-10_READ	-2.48	-2.81	0.00	-3.11	-2.54	-2.58	-2.44	-2.70	-2.59	-3.39	-2.94	0.00	-2.90	-2.81	0.00	-3.11	-2.40
TCGA-EI-6508-10A-01D-1733-10_READ	-2.59	-2.54	-2.52	0.00	-2.94	-2.74	-2.51	-2.61	-2.71	-3.56	-2.82	-2.88	-2.76	-2.80	-3.46	0.00	-2.41
TCGA-EI-6509-10A-01D-1733-10_READ	-2.48	-2.66	-2.72	-2.96	-2.66	-2.69	-2.40	-2.62	-2.41	0.00	0.00	0.00	0.00	-4.32	0.00	-2.62	-2.43
TCGA-EI-6510-10A-01D-1733-10_READ	-2.59	-2.92	-2.81	-2.98	-2.59	-2.57	-2.59	-2.65	-2.73	-3.48	-2.93	-2.59	0.00	-2.81	0.00	-3.17	-2.52
TCGA-EI-6511-10A-01D-1733-10_READ	-2.60	-2.88	-2.84	-2.85	-2.53	-2.71	-2.53	-2.69	-2.48	0.00	-3.17	-2.93	0.00	0.00	0.00	-2.79	-2.56
TCGA-EI-6512-10A-01D-1733-10_READ	-2.45	-2.69	-2.62	-2.98	-2.75	-2.73	-2.46	-2.61	-2.34	0.00	0.00	0.00	0.00	-4.36	0.00	-2.62	-2.41
TCGA-EI-6513-10A-01D-1733-10_READ	-2.42	-2.68	-2.59	-2.79	-2.64	0.00	-2.55	-2.75	-2.48	0.00	0.00	0.00	0.00	-2.54	-2.98	-4.21	-2.43
TCGA-EI-6514-10A-01D-1733-10_READ	-2.61	0.00	0.00	-2.78	-2.52	-2.54	-2.42	-2.63	-2.32	0.00	0.00	0.00	0.00	0.00	0.00	-2.64	-2.39
TCGA-EI-6881-10A-01D-1924-10_READ	-2.55	-2.55	-2.44	0.00	-2.82	-2.69	-2.44	-2.63	-2.51	0.00	-3.07	-2.78	0.00	0.00	-3.19	-2.91	-2.51
TCGA-EI-6882-10A-01D-1924-10_READ	-2.64	-2.72	-2.91	-2.94	-2.65	-2.57	-2.54	-2.68	0.00	-3.02	-2.65	-2.64	-2.80	-2.56	0.00	0.00	-2.57
TCGA-EI-6883-10A-01D-1924-10_READ	-2.69	0.00	0.00	-2.73	-2.67	-2.57	-2.54	-2.73	-2.76	-3.44	-3.22	-2.81	0.00	-2.94	0.00	-3.08	-2.47
TCGA-EI-6884-10A-01D-1924-10_READ	-2.53	-2.96	0.00	-2.79	-2.66	-2.77	-2.41	-2.56	-2.83	-3.21	-3.11	0.00	-2.90	-2.63	0.00	-2.90	-2.33
TCGA-EI-6885-10A-01D-1924-10_READ	-2.57	-2.88	-2.88	-2.92	-2.79	-2.73	-2.40	-2.58	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.38
TCGA-EI-6917-10A-01D-1924-10_READ	-2.58	0.00	0.00	-2.76	-2.56	-2.54	-2.47	-2.78	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.70	-2.42
TCGA-EI-7002-10A-01D-1924-10_READ	-2.55	0.00	0.00	-2.62	-2.52	-2.46	-2.40	-2.60	-2.44	0.00	0.00	0.00	0.00	0.00	-3.18	-2.87	-2.39
TCGA-EI-7004-10A-01D-1924-10_READ	-2.71	0.00	0.00	-2.51	-2.56	-2.48	-2.41	-2.73	-2.72	-3.39	-2.96	0.00	-2.71	-2.81	0.00	-3.06	-2.41
TCGA-EJ-5494-10A-01D-1577-08_PRAD	-2.61	-2.79	-2.80	-3.00	-2.53	-2.63	-2.70	-2.52	-2.57	0.00	-2.99	-2.77	0.00	0.00	0.00	-2.53	-2.56
TCGA-EJ-5495-10A-01D-1577-08_PRAD	-2.63	-4.76	-4.76	-2.89	-2.59	-2.66	-2.76	-2.59	-2.74	-3.38	-2.90	-4.46	-2.84	-2.75	-3.09	-4.46	-2.50
TCGA-EJ-5496-10A-01D-1577-08_PRAD	-2.53	-4.65	-4.35	-2.79	-2.51	-2.55	-2.59	-2.47	-2.50	0.00	0.00	0.00	-4.65	-4.35	0.00	-2.45	-2.50
TCGA-EJ-5497-10A-01D-1577-08_PRAD	-2.60	0.00	0.00	-2.69	-2.59	-2.63	-2.66	-2.57	-2.80	-3.41	-2.99	-4.69	-2.80	-2.70	0.00	-2.81	-2.52
TCGA-EJ-5498-10A-01D-1577-08_PRAD	-2.49	-4.67	-4.36	-2.87	-2.62	-2.55	-2.63	-2.53	-2.56	0.00	-4.67	0.00	0.00	-4.67	0.00	-2.60	-2.49
TCGA-EJ-5499-10A-01D-1577-08_PRAD	-2.49	-4.64	-4.64	-2.73	-2.52	-2.57	-2.60	-2.62	-2.60	0.00	0.00	-4.64	0.00	-4.64	0.00	-2.60	-2.47
TCGA-EJ-5501-10A-01D-1577-08_PRAD	-2.45	-2.55	-2.54	0.00	-4.06	-4.06	-2.59	-2.47	-2.53	0.00	-4.53	0.00	0.00	-4.23	-2.81	-4.23	-2.47
TCGA-EJ-5502-10A-01D-1577-08_PRAD	-2.56	-4.13	0.00	-2.66	-2.56	-2.57	-2.64	-2.53	-2.50	0.00	-4.61	-4.61	-4.61	-4.31	-3.12	-2.81	-2.59
TCGA-EJ-5503-10A-01D-1577-08_PRAD	-2.42	-2.56	-2.56	-4.04	-4.22	-4.22	-2.54	-2.48	-2.48	0.00	-4.52	0.00	0.00	0.00	-2.81	-4.04	-2.47
TCGA-EJ-5504-10A-01D-1577-08_PRAD	-2.57	-2.71	-2.62	-4.21	-2.74	-2.74	-2.70	-2.65	-2.62	0.00	-2.96	-2.75	0.00	0.00	-3.12	-2.78	-2.59
TCGA-EJ-5505-10A-01D-1577-08_PRAD	-2.58	0.00	-4.63	-2.67	-2.55	-2.55	-2.57	-2.53	-2.60	0.00	0.00	-4.63	0.00	-4.63	0.00	-2.50	-2.54
TCGA-EJ-5506-10A-01D-1577-08_PRAD	-2.51	0.00	-4.62	-2.88	-2.58	-2.59	-2.61	-2.56	-2.55	0.00	0.00	-4.32	0.00	-4.32	-3.09	-2.76	-2.51
TCGA-EJ-5507-10A-01D-1577-08_PRAD	-2.53	-4.19	0.00	-2.87	-2.55	-2.53	-2.54	-2.47	-2.48	0.00	0.00	-4.67	0.00	-4.67	0.00	-2.44	-2.49
TCGA-EJ-5508-10A-01D-1577-08_PRAD	-2.57	-4.72	-4.42	-2.87	-2.62	-2.64	-2.71	-2.59	-2.67	-3.42	-2.94	0.00	-2.80	-2.71	0.00	-2.80	-2.59
TCGA-EJ-5509-10A-01D-1577-08_PRAD	-2.53	-2.73	-2.79	-2.85	-2.49	-2.62	-2.67	-2.57	-2.67	0.00	-3.04	-2.71	0.00	-4.57	0.00	-2.52	-2.51
TCGA-EJ-5510-10A-01D-1577-08_PRAD	-2.49	-4.51	-4.51	-2.59	-2.54	-2.60	-2.73	-2.63	-2.63	0.00	0.00	0.00	-4.51	-2.65	0.00	-2.65	-2.48
TCGA-EJ-5511-10A-01D-1577-08_PRAD	-2.41	-2.69	-2.67	-2.90	-2.56	-2.59	-2.55	-2.45	-2.49	0.00	-4.56	0.00	0.00	-4.26	-3.01	-4.26	-2.58
TCGA-EJ-5512-10A-01D-1577-08_PRAD	-2.63	-2.82	-2.82	-3.03	-2.54	-2.66	-2.70	-2.71	-4.28	-3.30	-2.71	-2.82	-2.74	-2.65	0.00	-4.28	-2.59
TCGA-EJ-5514-10A-01D-1577-08_PRAD	-2.65	-2.83	-2.79	-3.03	-2.54	-2.64	-2.67	-2.52	-2.56	0.00	-3.03	-2.67	0.00	-4.13	-3.09	-2.80	-2.58
TCGA-EJ-5515-10A-01D-1577-08_PRAD	-2.57	-2.80	-2.77	-2.97	-2.50	-2.66	-2.63	-2.68	-2.62	0.00	-2.95	-2.73	-4.72	-4.72	-3.19	-2.84	-2.58
TCGA-EJ-5516-10A-01D-1577-08_PRAD	-2.54	0.00	-4.65	-2.84	-2.58	-2.60	-2.64	-2.52	-2.59	0.00	0.00	0.00	0.00	-4.65	0.00	-2.46	-2.53
TCGA-EJ-5517-10A-01D-1577-08_PRAD	-2.64	-2.80	-2.85	-2.97	-2.54	-2.59	-2.69	-2.59	-2.83	-3.35	-2.89	-2.57	0.00	-2.70	0.00	-2.82	-2.54
TCGA-EJ-5518-10A-01D-1577-08_PRAD	-2.56	-2.68	-2.64	-2.93	-2.64	-2.66	-2.58	-2.55	-2.58	0.00	-4.27	0.00	0.00	-4.57	-2.98	-2.70	-2.50
TCGA-EJ-5519-10A-01D-1577-08_PRAD	-2.63	-2.73	-2.69	-4.71	-2.62	-2.75	-2.72	-2.58	-2.76	-3.39	-2.71	-2.60	-2.85	-2.77	0.00	-2.74	-2.63
TCGA-EJ-5521-10A-01D-1577-08_PRAD	-2.59	-2.73	-2.76	-2.96	-2.72	-2.76	-2.66	-2.62	-2.79	-3.39	-2.92	-2.69	0.00	-2.70	0.00	-2.77	-2.59
TCGA-EJ-5522-10A-01D-1577-08_PRAD	-2.54	-2.84	-2.83	-3.08	-2.54	-2.66	-2.69	-2.63	-2.81	-3.54	-2.86	-2.79	-2.87	-2.78	0.00	-2.86	-2.56
TCGA-EJ-5524-10A-01D-1577-08_PRAD	-2.46	-4.68	-4.68	-2.79	-2.55	-2.61	-2.65	-2.45	-2.51	0.00	0.00	0.00	-4.68	-4.38	0.00	-2.45	-2.52
TCGA-EJ-5525-10A-01D-1577-08_PRAD	-2.58	-2.76	-2.78	-2.91	-2.50	-2.59	-2.72	-2.66	-2.63	0.00	-2.90	-2.69	-4.72	-4.72	-3.02	-4.42	-2.56
TCGA-EJ-5526-10A-01D-1577-08_PRAD	-2.60	0.00	0.00	-2.72	-2.64	-2.65	-2.65	-2.53	-2.79	-3.37	-2.90	0.00	-2.87	-2.74	0.00	-2.80	-2.56
TCGA-EJ-5527-10A-01D-1577-08_PRAD	-2.66	-2.82	-2.87	-3.08	-2.52	-2.69	-2.77	-2.69	-3.87	-3.29	-2.75	-2.68	-2.86	-2.67	0.00	-4.18	-2.64
TCGA-EJ-5530-10A-01D-1577-08_PRAD	-2.50	0.00	0.00	-2.82	-2.50	-2.56	-2.63	-2.54	-2.54	0.00	-4.57	0.00	0.00	0.00	0.00	-2.54	-2.50
TCGA-EJ-5531-10A-01D-1577-08_PRAD	-2.61	-2.77	-2.77	-3.01	-2.49	-2.61	-2.64	-2.63	-2.63	0.00	-2.99	-2.77	0.00	-4.17	0.00	-2.55	-2.53
TCGA-EJ-5532-10A-01D-1577-08_PRAD	-2.50	-2.57	-2.54	0.00	-4.52	-4.22	-2.72	-2.61	-2.60	0.00	-2.80	-4.52	-2.67	-2.56	0.00	-2.72	-2.44
TCGA-EJ-5542-10A-01D-1577-08_PRAD	-2.58	-3.59	-3.71	-2.70	-2.55	-2.58	-2.57	-2.46	-2.48	0.00	0.00	-4.67	-4.67	-4.67	-3.08	-2.79	-2.51
TCGA-EJ-7115-10A-01D-2114-08_PRAD	-2.52	-4.48	0.00	-2.75	-2.56	-2.57	-2.59	-2.54	-2.44	0.00	-4.48	0.00	-4.48	-4.48	0.00	-2.40	-2.46
TCGA-EJ-7123-10A-01D-1961-08_PRAD	-2.49	-4.60	-4.30	-2.69	-2.49	-2.54	-2.57	-2.57	-2.48	0.00	0.00	0.00	-4.60	-4.30	0.00	-2.50	-2.39
TCGA-EJ-7125-10A-01D-1961-08_PRAD	-2.54	0.00	0.00	-2.58	-2.52	-2.38	-2.59	-2.60	-2.59	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.48
TCGA-EJ-7218-10A-01D-A329-08_PRAD	-2.49	-2.75	-2.66	-2.81	-2.62	-2.62	-2.50	-2.57	-2.46	0.00	0.00	-4.49	0.00	0.00	0.00	-2.48	-2.38
TCGA-EJ-7312-10A-01D-A329-08_PRAD	-2.56	-2.73	-2.75	-2.91	-2.42	-2.54	-2.59	-2.72	-2.49	0.00	-2.99	-2.67	0.00	0.00	0.00	-2.73	-2.51
TCGA-EJ-7314-10A-01D-2114-08_PRAD	-2.45	-2.51	-2.48	-4.45	-4.45	-4.15	-2.52	-2.48	-2.49	-4.15	-4.45	-3.97	-4.45	-3.67	0.00	-2.53	-2.43
TCGA-EJ-7315-10A-01D-2114-08_PRAD	-2.51	-2.82	-2.65	-2.97	-2.52	-2.63	-2.65	-2.64	-4.61	-3.13	-2.64	-2.55	-2.84	-2.61	0.00	-4.61	-2.58
TCGA-EJ-7317-10A-01D-2114-08_PRAD	-2.45	0.00	-3.93	-2.58	-2.40	-2.43	-2.45	-2.51	-2.38	0.00	0.00	0.00	0.00	-4.11	0.00	-2.38	-2.38
TCGA-EJ-7318-10A-01D-A329-08_PRAD	-2.48	-2.71	-2.64	-2.80	-2.61	-2.58	-2.41	-2.63	-2.48	0.00	0.00	0.00	0.00	-4.44	0.00	-2.56	-2.38
TCGA-EJ-7321-10A-01D-2260-08_PRAD	-2.53	-2.70	-2.69	-2.82	-2.50	-2.54	-2.55	-2.55	-2.58	0.00	-2.87	-4.49	-2.79	-4.49	0.00	-2.71	-2.53
TCGA-EJ-7325-10A-01D-A329-08_PRAD	-2.62	-2.74	-2.70	-2.87	-2.68	-2.75	-2.63	-2.55	-2.54	0.00	0.00	-4.58	0.00	0.00	0.00	-2.58	-2.54
TCGA-EJ-7327-10A-01D-2114-08_PRAD	-2.40	-4.01	-3.64	-2.72	-2.55	-2.56	-2.58	-2.54	-2.52	0.00	0.00	0.00	0.00	-4.19	-2.97	-2.70	-2.50
TCGA-EJ-7328-10A-01D-2114-08_PRAD	-2.54	0.00	-4.48	-2.58	-2.52	-2.58	-2.57	-2.63	-2.62	-3.28	-2.94	0.00	-2.76	-2.62	0.00	-2.73	-2.49
TCGA-EJ-7330-10A-01D-2114-08_PRAD	-2.49	-2.71	-2.66	-4.01	-2.69	-2.76	-2.68	-2.61	-2.71	-3.41	-2.75	-2.68	-3.66	-2.74	-3.12	-3.84	-2.58
TCGA-EJ-7331-10A-01D-2114-08_PRAD	-2.60	-2.73	-2.77	-3.80	-2.51	-2.61	-2.60	-2.55	-2.48	0.00	-2.88	-2.74	0.00	-3.88	-3.14	-2.73	-2.51
TCGA-EJ-7781-10A-01D-2114-08_PRAD	-2.61	-2.67	-2.67	-4.14	-2.69	-2.75	-2.69	-2.59	-2.74	-3.44	-2.72	-2.78	-2.85	-2.75	-3.12	-4.01	-2.55
TCGA-EJ-7782-10A-01D-2114-08_PRAD	-2.62	-2.73	-2.76	-2.91	-2.56	-2.64	-2.68	-2.63	-2.64	0.00	-2.89	-2.73	-3.98	-4.28	-3.03	0.00	-2.53
TCGA-EJ-7783-10A-01D-2114-08_PRAD	-2.32	-2.64	-2.65	-2.84	-2.54	0.00	-2.46	-2.54	-2.41	0.00	-4.43	0.00	0.00	0.00	0.00	-2.46	-2.38
TCGA-EJ-7784-10A-01D-2114-08_PRAD	-2.37	0.00	0.00	-2.65	-2.41	-2.50	-2.54	-2.63	-2.40	0.00	0.00	0.00	0.00	-4.14	0.00	-2.48	-2.39
TCGA-EJ-7785-10A-01D-2114-08_PRAD	-2.59	-3.83	-4.53	-2.64	-2.58	-2.58	-2.65	-2.55	-2.73	-3.42	-2.93	0.00	-2.85	-2.75	0.00	-2.81	-2.50
TCGA-EJ-7786-10A-01D-2114-08_PRAD	-2.48	0.00	0.00	-2.64	-2.46	-2.51	-2.49	-2.58	-2.58	-3.25	-2.92	0.00	-2.96	-2.55	0.00	-2.72	-2.45
TCGA-EJ-7788-10A-01D-2114-08_PRAD	-2.57	-2.78	-2.82	-2.84	-2.50	-2.56	-2.62	-2.61	-2.68	-3.37	-2.78	-2.60	0.00	-2.72	-3.04	0.00	-2.45
TCGA-EJ-7789-10A-01D-2114-08_PRAD	-2.51	-2.65	-2.66	-2.75	-2.59	-2.60	-2.55	-2.48	-2.43	0.00	0.00	0.00	-4.48	0.00	-2.95	-2.69	-2.40
TCGA-EJ-7791-10A-01D-2115-08_PRAD	-2.58	-3.96	-3.96	-2.79	-2.57	-2.62	-2.63	-2.55	-2.57	0.00	0.00	0.00	0.00	-4.56	0.00	-2.38	-2.52
TCGA-EJ-7792-10A-01D-2115-08_PRAD	-2.60	-4.08	-4.26	-2.85	-2.59	-2.61	-2.65	-2.54	-2.71	-3.41	-2.91	0.00	-2.78	-2.70	-2.99	0.00	-2.58
TCGA-EJ-7793-10A-01D-2260-08_PRAD	-2.57	-4.55	-4.25	-2.62	-2.54	-2.59	-2.58	-2.56	-2.65	-3.27	-2.91	-4.25	-2.76	-2.71	0.00	-2.71	-2.54
TCGA-EJ-7794-10A-01D-2115-08_PRAD	-2.50	-2.71	-2.72	-2.78	-2.65	-2.68	-2.61	-2.71	-2.63	0.00	-2.79	0.00	-2.79	-2.64	0.00	-2.65	-2.45
TCGA-EJ-7797-10A-01D-2260-08_PRAD	-2.63	-2.73	-2.79	-2.88	-2.48	-2.62	-2.59	-2.62	-2.70	-3.31	-2.78	-2.64	-4.56	-2.72	0.00	-2.80	-2.51
TCGA-EJ-8468-10A-01D-2395-08_PRAD	-2.70	-2.78	-2.80	-2.92	-2.56	-2.69	-2.73	-2.65	-2.74	-3.48	-2.78	-2.59	-4.33	-2.73	0.00	-2.82	-2.59

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EJ-8469-10A-01D-2395-08_PRAD	-2.55	-4.22	-4.52	-2.62	-2.59	-2.60	-2.59	-2.41	-2.46	0.00	-4.52	-4.22	0.00	0.00	0.00	-2.41	-2.52
TCGA-EJ-8470-10A-01D-2395-08_PRAD	-2.55	0.00	0.00	-2.64	-2.60	-2.58	-2.56	-2.55	-2.72	-3.34	-2.93	0.00	-2.73	-2.69	-3.08	-4.64	-2.53
TCGA-EJ-8472-10A-01D-2395-08_PRAD	-2.49	0.00	-4.00	-2.73	-2.54	-2.55	-2.54	-2.57	-2.48	0.00	-4.17	-4.17	0.00	0.00	-2.96	-2.66	-2.46
TCGA-EJ-8474-10A-01D-2395-08_PRAD	-2.61	-3.75	-3.89	-2.81	-2.66	-2.64	-2.66	-2.58	-2.67	-3.36	-2.89	0.00	-2.75	-2.69	-3.12	0.00	-2.58
TCGA-EJ-A46B-10A-01D-A25A-08_PRAD	-2.56	-2.73	-2.71	-2.85	-2.48	-2.64	-2.67	-2.56	-2.59	-4.54	-3.01	-2.75	-4.06	-4.06	-3.13	-2.74	-2.52
TCGA-EJ-A46D-10A-01D-A25A-08_PRAD	-2.40	0.00	0.00	-2.55	-2.59	-2.53	-2.60	-2.47	-2.44	0.00	0.00	0.00	0.00	-4.21	-3.01	-2.69	-2.45
TCGA-EJ-A46E-10A-01D-A25A-08_PRAD	-2.64	-2.74	-2.74	-2.88	-2.49	-2.62	-2.65	-2.57	-2.51	0.00	-2.92	-2.73	0.00	0.00	-3.15	-2.75	-2.49
TCGA-EJ-A46F-10A-01D-A25A-08_PRAD	-2.56	-2.70	-2.68	-2.79	-2.67	-2.68	-2.61	-2.58	-2.47	-4.52	-4.05	-4.52	-4.22	-3.92	0.00	-2.55	-2.47
TCGA-EJ-A46G-10A-01D-A26K-08_PRAD	-2.46	-2.61	-2.64	-2.75	-2.53	-2.58	-2.41	-2.51	-2.38	0.00	0.00	0.00	0.00	0.00	-2.82	-4.03	-2.31
TCGA-EJ-A46H-10A-01D-A26K-08_PRAD	-2.47	-4.37	-3.77	-2.66	-2.42	-2.45	-2.46	-2.51	-2.43	0.00	-4.07	-3.67	-4.37	-4.07	-2.97	-2.76	-2.36
TCGA-EJ-A46I-10A-01D-A26K-08_PRAD	-2.42	0.00	0.00	-2.53	-2.47	-2.42	-2.45	-2.45	-2.35	0.00	-4.29	0.00	0.00	-3.99	0.00	-2.37	-2.38
TCGA-EJ-A65B-10A-01D-A30H-08_PRAD	-2.43	0.00	0.00	-2.62	-2.44	-2.53	-2.49	-2.43	-2.44	0.00	0.00	0.00	0.00	-4.39	-3.04	-2.68	-2.40
TCGA-EJ-A65D-10A-01D-A30H-08_PRAD	-2.38	-2.63	-2.62	-2.80	-2.60	-2.60	-2.47	-2.50	-2.41	0.00	0.00	0.00	0.00	-4.64	0.00	-2.42	-2.38
TCGA-EJ-A65E-10A-01D-A29Q-08_PRAD	-2.67	-2.88	-2.82	-2.99	-2.66	-2.69	-2.72	-2.62	-2.66	0.00	-3.06	-2.81	0.00	-4.15	-3.17	-2.92	-2.62
TCGA-EJ-A65F-10A-01D-A30X-08_PRAD	-2.66	-2.82	-2.85	-3.04	-2.60	-2.69	-2.70	-2.65	-2.62	0.00	-3.06	-2.78	0.00	-4.61	-3.23	-2.89	-2.64
TCGA-EJ-A65G-10A-01D-A29Q-08_PRAD	-2.50	-2.68	-2.64	-2.89	-2.64	-2.62	-2.57	-2.54	-2.43	0.00	0.00	0.00	0.00	-4.58	0.00	-2.55	-2.43
TCGA-EJ-A65J-10A-01D-A30X-08_PRAD	-2.61	0.00	0.00	-2.65	-2.67	-2.70	-2.71	-2.67	-2.79	-3.52	-2.97	0.00	-2.85	-2.74	-3.22	0.00	-2.62
TCGA-EJ-A65M-10A-01D-A29Q-08_PRAD	-2.55	0.00	-2.68	-2.88	-2.47	-2.51	-2.56	-2.65	-2.53	0.00	-2.94	0.00	-2.75	0.00	0.00	-2.60	-2.46
TCGA-EJ-A6RA-10A-01D-A33W-08_PRAD	-2.49	0.00	0.00	-2.71	-2.59	-2.57	-2.63	-2.58	-2.69	-3.28	-2.87	0.00	-2.80	-2.64	0.00	-2.76	-2.52
TCGA-EJ-A6RC-10A-01D-A329-08_PRAD	-2.47	-2.54	-2.49	0.00	-2.62	-2.62	-2.59	-2.61	-2.44	0.00	-3.01	-2.66	0.00	0.00	0.00	-2.47	-2.43
TCGA-EJ-A7NF-10A-01D-A33W-08_PRAD	-2.49	0.00	0.00	-2.51	-2.45	-2.49	-2.48	-2.55	-2.55	0.00	0.00	0.00	0.00	-4.40	0.00	-2.47	-2.41
TCGA-EJ-A7NG-10A-01D-A33W-08_PRAD	-2.49	-2.84	-2.75	-2.87	-2.49	-2.63	-2.63	-2.69	-2.72	-3.34	-2.78	-2.61	0.00	-2.69	0.00	-2.77	-2.51
TCGA-EJ-A7NH-10A-01D-A33W-08_PRAD	-2.52	0.00	0.00	-2.71	-2.52	-2.55	-2.56	-2.55	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.34	-2.47
TCGA-EJ-A7NM-10A-01D-A33W-08_PRAD	-2.51	-2.70	-2.66	-2.91	-2.63	-2.72	-2.57	-2.49	-2.61	-3.32	-2.91	0.00	-2.82	-2.56	-3.03	0.00	-2.44
TCGA-EJ-A7NN-10A-01D-A33W-08_PRAD	-2.47	0.00	0.00	-2.67	-2.49	-2.47	-2.47	-2.59	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.42
TCGA-EK-A2GZ-10A-01D-A17W-09_CESC	-2.65	-2.47	-2.51	-3.96	-3.96	-3.73	-2.40	-2.45	-2.38	0.00	-4.43	-4.43	0.00	0.00	-2.72	-4.43	-2.51
TCGA-EK-A2H0-10A-01D-A17W-09_CESC	-2.78	0.00	0.00	-2.89	-2.43	-2.47	-2.40	-2.40	-2.47	0.00	0.00	-4.54	0.00	-4.24	-2.95	-2.65	-2.54
TCGA-EK-A2H1-10A-01D-A17W-09_CESC	-2.76	-4.51	0.00	-2.97	-2.51	-2.48	-2.46	-2.43	-2.37	0.00	0.00	0.00	0.00	0.00	-2.88	-2.61	-2.56
TCGA-EK-A2IP-10A-01D-A17W-09_CESC	-2.73	-4.04	0.00	-2.92	-2.47	-2.48	-2.45	-2.57	-2.32	0.00	0.00	0.00	0.00	-4.52	0.00	-2.52	-2.60
TCGA-EK-A2PG-10A-01D-A18J-09_CESC	-2.80	-2.66	-2.63	-3.41	-2.76	-2.63	-2.49	-2.49	-2.58	-3.30	-2.79	-4.45	-2.70	-2.58	-3.00	-4.45	-2.61
TCGA-EK-A2PI-10A-01D-A18J-09_CESC	-2.74	-2.41	-2.48	0.00	-3.94	-4.42	-2.45	-2.42	-2.43	-4.42	-4.12	-4.42	-4.42	-4.42	-2.78	-2.66	-2.56
TCGA-EK-A2PK-10A-01D-A18J-09_CESC	-2.81	-2.65	-2.69	-3.16	-2.66	-2.62	-2.47	-2.50	-2.36	-4.44	0.00	-4.44	0.00	0.00	-2.87	-2.73	-2.61
TCGA-EK-A2PL-10A-01D-A18J-09_CESC	-2.83	-2.56	-2.54	-4.44	-2.76	-2.65	-2.51	-2.58	-2.39	0.00	-2.79	-2.75	-4.44	-4.44	-2.95	-2.77	-2.59
TCGA-EK-A2PM-10A-01D-A18J-09_CESC	-2.74	-4.12	0.00	-2.92	-2.55	-2.49	-2.50	-2.49	-2.34	0.00	0.00	-4.42	0.00	-4.42	-2.89	-2.71	-2.60
TCGA-EK-A2R7-10A-01D-A18J-09_CESC	-2.81	-4.43	0.00	-2.96	-2.55	-2.58	-2.54	-2.59	-2.65	-3.48	-2.87	0.00	-2.73	-2.68	-2.84	-4.43	-2.69
TCGA-EK-A2R8-10A-01D-A18J-09_CESC	-2.69	-2.56	-2.56	-3.21	-2.47	-2.53	-2.52	-2.66	-2.43	0.00	-4.05	-4.36	-4.36	-4.36	-2.85	-4.05	-2.60
TCGA-EK-A2R9-10A-01D-A18J-09_CESC	-2.83	-2.63	-2.59	0.00	-2.76	-2.74	-2.56	-2.59	-2.70	-3.40	-2.59	-2.77	-2.84	-2.77	-3.04	0.00	-2.61
TCGA-EK-A2RA-10A-01D-A18J-09_CESC	-2.73	-2.72	-2.81	-3.38	-2.69	-2.72	-2.46	-2.47	-2.58	-3.50	-2.79	0.00	-2.77	-2.69	0.00	-2.73	-2.61
TCGA-EK-A2RB-10A-01D-A18J-09_CESC	-2.82	-2.75	-2.77	-3.32	-2.57	-2.60	-2.57	-2.61	-2.65	-3.43	-2.65	-2.76	-2.81	-2.73	0.00	-2.82	-2.67
TCGA-EK-A2RC-10A-01D-A18J-09_CESC	-2.80	-4.37	0.00	-3.07	-2.48	-2.47	-2.43	-2.51	-2.34	0.00	0.00	-4.07	0.00	-4.37	0.00	-2.51	-2.55
TCGA-EK-A2RD-10A-01D-A20U-09_CESC	-2.78	-4.45	-4.15	-3.12	-2.48	-2.54	-2.52	-2.55	-2.38	-4.45	-3.97	-4.45	0.00	-4.15	0.00	-2.54	-2.51
TCGA-EK-A2RE-10A-01D-A18J-09_CESC	-2.79	-4.06	-4.36	-3.08	-2.44	-2.48	-2.46	-2.54	-2.27	0.00	0.00	-4.36	-4.36	0.00	0.00	-2.51	-2.51
TCGA-EK-A2RJ-10A-01D-A18J-09_CESC	-2.83	-2.74	-2.76	-3.36	-2.51	-2.59	-2.51	-2.61	-2.73	-3.42	-2.74	-2.60	0.00	-2.73	0.00	-2.78	-2.57
TCGA-EK-A2RK-10A-01D-A18J-09_CESC	-2.73	-4.10	-4.41	-2.97	-2.52	-2.52	-2.52	-2.39	-2.37	-3.93	0.00	-4.10	0.00	-4.41	0.00	-2.80	-2.56
TCGA-EK-A2RL-10A-01D-A18J-09_CESC	-2.88	-2.59	-2.64	-4.50	-2.91	-2.69	-2.53	-2.55	-2.67	-3.29	-2.66	-2.73	-2.81	-2.98	0.00	-2.85	-2.65
TCGA-EK-A2RN-10A-01D-A20U-09_CESC	-2.74	0.00	-4.47	-3.09	-2.52	-2.53	-2.56	-2.44	-2.32	0.00	0.00	0.00	-4.47	0.00	-2.99	-2.76	-2.57
TCGA-EK-A2RO-10A-01D-A18J-09_CESC	-2.69	-2.70	-2.75	-3.13	-2.63	-2.67	-2.46	-2.43	-2.31	0.00	-4.45	-4.45	0.00	-4.15	0.00	-2.35	-2.56
TCGA-EK-A3GK-10A-01D-A20U-09_CESC	-2.87	-2.76	-2.74	-3.24	-2.64	-2.74	-2.51	-2.57	-2.60	-3.36	-2.81	0.00	-2.77	-2.70	-2.92	-4.47	-2.60
TCGA-EK-A3GM-10A-01D-A20U-09_CESC	-2.73	-2.69	-2.73	-3.15	-2.76	-2.72	-2.64	-2.67	-2.62	0.00	-2.80	0.00	-2.73	-2.72	0.00	-2.72	-2.59
TCGA-EK-A3GN-10A-01D-A20U-09_CESC	-2.89	-2.73	-2.84	-3.27	-2.53	-2.54	-2.54	-2.59	-2.69	-3.36	-2.71	-2.86	-2.76	-2.77	0.00	-2.83	-2.63
TCGA-EL-A3CL-10A-01D-A19M-08_THCA	-2.48	0.00	-4.50	-2.67	-2.45	-2.51	-2.48	-2.62	-2.45	0.00	0.00	0.00	-4.50	0.00	0.00	-2.54	-2.36
TCGA-EL-A3CM-10A-01D-A19M-08_THCA	-2.52	-4.13	0.00	-2.59	-2.49	-2.56	-2.56	-2.55	-2.53	0.00	-4.43	0.00	0.00	-4.43	0.00	-2.56	-2.45
TCGA-EL-A3CN-10A-01D-A20C-08_THCA	-2.50	-2.57	-2.57	-4.52	0.00	-4.22	-2.66	-2.74	-2.66	-3.22	-2.72	0.00	-2.62	-2.47	0.00	-2.72	-2.41
TCGA-EL-A3CO-10A-01D-A19M-08_THCA	-2.60	-2.75	-2.68	-2.89	-2.46	-2.60	-2.60	-2.58	-2.60	0.00	-2.93	-2.80	0.00	-4.34	0.00	-2.50	-2.45
TCGA-EL-A3CP-10A-01D-A19M-08_THCA	-2.56	-2.73	-2.72	-2.89	-2.52	-2.53	-2.61	-2.58	-2.50	0.00	-3.01	-2.72	0.00	-4.06	-3.14	-2.81	-2.42
TCGA-EL-A3CR-10A-01D-A202-08_THCA	-2.53	0.00	-4.20	-2.61	-2.56	-2.58	-2.57	-2.48	-2.45	0.00	0.00	0.00	0.00	0.00	-3.02	-2.69	-2.49
TCGA-EL-A3CS-10A-01D-A19M-08_THCA	-2.54	-4.52	-4.22	-2.57	-2.51	-2.54	-2.57	-2.53	-2.49	0.00	0.00	0.00	0.00	-4.52	0.00	-2.56	-2.39
TCGA-EL-A3CT-10A-01D-A202-08_THCA	-2.60	0.00	0.00	-2.66	-2.59	-2.66	-2.51	-2.56	-2.66	-3.49	-2.85	0.00	-2.84	-2.71	0.00	-2.77	-2.55
TCGA-EL-A3CU-10A-01D-A19M-08_THCA	-2.52	-2.78	-2.71	-2.91	-2.47	-2.58	-2.63	-2.63	-2.50	0.00	-3.01	-2.75	-3.85	-3.65	-3.11	-3.00	-2.46
TCGA-EL-A3CV-10A-01D-A19M-08_THCA	-2.47	-2.66	-2.64	-2.77	-2.62	-2.61	-2.52	-2.57	-2.35	0.00	0.00	0.00	0.00	0.00	-2.93	-3.78	-2.37
TCGA-EL-A3CW-10A-01D-A19M-08_THCA	-2.48	-2.67	-2.69	-2.80	-2.59	-2.65	-2.46	-2.57	-2.41	0.00	0.00	-4.52	-4.52	0.00	-3.20	-2.73	-2.37
TCGA-EL-A3CX-10A-01D-A19M-08_THCA	-2.53	-3.98	-3.85	-2.74	-2.52	-2.52	-2.55	-2.50	-2.51	-4.46	-4.46	-4.15	-3.85	-4.15	-3.04	-2.77	-2.52
TCGA-EL-A3CY-10A-01D-A19M-08_THCA	-2.44	0.00	0.00	-2.54	-2.49	-2.52	-2.53	-2.55	-2.51	0.00	0.00	-4.53	-4.53	-4.53	-3.09	-2.69	-2.36
TCGA-EL-A3CZ-10A-01D-A19M-08_THCA	-2.47	0.00	0.00	-2.65	-2.46	-2.48	-2.53	-2.58	-2.51	-4.51	-4.51	-4.51	-4.51	-4.03	0.00	-2.40	-2.40
TCGA-EL-A3D0-10A-01D-A202-08_THCA	-2.55	-4.51	0.00	-2.71	-2.57	-2.61	-2.63	-2.56	-2.63	-3.34	-2.81	0.00	-2.73	-2.66	-3.07	-4.51	-2.54
TCGA-EL-A3D1-10A-01D-A19M-08_THCA	-2.45	-2.62	-2.64	-2.84	-2.64	-2.62	-2.60	-2.80	-3.84	-3.36	-2.63	-4.23	-2.59	-2.48	0.00	-4.06	-2.44
TCGA-EL-A3D4-10A-01D-A19M-08_THCA	-2.47	-4.22	-4.22	-2.58	-2.46	-2.50	-2.51	-2.54	-2.42	0.00	-4.52	0.00	0.00	0.00	-3.24	-2.65	-2.41
TCGA-EL-A3D5-10A-01D-A202-08_THCA	-2.60	-2.69	-2.72	-2.88	-2.67	-2.75	-2.66	-2.64	-2.66	-3.27	-2.85	0.00	-2.77	-2.71	0.00	-2.73	-2.58
TCGA-EL-A3D6-10A-01D-A202-08_THCA	-2.58	0.00	0.00	-2.85	-2.60	-2.61	-2.62	-2.50	-2.66	-3.23	-2.89	-2.74	0.00	-2.72	-3.06	0.00	-2.54
TCGA-EL-A3GO-10A-01D-A202-08_THCA	-2.59	-2.74	-2.67	-2.81	-2.64	-2.66	-2.59	-2.45	-2.45	0.00	0.00	0.00	0.00	0.00	-2.96	-2.73	-2.53
TCGA-EL-A3GP-10A-01D-A202-08_THCA	-2.60	-2.61	-2.74	-4.57	-2.70	-2.75	-2.71	-2.82	-2.73	0.00	-2.64	-2.71	-2.73	-2.71	0.00	-2.75	-2.54
TCGA-EL-A3GQ-10A-01D-A202-08_THCA	-2.51	-2.63	-2.67	-2.79	-2.63	-2.63	-2.58	-2.48	-2.45	0.00	-4.45	0.00	0.00	-4.15	-3.02	-2.70	-2.42
TCGA-EL-A3GR-10A-01D-A202-08_THCA	-2.56	-2.66	-2.67	-2.89	-2.60	-2.67	-2.60	-2.46	-2.48	0.00	0.00	0.00	0.00	-4.50	-2.99	-2.64	-2.50
TCGA-EL-A3GS-10A-01D-A20C-08_THCA	-2.55	-2.66	-2.69	-2.84	-2.63	-2.66	-2.60	-2.49	-2.52	0.00	0.00	-4.52	-4.52	-4.52	-3.06	-2.63	-2.44
TCGA-EL-A3GV-10A-01D-A21A-08_THCA	-2.55	-4.47	0.00	-2.75	-2.52	-2.57	-2.61	-2.55	-2.78	-3.33	-2.80	0.00	-2.80	-2.63	0.00	-2.73	-2.49
TCGA-EL-A3GW-10A-01D-A202-08_THCA	-2.54	-2.60	-2.69	-4.49	-2.68	-2.68	-2.61	-2.47	-2.72	-3.21	-2.86	0.00	-2.72	-2.69	0.00	-2.71	-2.49
TCGA-EL-A3GX-10A-01D-A202-08_THCA	-2.60	-2.79	-2.74	-2.89	-2.75	-2.73	-2.67	-2.67	-2.68	-3.35	-2.95	0.00	-2.79	-2.71	0.00	-2.78	-2.58
TCGA-EL-A3GY-10A-01D-A202-08_THCA	-2.61	-4.56	0.00	-2.64	-2.55	-2.61	-2.64	-2.62	-2.68	-3.33	-2.85	0.00	-2.72	-2.70	0.00	-2.71	-2.59
TCGA-EL-A3H3-10A-01D-A202-08_THCA	-2.53	-2.70	-2.67	-2.83	-2.62	-2.67	-2.54	-2.46	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.53
TCGA-EL-A3H4-10A-01D-A202-08_THCA	-2.63	-4.57	0.00	-2.64	-2.59	-2.65	-2.63	-2.43	-2.49	0.00	-2.81	0.00	-2.76	-4.57	-3.09	-2.76	-2.57
TCGA-EL-A3H5-10A-01D-A202-08_THCA	-2.67	-2.68	-2.68	-4.62	-2.62	-2.69	-2.69	-2.60	-2.76	-3.39	-2.64	-2.68	-2.80	-2.77	-3.16	-4.62	-2.61
TCGA-EL-A3H8-10A-01D-A20C-08_THCA	-2.51	0.00	-4.20	-2.57	-2.50	-2.53	-2.60	-2.64	-4.50	-3.12	-2.72	-4.50	-2.68	-2.54	0.00	-4.20	-2.48
TCGA-EL-A4KG-10A-01D-A25A-08_THCA	-2.59	-2.65	-2.68	-2.85	-2.70	-2.74	-2.55	-2.46	-2.47	0.00	0.00	0.00	0.00	0.00	-3.09	-2.70	-2.51
TCGA-EL-A4KH-10A-01D-A25A-08_THCA	-2.57	0.00	-4.42	-2.58	-2.54	-2.59	-2.57	-2.49	-2.46	0.00	-4.42	0.00	0.00	-3.82	0.00	-2.41	-2.49
TCGA-EL-A4KI-10A-01D-A25A-08_THCA	-2.58	0.00	0.00	-2.71	-2.63	-2.61	-2.65	-2.50	-2.71	-3.47	-2.93	0.00	-2.86	-2.69	0.00	-2.74	-2.57
TCGA-EM-A1CS-10A-01D-A13W-08_THCA	-2.43	-2.75	-2.68	-2.84	-2.63	-2.65	-2.48	-2.45	-2.40	0.00	0.00	-4.37	0.00	0.00	-3.04	-2.72	-2.24
TCGA-EM-A1CT-10A-01D-A13W-08_THCA	-2.45	-4.45	0.00	-2.76	-2.52	-2.48	-2.59	-2.56	-2.68	-3.43	-2.97	0.00	-2.85	-2.69	-3.09	0.00	-2.38
TCGA-EM-A1CU-10A-02D-A13W-08_THCA	-2.52	-2.73	-2.76	-2.89	-2.46	-2.56	-2.55	-2.61	-2.49	0.00	-3.01	-2.70	-4.44	-4.27	-3.08	-2.77	-2.42
TCGA-EM-A1CV-10A-01D-A13W-08_THCA	-2.49	-2.57	-2.59	-4.67	-2.70	-2.71	-2.53	-2.53	-2.72	-3.36	-2.80	-2.56	0.00	-2.67	-3.16	-4.67	-2.43
TCGA-EM-A1CW-10A-01D-A13W-08_THCA	-2.44	-2.64	-2.62	-2.88	-2.61	-2.66	-2.45	-2.56	-2.39	0.00	-4.68	-4.38	0.00	-4.68	0.00	-2.53	-2.37
TCGA-EM-A1YA-10A-01D-A14W-08_THCA	-2.49	-4.52	0.00	-2.67	-2.53	-2.56	-2.61	-2.56	-2.62	-3.35	-2.89	0.00	-2.78	-2.71	-3.13	-4.52	-2.47
TCGA-EM-A1YB-10A-01D-A14W-08_THCA	-2.50	-3.84	-4.14	-2.76	-2.56	-2.48	-2.55	-2.50	-2.42	0.00	0.00	-4.44	-3.96	-3.54	0.00	-2.46	-2.42
TCGA-EM-A22I-10A-01D-A17V-08_THCA	-2.56	-2.72	-2.70	-2.94	-2.73	-2.75	-2.61	-2.58	-2.70	-3.42	-2.88	0.00	-2.70	-2.70	-3.10	-4.62	-2.53
TCGA-EM-A22J-10A-01D-A17V-08_THCA	-2.56	0.00	-2.71	-2.98	-2.51	-2.61	-2.62	-2.60	-2.59	0.00	-2.93	0.00	-2.78	-3.96	-3.22	-2.84	-2.52
TCGA-EM-A22K-10A-01D-A17V-08_THCA	-2.47	0.00	0.00	-2.57	-2.50	-2.54	-2.57	-2.50	-2.47	0.00	0.00	0.00	0.00	0.00	-2.98	-2.70	-2.43
TCGA-EM-A22L-10A-01D-A17V-08_THCA	-2.48	-2.71	-2.65	-2.85	-2.60	-2.70	-2.50	-2.48	-2.49	0.00	-4.46	0.00	0.00	0.00	-3.03	-2.66	-2.45

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EM-A22M-10A-01D-A17V-08_THCA	-2.59	-2.79	-2.72	-2.93	-2.58	-2.64	-2.67	-2.62	-2.72	-3.44	-2.71	-2.75	-2.88	-2.72	0.00	-2.83	-2.57
TCGA-EM-A22N-10A-01D-A17V-08_THCA	-2.56	0.00	0.00	-2.60	-2.52	-2.59	-2.61	-2.50	-2.47	0.00	0.00	0.00	0.00	-4.52	-3.08	-2.73	-2.49
TCGA-EM-A22O-10A-01D-A17V-08_THCA	-2.60	0.00	-4.69	-2.81	-2.59	-2.63	-2.65	-2.58	-2.72	-3.39	-2.95	-4.69	-2.79	-2.68	-3.16	0.00	-2.56
TCGA-EM-A22P-10A-01D-A19M-08_THCA	-2.45	0.00	-4.53	-2.57	-2.47	-2.50	-2.59	-2.49	-2.42	0.00	0.00	0.00	0.00	0.00	-3.15	-2.69	-2.39
TCGA-EM-A22Q-10A-01D-A17V-08_THCA	-2.69	-2.79	-2.82	-2.92	-2.57	-2.65	-2.71	-2.73	-4.68	-3.28	-2.71	-2.82	-2.71	-2.63	0.00	0.00	-2.60
TCGA-EM-A2CJ-10A-01D-A17V-08_THCA	-2.54	-2.58	-2.56	0.00	-2.65	-2.66	-2.71	-2.77	-2.70	0.00	-2.66	-2.57	0.00	-2.61	-3.07	0.00	-2.50
TCGA-EM-A2CK-10A-01D-A17V-08_THCA	-2.56	-2.77	-2.74	-2.92	-2.51	-2.64	-2.63	-2.60	-2.60	0.00	-2.88	-2.76	0.00	-4.57	-2.99	0.00	-2.58
TCGA-EM-A2CL-10A-01D-A17V-08_THCA	-2.51	-2.63	-2.54	-4.61	-4.61	-4.14	-2.55	-2.60	-2.68	-3.29	-2.77	-4.61	-2.75	-2.71	0.00	-2.78	-2.47
TCGA-EM-A2CM-10A-01D-A17V-08_THCA	-2.53	0.00	0.00	-2.55	-2.53	-2.59	-2.55	-2.48	-2.52	0.00	-4.19	0.00	0.00	0.00	-2.94	-2.68	-2.45
TCGA-EM-A2CN-10B-01D-A19M-08_THCA	-2.49	-4.20	0.00	-2.54	-2.51	-2.48	-2.51	-2.57	-2.44	0.00	0.00	0.00	0.00	-4.51	0.00	-2.50	-2.37
TCGA-EM-A2CO-10A-01D-A19M-08_THCA	-2.46	-4.49	0.00	-2.70	-2.46	-2.50	-2.52	-2.55	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.35
TCGA-EM-A2CP-10A-01D-A17V-08_THCA	-2.48	0.00	-4.41	-2.67	-2.46	-2.46	-2.49	-2.46	-2.46	0.00	0.00	-4.41	0.00	0.00	-3.11	-2.62	-2.47
TCGA-EM-A2CQ-10A-01D-A17V-08_THCA	-2.51	0.00	0.00	-2.72	-2.53	-2.58	-2.55	-2.46	-2.47	0.00	0.00	0.00	0.00	0.00	-3.01	-2.73	-2.44
TCGA-EM-A2CR-10A-01D-A17V-08_THCA	-2.51	-2.86	-2.79	-2.94	-2.53	-2.60	-2.63	-2.56	-2.76	-3.52	-2.71	-2.64	-4.56	-2.68	-3.18	0.00	-2.56
TCGA-EM-A2CS-10A-01D-A19M-08_THCA	-2.52	-2.69	-2.64	-2.87	-2.60	-2.65	-2.55	-2.45	-2.48	0.00	-3.93	-4.41	-3.93	-3.93	-2.95	-2.65	-2.46
TCGA-EM-A2CT-10A-01D-A17V-08_THCA	-2.45	-2.70	-2.60	-2.78	-2.73	-2.67	-2.48	-2.45	-2.39	0.00	-4.45	-4.45	0.00	0.00	-2.91	-2.76	-2.39
TCGA-EM-A2CU-10A-01D-A17V-08_THCA	-2.51	-2.71	-2.67	-2.78	-2.66	-2.67	-2.58	-2.50	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.47
TCGA-EM-A2OV-10A-01D-A202-08_THCA	-2.56	0.00	0.00	-2.74	-2.49	-2.57	-2.61	-2.56	-2.58	0.00	0.00	0.00	0.00	0.00	-2.87	-4.20	-2.50
TCGA-EM-A2OW-10A-01D-A202-08_THCA	-2.55	0.00	0.00	-2.53	-2.53	-2.57	-2.45	-2.58	-2.58	0.00	0.00	0.00	0.00	-4.21	0.00	-2.53	-2.45
TCGA-EM-A2OX-10A-01D-A202-08_THCA	-2.43	-2.52	-2.51	0.00	0.00	0.00	-2.51	-2.45	-2.45	0.00	0.00	0.00	0.00	0.00	-3.04	-2.65	-2.47
TCGA-EM-A2OY-10A-01D-A202-08_THCA	-2.47	-4.57	0.00	-2.76	-2.58	-2.60	-2.69	-2.60	-2.68	-3.26	-2.79	-4.57	-2.79	-2.71	0.00	-2.84	-2.54
TCGA-EM-A2OZ-10A-01D-A202-08_THCA	-2.52	0.00	-4.20	-2.76	-2.52	-2.52	-2.58	-2.50	-2.52	0.00	0.00	0.00	0.00	0.00	-2.98	-2.72	-2.53
TCGA-EM-A2P0-10A-01D-A202-08_THCA	-2.60	0.00	0.00	-2.61	-2.60	-2.61	-2.68	-2.55	-2.75	-3.32	-2.76	0.00	-2.80	-2.69	0.00	-2.75	-2.57
TCGA-EM-A2P1-10A-01D-A202-08_THCA	-2.57	-2.70	-2.71	-2.89	-2.69	-2.66	-2.59	-2.54	-2.71	-3.33	-2.95	0.00	-2.88	-2.66	0.00	-2.76	-2.54
TCGA-EM-A2P2-10A-01D-A202-08_THCA	-2.54	0.00	-4.53	-2.63	-2.55	-2.57	-2.58	-2.61	-2.59	0.00	0.00	-4.53	0.00	0.00	0.00	-2.57	-2.49
TCGA-EM-A2P3-10A-01D-A202-08_THCA	-2.55	0.00	-4.52	-2.75	-2.51	-2.55	-2.55	-2.56	-2.55	0.00	-4.52	0.00	0.00	0.00	-3.00	-2.66	-2.51
TCGA-EM-A3AI-10A-01D-A202-08_THCA	-2.66	-2.74	-2.78	-3.02	-2.51	-2.66	-2.70	-2.49	-2.51	0.00	-2.92	-2.74	0.00	0.00	-3.11	-2.75	-2.56
TCGA-EM-A3AJ-10A-01D-A202-08_THCA	-2.50	-2.65	-2.67	-2.84	-2.63	-2.64	-2.63	-2.46	-2.49	0.00	0.00	0.00	0.00	-4.52	0.00	-2.44	-2.52
TCGA-EM-A3AK-10A-01D-A202-08_THCA	-2.52	-2.67	-2.64	-2.80	-2.65	-2.59	-2.57	-2.59	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.44
TCGA-EM-A3AL-10A-01D-A202-08_THCA	-2.55	-2.64	-2.65	-2.91	-2.65	-2.65	-2.57	-2.42	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.46
TCGA-EM-A3AN-10A-01D-A202-08_THCA	-2.52	0.00	0.00	-2.60	-2.57	-2.53	-2.58	-2.59	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.49
TCGA-EM-A3AO-10A-01D-A202-08_THCA	-2.56	0.00	0.00	-2.59	-2.55	-2.61	-2.63	-2.51	-2.50	0.00	0.00	0.00	0.00	0.00	-3.01	-2.66	-2.52
TCGA-EM-A3AP-10A-01D-A20C-08_THCA	-2.33	-4.33	-4.03	-2.66	-2.41	-2.39	-2.59	-2.56	-2.38	0.00	0.00	0.00	0.00	-4.33	-3.01	-2.73	-2.38
TCGA-EM-A3AQ-10A-01D-A20C-08_THCA	-2.56	-4.29	-4.59	-2.65	-2.62	-2.57	-2.63	-2.57	-2.71	-3.31	-2.88	0.00	-2.80	-2.69	-3.05	-4.11	-2.56
TCGA-EM-A3AR-10A-01D-A20C-08_THCA	-2.50	-4.53	-4.53	-2.58	-2.55	-2.55	-2.61	-2.54	-2.63	0.00	0.00	0.00	0.00	-4.53	0.00	-2.34	-2.44
TCGA-EM-A3FJ-10A-01D-A21A-08_THCA	-2.48	-2.70	-2.72	-2.78	-2.61	-2.64	-2.56	-2.50	-2.52	0.00	0.00	-4.46	0.00	0.00	-3.00	-2.68	-2.39
TCGA-EM-A3FK-10A-01D-A21A-08_THCA	-2.49	-2.71	-2.84	-2.73	-2.62	-2.57	-2.51	-2.63	-2.43	-4.44	0.00	0.00	0.00	-4.14	0.00	-2.48	-2.34
TCGA-EM-A3FL-10A-01D-A21A-08_THCA	-2.42	-2.72	-2.72	-2.92	-2.61	-2.70	-2.61	-2.51	-2.75	-3.32	-2.82	0.00	-2.79	-2.68	-3.03	-4.52	-2.50
TCGA-EM-A3FM-10A-01D-A21A-08_THCA	-2.55	0.00	0.00	-2.73	-2.59	-2.58	-2.56	-2.63	-2.66	-3.48	-2.91	0.00	-2.85	-2.68	-3.02	0.00	-2.42
TCGA-EM-A3FN-10A-01D-A21A-08_THCA	-2.62	-2.85	-2.82	-2.93	-2.61	-2.64	-2.63	-2.66	-2.74	-3.32	-2.71	-2.73	-2.74	-2.82	0.00	-2.74	-2.59
TCGA-EM-A3FO-10A-01D-A21A-08_THCA	-2.48	-2.74	-2.69	-2.81	-2.60	-2.56	-2.54	-2.48	-2.49	0.00	0.00	0.00	0.00	0.00	-3.02	-2.62	-2.41
TCGA-EM-A3FP-10A-01D-A21A-08_THCA	-2.51	-4.21	0.00	-2.71	-2.53	-2.60	-2.59	-2.58	-2.65	-3.40	-2.85	0.00	-2.80	-2.61	-3.01	0.00	-2.50
TCGA-EM-A3FQ-10A-01D-A21A-08_THCA	-2.50	-2.70	-2.73	-2.86	-2.63	-2.62	-2.52	-2.42	-2.45	0.00	0.00	0.00	0.00	0.00	-2.94	-2.65	-2.42
TCGA-EM-A3FR-10A-01D-A21Z-08_THCA	-2.49	-2.63	-2.66	-2.74	-2.55	-2.60	-2.51	-2.56	-2.45	0.00	-4.46	-4.46	0.00	0.00	-2.91	-4.46	-2.48
TCGA-EM-A3O3-10A-01D-A21Z-08_THCA	-2.57	-2.70	-2.72	-2.88	-2.62	-2.67	-2.60	-2.53	-2.66	-3.15	-2.82	-2.68	0.00	-2.66	-3.02	-4.53	-2.50
TCGA-EM-A3O6-10A-01D-A21Z-08_THCA	-2.57	-4.52	0.00	-2.77	-2.56	-2.60	-2.61	-2.61	-2.58	-3.14	-2.84	0.00	-2.79	-2.62	0.00	-2.79	-2.49
TCGA-EM-A3O7-10A-01D-A21Z-08_THCA	-2.55	-2.58	-2.62	0.00	-2.64	-2.65	-2.58	-2.64	-2.55	0.00	-2.84	-2.67	0.00	-4.23	-2.98	0.00	-2.49
TCGA-EM-A3O8-10A-01D-A21Z-08_THCA	-2.55	-2.66	-2.64	-4.28	-2.69	-2.70	-2.62	-2.57	-2.69	-3.26	-2.68	-2.71	-2.72	-2.69	-3.04	0.00	-2.58
TCGA-EM-A3O9-10A-01D-A21Z-08_THCA	-2.63	-2.64	-2.68	-4.09	-2.63	-2.64	-2.66	-2.54	-2.73	-3.22	-2.67	-2.58	0.00	-2.72	0.00	-2.72	-2.52
TCGA-EM-A3OA-10A-01D-A21Z-08_THCA	-2.48	-2.67	-2.64	-2.78	-2.59	-2.60	-2.50	-2.55	-2.51	0.00	0.00	-4.45	0.00	-4.45	-2.91	0.00	-2.44
TCGA-EM-A3OB-10A-01D-A21Z-08_THCA	-2.61	-2.49	-2.65	-4.10	-2.62	-2.61	-2.65	-2.49	-2.52	0.00	-2.81	-2.63	0.00	-4.58	-3.08	-2.72	-2.52
TCGA-EM-A3SU-10A-01D-A22Z-08_THCA	-2.56	-2.61	-2.55	0.00	-2.66	-2.73	-2.56	-2.59	0.00	-3.11	-2.57	-2.66	-2.62	-2.54	0.00	0.00	-2.57
TCGA-EM-A3SX-10A-01D-A22Z-08_THCA	-2.38	-2.41	-2.46	0.00	0.00	0.00	-2.42	-2.34	-2.36	0.00	0.00	0.00	0.00	0.00	-2.94	-2.66	-2.39
TCGA-EM-A3SY-10A-01D-A22Z-08_THCA	-2.45	0.00	0.00	-2.67	-2.42	-2.44	-2.45	-2.50	-2.36	0.00	0.00	0.00	0.00	-4.31	0.00	-2.57	-2.53
TCGA-EM-A3SZ-10A-01D-A22Z-08_THCA	-2.48	-4.39	-4.39	-2.55	-2.50	-2.50	-2.54	-2.59	-2.57	-4.39	0.00	-3.69	-4.39	0.00	0.00	-2.52	-2.48
TCGA-EM-A4FF-10A-01D-A25A-08_THCA	-2.37	0.00	0.00	-2.62	-2.41	-2.41	-2.46	-2.55	-2.38	0.00	0.00	0.00	0.00	0.00	-2.88	0.00	-2.32
TCGA-EM-A4FH-10A-01D-A25A-08_THCA	-2.55	-2.65	-2.65	-2.80	-2.65	-2.65	-2.54	-2.47	-2.51	0.00	-4.09	0.00	0.00	-3.61	-2.91	-2.69	-2.50
TCGA-EM-A4FK-10A-01D-A25A-08_THCA	-2.47	-2.45	-2.47	-3.51	-3.81	-3.81	-2.49	-2.43	-2.49	0.00	0.00	0.00	0.00	0.00	-2.89	-2.73	-2.43
TCGA-EM-A4FM-10A-01D-A25A-08_THCA	-2.52	-2.51	-2.53	-4.09	-2.65	-2.64	-2.72	-2.74	-3.61	-3.39	-2.54	-2.68	-2.53	-2.55	0.00	0.00	-2.48
TCGA-EM-A4FN-10A-01D-A25A-08_THCA	-2.61	-2.61	-2.58	-3.89	-2.75	-2.72	-2.66	-2.63	-2.70	-3.41	-2.73	-2.68	-4.19	-2.70	0.00	-2.73	-2.63
TCGA-EM-A4FO-10A-01D-A25A-08_THCA	-2.59	-3.95	0.00	-2.82	-2.59	-2.65	-2.64	-2.56	-2.67	-3.43	-2.93	-4.13	-2.76	-2.63	-3.13	-3.83	-2.56
TCGA-EM-A4FQ-10A-01D-A25A-08_THCA	-2.60	-2.72	-2.74	-2.98	-2.50	-2.63	-2.67	-2.52	-2.59	0.00	-2.82	-2.76	-4.49	0.00	0.00	-2.46	-2.54
TCGA-EM-A4FR-10A-01D-A25A-08_THCA	-2.58	-4.14	-4.14	-2.66	-2.58	-2.60	-2.55	-2.47	-2.72	-3.44	0.00	0.00	0.00	0.00	-3.04	-2.66	-2.55
TCGA-EM-A4FU-10A-01D-A25A-08_THCA	-2.61	-4.47	0.00	-2.62	-2.61	-2.58	-2.61	-2.51	-2.60	0.00	0.00	0.00	0.00	-4.17	-2.99	-2.73	-2.57
TCGA-EM-A4FV-10A-01D-A25A-08_THCA	-2.65	-2.75	-2.79	-2.98	-2.55	-2.67	-2.65	-2.60	-2.69	-3.58	-2.73	-2.81	-2.93	-2.77	-3.31	-3.71	-2.61
TCGA-EM-A4G1-10A-01D-A25A-08_THCA	-2.63	-2.75	-2.75	-3.07	-2.57	-2.63	-2.67	-2.54	-2.69	-4.47	-3.02	-2.77	-4.16	-4.47	0.00	-2.49	-2.61
TCGA-EO-A1Y5-10A-01D-A159-09_UCEC	-2.96	0.00	-4.56	-2.92	-2.56	-2.60	-2.57	-2.68	-2.74	-3.36	-2.87	0.00	-2.81	-2.78	0.00	-2.90	-2.71
TCGA-EO-A1Y7-10A-01D-A159-09_UCEC	-2.83	0.00	-4.48	-2.91	-2.47	-2.55	-2.50	-2.51	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.59
TCGA-EO-A1Y8-10A-01D-A159-09_UCEC	-2.99	0.00	0.00	-2.84	-2.65	-2.68	-2.61	-2.76	-2.61	0.00	0.00	0.00	0.00	-4.72	0.00	-2.68	-2.72
TCGA-EO-A22U-10B-01D-A17W-09_UCEC	-2.68	-2.59	-2.75	-3.13	-2.67	-2.59	-2.47	-2.38	-2.36	0.00	0.00	0.00	0.00	0.00	-2.81	-2.73	-2.49
TCGA-EO-A22X-10A-01D-A17W-09_UCEC	-2.85	-2.65	-2.68	-3.20	-2.67	-2.64	-2.46	-2.43	-2.40	0.00	0.00	0.00	-4.43	0.00	0.00	-2.48	-2.55
TCGA-EO-A22Y-10A-01D-A17W-09_UCEC	-2.77	-2.68	-2.66	-3.18	-2.68	-2.66	-2.50	-2.45	-2.39	-4.45	-3.98	0.00	-4.15	-3.98	0.00	-2.45	-2.63
TCGA-EO-A2CG-10A-01D-A17W-09_UCEC	-2.92	-2.86	-2.83	-3.35	-2.54	-2.68	-2.65	-2.70	-4.17	-3.47	-2.60	-2.85	-2.66	-2.71	0.00	-4.65	-2.73
TCGA-EO-A2CH-10A-01D-A17W-09_UCEC	-2.74	-2.64	-2.71	-3.27	-2.77	-2.68	-2.49	-2.48	-2.41	0.00	0.00	-4.38	0.00	0.00	0.00	-2.48	-2.57
TCGA-EO-A3AS-10A-01D-A19Y-09_UCEC	-2.94	-2.64	-2.68	0.00	-2.71	-2.65	-2.68	-2.57	-2.71	-3.48	-2.58	-2.65	-2.88	-2.78	-3.03	-4.15	-2.73
TCGA-EO-A3AU-10A-01D-A19Y-09_UCEC	-2.72	0.00	0.00	-2.99	-2.53	-2.48	-2.44	-2.55	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.62
TCGA-EO-A3AV-10A-01D-A19Y-09_UCEC	-2.78	-4.54	-4.24	-2.94	-2.52	-2.53	-2.49	-2.56	-2.42	0.00	0.00	0.00	0.00	-4.54	-3.11	-2.71	-2.63
TCGA-EO-A3AY-10A-01D-A19Y-09_UCEC	-2.68	-2.62	-2.66	-3.12	-2.59	-2.58	-2.45	-2.59	-2.35	0.00	0.00	0.00	-4.46	-4.16	0.00	-2.58	-2.55
TCGA-EO-A3AZ-10A-01D-A19Y-09_UCEC	-2.71	-2.38	-2.40	0.00	0.00	-3.78	-2.39	-2.65	-2.35	0.00	0.00	0.00	-4.39	-4.39	-3.06	-2.80	-2.40
TCGA-EO-A3B0-10A-01D-A19Y-09_UCEC	-2.86	-2.83	-2.83	-3.35	-2.51	-2.58	-2.58	-2.51	-2.76	0.00	-2.88	-2.81	0.00	-4.22	-2.97	-2.85	-2.68
TCGA-EO-A3B1-10A-01D-A19Y-09_UCEC	-2.82	-2.74	-2.74	-3.20	-2.74	-2.69	-2.58	-2.65	-2.67	-3.43	-2.87	-4.24	-2.79	-2.82	0.00	-2.81	-2.69
TCGA-EO-A3KU-10A-01D-A22A-09_UCEC	-2.75	-4.01	-3.88	-2.99	-2.50	-2.66	-2.54	-2.46	-2.46	0.00	-4.18	-4.49	0.00	-4.18	-3.12	-2.81	-2.62
TCGA-EO-A3KW-10A-01D-A22A-09_UCEC	-2.91	-2.90	-3.04	-3.27	-2.65	-2.70	-2.55	-2.49	-2.63	-3.49	-3.01	-3.03	-4.63	-4.03	-3.09	-2.92	-2.72
TCGA-EO-A3KX-10A-01D-A22A-09_UCEC	-2.81	-3.72	-3.94	-2.96	-2.57	-2.58	-2.56	-2.59	-2.65	-3.42	-2.94	-3.94	-2.80	-2.77	0.00	-2.84	-2.64
TCGA-EO-A3L0-10A-01D-A22A-09_UCEC	-2.81	-2.70	-2.72	-3.22	-2.67	-2.75	-2.62	-2.74	-2.59	0.00	-2.73	0.00	-2.72	-2.72	0.00	-2.64	-2.60
TCGA-EP-A12J-10A-01D-A12Z-10_LIHC	-2.37	-2.79	-2.67	-2.83	-2.48	-2.53	-2.37	-2.68	-2.42	0.00	-3.06	-2.87	0.00	0.00	-3.33	-3.22	-2.39
TCGA-EP-A26S-10A-01D-A16V-10_LIHC	-2.55	0.00	0.00	-2.62	-2.49	-2.50	-2.44	-2.72	-2.96	-3.12	-3.03	0.00	-2.91	-2.73	0.00	-2.76	-2.39
TCGA-EP-A2KA-10A-01D-A183-10_LIHC	-2.39	-2.66	-2.64	-2.71	-2.64	-2.67	-2.31	-2.46	-2.28	0.00	0.00	0.00	0.00	0.00	-3.31	-2.71	-2.24
TCGA-EP-A2KB-10A-01D-A183-10_LIHC	-2.44	-2.64	-2.54	-2.84	-2.73	-2.49	-2.24	-2.49	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.23
TCGA-EP-A2KC-10A-01D-A20W-10_LIHC	-2.43	-2.51	-2.36	-4.36	-2.40	-2.32	-2.33	-2.42	-2.55	0.00	-2.59	-2.57	-2.62	0.00	-2.91	-2.77	-2.42
TCGA-EP-A3JL-10A-01D-A20W-10_LIHC	-2.41	0.00	0.00	-2.70	-2.26	-2.33	-2.23	-2.37	-2.27	0.00	0.00	0.00	0.00	0.00	-2.87	-2.73	-2.36
TCGA-EP-A3RK-10A-01D-A22F-10_LIHC	-2.44	-2.57	-2.72	-3.02	-2.79	-2.59	-2.36	-2.56	-2.25	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.37
TCGA-EQ-5647-10A-01D-1600-08_STAD	-2.56	-4.32	-4.62	-2.81	-2.52	-2.56	-2.56	-2.56	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.62	-2.51
TCGA-EQ-8122-10A-01D-2341-08_STAD	-2.58	0.00	-4.59	-2.60	-2.56	-2.55	-2.59	-2.60	-2.47	0.00	0.00	0.00	0.00	-4.59	0.00	-2.41	-2.52
TCGA-EQ-A4SO-10A-01D-A25E-08_STAD	-2.67	0.00	0.00	-2.89	-2.63	-2.62	-2.68	-2.58	-2.78	-3.48	-2.82	0.00	-2.76	-2.76	-3.03	0.00	-2.59
TCGA-ER-A193-10A-01D-A199-08_SKCM	-2.52	-2.74	-2.79	-2.82	-2.53	-2.56	-2.60	-2.60	-2.49	0.00	-3.14	-2.90	0.00	-4.59	0.00	-2.57	-2.44

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-ER-A194-10A-01D-A199-08_SKCM	-2.49	0.00	-4.47	-2.59	-2.54	-2.56	-2.54	-2.53	-2.43	0.00	0.00	0.00	0.00	-4.17	-3.00	-2.69	-2.43
TCGA-ER-A195-10A-01D-A198-08_SKCM	-2.50	-2.71	-2.71	-2.86	-2.74	-2.67	-2.60	-2.54	-2.67	-3.40	-2.84	0.00	-2.77	-2.61	0.00	-2.74	-2.47
TCGA-ER-A196-10A-01D-A199-08_SKCM	-2.45	-2.69	-2.67	-2.82	-2.61	-2.64	-2.50	-2.56	-2.45	0.00	0.00	0.00	-4.51	-4.51	-3.08	-2.65	-2.44
TCGA-ER-A197-10A-01D-A199-08_SKCM	-2.55	-2.71	-2.72	-2.90	-2.52	-2.59	-2.65	-2.48	-2.72	-3.47	-2.82	-2.79	-2.81	-2.69	-3.24	0.00	-2.52
TCGA-ER-A198-10A-01D-A198-08_SKCM	-2.48	0.00	0.00	-2.68	-2.53	-2.53	-2.55	-2.51	-2.63	-3.36	-2.99	0.00	-2.87	-2.66	-3.24	0.00	-2.40
TCGA-ER-A199-10A-01D-A199-08_SKCM	-2.33	-2.60	-2.74	-2.72	-2.60	-2.69	-2.50	-2.55	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.34
TCGA-ER-A19A-10A-01D-A199-08_SKCM	-2.40	0.00	0.00	-2.52	-2.45	-2.50	-2.48	-2.48	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.37
TCGA-ER-A19B-10A-01D-A198-08_SKCM	-2.37	-2.68	-2.71	-2.74	-2.55	-2.67	-2.48	-2.49	-2.43	0.00	0.00	0.00	0.00	0.00	-3.14	-2.77	-2.28
TCGA-ER-A19C-10A-01D-A198-08_SKCM	-2.46	-2.85	-2.82	-2.73	-2.64	-2.60	-2.73	-2.63	-2.86	-3.46	-2.76	-2.58	0.00	-2.76	0.00	-2.92	-2.45
TCGA-ER-A19D-10A-01D-A199-08_SKCM	-2.56	-2.87	-2.67	-2.92	-2.47	-2.62	-2.63	-2.67	-2.80	-3.49	-2.74	-2.76	-2.80	-2.72	0.00	-2.78	-2.51
TCGA-ER-A19E-10A-01D-A199-08_SKCM	-2.43	0.00	-4.45	-2.56	-2.55	-2.49	-2.57	-2.51	-2.57	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.47
TCGA-ER-A19F-10A-01D-A198-08_SKCM	-2.43	0.00	-4.10	-2.51	-2.48	-2.49	-2.54	-2.44	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.41
TCGA-ER-A19G-10A-01D-A198-08_SKCM	-2.52	-2.84	-2.91	-2.93	-2.47	-2.61	-2.61	-2.64	-3.79	-3.21	-2.62	-2.61	-2.91	-2.67	0.00	-4.57	-2.56
TCGA-ER-A19H-10A-01D-A198-08_SKCM	-2.43	-2.84	-2.75	-2.86	-2.50	-2.64	-2.60	-2.61	-2.54	0.00	-3.17	-2.83	0.00	0.00	0.00	-2.69	-2.40
TCGA-ER-A19J-10A-01D-A198-08_SKCM	-2.44	-2.61	-2.59	0.00	-2.70	-2.80	-2.51	-2.59	-2.53	0.00	-2.99	-2.74	0.00	0.00	-3.10	-2.76	-2.42
TCGA-ER-A19K-10A-01D-A199-08_SKCM	-2.52	-2.58	-2.61	0.00	-4.47	-4.47	-2.57	-2.48	-2.59	-3.32	-2.76	0.00	-2.75	-2.64	0.00	-2.64	-2.45
TCGA-ER-A19L-10A-01D-A199-08_SKCM	-2.41	0.00	0.00	-2.55	-2.46	-2.53	-2.56	-2.49	-2.63	-3.45	-3.08	0.00	-2.86	-2.73	0.00	-2.79	-2.42
TCGA-ER-A19M-10A-01D-A23B-08_SKCM	-2.69	-2.79	-2.78	-2.94	-2.55	-2.64	-2.68	-2.62	-2.72	-3.31	-2.71	-2.81	-2.84	-2.75	-3.14	-4.05	-2.64
TCGA-ER-A19N-10A-01D-A199-08_SKCM	-2.48	0.00	-4.50	-2.57	-2.66	-2.56	-2.56	-2.60	-2.72	-3.59	-3.06	0.00	-2.85	-2.69	0.00	-2.86	-2.45
TCGA-ER-A19O-10A-01D-A199-08_SKCM	-2.31	-2.50	-2.46	-4.38	-4.38	-4.38	-2.50	-2.47	-2.37	0.00	0.00	0.00	0.00	-4.38	-3.30	-2.77	-2.27
TCGA-ER-A19P-10A-01D-A198-08_SKCM	-2.44	0.00	0.00	-2.57	-2.55	-2.56	-2.63	-2.54	-2.67	-3.43	-2.83	0.00	-2.80	-2.68	-3.26	0.00	-2.47
TCGA-ER-A19Q-10A-01D-A199-08_SKCM	-2.54	-2.59	-2.54	0.00	-2.70	-2.70	-2.64	-2.53	-2.55	0.00	-2.82	-2.72	0.00	0.00	-2.99	-2.67	-2.50
TCGA-ER-A19S-10A-01D-A198-08_SKCM	-2.54	-2.74	-2.72	-2.89	-2.50	-2.60	-2.67	-2.57	-2.49	0.00	-2.87	-2.74	0.00	0.00	0.00	-2.44	-2.52
TCGA-ER-A19T-10A-01D-A19A-08_SKCM	-2.44	-2.70	-2.90	-2.80	-2.53	-2.64	-2.60	-2.49	-2.57	0.00	-3.08	-2.92	0.00	-4.49	0.00	-2.59	-2.48
TCGA-ER-A19W-10A-01D-A23B-08_SKCM	-2.47	-2.70	-2.69	-2.99	-2.45	-2.61	-2.60	-2.59	-2.56	0.00	-2.97	-2.71	0.00	0.00	-3.18	-2.76	-2.48
TCGA-ER-A1A1-10A-01D-A199-08_SKCM	-2.42	-2.67	-2.63	-2.87	-2.67	-2.76	-2.52	-2.49	-2.47	0.00	0.00	0.00	0.00	-4.51	-2.96	-2.72	-2.33
TCGA-ER-A2NB-10A-01D-A198-08_SKCM	-2.55	-2.75	-2.71	-2.85	-2.46	-2.60	-2.60	-2.62	-2.74	-3.38	-2.70	-2.59	0.00	-2.76	0.00	-2.77	-2.56
TCGA-ER-A2NC-10A-01D-A199-08_SKCM	-2.55	-2.80	-2.76	-2.96	-2.54	-2.65	-2.66	-2.66	-2.71	-3.50	-2.74	-2.68	0.00	-2.72	0.00	-2.79	-2.59
TCGA-ER-A2ND-10A-01D-A198-08_SKCM	-2.45	-2.75	-2.76	-2.96	-2.51	-2.59	-2.53	-2.54	-2.50	0.00	-3.06	-2.79	0.00	-4.55	0.00	-2.45	-2.39
TCGA-ER-A2NE-10A-01D-A198-08_SKCM	-2.43	-2.80	-2.72	-2.85	-2.54	-2.55	-2.67	-2.53	-2.54	-4.55	-3.21	-2.85	0.00	-4.25	0.00	-2.62	-2.42
TCGA-ER-A2NF-10A-01D-A19A-08_SKCM	-2.42	0.00	-4.24	-2.75	-2.54	-2.60	-2.65	-2.55	-2.72	-3.40	-2.90	0.00	-2.80	-2.65	-3.07	-4.24	-2.52
TCGA-ER-A2NG-10A-01D-A198-08_SKCM	-2.55	-2.60	-2.59	-4.44	-2.79	-2.77	-2.57	-2.46	-2.55	-3.48	-3.01	-2.75	0.00	0.00	-3.14	-2.72	-2.51
TCGA-ER-A2NH-10A-01D-A198-08_SKCM	-2.43	-2.67	-2.65	-2.75	-2.65	-2.71	-2.42	-2.52	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.39
TCGA-ER-A3ES-10A-01D-A20D-08_SKCM	-2.50	0.00	-4.43	-2.60	-2.48	-2.50	-2.49	-2.54	-2.44	0.00	0.00	-3.96	0.00	0.00	-2.84	-4.43	-2.45
TCGA-ER-A3ET-10A-01D-A20D-08_SKCM	-2.61	-2.77	-2.71	-2.84	-2.49	-2.56	-2.65	-2.52	-2.50	0.00	-2.93	-2.71	0.00	0.00	-3.08	-2.79	-2.54
TCGA-ER-A3EV-10A-01D-A20D-08_SKCM	-2.52	0.00	-4.46	-2.67	-2.46	-2.50	-2.54	-2.53	-2.54	0.00	0.00	-4.46	0.00	-4.46	0.00	-2.53	-2.39
TCGA-ER-A3PL-10A-01D-A23B-08_SKCM	-2.57	-4.60	-4.60	-2.75	-2.44	-2.54	-2.59	-2.66	-2.63	-3.25	-2.92	0.00	-2.71	-2.65	0.00	-2.77	-2.45
TCGA-ER-A42H-10A-01D-A24R-08_SKCM	-2.56	0.00	0.00	-2.76	-2.57	-2.59	-2.58	-2.55	-2.59	0.00	0.00	0.00	-4.21	0.00	0.00	-2.42	-2.54
TCGA-ER-A42K-10A-01D-A24R-08_SKCM	-2.50	-3.82	-4.05	-2.64	-2.61	-2.65	-2.62	-2.65	-2.70	-3.29	-2.83	0.00	-2.80	-2.70	0.00	-2.70	-2.60
TCGA-ER-A42L-10A-01D-A24R-08_SKCM	-2.64	0.00	-4.51	-2.65	-2.59	-2.60	-2.61	-2.63	-2.48	0.00	-4.51	0.00	-4.51	0.00	0.00	-2.65	-2.55
TCGA-ET-A25G-10A-01D-A16O-08_THCA	-2.47	-2.74	-2.72	-2.80	-2.66	-2.63	-2.54	-2.45	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.44
TCGA-ET-A25I-10A-01D-A16O-08_THCA	-2.48	-2.67	-2.70	-2.80	-2.68	-2.68	-2.50	-2.55	-2.55	-3.44	-4.59	0.00	0.00	0.00	0.00	-2.58	-2.47
TCGA-ET-A25K-10A-01D-A16O-08_THCA	-2.50	-2.69	-2.73	-2.86	-2.70	-2.66	-2.70	-2.71	-4.30	-3.37	-2.69	-2.69	-2.77	-2.51	0.00	0.00	-2.46
TCGA-ET-A25O-10A-01D-A17V-08_THCA	-2.65	-4.64	0.00	-2.75	-2.49	-2.62	-2.68	-2.54	-2.65	-3.52	-2.89	-2.82	0.00	-4.34	-3.16	-2.89	-2.60
TCGA-ET-A25R-10A-01D-A16O-08_THCA	-2.49	0.00	0.00	-2.70	-2.49	-2.55	-2.53	-2.57	-2.43	0.00	-4.51	0.00	0.00	-4.51	0.00	-2.42	-2.37
TCGA-ET-A2MZ-10A-01D-A19M-08_THCA	-2.46	-2.70	-2.67	-2.82	-2.63	-2.60	-2.53	-2.47	-2.43	0.00	0.00	-4.53	0.00	0.00	-3.11	-2.65	-2.40
TCGA-ET-A2N0-10A-01D-A18F-08_THCA	-2.47	-4.53	-4.53	-2.71	-2.46	-2.57	-2.54	-2.55	-2.75	-3.33	-2.99	0.00	-2.86	-2.72	0.00	-2.79	-2.37
TCGA-ET-A2N1-10A-01D-A18F-08_THCA	-2.53	-2.72	-2.76	-2.94	-2.51	-2.56	-2.61	-2.62	-2.55	0.00	-2.91	-2.75	0.00	0.00	0.00	-2.61	-2.54
TCGA-ET-A2N3-10A-01D-A23K-08_THCA	-2.43	0.00	0.00	-2.60	-2.43	-2.46	-2.48	-2.56	-2.63	-3.47	-2.91	0.00	-2.76	-2.54	0.00	-2.75	-2.37
TCGA-ET-A2N4-10A-01D-A19M-08_THCA	-2.56	-2.71	-2.71	-2.87	-2.47	-2.55	-2.53	-2.52	-2.52	0.00	-2.92	-2.74	0.00	-4.31	0.00	-2.56	-2.43
TCGA-ET-A39I-10A-01D-A19M-08_THCA	-2.46	-2.70	-2.64	-2.84	-2.65	-2.71	-2.46	-2.51	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.37
TCGA-ET-A39J-10A-01D-A19M-08_THCA	-2.44	-2.58	-2.66	-2.80	-2.56	-2.62	-2.42	-2.61	-2.38	0.00	0.00	0.00	0.00	-3.98	-3.03	-4.16	-2.34
TCGA-ET-A39K-10A-01D-A19M-08_THCA	-2.55	0.00	-4.23	-2.71	-2.50	-2.57	-2.58	-2.58	-2.61	-3.21	-2.87	0.00	-2.79	-2.68	0.00	-2.79	-2.44
TCGA-ET-A39L-10A-01D-A19M-08_THCA	-2.42	-4.05	0.00	-2.53	-2.47	-2.45	-2.46	-2.62	-2.43	0.00	-4.52	0.00	-3.92	-4.22	0.00	-2.54	-2.30
TCGA-ET-A39M-10A-01D-A19M-08_THCA	-2.62	-2.90	-2.77	-2.96	-2.52	-2.65	-2.65	-2.69	-2.71	-3.34	-2.69	-2.79	-2.79	-2.77	0.00	-2.78	-2.55
TCGA-ET-A39N-10A-01D-A19M-08_THCA	-2.44	-2.72	-2.72	-2.76	-2.63	-2.67	-2.45	-2.46	-2.44	0.00	0.00	0.00	0.00	-4.52	-3.13	-2.82	-2.42
TCGA-ET-A39O-10A-01D-A19M-08_THCA	-2.46	-4.22	0.00	-2.73	-2.46	-2.44	-2.47	-2.47	-2.39	0.00	0.00	0.00	-3.75	-3.75	-3.18	-2.81	-2.40
TCGA-ET-A39P-10A-01D-A19M-08_THCA	-2.54	-2.78	-2.68	-2.93	-2.45	-2.53	-2.53	-2.64	-2.51	0.00	-2.97	-2.74	0.00	0.00	-3.25	-2.82	-2.40
TCGA-ET-A39R-10A-01D-A19M-08_THCA	-2.57	-2.71	-2.70	-2.89	-2.67	-2.68	-2.60	-2.67	-2.74	-3.37	-2.89	-4.62	-2.75	-2.66	0.00	-2.74	-2.48
TCGA-ET-A39S-10A-01D-A19M-08_THCA	-2.48	-4.05	-4.53	-2.63	-2.43	-2.45	-2.46	-2.54	-2.46	0.00	0.00	-4.05	0.00	-4.23	-3.06	-2.83	-2.38
TCGA-ET-A39T-10A-01D-A19M-08_THCA	-2.47	-2.71	-2.59	-2.78	-2.64	-2.73	-2.49	-2.55	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.39
TCGA-ET-A3BN-10A-01D-A19M-08_THCA	-2.46	-4.56	0.00	-2.70	-2.46	-2.45	-2.47	-2.65	-2.63	-3.16	-3.06	0.00	-2.77	-2.63	0.00	-2.89	-2.40
TCGA-ET-A3BO-10A-01D-A19M-08_THCA	-2.50	-2.66	-2.67	-2.86	-2.64	-2.67	-2.53	-2.47	-2.41	0.00	0.00	-4.57	0.00	0.00	-3.02	-2.73	-2.43
TCGA-ET-A3BP-10A-01D-A19M-08_THCA	-2.42	0.00	0.00	-2.80	-2.52	-2.60	-2.59	-2.50	-2.68	-3.36	-2.84	0.00	-2.79	-2.67	0.00	-2.82	-2.42
TCGA-ET-A3BQ-10A-01D-A202-08_THCA	-2.58	0.00	-4.52	-2.79	-2.54	-2.58	-2.62	-2.50	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.61	-2.52
TCGA-ET-A3BS-10A-01D-A202-08_THCA	-2.55	-2.74	-2.74	-2.88	-2.70	-2.71	-2.59	-2.61	-2.75	-3.33	-2.81	0.00	-2.82	-2.69	0.00	-2.67	-2.51
TCGA-ET-A3BT-10A-01D-A19M-08_THCA	-2.46	-3.80	-3.66	-2.65	-2.45	-2.43	-2.39	-2.46	-2.41	0.00	0.00	0.00	-4.50	0.00	-3.07	-2.75	-2.41
TCGA-ET-A3BU-10A-01D-A19M-08_THCA	-2.53	-2.71	-2.68	-2.83	-2.59	-2.67	-2.58	-2.63	-2.70	-3.24	-2.94	-2.72	-4.26	-2.61	0.00	-2.70	-2.41
TCGA-ET-A3BV-10A-01D-A19M-08_THCA	-2.44	-4.51	0.00	-2.67	-2.45	-2.48	-2.51	-2.46	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.41
TCGA-ET-A3BW-10A-01D-A19M-08_THCA	-2.45	-4.56	-3.96	-2.67	-2.40	-2.52	-2.43	-2.59	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.30
TCGA-ET-A3BX-10A-01D-A19M-08_THCA	-2.46	-4.03	-4.03	-2.69	-2.47	-2.49	-2.49	-2.58	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.37
TCGA-ET-A3DO-10A-01D-A19M-08_THCA	-2.50	-2.70	-2.69	-2.88	-2.72	-2.70	-2.54	-2.48	-2.63	-3.37	-2.96	0.00	-2.80	-2.69	-3.23	0.00	-2.43
TCGA-ET-A3DQ-10A-01D-A19M-08_THCA	-2.39	-3.92	-4.53	-2.55	-2.42	-2.50	-2.51	-2.51	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.38
TCGA-ET-A3DR-10A-01D-A19M-08_THCA	-2.53	-4.67	0.00	-2.74	-2.50	-2.60	-2.57	-2.55	-2.49	0.00	-4.37	0.00	-4.37	-3.97	0.00	-2.60	-2.41
TCGA-ET-A3DS-10A-01D-A19M-08_THCA	-2.49	-2.59	-2.53	-3.79	-2.62	-2.67	-2.54	-2.63	-2.49	0.00	-2.83	-2.70	0.00	0.00	-2.97	-4.09	-2.44
TCGA-ET-A3DT-10A-01D-A19M-08_THCA	-2.51	-2.54	-2.50	-4.51	-3.91	-4.04	-2.56	-2.57	-2.58	-3.34	-2.91	0.00	-2.83	-2.64	-3.13	0.00	-2.39
TCGA-ET-A3DU-10A-01D-A19M-08_THCA	-2.45	-2.46	-2.43	-3.80	-3.46	-3.65	-2.41	-2.50	-2.40	0.00	0.00	0.00	0.00	0.00	-2.77	-4.50	-2.35
TCGA-ET-A40P-10A-01D-A23K-08_THCA	-2.54	-4.64	-4.34	-2.89	-2.62	-2.65	-2.74	-2.70	-2.78	-3.34	-2.90	0.00	-2.80	-2.76	0.00	-2.75	-2.61
TCGA-ET-A40Q-10A-01D-A23K-08_THCA	-2.44	0.00	-4.69	-2.62	-2.43	-2.45	-2.48	-2.49	-2.41	0.00	0.00	0.00	0.00	-4.69	-3.03	-2.71	-2.36
TCGA-ET-A40R-10A-01D-A23K-08_THCA	-2.69	-2.88	-2.84	-3.01	-2.62	-2.77	-2.72	-2.62	-2.67	0.00	-2.92	-2.89	-4.22	-4.53	0.00	-2.59	-2.63
TCGA-ET-A40S-10A-01D-A23K-08_THCA	-2.63	-2.68	-2.70	-2.87	-2.64	-2.73	-2.66	-2.51	-2.51	0.00	0.00	0.00	0.00	-4.27	-3.07	-2.71	-2.55
TCGA-ET-A40T-10A-01D-A23K-08_THCA	-2.46	-3.76	-3.83	-2.65	-2.58	-2.67	-2.66	-2.43	-2.54	-4.13	-4.00	-3.76	-4.30	-3.56	-3.11	-2.68	-2.59
TCGA-ET-A4KN-10A-01D-A25A-08_THCA	-2.49	-4.43	-3.73	-2.85	-2.58	-2.57	-2.59	-2.62	-2.69	-3.38	-2.88	0.00	-2.77	-2.65	0.00	-2.77	-2.56
TCGA-ET-A4KQ-10A-01D-A25A-08_THCA	-2.59	0.00	-4.39	-2.75	-2.57	-2.57	-2.54	-2.48	-2.59	0.00	-4.39	0.00	-3.69	-3.79	0.00	-2.42	-2.54
TCGA-EU-5904-10A-01D-1669-08_KIRC	-2.52	-2.67	-2.69	-2.88	-2.59	-2.63	-2.55	-2.43	-2.48	0.00	0.00	0.00	0.00	0.00	-3.04	-2.71	-2.43
TCGA-EU-5905-10A-01D-1669-08_KIRC	-2.52	-4.52	-4.52	-2.63	-2.49	-2.55	-2.58	-2.54	-2.53	0.00	0.00	0.00	-4.52	-4.52	0.00	-2.63	-2.41
TCGA-EU-5906-10A-01D-1669-08_KIRC	-2.48	-4.55	0.00	-2.71	-2.51	-2.56	-2.55	-2.49	-2.46	0.00	-4.55	0.00	0.00	-4.55	-3.01	-2.65	-2.41
TCGA-EU-5907-10A-01D-1669-08_KIRC	-2.62	-2.80	-2.79	-2.96	-2.52	-2.60	-2.64	-2.55	-2.75	-3.29	-2.80	-2.76	-2.83	-2.68	-3.27	-4.18	-2.50
TCGA-EV-5901-10A-01D-1589-08_KIRP	-2.39	-4.23	-4.06	-2.60	-2.51	-2.49	-2.57	-2.43	-2.48	0.00	0.00	0.00	0.00	0.00	-3.01	-2.69	-2.52
TCGA-EV-5902-10A-01D-1589-08_KIRP	-2.52	0.00	-4.08	-2.80	-2.52	-2.53	-2.57	-2.57	-2.52	0.00	0.00	-4.26	0.00	-4.56	0.00	-2.50	-2.48
TCGA-EV-5903-10A-01D-1589-08_KIRP	-2.50	-4.07	-4.55	-2.62	-2.55	-2.53	-2.56	-2.62	-2.44	0.00	-4.55	0.00	0.00	-4.07	0.00	-2.58	-2.52
TCGA-EW-A1IW-10A-01D-A13O-09_BRCA	-2.98	0.00	0.00	-3.00	-2.58	-2.60	-2.50	-2.68	-2.53	0.00	0.00	-4.45	0.00	0.00	-3.17	-2.83	-2.62
TCGA-EW-A1IX-10A-01D-A142-09_BRCA	-2.87	0.00	0.00	-2.92	-2.56	-2.56	-2.52	-2.61	-2.49	0.00	0.00	0.00	0.00	0.00	-3.16	-2.79	-2.67
TCGA-EW-A1IY-10A-01D-A13O-09_BRCA	-2.85	0.00	0.00	-2.92	-2.60	-2.62	-2.63	-2.65	-2.78	-3.36	-2.89	0.00	-2.77	-2.78	-3.12	0.00	-2.76
TCGA-EW-A1IZ-10A-01D-A13O-09_BRCA	-2.88	-2.73	-2.70	-3.01	-2.77	-2.73	-2.48	-2.60	-2.50	0.00	0.00	0.00	0.00	0.00	-3.03	-2.87	-2.60
TCGA-EW-A1J1-10A-01D-A13O-09_BRCA	-2.94	-2.83	-2.85	-3.19	-2.58	-2.68	-2.65	-2.69	-2.68	0.00	-2.97	-2.84	0.00	0.00	-3.19	-2.91	-2.74

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EW-A1J3-10A-01D-A13O-09_BRCA	-2.99	-2.70	-2.73	0.00	-2.79	-2.86	-2.68	-2.81	-2.67	0.00	-3.02	-2.84	-4.78	0.00	-3.21	-2.87	-2.88
TCGA-EW-A1J5-10A-01D-A13O-09_BRCA	-2.85	-2.75	-2.74	-3.11	-2.77	-2.75	-2.55	-2.62	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.73	-2.70
TCGA-EW-A1J6-10A-01D-A13O-09_BRCA	-2.98	-4.67	0.00	-2.94	-2.63	-2.63	-2.59	-2.58	-2.59	0.00	0.00	0.00	0.00	0.00	-3.07	-2.90	-2.76
TCGA-EW-A1OV-10A-01D-A142-09_BRCA	-3.07	-2.92	-2.93	-3.31	-2.74	-2.82	-2.72	-2.72	-2.78	0.00	-3.10	-2.95	0.00	0.00	0.00	-2.75	-2.82
TCGA-EW-A1OX-10A-01D-A142-09_BRCA	-3.01	0.00	0.00	-2.95	-2.62	-2.62	-2.53	-2.71	-2.62	0.00	0.00	0.00	0.00	0.00	0.00	-2.65	-2.73
TCGA-EW-A1OZ-10A-01D-A142-09_BRCA	-2.99	0.00	-2.81	-3.08	-2.54	-2.67	-2.55	-2.71	-2.61	0.00	-2.91	0.00	-2.83	0.00	-3.08	-2.99	-2.78
TCGA-EW-A1P0-10A-01D-A142-09_BRCA	-3.14	-4.65	0.00	-3.04	-2.80	-2.84	-2.75	-3.02	-2.74	0.00	0.00	0.00	0.00	0.00	-3.40	-3.05	-2.88
TCGA-EW-A1P1-10A-01D-A14G-09_BRCA	-3.04	-2.85	-2.88	-3.16	-2.62	-2.66	-2.56	-2.65	-2.59	0.00	-2.97	-2.82	0.00	-4.56	-3.19	-3.07	-2.79
TCGA-EW-A1P3-10A-01D-A142-09_BRCA	-3.02	0.00	0.00	-2.83	-2.63	-2.62	-2.61	-2.58	-2.81	-3.38	-2.87	0.00	-2.92	-2.72	0.00	-2.98	-2.68
TCGA-EW-A1P4-10A-01D-A142-09_BRCA	-3.02	-2.62	-2.64	0.00	-2.87	-2.81	-2.63	-2.60	-2.54	0.00	-2.95	-2.91	0.00	0.00	0.00	-2.61	-2.73
TCGA-EW-A1P5-10A-01D-A142-09_BRCA	-2.94	-2.69	-2.75	-3.04	-2.75	-2.81	-2.59	-2.72	-2.78	-3.41	-2.93	-2.76	0.00	-2.79	0.00	-2.82	-2.65
TCGA-EW-A1P6-10A-01D-A142-09_BRCA	-3.09	-2.81	-2.77	-3.14	-2.81	-2.82	-2.59	-2.69	-2.94	-3.33	-2.97	0.00	-2.83	-2.94	0.00	-2.94	-2.77
TCGA-EW-A1P7-10A-01D-A142-09_BRCA	-3.21	-2.75	-2.82	-3.18	-2.83	-2.85	-2.56	-2.67	-2.56	0.00	0.00	0.00	0.00	0.00	-3.01	0.00	-2.65
TCGA-EW-A1P8-10A-01D-A142-09_BRCA	-2.89	-2.69	-2.70	-3.05	-2.79	-2.75	-2.59	-2.70	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.68	-2.70
TCGA-EW-A1PA-10A-01D-A142-09_BRCA	-2.92	0.00	0.00	-2.88	-2.62	-2.62	-2.56	-2.72	-2.81	-3.27	-3.07	-2.70	-4.45	-2.76	0.00	-2.89	-2.69
TCGA-EW-A1PB-10A-01D-A142-09_BRCA	-2.88	0.00	-4.52	-2.85	-2.58	-2.67	-2.66	-2.62	-2.60	-4.52	0.00	-4.52	0.00	0.00	-3.12	-2.96	-2.74
TCGA-EW-A1PC-10A-01D-A21Q-09_BRCA	-2.67	-2.70	-4.10	-3.12	-2.76	-2.68	-2.73	-2.78	-2.59	-4.40	-2.92	-4.10	-2.76	-2.69	0.00	-2.86	-2.61
TCGA-EW-A1PD-10A-01D-A142-09_BRCA	-3.23	-2.71	-2.74	-4.58	-2.74	-2.73	-2.65	-2.63	-2.68	-3.40	-2.84	-2.77	0.00	-4.58	0.00	-2.66	-2.79
TCGA-EW-A1PE-10A-01D-A142-09_BRCA	-2.90	0.00	0.00	-2.96	-2.61	-2.64	-2.62	-2.60	-2.64	-4.52	0.00	0.00	0.00	-4.52	-3.20	-2.89	-2.75
TCGA-EW-A1PG-10A-01D-A142-09_BRCA	-3.14	0.00	0.00	-2.97	-2.64	-2.71	-2.57	-2.70	-2.86	-3.53	-3.08	0.00	-2.80	-2.88	0.00	-3.07	-2.81
TCGA-EW-A1PH-10A-01D-A14K-09_BRCA	-3.05	-2.76	-2.68	-3.02	-2.56	-2.61	-2.59	-2.78	-2.63	-4.71	-2.92	-2.76	0.00	0.00	0.00	-2.69	-2.74
TCGA-EW-A2FR-10A-01D-A21Q-09_BRCA	-2.82	-4.17	-4.17	-3.02	-2.51	-2.45	-2.50	-2.55	-2.40	-4.47	0.00	0.00	-3.99	-3.99	-2.75	-3.69	-2.55
TCGA-EW-A2FS-10A-01D-A17D-09_BRCA	-2.82	0.00	0.00	-2.76	-2.48	-2.64	-2.64	-2.76	-2.52	0.00	0.00	0.00	0.00	0.00	-3.00	0.00	-2.65
TCGA-EW-A2FV-10A-01D-A17D-09_BRCA	-2.75	-4.43	0.00	-2.63	-2.88	-2.56	-2.44	-2.34	-2.43	0.00	0.00	-4.43	0.00	0.00	-3.20	-3.07	-2.49
TCGA-EW-A2FW-10A-01D-A17D-09_BRCA	-2.86	-4.43	-4.43	-2.82	-2.61	-2.61	-2.57	-2.67	-2.77	-3.35	-2.78	0.00	-2.85	-2.78	-3.20	0.00	-2.72
TCGA-EW-A3E8-10A-01D-A243-09_BRCA	-2.81	-2.60	-2.74	-3.30	-2.68	-2.75	-2.69	-2.85	-3.46	-3.41	-2.66	-4.11	-2.50	-2.57	0.00	-3.46	-2.56
TCGA-EW-A3U0-10A-01D-A22A-09_BRCA	-2.89	-2.79	-2.84	-3.32	-2.52	-2.71	-2.65	-2.61	-2.77	-3.54	-2.75	-2.87	-2.87	-2.80	-3.24	-4.49	-2.67
TCGA-EW-A423-10A-01D-A243-09_BRCA	-2.83	0.00	-4.31	-3.10	-2.48	-2.53	-2.46	-2.50	-2.33	0.00	-4.31	-4.00	0.00	0.00	-3.05	-2.79	-2.58
TCGA-EX-A1H5-10A-01D-A13W-08_CESC	-2.39	-4.65	-4.35	-2.59	-2.43	-2.50	-2.46	-2.54	-2.39	0.00	-4.65	0.00	0.00	0.00	-3.03	-2.70	-2.32
TCGA-EX-A1H6-10A-01D-A22X-09_CESC	-2.77	-2.63	-2.67	-3.19	-2.70	-2.66	-2.41	-2.45	-2.37	0.00	-4.45	0.00	0.00	0.00	-2.84	-2.68	-2.55
TCGA-EX-A3L1-10A-01D-A21Q-09_CESC	-2.89	-2.58	-2.61	0.00	-2.77	-2.78	-2.53	-2.55	-2.66	-3.43	-2.68	-2.57	-4.58	-2.70	-2.99	-4.28	-2.58
TCGA-EX-A449-10A-01D-A243-09_CESC	-2.90	-4.02	-4.50	-2.94	-2.56	-2.62	-2.45	-2.37	-2.40	-3.60	-4.50	0.00	0.00	0.00	-2.93	-2.95	-2.65
TCGA-EY-A1G7-10A-01D-A13O-09_UCEC	-2.79	-2.55	-2.55	-4.46	-2.66	-2.71	-2.50	-2.51	-2.40	0.00	-2.87	-2.81	0.00	0.00	0.00	-2.55	-2.52
TCGA-EY-A1G8-10A-01D-A13O-09_UCEC	-2.84	-2.80	-2.82	-3.26	-2.51	-2.57	-2.55	-2.66	-2.67	-3.43	-2.74	-2.61	0.00	-2.76	0.00	-2.79	-2.64
TCGA-EY-A1GC-10A-01D-A13O-09_UCEC	-2.77	0.00	-4.17	-2.86	-2.48	-2.53	-2.43	-2.55	-2.33	0.00	0.00	-4.17	0.00	-4.47	0.00	-2.54	-2.58
TCGA-EY-A1GD-10A-01D-A13O-09_UCEC	-2.84	-4.46	0.00	-2.96	-2.50	-2.55	-2.44	-2.59	-2.33	0.00	0.00	0.00	0.00	0.00	-2.74	0.00	-2.58
TCGA-EY-A1GE-10A-01D-A13O-09_UCEC	-2.70	-2.63	-2.60	-3.36	-2.63	-2.66	-2.42	-2.51	-2.35	0.00	0.00	0.00	0.00	-4.36	-2.88	-2.77	-2.50
TCGA-EY-A1GF-10A-01D-A13O-09_UCEC	-2.76	-2.66	-2.69	-3.18	-2.67	-2.69	-2.54	-2.54	-2.44	0.00	0.00	0.00	0.00	0.00	-2.95	-2.75	-2.61
TCGA-EY-A1GH-10A-01D-A13O-09_UCEC	-2.72	-2.58	-2.70	-3.17	-2.61	-2.61	-2.42	-2.46	-2.31	0.00	-4.08	-4.38	0.00	0.00	-2.89	-2.70	-2.57
TCGA-EY-A1GI-10A-01D-A13O-09_UCEC	-2.69	-3.94	0.00	-2.93	-2.49	-2.47	-2.45	-2.50	-2.43	0.00	0.00	0.00	-4.42	0.00	-2.71	-4.42	-2.53
TCGA-EY-A1GJ-10A-01D-A142-09_UCEC	-2.91	-2.76	-2.80	-3.28	-2.49	-2.64	-2.51	-2.62	-2.54	0.00	-2.82	-2.79	0.00	0.00	-2.87	0.00	-2.69
TCGA-EY-A1GK-10A-01D-A13O-09_UCEC	-2.81	-4.45	0.00	-2.81	-2.51	-2.52	-2.48	-2.43	-2.41	0.00	0.00	-4.45	0.00	-4.45	-2.88	-2.76	-2.55
TCGA-EY-A1GL-10A-01D-A13O-09_UCEC	-2.74	-2.65	-2.67	-3.16	-2.68	-2.63	-2.42	-2.44	-2.37	0.00	0.00	-4.12	0.00	0.00	-2.93	-2.71	-2.54
TCGA-EY-A1GM-10A-01D-A14G-09_UCEC	-2.78	-2.74	-2.81	-3.27	-2.46	-2.62	-2.57	-2.64	-2.53	0.00	-2.86	-2.76	0.00	0.00	-2.88	0.00	-2.68
TCGA-EY-A1GO-10A-01D-A14G-09_UCEC	-2.83	-2.72	-2.70	-3.41	-2.85	-2.75	-2.70	-2.68	-3.85	-3.50	-2.59	-2.68	-2.75	-2.51	0.00	-4.45	-2.55
TCGA-EY-A1GP-10A-01D-A13O-09_UCEC	-2.89	-2.71	-2.71	-3.29	-2.54	-2.45	-2.57	-2.54	-2.44	0.00	-2.85	0.00	-2.78	0.00	-2.95	0.00	-2.81
TCGA-EY-A1GQ-10A-01D-A13O-09_UCEC	-2.79	-4.43	-3.95	-3.00	-2.48	-2.49	-2.47	-2.53	-2.40	0.00	-4.13	0.00	-4.13	-3.83	0.00	-2.51	-2.50
TCGA-EY-A1GR-10A-01D-A13O-09_UCEC	-2.80	-2.70	-2.67	-3.28	-2.50	-2.54	-2.51	-2.47	-2.38	0.00	-2.80	0.00	-2.75	-4.53	0.00	-2.79	-2.82
TCGA-EY-A1GS-10A-01D-A13O-09_UCEC	-2.93	-2.74	-2.74	-3.12	-2.79	-2.72	-2.51	-2.65	-2.56	0.00	0.00	0.00	0.00	0.00	-2.83	-2.85	-2.65
TCGA-EY-A1GT-10A-01D-A13O-09_UCEC	-2.69	-2.62	-2.63	-3.16	-2.58	-2.61	-2.40	-2.53	-2.34	0.00	0.00	0.00	0.00	-4.04	0.00	-2.46	-2.48
TCGA-EY-A1GU-10A-01D-A13O-09_UCEC	-2.80	0.00	-4.44	-3.08	-2.48	-2.42	-2.51	-2.55	-2.40	0.00	0.00	0.00	0.00	0.00	-2.78	0.00	-2.57
TCGA-EY-A1GV-10A-01D-A13O-09_UCEC	-2.86	-2.59	-2.55	-4.53	-2.57	-2.62	-2.55	-2.53	-2.47	0.00	-2.66	-2.58	0.00	0.00	-3.07	-2.80	-2.69
TCGA-EY-A1GW-10A-01D-A13O-09_UCEC	-2.85	-2.53	-2.58	0.00	-2.54	-2.52	-2.55	-2.63	-2.40	0.00	-2.67	-2.59	0.00	-4.52	0.00	-2.45	-2.65
TCGA-EY-A1GX-10A-01D-A13O-09_UCEC	-2.77	-4.44	-4.14	-3.06	-2.51	-2.40	-2.38	-2.39	-2.35	0.00	0.00	0.00	0.00	-3.97	-2.95	-2.74	-2.51
TCGA-EY-A1H0-10A-01D-A13O-09_UCEC	-2.86	-2.54	-2.60	0.00	-2.73	-2.71	-2.56	-2.48	-2.46	0.00	-2.82	-2.75	0.00	-4.59	-2.87	-2.83	-2.62
TCGA-EY-A210-10A-01D-A159-09_UCEC	-2.85	0.00	-2.78	-3.32	-2.42	-2.53	-2.58	-2.55	-2.42	0.00	-2.89	0.00	-2.78	0.00	-3.08	-2.93	-2.65
TCGA-EY-A212-10A-01D-A14K-09_UCEC	-2.93	-2.70	-2.78	-3.11	-2.73	-2.68	-2.48	-2.66	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.65	-2.74
TCGA-EY-A214-10A-01D-A159-09_UCEC	-2.70	-2.52	-2.51	-4.40	-2.70	-2.65	-2.50	-2.54	-2.48	0.00	-2.85	-2.70	0.00	0.00	0.00	-2.62	-2.56
TCGA-EY-A215-10A-01D-A14K-09_UCEC	-2.84	-2.75	-2.75	-3.26	-2.52	-2.60	-2.54	-2.55	-2.54	0.00	-2.79	-2.76	0.00	-4.11	-2.94	-2.83	-2.65
TCGA-EY-A2OM-10A-01D-A18P-09_UCEC	-2.77	-2.67	-2.71	-3.16	-2.56	-2.70	-2.74	-2.78	-2.59	0.00	-2.82	0.00	-2.65	-2.61	0.00	-2.77	-2.56
TCGA-EY-A2ON-10A-01D-A18P-09_UCEC	-2.80	0.00	0.00	-3.08	-2.58	-2.49	-2.52	-2.54	-2.38	0.00	0.00	0.00	0.00	-4.44	-2.68	0.00	-2.53
TCGA-EY-A2OO-10A-01D-A19Y-09_UCEC	-2.91	-2.85	-2.80	-3.32	-2.62	-2.62	-2.64	-2.68	-2.85	-3.58	-2.67	-2.65	0.00	-2.81	0.00	-2.85	-2.68
TCGA-EY-A2OP-10A-01D-A19Y-09_UCEC	-2.96	-2.60	-2.59	-4.19	-2.79	-2.84	-2.57	-2.62	-2.48	0.00	-2.87	-2.85	-4.49	0.00	-2.99	-2.94	-2.72
TCGA-EY-A2OQ-10A-01D-A19Y-09_UCEC	-2.75	-4.06	-3.93	-3.03	-2.54	-2.53	-2.57	-2.49	-2.36	0.00	0.00	0.00	-4.53	-4.23	0.00	-2.47	-2.62
TCGA-EY-A3L3-10A-01D-A22A-09_UCEC	-2.90	-2.86	-2.82	-3.45	-2.51	-2.67	-2.56	-2.61	-2.64	-3.49	-2.71	-2.78	-2.84	-2.71	-2.99	-4.60	-2.71
TCGA-EY-A3QX-10A-01D-A22A-09_UCEC	-2.84	-2.82	-2.92	-3.27	-2.53	-2.63	-2.58	-2.64	-2.75	-3.48	-2.84	-2.86	-2.80	-2.89	0.00	-2.87	-2.67
TCGA-EY-A4KR-10A-01D-A27P-09_UCEC	-2.72	-4.16	0.00	-2.84	-2.50	-2.57	-2.47	-2.56	-2.49	0.00	-4.46	0.00	-4.46	0.00	-2.76	-4.16	-2.58
TCGA-EY-A547-10A-01D-A27P-09_UCEC	-2.79	-4.60	-4.60	-2.96	-2.47	-2.57	-2.59	-2.52	-2.39	0.00	0.00	0.00	-4.60	-4.30	-2.90	-2.72	-2.63
TCGA-EY-A548-10A-01D-A27P-09_UCEC	-2.62	-2.45	-2.63	0.00	-4.40	-4.10	-3.80	-4.40	-3.70	0.00	-2.49	0.00	-2.45	-2.37	0.00	-4.40	-2.54
TCGA-EY-A549-10A-01D-A27P-09_UCEC	-2.71	-4.45	0.00	-3.05	-2.46	-2.52	-2.48	-2.45	-2.45	0.00	0.00	0.00	-3.97	0.00	0.00	-2.39	-2.58
TCGA-EY-A54A-10A-01D-A27P-09_UCEC	-2.77	-2.78	-4.28	-3.28	-2.60	-2.58	-2.64	-2.62	-2.64	-3.46	-2.60	-2.85	-2.83	-2.77	-2.89	0.00	-2.71
TCGA-EY-A5W2-10A-01D-A31U-09_UCEC	-2.84	0.00	0.00	-3.19	-2.65	-2.45	-2.48	-2.53	-2.36	0.00	0.00	0.00	0.00	0.00	-2.63	0.00	-2.49
TCGA-EZ-7264-10A-01D-2024-08_LGG	-2.63	-2.76	-2.74	-2.92	-2.51	-2.60	-2.68	-2.67	-3.62	-3.14	-2.70	-2.79	-2.69	-2.63	0.00	0.00	-2.54
TCGA-F1-6177-10A-01D-1800-08_STAD	-2.62	-2.75	-2.79	-2.93	-2.50	-2.65	-2.68	-2.57	-2.68	-3.40	-2.66	-2.78	-2.80	-2.75	-3.11	-4.60	-2.57
TCGA-F1-6874-10A-01D-1882-08_STAD	-2.51	-2.69	-2.69	-2.86	-2.65	-2.64	-2.71	-2.74	-2.70	0.00	-2.75	0.00	-2.70	-2.64	0.00	-2.70	-2.49
TCGA-F1-A448-10A-01D-A24F-08_STAD	-2.51	-2.62	-2.63	-2.88	-2.62	-2.69	-2.59	-2.58	-2.57	-4.17	-3.57	0.00	-3.63	-3.39	-2.93	0.00	-2.49
TCGA-F1-A72C-10A-01D-A33W-08_STAD	-2.51	0.00	0.00	-2.69	-2.51	-2.53	-2.53	-2.56	-2.49	0.00	0.00	0.00	0.00	0.00	-2.87	0.00	-2.45
TCGA-F2-A44G-10A-01D-A26I-08_PAAD	-2.60	-4.61	0.00	-2.66	-2.54	-2.57	-2.62	-2.66	0.00	-3.09	-2.69	0.00	-2.69	-2.58	0.00	0.00	-2.45
TCGA-F2-A44H-10A-01D-A26I-08_PAAD	-2.43	-4.34	-4.34	-2.65	-2.46	-2.43	-2.40	-2.48	-2.41	0.00	0.00	0.00	0.00	0.00	-2.89	0.00	-2.38
TCGA-F4-6459-10A-01D-1771-10_COAD	-2.47	0.00	0.00	-2.54	-2.58	-2.52	-2.46	-2.56	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.50
TCGA-F4-6460-10B-01D-1771-10_COAD	-2.57	0.00	0.00	-2.68	-2.54	-2.59	-2.47	-2.65	-2.71	-3.39	-3.15	0.00	-2.90	-2.80	-3.03	0.00	-2.51
TCGA-F4-6461-10A-01D-1806-10_COAD	-2.54	0.00	0.00	-2.64	-2.43	-2.49	-2.45	-2.34	-2.32	0.00	0.00	0.00	0.00	0.00	-3.09	-2.76	-2.45
TCGA-F4-6463-10A-01D-1719-10_COAD	-2.49	-2.52	-2.67	-3.07	-2.54	-2.44	-2.44	-2.50	-2.30	0.00	-3.11	-2.86	0.00	0.00	-3.37	-2.86	-2.35
TCGA-F4-6569-10A-01D-1771-10_COAD	-2.58	0.00	-4.26	-2.60	-2.61	-2.62	-2.43	-2.55	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.40
TCGA-F4-6570-10A-01D-1771-10_COAD	-2.37	-2.72	-2.81	-2.81	-2.74	0.00	-2.64	-2.94	-2.58	0.00	0.00	0.00	0.00	-2.71	0.00	-2.86	-2.61
TCGA-F4-6703-10A-01D-1835-10_COAD	-2.75	0.00	0.00	-2.72	-2.75	-2.60	-2.67	-2.70	-2.97	-3.34	-3.27	0.00	-3.00	-2.94	0.00	-3.00	-2.42
TCGA-F4-6805-10A-01D-1835-10_COAD	-2.77	-2.63	-2.61	0.00	-2.78	-2.64	-2.56	-2.71	-2.83	-3.33	-2.81	-2.67	0.00	-2.87	0.00	-2.96	-2.53
TCGA-F4-6806-10A-01D-1835-10_COAD	-2.46	-3.01	-3.08	-2.81	-2.81	-2.91	-2.50	-2.67	-2.76	-3.24	-3.04	0.00	-2.99	-2.87	-3.29	0.00	-2.53
TCGA-F4-6807-10A-01D-1835-10_COAD	-2.50	0.00	0.00	-2.60	-2.46	-2.54	-2.42	-2.61	-2.45	0.00	0.00	0.00	0.00	-4.18	0.00	-2.66	-2.38
TCGA-F4-6808-10A-01D-1835-10_COAD	-2.35	0.00	0.00	-2.60	-2.45	-2.77	-2.68	-2.96	0.00	-3.17	-2.87	0.00	-2.73	-2.51	0.00	0.00	-2.49
TCGA-F4-6809-10A-01D-1835-10_COAD	-2.40	0.00	0.00	-2.58	-2.48	-2.60	-2.50	-2.68	-2.55	0.00	0.00	0.00	0.00	-2.67	0.00	-2.80	-2.47
TCGA-F4-6854-10A-01D-1924-10_COAD	-2.62	0.00	-4.15	-2.75	-2.62	-2.75	-2.66	-2.59	0.00	-3.15	-2.77	0.00	-2.85	-2.69	0.00	0.00	-2.43
TCGA-F4-6855-10A-01D-1924-10_COAD	-2.61	-2.76	-2.99	-3.11	-2.69	-2.55	-2.76	-2.70	-2.88	-3.38	-2.73	-2.84	-3.02	-2.90	0.00	-3.14	-2.45
TCGA-F4-6856-10A-01D-1924-10_COAD	-2.52	-3.19	-3.03	-2.84	-2.99	-2.71	-2.56	-2.47	-2.65	-3.10	-3.03	0.00	-2.94	-2.78	0.00	-2.99	-2.45
TCGA-F5-6464-10A-01D-1733-10_READ	-2.57	0.00	0.00	-2.85	-2.60	-2.58	-2.54	-2.60	-2.73	-3.37	-2.93	0.00	-2.90	-2.84	0.00	-3.04	-2.43
TCGA-F5-6465-10A-01D-1733-10_READ	-2.52	-2.74	-2.75	-3.05	-2.66	-2.91	-2.48	-2.59	-2.59	-3.33	-3.01	0.00	-2.84	-2.74	-3.07	0.00	-2.46

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-F5-6571-10A-01D-1826-10_READ	-2.54	0.00	0.00	-2.77	-2.67	-2.54	-2.61	-2.64	-2.77	-3.21	-3.18	0.00	-2.97	-2.76	-3.15	0.00	-2.56
TCGA-F5-6702-10A-01D-1826-10_READ	-2.64	-2.54	-2.60	0.00	-2.86	-2.94	-2.55	-2.66	-2.43	0.00	-2.88	-2.73	0.00	0.00	-3.10	-2.98	-2.47
TCGA-F5-6812-10A-01D-1826-10_READ	-2.43	-2.80	-2.80	-2.76	-2.84	-2.84	-2.45	-2.48	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.41
TCGA-F5-6813-10A-01D-1826-10_READ	-2.44	-2.64	-2.73	-2.90	-2.90	-2.81	-2.43	-2.53	-2.36	0.00	0.00	0.00	0.00	0.00	-3.13	-3.10	-2.34
TCGA-F5-6814-10A-01D-1924-10_READ	-2.81	-2.56	-2.52	0.00	-2.80	-2.65	-2.59	-2.75	-2.80	-3.31	-2.70	-2.64	-2.94	-2.81	0.00	-2.97	-2.60
TCGA-F5-6861-10A-01D-1924-10_READ	-2.51	-2.73	-2.73	-2.73	-2.97	-2.71	-2.35	-2.50	-2.44	0.00	0.00	0.00	0.00	0.00	-2.78	0.00	-2.43
TCGA-F5-6863-10A-01D-1924-10_READ	-2.54	-2.94	-2.92	-2.99	-2.62	-2.51	-2.43	-2.65	-2.60	0.00	-3.16	-2.77	0.00	0.00	0.00	-2.60	-2.49
TCGA-F5-6864-10A-01D-1924-10_READ	-2.63	0.00	0.00	-2.69	-2.49	-2.49	-2.42	-2.61	-2.40	0.00	0.00	0.00	0.00	0.00	-3.29	-2.90	-2.38
TCGA-F7-7848-10A-01D-2129-08_HNSC	-2.38	-2.67	0.00	-2.81	-2.38	-2.61	-2.65	-2.65	-3.87	-3.30	-2.78	-4.47	-2.74	-2.52	0.00	-3.63	-2.59
TCGA-F7-8298-10A-01D-2394-08_HNSC	-2.63	-3.93	-4.06	-2.76	-2.59	-2.62	-2.63	-2.64	-2.70	-3.31	-2.99	0.00	-2.74	-2.70	0.00	-2.69	-2.54
TCGA-F7-8489-10A-01D-2394-08_HNSC	-2.66	-2.77	-2.78	-2.95	-2.50	-2.67	-2.69	-2.62	-2.75	-3.49	-2.78	-2.66	0.00	-2.75	-3.14	-4.13	-2.64
TCGA-F7-A50G-10A-01D-A25Y-08_HNSC	-2.43	-2.65	-2.64	-2.76	-2.37	-2.64	-2.62	-2.72	-2.64	0.00	-2.87	-2.64	0.00	-2.59	0.00	-2.63	-2.49
TCGA-F7-A624-10A-01D-A30H-08_HNSC	-2.53	-2.54	-2.54	0.00	-2.65	-2.73	-2.51	-2.51	-2.66	-3.30	-2.68	-2.54	0.00	-2.67	-3.07	0.00	-2.48
TCGA-F9-A4JJ-10A-01D-A25F-10_KIRP	-2.31	0.00	-4.06	-2.72	-2.36	-2.33	-2.33	-2.41	-2.28	0.00	0.00	0.00	0.00	0.00	-2.79	-2.52	-2.33
TCGA-FA-8693-10A-01D-2397-10_DLBC	-2.38	0.00	0.00	-2.52	-2.39	-2.25	-2.32	-2.39	-2.22	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.31
TCGA-FA-A4BB-10A-01D-A31X-10_DLBC	-2.47	0.00	0.00	-2.40	-2.47	-2.26	-2.33	-2.35	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-2.43
TCGA-FA-A6HN-10A-01D-A31X-10_DLBC	-2.35	0.00	0.00	-2.86	-2.67	-2.36	-2.36	-2.41	-2.61	-4.09	-2.88	0.00	-2.60	-2.60	0.00	0.00	-2.45
TCGA-FA-A6HO-10A-01D-A31X-10_DLBC	-2.40	0.00	0.00	-2.58	-2.35	-2.37	-2.28	-2.43	-2.29	0.00	0.00	0.00	-4.08	0.00	0.00	0.00	-2.43
TCGA-FB-A4P5-10A-01D-A26I-08_PAAD	-2.44	-2.72	-2.67	-2.88	-2.57	-2.61	-2.51	-2.42	-2.34	0.00	-4.36	-3.88	0.00	-4.36	-2.89	-2.65	-2.38
TCGA-FB-A4P6-10A-01D-A26I-08_PAAD	-2.39	0.00	0.00	-2.52	-2.44	-2.42	-2.46	-2.49	-2.49	0.00	0.00	0.00	-4.38	-4.08	0.00	-2.45	-2.35
TCGA-FB-A545-10A-01D-A26I-08_PAAD	-2.50	0.00	0.00	-2.69	-2.53	-2.52	-2.53	-2.56	-2.64	-3.44	-2.83	0.00	-2.76	-2.60	0.00	-2.66	-2.43
TCGA-FB-A5VM-10A-01D-A32N-08_PAAD	-2.50	-2.60	-2.69	-2.80	-2.61	-2.68	-2.53	-2.49	-2.38	0.00	0.00	0.00	0.00	0.00	-3.04	-2.66	-2.49
TCGA-FB-A78T-10A-01D-A32N-08_PAAD	-2.52	0.00	0.00	-2.62	-2.54	-2.53	-2.59	-2.53	-2.47	0.00	0.00	0.00	0.00	0.00	-2.97	-2.66	-2.46
TCGA-FB-A7DR-10A-01D-A33W-08_PAAD	-2.48	0.00	-4.47	-2.69	-2.58	-2.56	-2.65	-2.63	-2.67	-3.42	-2.81	0.00	-2.79	-2.73	0.00	-2.74	-2.57
TCGA-FC-7708-10A-01D-2115-08_PRAD	-2.40	-2.62	-2.69	-2.79	-2.34	-2.54	-2.68	-2.70	-2.57	0.00	-2.81	-2.63	-4.45	-2.49	0.00	0.00	-2.47
TCGA-FC-7961-10A-01D-A29Q-08_PRAD	-2.50	0.00	-4.63	-2.56	-2.54	-2.51	-2.47	-2.49	-2.45	0.00	0.00	0.00	0.00	0.00	-2.95	-2.74	-2.46
TCGA-FC-A4JI-10A-01D-A25A-08_PRAD	-2.52	-2.70	-2.64	-2.71	-2.70	-2.61	-2.53	-2.49	-2.46	0.00	-4.45	-4.15	-4.45	-3.55	-2.94	-2.68	-2.45
TCGA-FC-A5OB-10A-01D-A29Q-08_PRAD	-2.54	-2.68	-2.70	-2.83	-2.69	-2.72	-2.51	-2.60	0.00	-3.19	-2.69	0.00	-2.60	-2.53	0.00	0.00	-2.48
TCGA-FC-A66V-10A-01D-A30H-08_PRAD	-2.47	0.00	0.00	-2.66	-2.46	-2.45	-2.50	-2.46	-2.42	0.00	0.00	0.00	0.00	0.00	-3.08	-2.74	-2.38
TCGA-FC-A6HD-10A-01D-A31J-08_PRAD	-2.44	0.00	0.00	-2.75	-2.61	-2.58	-2.58	-2.56	-2.65	-3.28	-2.86	-2.71	0.00	-2.67	0.00	-2.67	-2.53
TCGA-FD-A3B3-10A-01D-A202-08_BLCA	-2.49	-4.43	-4.43	-2.64	-2.46	-2.51	-2.51	-2.68	-2.73	-3.35	-3.05	0.00	-2.79	-2.70	0.00	-2.75	-2.46
TCGA-FD-A3B4-10A-01D-A202-08_BLCA	-2.52	-2.64	0.00	-2.82	-2.65	-2.68	-2.67	-2.76	-3.79	-3.24	-2.74	0.00	-2.54	-2.48	0.00	0.00	-2.45
TCGA-FD-A3B5-10A-01D-A20D-08_BLCA	-2.54	0.00	-2.70	-2.83	-2.44	-2.50	-2.57	-2.64	-2.55	0.00	-2.81	0.00	-2.78	0.00	-2.94	-4.19	-2.47
TCGA-FD-A3B6-10A-01D-A20D-08_BLCA	-2.47	-2.65	-2.70	-2.80	-2.53	-2.63	-2.53	-2.47	-2.45	0.00	0.00	-4.15	0.00	-4.15	-3.04	-2.65	-2.42
TCGA-FD-A3B7-10A-01D-A20D-08_BLCA	-2.53	0.00	0.00	-2.50	-2.50	-2.52	-2.51	-2.57	-2.43	0.00	-4.46	0.00	0.00	0.00	-3.05	-2.68	-2.41
TCGA-FD-A3B8-10A-01D-A20D-08_BLCA	-2.54	-2.77	-2.71	-2.86	-2.49	-2.53	-2.59	-2.69	-2.59	0.00	-2.82	-2.67	0.00	-4.49	0.00	-2.59	-2.47
TCGA-FD-A3N5-10A-01D-A21A-08_BLCA	-2.47	0.00	-3.95	-2.70	-2.48	-2.51	-2.59	-2.49	-2.42	0.00	0.00	-4.43	0.00	-4.13	-2.95	-2.58	-2.40
TCGA-FD-A3N6-10A-01D-A21A-08_BLCA	-2.48	-4.16	0.00	-2.73	-2.52	-2.57	-2.56	-2.53	-2.52	0.00	-2.97	-2.81	0.00	0.00	-3.06	-2.71	-2.43
TCGA-FD-A3NA-10A-01D-A21A-08_BLCA	-2.36	-2.78	-2.75	-2.83	-2.55	-2.64	-2.55	-2.51	-2.43	0.00	0.00	0.00	0.00	-3.90	-3.01	-2.66	-2.43
TCGA-FD-A3SJ-10A-01D-A22Z-08_BLCA	-2.44	0.00	-4.60	-2.55	-2.44	-2.45	-2.46	-2.48	-2.42	0.00	0.00	0.00	0.00	0.00	-2.94	-2.73	-2.37
TCGA-FD-A3SL-10A-01D-A22Z-08_BLCA	-2.42	-2.64	-2.64	-2.91	-2.65	-2.56	-2.45	-2.49	-2.42	0.00	0.00	0.00	0.00	-4.59	-3.05	-2.75	-2.35
TCGA-FD-A3SM-10A-01D-A22Z-08_BLCA	-2.42	-2.68	0.00	-2.88	-2.43	-2.52	-2.61	-2.57	0.00	-3.18	-2.69	0.00	-2.57	-2.50	0.00	0.00	-2.47
TCGA-FD-A3SN-10A-01D-A22Z-08_BLCA	-2.42	0.00	0.00	-2.56	-2.45	-2.43	-2.52	-2.46	-2.45	0.00	0.00	0.00	0.00	0.00	-3.04	-2.72	-2.41
TCGA-FD-A3SO-10A-01D-A22Z-08_BLCA	-2.45	-2.69	-2.70	-2.85	-2.64	-2.64	-2.54	-2.51	-2.61	-3.48	-2.96	0.00	-2.73	-2.61	-2.94	0.00	-2.42
TCGA-FD-A3SP-10A-01D-A22Z-08_BLCA	-2.44	-2.60	-2.66	-2.80	-2.62	-2.60	-2.52	-2.39	-2.45	0.00	0.00	0.00	-4.61	0.00	-2.98	-2.70	-2.36
TCGA-FD-A3SQ-10A-01D-A22Z-08_BLCA	-2.57	0.00	0.00	-2.73	-2.44	-2.52	-2.54	-2.53	-2.78	-3.39	-2.72	-2.73	-2.79	-2.74	0.00	-2.85	-2.51
TCGA-FD-A3SR-10A-01D-A22Z-08_BLCA	-2.53	-2.78	-2.80	-2.98	-2.49	-2.56	-2.60	-2.59	-2.69	-3.46	-2.70	-2.54	0.00	-2.66	0.00	-2.80	-2.44
TCGA-FD-A3SS-10A-01D-A22Z-08_BLCA	-2.49	0.00	-4.75	-2.82	-2.42	-2.52	-2.53	-2.53	0.00	-3.19	-2.64	-2.78	-2.62	-2.57	0.00	0.00	-2.52
TCGA-FD-A43N-10A-01D-A23U-08_BLCA	-2.50	-4.40	-3.80	-2.76	-2.52	-2.56	-2.57	-2.44	-2.49	0.00	-4.10	-4.40	0.00	0.00	-3.04	-2.67	-2.47
TCGA-FD-A43P-10A-01D-A23U-08_BLCA	-2.66	-3.91	-2.72	-2.96	-2.57	-2.59	-2.66	-2.68	-2.58	0.00	-2.66	-2.66	-2.83	-4.21	-2.95	-4.04	-2.59
TCGA-FD-A43S-10A-01D-A23U-08_BLCA	-2.61	-2.73	-2.73	-2.89	-2.50	-2.63	-2.65	-2.60	-2.52	0.00	-2.93	-2.72	0.00	0.00	0.00	-2.66	-2.56
TCGA-FD-A43U-10A-01D-A23U-08_BLCA	-2.57	-2.72	-2.69	-2.89	-2.67	-2.67	-2.64	-2.46	-2.45	-4.49	0.00	0.00	0.00	-3.72	0.00	-2.39	-2.55
TCGA-FD-A43X-10A-01D-A23U-08_BLCA	-2.53	0.00	0.00	-2.60	-2.48	-2.52	-2.57	-2.57	-2.58	-3.31	-2.85	0.00	-2.79	-2.66	0.00	-2.79	-2.46
TCGA-FD-A43Y-10A-01D-A26K-08_BLCA	-2.36	-3.90	-3.68	-2.57	-2.38	-2.43	-2.58	-2.48	-2.38	0.00	-4.37	-4.37	0.00	0.00	0.00	-2.40	-2.36
TCGA-FD-A5BR-10A-01D-A26K-08_BLCA	-2.40	0.00	0.00	-2.55	-2.52	-2.52	-2.50	-2.57	-2.57	-3.31	-2.90	0.00	-2.69	-2.62	-3.01	-3.79	-2.41
TCGA-FD-A5BS-10A-01D-A26K-08_BLCA	-2.54	-2.77	-2.70	0.00	-2.45	-2.54	-2.57	-2.60	-2.74	-3.73	-2.67	-2.70	-2.81	-2.76	0.00	-2.80	-2.46
TCGA-FD-A5BT-10A-01D-A26K-08_BLCA	-2.45	-2.62	-2.64	-2.80	-2.60	-2.55	-2.45	-2.50	-2.35	0.00	-4.38	0.00	-3.78	-3.78	-2.93	-2.68	-2.34
TCGA-FD-A5BU-10A-01D-A26K-08_BLCA	-2.49	-2.54	-2.48	-4.44	-2.61	-2.66	-2.66	-2.70	-2.53	0.00	-2.68	-2.68	-2.75	-2.65	-2.90	-3.84	-2.44
TCGA-FD-A5BV-10A-01D-A26K-08_BLCA	-2.47	-2.54	-2.51	-3.94	-2.66	-2.61	-2.62	-2.69	-3.46	-3.27	-2.51	-2.54	-2.74	-2.41	0.00	0.00	-2.41
TCGA-FD-A5BX-10A-01D-A26K-08_BLCA	-2.53	-2.76	-2.78	-2.91	-2.49	-2.59	-2.60	-2.60	-2.67	-3.27	-2.68	-2.74	-2.78	-2.77	0.00	-2.71	-2.50
TCGA-FD-A5BY-10A-01D-A289-08_BLCA	-2.49	-2.67	-2.63	-2.83	-2.61	-2.65	-2.52	-2.55	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.41
TCGA-FD-A5BZ-10A-01D-A289-08_BLCA	-2.57	-2.75	-2.67	-2.88	-2.49	-2.61	-2.60	-2.60	-2.58	0.00	-2.90	-2.80	0.00	0.00	0.00	-2.48	-2.46
TCGA-FD-A5C0-10A-01D-A289-08_BLCA	-2.52	0.00	0.00	-2.68	-2.48	-2.50	-2.54	-2.52	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.44
TCGA-FD-A5C1-10A-01D-A289-08_BLCA	-2.56	-2.83	-2.68	-2.88	-2.49	-2.63	-2.62	-2.54	-2.53	0.00	-2.87	-2.73	0.00	0.00	0.00	-2.49	-2.45
TCGA-FD-A62N-10A-01D-A30H-08_BLCA	-2.54	-2.77	-2.71	-2.90	-2.46	-2.59	-2.63	-2.63	-2.69	-3.64	-2.74	-2.59	0.00	-2.74	0.00	-2.79	-2.49
TCGA-FD-A62O-10A-01D-A30H-08_BLCA	-2.53	-2.77	-2.75	-2.93	-2.52	-2.53	-2.56	-2.61	-2.66	-3.42	-2.71	-2.56	0.00	-2.70	-3.11	0.00	-2.46
TCGA-FD-A62P-10A-01D-A30H-08_BLCA	-2.37	-2.41	-2.42	0.00	-4.58	0.00	-2.43	-2.44	-2.34	0.00	0.00	0.00	0.00	0.00	-2.96	-2.62	-2.32
TCGA-FD-A62S-10A-01D-A30H-08_BLCA	-2.45	-2.74	-2.67	-2.93	-2.48	-2.52	-2.51	-2.59	-2.47	0.00	-2.92	0.00	-2.78	-4.66	0.00	-2.58	-2.40
TCGA-FD-A6TA-10A-21D-A339-08_BLCA	-2.48	0.00	0.00	-2.62	-2.49	-2.51	-2.54	-2.61	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.42
TCGA-FD-A6TB-10A-21D-A339-08_BLCA	-2.42	0.00	0.00	-2.62	-2.51	-2.56	-2.55	-2.50	-2.54	0.00	0.00	0.00	0.00	-4.45	-3.09	-2.77	-2.49
TCGA-FD-A6TC-10A-21D-A339-08_BLCA	-2.56	-2.67	-2.68	-2.89	-2.66	-2.66	-2.56	-2.43	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.52
TCGA-FD-A6TD-10A-21D-A339-08_BLCA	-2.49	0.00	0.00	-2.60	-2.46	-2.48	-2.51	-2.55	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.47
TCGA-FD-A6TE-10A-21D-A339-08_BLCA	-2.55	-2.77	-2.72	-2.88	-2.49	-2.64	-2.59	-2.59	-2.59	0.00	-2.95	-2.69	0.00	0.00	0.00	-2.51	-2.54
TCGA-FD-A6TF-10A-21D-A329-08_BLCA	-2.55	-2.71	-2.75	-2.94	-2.49	-2.55	-2.51	-2.63	-2.49	0.00	-3.00	-2.68	0.00	-4.23	0.00	-2.54	-2.50
TCGA-FD-A6TG-10A-01D-A329-08_BLCA	-2.63	-2.79	-2.76	-3.02	-2.47	-2.59	-2.65	-2.66	-2.70	-3.41	-2.81	-2.74	-2.78	-2.73	-3.17	0.00	-2.53
TCGA-FD-A6TH-10A-01D-A329-08_BLCA	-2.58	-2.85	-2.73	-2.89	-2.48	-2.55	-2.62	-2.55	-2.66	-3.31	-2.73	-2.60	-4.56	-2.76	-3.26	0.00	-2.50
TCGA-FD-A6TI-10A-01D-A329-08_BLCA	-2.55	-2.76	-2.75	-2.97	-2.54	-2.52	-2.50	-2.60	-2.48	0.00	-3.06	-2.71	0.00	0.00	-3.23	-2.83	-2.48
TCGA-FD-A6TK-10A-21D-A339-08_BLCA	-2.43	-2.40	-2.43	0.00	0.00	0.00	-2.44	-2.40	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.34	-2.31
TCGA-FE-A22Z-10A-01D-A17V-08_THCA	-2.55	-2.60	-2.63	0.00	-2.68	-2.64	-2.61	-2.45	-2.53	0.00	-2.88	-2.73	0.00	-4.51	-3.08	-2.71	-2.48
TCGA-FE-A230-10A-01D-A14W-08_THCA	-2.47	-2.61	-2.64	-2.85	-2.61	-2.61	-2.52	-2.58	-2.35	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.41
TCGA-FE-A231-10A-01D-A14W-08_THCA	-2.53	0.00	0.00	-2.57	-2.43	-2.51	-2.51	-2.55	-2.42	0.00	0.00	0.00	-4.47	-3.87	0.00	-2.59	-2.41
TCGA-FE-A232-10A-01D-A14W-08_THCA	-2.54	-2.78	-2.76	-2.89	-2.49	-2.62	-2.64	-2.60	-2.70	-3.43	-2.75	-2.75	-2.85	-2.77	-3.24	-4.28	-2.54
TCGA-FE-A233-10A-01D-A14W-08_THCA	-2.48	-2.72	-2.58	-2.85	-2.58	-2.61	-2.67	-2.72	-2.49	0.00	-2.76	0.00	-2.66	-2.60	0.00	-2.80	-2.44
TCGA-FE-A234-10A-01D-A14W-08_THCA	-2.51	-2.70	-2.68	-2.82	-2.65	-2.65	-2.57	-2.53	0.00	-3.07	-2.63	0.00	-2.60	-2.50	0.00	-4.18	-2.46
TCGA-FE-A235-10A-01D-A16O-08_THCA	-2.42	0.00	-4.53	-2.82	-2.61	-2.61	-2.48	-2.49	-2.49	0.00	0.00	0.00	0.00	0.00	-3.04	-2.77	-2.39
TCGA-FE-A236-10A-01D-A16O-08_THCA	-2.47	0.00	-4.57	-2.62	-2.44	-2.49	-2.51	-2.49	-2.56	0.00	0.00	0.00	0.00	-4.57	0.00	-2.46	-2.42
TCGA-FE-A237-10A-01D-A16O-08_THCA	-2.48	0.00	0.00	-2.67	-2.48	-2.48	-2.53	-2.62	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.41
TCGA-FE-A23A-10A-01D-A17V-08_THCA	-2.48	-2.73	-2.73	-2.91	-2.51	-2.63	-2.57	-2.65	-2.61	0.00	-2.85	-2.73	0.00	0.00	-2.97	0.00	-2.52
TCGA-FE-A3PA-10A-01D-A21Z-08_THCA	-2.46	-4.45	-4.45	-2.61	-2.50	-2.46	-2.57	-2.60	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.48
TCGA-FE-A3PB-10A-01D-A21Z-08_THCA	-2.43	-2.71	-2.76	-2.87	-2.45	-2.60	-2.65	-2.59	-2.53	0.00	-2.90	-2.76	0.00	-4.56	0.00	-2.45	-2.54
TCGA-FE-A3PC-10A-01D-A21Z-08_THCA	-2.46	-4.18	0.00	-2.75	-2.47	-2.47	-2.52	-2.44	-2.55	0.00	0.00	0.00	-4.48	0.00	-3.06	-2.63	-2.45
TCGA-FE-A3PD-10A-01D-A21Z-08_THCA	-2.41	0.00	0.00	-2.77	-2.55	-2.56	-2.56	-2.50	-2.63	-3.24	-2.92	0.00	-2.72	-2.62	0.00	-2.65	-2.46
TCGA-FF-8041-10A-01D-2210-10_DLBC	-2.43	0.00	-4.33	-2.81	-2.38	-2.36	-2.29	-2.54	-2.51	-3.37	-2.85	-2.57	0.00	-2.63	0.00	0.00	-2.37
TCGA-FF-8042-10A-01D-2210-10_DLBC	-2.29	-2.47	-2.53	-2.83	-2.53	-2.53	-2.32	-2.60	-2.44	0.00	-2.81	-2.48	0.00	-2.50	0.00	0.00	-2.34
TCGA-FF-8043-10A-01D-2210-10_DLBC	-2.39	0.00	-4.38	-2.80	-2.39	-2.32	-2.31	-2.41	-2.51	-3.33	-3.12	-2.58	0.00	-2.61	0.00	0.00	-2.29
TCGA-FF-8046-10A-01D-2210-10_DLBC	-2.43	-2.27	-2.29	0.00	-2.60	-2.57	-2.51	-2.66	-2.52	0.00	-2.48	-2.53	-2.62	-2.46	0.00	-2.67	-2.22

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-FG-5962-10A-01D-1893-08_LGG	-2.55	-4.28	0.00	-2.58	-2.49	-2.60	-2.63	-2.50	-2.58	0.00	0.00	-4.58	0.00	0.00	0.00	-2.44	-2.49
TCGA-FG-5963-10A-01D-1705-08_LGG	-2.59	-4.47	0.00	-2.75	-2.50	-2.55	-2.55	-2.63	-2.68	-3.32	-2.95	0.00	-2.78	-2.62	0.00	-2.77	-2.46
TCGA-FG-5964-10A-01D-1705-08_LGG	-2.42	-4.52	-4.22	-2.78	-2.47	-2.51	-2.54	-2.58	-2.64	-3.40	-2.97	0.00	-2.75	-2.65	0.00	-2.77	-2.45
TCGA-FG-5965-10A-01D-1893-08_LGG	-2.62	-2.83	-2.85	-2.92	-2.53	-2.69	-2.70	-2.70	-4.67	-3.31	-2.70	-2.66	-2.83	-2.66	0.00	0.00	-2.60
TCGA-FG-6688-10A-01D-1893-08_LGG	-2.55	0.00	-4.25	-2.70	-2.53	-2.57	-2.57	-2.57	-2.53	0.00	-4.55	0.00	0.00	0.00	-2.96	-4.55	-2.45
TCGA-FG-6689-10A-01D-1893-08_LGG	-2.55	-2.73	-2.75	-2.87	-2.66	-2.75	-2.63	-2.69	-2.71	-3.35	-2.91	0.00	-2.78	-2.68	0.00	-2.79	-2.55
TCGA-FG-6690-10A-01D-1893-08_LGG	-2.68	-2.81	-2.81	-3.04	-2.55	-2.71	-2.68	-2.57	-2.84	-3.36	-2.81	-2.79	-2.84	-2.79	-3.17	0.00	-2.62
TCGA-FG-6691-10A-01D-1893-08_LGG	-2.50	-4.61	-4.61	-2.72	-2.56	-2.61	-2.58	-2.65	-2.44	0.00	0.00	0.00	0.00	-4.61	0.00	-2.57	-2.42
TCGA-FG-6692-10A-01D-1893-08_LGG	-2.40	0.00	0.00	-2.62	-2.56	-2.60	-2.61	-2.57	-2.46	0.00	0.00	-4.60	-4.60	-4.00	0.00	-2.56	-2.44
TCGA-FG-7634-10A-01D-2086-08_LGG	-2.43	-2.64	-2.62	-2.70	-2.54	-4.39	-2.51	-2.47	-2.42	0.00	0.00	0.00	0.00	0.00	-3.05	-2.63	-2.38
TCGA-FG-7636-10A-01D-2086-08_LGG	-2.44	-2.64	-2.65	-2.78	-2.65	-2.62	-2.51	-2.53	-2.50	0.00	0.00	0.00	0.00	-4.43	-3.03	-2.70	-2.45
TCGA-FG-7637-10A-01D-2086-08_LGG	-2.43	0.00	-4.52	-2.60	-2.56	-2.54	-2.61	-2.63	-2.63	-3.26	-2.77	-2.71	0.00	-2.64	0.00	-2.74	-2.53
TCGA-FG-7638-10A-01D-2086-08_LGG	-2.57	0.00	-4.50	-2.84	-2.59	-2.55	-2.59	-2.59	-2.74	-3.22	-2.89	0.00	-2.80	-2.67	0.00	-2.66	-2.49
TCGA-FG-7641-10A-01D-2253-08_LGG	-2.41	0.00	0.00	-2.58	-2.55	-2.53	-2.56	-2.56	-2.64	-3.29	-2.79	0.00	-2.76	-2.66	-3.16	0.00	-2.49
TCGA-FG-7643-10A-01D-2086-08_LGG	-2.52	-4.46	0.00	-2.54	-2.54	-2.62	-2.55	-2.65	-2.65	-3.38	-2.85	-4.46	-2.79	-2.66	0.00	-2.75	-2.48
TCGA-FG-8181-10A-01D-2253-08_LGG	-2.51	-2.71	-2.68	-2.73	-2.61	-2.62	-2.52	-2.51	-2.44	0.00	0.00	-4.43	0.00	0.00	0.00	-2.37	-2.45
TCGA-FG-8182-10A-01D-2253-08_LGG	-2.48	0.00	-4.45	-2.73	-2.51	-2.51	-2.54	-2.42	-2.40	0.00	0.00	0.00	0.00	0.00	-2.98	-2.67	-2.47
TCGA-FG-8185-10A-01D-2253-08_LGG	-2.48	0.00	-4.46	-2.63	-2.47	-2.51	-2.51	-2.56	-2.40	0.00	-4.46	0.00	0.00	-4.46	0.00	-2.38	-2.46
TCGA-FG-8186-10A-01D-2253-08_LGG	-2.50	-2.64	-2.63	-2.76	-2.59	-2.61	-2.56	-2.49	-2.50	0.00	0.00	0.00	0.00	0.00	-2.94	-2.71	-2.43
TCGA-FG-8187-10A-01D-2253-08_LGG	-2.54	-2.71	-2.73	-2.81	-2.67	-2.67	-2.62	-2.59	-3.95	-3.09	-2.72	0.00	-2.66	-2.54	0.00	-4.25	-2.46
TCGA-FG-8188-10A-01D-2253-08_LGG	-2.54	-2.76	-2.69	-2.73	-2.63	-2.67	-2.61	-2.60	-2.62	-3.48	-2.84	-4.48	-2.82	-2.69	-2.99	0.00	-2.46
TCGA-FG-8189-10A-01D-A289-08_LGG	-2.44	0.00	0.00	-2.54	-2.54	-2.53	-2.47	-2.52	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.42
TCGA-FG-8191-10A-01D-2253-08_LGG	-2.61	-4.22	0.00	-2.70	-2.51	-2.56	-2.61	-2.69	-2.71	-3.37	-2.90	0.00	-2.72	-2.65	0.00	-2.71	-2.43
TCGA-FG-A4MT-10A-01D-A26K-08_LGG	-2.43	-4.38	-4.08	-2.63	-2.49	-2.47	-2.48	-2.42	-2.39	0.00	0.00	0.00	0.00	0.00	-3.00	-2.57	-2.40
TCGA-FG-A4MU-10A-01D-A289-08_LGG	-2.51	0.00	0.00	-2.61	-2.52	-2.52	-2.50	-2.47	-2.44	0.00	0.00	0.00	0.00	-4.53	0.00	-2.42	-2.44
TCGA-FG-A4MW-10A-01D-A26K-08_LGG	-2.47	-2.70	-2.66	-2.83	-2.59	-2.69	-2.51	-2.57	-2.66	-3.40	-2.84	0.00	-2.78	-2.61	0.00	-2.71	-2.44
TCGA-FG-A4MX-10A-01D-A26K-08_LGG	-2.46	-3.95	-4.42	-2.59	-2.50	-2.51	-2.53	-2.55	-2.71	-3.31	-2.96	-2.68	-3.95	-2.74	0.00	-2.70	-2.42
TCGA-FG-A4MY-10A-01D-A26K-08_LGG	-2.50	-2.59	-2.57	-4.18	-2.67	-2.63	-2.59	-2.61	-2.71	-3.30	-2.70	-2.74	-2.78	-2.66	0.00	-2.70	-2.46
TCGA-FG-A60J-10A-01D-A289-08_LGG	-2.46	0.00	0.00	-2.51	-2.49	-2.57	-2.52	-2.57	-2.55	0.00	0.00	0.00	-4.45	0.00	0.00	-2.55	-2.46
TCGA-FG-A60K-10A-01D-A29Q-08_LGG	-2.55	-2.74	-2.70	-2.86	-2.66	-2.69	-2.52	-2.58	-2.64	-3.24	-2.96	0.00	-2.71	-2.65	-3.02	0.00	-2.43
TCGA-FG-A60L-10A-01D-A31J-08_LGG	-2.58	0.00	0.00	-2.85	-2.57	-2.60	-2.61	-2.56	-2.72	-3.21	-2.83	0.00	-2.75	-2.62	0.00	-2.79	-2.56
TCGA-FG-A6IZ-10A-01D-A31J-08_LGG	-2.38	-4.13	-4.43	-2.71	-2.50	-2.55	-2.54	-2.48	-2.57	0.00	0.00	0.00	0.00	0.00	-3.00	-2.68	-2.53
TCGA-FG-A6J1-10A-01D-A31J-08_LGG	-2.54	0.00	0.00	-2.72	-2.54	-2.49	-2.55	-2.56	-2.49	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.47
TCGA-FG-A6J3-10A-01D-A31J-08_LGG	-2.47	-4.54	0.00	-2.69	-2.63	-2.63	-2.64	-2.62	-2.69	-3.17	-2.79	0.00	-2.75	-2.66	0.00	-2.74	-2.57
TCGA-FG-A713-10A-01D-A329-08_LGG	-2.53	0.00	-4.43	-2.77	-2.53	-2.54	-2.66	-2.59	0.00	-3.20	-2.68	0.00	-2.65	-2.51	0.00	0.00	-2.46
TCGA-FI-A2CX-10A-01D-A17D-09_UCEC	-2.77	-2.73	-2.73	-3.34	-2.48	-2.58	-2.53	-2.59	-2.41	0.00	-2.83	-2.75	0.00	-4.54	-2.89	-2.79	-2.66
TCGA-FI-A2CY-10A-01D-A17D-09_UCEC	-2.79	0.00	0.00	-2.90	-2.49	-2.56	-2.53	-2.44	-2.29	0.00	0.00	0.00	0.00	0.00	-2.91	-2.84	-2.60
TCGA-FI-A2D0-10A-01D-A17D-09_UCEC	-2.72	0.00	0.00	-3.08	-2.50	-2.50	-2.51	-2.42	-2.37	0.00	0.00	-4.21	0.00	0.00	0.00	-2.40	-2.62
TCGA-FI-A2D2-10A-01D-A17D-09_UCEC	-2.95	0.00	0.00	-2.75	-2.57	-2.55	-2.50	-2.66	-2.58	0.00	0.00	0.00	0.00	-4.54	0.00	-2.62	-2.66
TCGA-FI-A2D4-10A-01D-A17D-09_UCEC	-2.84	-4.15	-4.45	-3.11	-2.48	-2.51	-2.53	-2.45	-2.47	0.00	0.00	0.00	0.00	-4.45	0.00	-2.46	-2.58
TCGA-FI-A2D5-10A-01D-A17D-09_UCEC	-2.66	-4.51	-4.20	-2.94	-2.51	-2.52	-2.50	-2.52	-2.63	-3.36	-2.81	0.00	-2.73	-2.67	-2.94	0.00	-2.64
TCGA-FI-A2D6-10A-01D-A17D-09_UCEC	-2.82	-4.48	0.00	-3.03	-2.50	-2.56	-2.49	-2.50	-2.33	0.00	-4.48	-4.48	0.00	-4.48	-2.89	-2.65	-2.61
TCGA-FI-A2EU-10A-01D-A17D-09_UCEC	-2.88	-2.68	-2.73	-3.02	-2.80	-2.81	-2.58	-2.64	-2.73	-3.36	-2.81	0.00	-2.81	-2.73	0.00	-2.83	-2.70
TCGA-FI-A2EW-10A-01D-A17D-09_UCEC	-2.99	-2.76	-2.92	-3.08	-2.58	-2.69	-2.59	-2.78	-2.63	-4.63	-3.06	-2.81	0.00	0.00	-3.06	0.00	-2.72
TCGA-FI-A2EX-10A-01D-A17D-09_UCEC	-3.02	-2.80	-2.89	-3.12	-2.96	-2.93	-2.51	-2.69	-2.92	-3.00	-3.22	0.00	-2.87	-2.79	-3.35	0.00	-2.81
TCGA-FI-A2EY-10A-01D-A18P-09_UCEC	-2.83	-2.78	-2.84	-3.30	-2.55	-2.68	-2.67	-2.69	-2.75	-3.47	-2.68	-2.83	-2.78	-2.83	0.00	-2.80	-2.71
TCGA-FI-A2F4-10B-01D-A17D-09_UCEC	-2.83	0.00	-4.52	-2.99	-2.48	-2.56	-2.48	-2.48	-2.39	0.00	0.00	0.00	0.00	0.00	-2.85	-2.70	-2.55
TCGA-FI-A2F8-10B-01D-A17D-09_UCEC	-3.08	-2.69	-2.72	-4.16	-2.74	-2.74	-2.70	-2.81	-2.96	-3.30	-2.69	-2.79	-2.96	-2.96	0.00	-3.06	-2.88
TCGA-FI-A2F9-10B-01D-A17D-09_UCEC	-2.79	-2.64	-2.66	-3.36	-2.70	-2.71	-2.48	-2.57	-2.36	0.00	0.00	0.00	0.00	0.00	-2.70	-4.00	-2.57
TCGA-FI-A3PV-10A-01D-A22A-09_UCEC	-2.80	0.00	-4.54	-3.00	-2.53	-2.57	-2.52	-2.57	-2.40	0.00	0.00	0.00	0.00	0.00	-2.98	-2.81	-2.63
TCGA-FI-A3PX-10A-01D-A22A-09_UCEC	-2.80	-2.85	-3.52	-3.22	-2.58	-2.55	-2.56	-2.55	-2.73	-3.52	-2.94	-4.22	-2.85	-2.82	0.00	-2.83	-2.57
TCGA-FJ-A3Z7-10A-01D-A23K-08_BLCA	-2.52	-2.64	-4.04	-2.88	-2.38	-2.48	-2.53	-2.45	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.40	-2.40
TCGA-FJ-A3Z9-10A-01D-A26K-08_BLCA	-2.52	-4.17	-4.47	-2.72	-2.49	-2.52	-2.57	-2.46	-2.58	-3.24	-2.90	-4.17	-2.68	-2.59	0.00	-2.75	-2.47
TCGA-FJ-A3ZE-10A-01D-A23K-08_BLCA	-2.45	-4.15	-3.98	-2.72	-2.55	-2.56	-2.59	-2.49	-2.57	0.00	-4.45	-4.45	0.00	0.00	0.00	-2.53	-2.49
TCGA-FJ-A3ZF-10A-01D-A23K-08_BLCA	-2.62	-3.46	-3.62	-2.67	-2.56	-2.65	-2.66	-2.57	-2.74	-3.35	-2.81	-3.46	-2.77	-2.71	0.00	-2.85	-2.59
TCGA-FK-A3S3-10A-01D-A22D-08_THCA	-2.52	0.00	-4.51	-2.62	-2.56	-2.54	-2.54	-2.45	-2.48	0.00	-4.51	0.00	0.00	-4.21	-2.99	-2.67	-2.50
TCGA-FK-A3SB-10A-01D-A22D-08_THCA	-2.56	-4.56	-4.08	-2.86	-2.61	-2.42	-2.55	-2.56	-2.67	-3.24	-2.84	0.00	0.00	-3.86	0.00	-2.47	-2.54
TCGA-FK-A3SD-10A-01D-A22D-08_THCA	-2.58	-2.76	-2.77	-2.86	-2.48	-2.66	-2.64	-2.58	-2.72	-3.31	-2.70	-2.77	-2.86	-2.72	-3.07	0.00	-2.53
TCGA-FK-A3SE-10A-01D-A22D-08_THCA	-2.55	0.00	-4.49	-2.77	-2.53	-2.53	-2.56	-2.62	-2.66	-3.38	-2.86	-4.49	-2.78	-2.63	0.00	-2.69	-2.49
TCGA-FK-A3SG-10A-01D-A22D-08_THCA	-2.52	-4.64	-4.04	-2.72	-2.50	-2.58	-2.67	-2.63	-2.76	-3.18	-2.81	-2.80	-2.90	-2.73	0.00	-2.85	-2.55
TCGA-FK-A3SH-10A-01D-A22D-08_THCA	-2.53	-2.73	-2.72	-2.90	-2.53	-2.63	-2.65	-2.65	-2.58	0.00	-2.87	-2.71	0.00	-3.85	-2.98	-4.25	-2.48
TCGA-FK-A4UB-10A-01D-A25A-08_THCA	-2.65	-2.77	-2.69	-2.94	-2.56	-2.69	-2.69	-2.65	-2.76	-3.48	-2.78	-2.73	0.00	-2.77	0.00	-2.87	-2.61
TCGA-FN-7833-10A-01D-2086-08_LGG	-2.56	-2.79	-2.76	-2.86	-2.47	-2.62	-2.62	-2.58	-2.51	0.00	-2.94	-2.73	0.00	-4.52	-3.02	-2.72	-2.51
TCGA-FP-7735-10A-01D-2053-08_STAD	-2.51	-2.70	-2.67	-2.81	-2.48	-2.53	-2.57	-2.59	-2.57	0.00	-2.91	-2.70	0.00	-4.16	-3.08	-2.94	-2.57
TCGA-FP-7829-10A-01D-2053-08_STAD	-2.50	-2.66	-2.67	-2.79	-2.58	-2.57	-2.53	-2.46	-2.41	0.00	0.00	0.00	0.00	-4.41	0.00	-2.37	-2.39
TCGA-FP-7916-10A-01D-2201-08_STAD	-2.54	0.00	0.00	-2.55	-2.53	-2.55	-2.53	-2.56	-2.65	-3.25	-2.93	-4.27	-2.85	-2.68	-3.19	0.00	-2.42
TCGA-FP-7998-10A-01D-2201-08_STAD	-2.53	-2.75	-2.69	-2.76	-2.62	-2.66	-2.58	-2.61	-2.68	-3.41	-2.91	0.00	-2.80	-2.67	-3.16	-4.52	-2.45
TCGA-FP-8099-10A-01D-2341-08_STAD	-2.39	0.00	-4.10	-2.70	-2.50	-2.53	-2.52	-2.47	-2.49	0.00	0.00	0.00	0.00	0.00	-3.03	-2.71	-2.49
TCGA-FP-8211-10A-01D-2341-08_STAD	-2.55	0.00	0.00	-2.56	-2.55	-2.53	-2.62	-2.46	-2.53	0.00	0.00	0.00	0.00	-4.58	0.00	-2.61	-2.48
TCGA-FP-8631-10A-01D-2394-08_STAD	-2.42	-2.57	-2.56	-4.46	-3.76	-3.68	-2.55	-2.36	-2.45	0.00	-3.86	0.00	-4.46	-3.76	-2.95	-2.58	-2.50
TCGA-FP-A4BF-10A-01D-A24F-08_STAD	-2.42	-3.97	-3.54	-2.73	-2.50	-2.56	-2.57	-2.46	-2.43	0.00	-3.97	-4.14	-4.45	-3.84	0.00	-2.47	-2.51
TCGA-FR-A2OS-10B-01D-A21A-08_SKCM	-2.44	0.00	-4.44	-2.55	-2.48	-2.51	-2.53	-2.63	-2.45	0.00	0.00	-4.44	0.00	-4.14	0.00	-2.52	-2.43
TCGA-FR-A3R1-10B-01D-A23B-08_SKCM	-2.47	-2.64	-2.62	-3.96	-2.73	-2.72	-2.68	-2.51	-2.60	-3.26	-2.98	-2.69	0.00	0.00	-2.96	-4.56	-2.60
TCGA-FR-A3YN-10A-01D-A23B-08_SKCM	-2.47	0.00	0.00	-2.60	-2.47	-2.50	-2.47	-2.50	-2.50	0.00	0.00	0.00	0.00	-4.50	-3.06	-2.76	-2.44
TCGA-FR-A3YO-10A-01D-A23B-08_SKCM	-2.56	-2.75	-2.76	-2.97	-2.54	-2.70	-2.73	-2.60	-2.75	-3.34	-2.75	-2.73	-2.83	-2.74	-3.20	0.00	-2.66
TCGA-FR-A44A-10A-01D-A24R-08_SKCM	-2.63	0.00	-4.26	-2.72	-2.68	-2.67	-2.66	-2.37	-2.56	-3.28	0.00	0.00	0.00	-4.26	-3.06	-2.74	-2.62
TCGA-FR-A69P-10A-01D-A30X-08_SKCM	-2.61	0.00	0.00	-2.76	-2.59	-2.64	-2.67	-2.65	-2.62	0.00	0.00	0.00	0.00	0.00	0.00	-2.69	-2.57
TCGA-FR-A726-10A-01D-A32N-08_SKCM	-2.58	0.00	0.00	-2.81	-2.57	-2.62	-2.64	-2.58	-2.50	0.00	0.00	0.00	0.00	0.00	-3.11	-2.77	-2.53
TCGA-FR-A728-10A-01D-A32N-08_SKCM	-2.61	0.00	0.00	-2.95	-2.62	-2.63	-2.67	-2.65	-2.77	-3.34	-2.94	0.00	-2.78	-2.74	0.00	-2.85	-2.54
TCGA-FS-A1YW-10A-01D-A199-08_SKCM	-2.37	-4.59	-4.59	-2.51	-2.48	-2.57	-2.52	-2.49	-2.41	0.00	0.00	0.00	0.00	-4.28	0.00	-2.60	-2.44
TCGA-FS-A1YX-10A-01D-A199-08_SKCM	-2.50	0.00	0.00	-2.77	-2.52	-2.56	-2.59	-2.60	-2.71	-3.47	-2.82	-2.68	0.00	-2.69	0.00	-2.68	-2.49
TCGA-FS-A1YY-10A-01D-A199-08_SKCM	-2.38	0.00	0.00	-2.53	-2.61	-2.61	-2.76	-2.54	-2.86	-3.15	-2.86	0.00	-3.05	-2.82	0.00	-2.73	-2.35
TCGA-FS-A1Z0-10A-01D-A199-08_SKCM	-2.55	-4.52	-4.52	-2.66	-2.62	-2.56	-2.57	-2.52	-2.78	-3.41	-2.95	0.00	-2.88	-2.71	0.00	-2.73	-2.49
TCGA-FS-A1Z3-10A-01D-A199-08_SKCM	-2.43	0.00	0.00	-2.56	-2.43	-2.50	-2.48	-2.45	-2.47	0.00	0.00	0.00	0.00	0.00	-3.00	-2.68	-2.36
TCGA-FS-A1Z4-10A-01D-A199-08_SKCM	-2.46	0.00	0.00	-2.54	-2.53	-2.54	-2.54	-2.42	-2.44	0.00	0.00	0.00	0.00	0.00	-2.94	-2.68	-2.46
TCGA-FS-A1Z7-10A-01D-A199-08_SKCM	-2.37	0.00	0.00	-2.66	-2.47	-2.46	-2.55	-2.42	-2.41	0.00	0.00	0.00	0.00	0.00	-3.21	-2.73	-2.34
TCGA-FS-A1ZA-10A-01D-A199-08_SKCM	-2.43	-2.72	-2.83	-2.81	-2.47	-2.59	-2.55	-2.65	-2.61	0.00	-2.98	-2.86	0.00	0.00	0.00	-2.51	-2.44
TCGA-FS-A1ZB-10A-01D-A199-08_SKCM	-2.46	0.00	-4.26	-2.54	-2.51	-2.58	-2.59	-2.49	-2.67	-3.44	-3.00	0.00	-2.86	-2.65	-3.28	-4.26	-2.39
TCGA-FS-A1ZC-10A-01D-A199-08_SKCM	-2.35	0.00	0.00	-2.45	-2.37	-2.68	-2.66	-2.61	-2.62	0.00	0.00	0.00	0.00	-2.53	0.00	-2.64	-2.51
TCGA-FS-A1ZD-10A-01D-A199-08_SKCM	-2.36	-2.81	-2.78	-2.76	-2.68	-2.65	-2.59	-2.54	-2.45	0.00	0.00	0.00	0.00	0.00	-2.98	0.00	-2.31
TCGA-FS-A1ZE-10A-01D-A199-08_SKCM	-2.34	0.00	-4.18	-2.58	-2.45	-2.51	-2.48	-2.52	-2.52	-4.48	0.00	0.00	0.00	-4.48	0.00	-2.59	-2.34
TCGA-FS-A1ZF-10A-01D-A199-08_SKCM	-2.35	-2.71	-2.75	-2.81	-2.73	-2.68	-2.44	-2.53	-2.46	0.00	0.00	0.00	0.00	0.00	-2.97	0.00	-2.38
TCGA-FS-A1ZG-10A-01D-A199-08_SKCM	-2.33	-2.77	-2.78	-2.80	-2.77	-2.70	-2.48	-2.51	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.35
TCGA-FS-A1ZH-10A-01D-A199-08_SKCM	-2.45	0.00	-4.56	-2.64	-2.48	-2.54	-2.51	-2.61	-4.56	-3.14	-2.75	0.00	-2.63	-2.47	0.00	0.00	-2.40
TCGA-FS-A1ZJ-10A-01D-A199-08_SKCM	-2.52	-2.64	-2.66	-2.78	-2.59	-2.63	-2.53	-2.47	-2.41	0.00	0.00	0.00	0.00	0.00	-2.95	-2.76	-2.43
TCGA-FS-A1ZK-10A-01D-A199-08_SKCM	-2.45	-2.70	-2.67	-2.88	-2.66	-2.62	-2.56	-2.43	-2.44	-4.47	0.00	0.00	0.00	0.00	-3.09	-2.79	-2.47

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-FS-A1ZM-10A-01D-A199-08_SKCM	-2.46	-2.80	-2.78	-2.82	-2.48	-2.59	-2.63	-2.66	-2.71	-3.52	-2.76	-2.69	0.00	-2.70	0.00	-2.82	-2.43
TCGA-FS-A1ZN-10A-01D-A199-08_SKCM	-2.56	-2.76	-2.75	-2.85	-2.46	-2.62	-2.61	-2.62	-2.59	0.00	-2.90	-2.76	0.00	0.00	0.00	-2.59	-2.41
TCGA-FS-A1ZP-10A-01D-A199-08_SKCM	-2.51	-2.87	-2.74	-2.90	-2.56	-2.61	-2.58	-2.56	-2.77	-3.48	-2.78	-2.61	0.00	-2.69	0.00	-2.81	-2.48
TCGA-FS-A1ZQ-10A-01D-A199-08_SKCM	-2.46	-2.74	-2.76	-2.89	-2.50	-2.57	-2.63	-2.61	-2.57	0.00	-3.10	-2.72	0.00	0.00	0.00	-2.54	-2.48
TCGA-FS-A1ZR-10A-01D-A199-08_SKCM	-2.53	-2.80	-2.87	-2.98	-2.58	-2.69	-2.75	-2.75	-2.91	-3.31	-2.72	-2.83	-2.88	-2.75	0.00	-2.89	-2.58
TCGA-FS-A1ZS-10A-01D-A199-08_SKCM	-2.39	0.00	0.00	-2.63	-2.52	-2.55	-2.50	-2.50	-2.45	0.00	0.00	0.00	0.00	-4.01	-3.31	-2.88	-2.36
TCGA-FS-A1ZT-10A-01D-A199-08_SKCM	-2.44	0.00	0.00	-2.63	-2.48	-2.55	-2.55	-2.58	-2.77	-3.27	-3.11	0.00	-3.05	-2.70	0.00	-2.79	-2.40
TCGA-FS-A1ZU-10A-01D-A198-08_SKCM	-2.35	0.00	0.00	-2.67	-2.42	-2.47	-2.46	-2.55	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.48	-2.38
TCGA-FS-A1ZW-10A-01D-A199-08_SKCM	-2.48	-2.74	-2.81	-2.96	-2.50	-2.53	-2.57	-2.56	-2.74	-3.41	-2.82	-2.57	0.00	-2.70	0.00	-2.83	-2.43
TCGA-FS-A1ZY-10A-01D-A199-08_SKCM	-2.48	-2.66	-2.73	-2.88	-2.68	-2.66	-2.52	-2.54	-2.43	0.00	0.00	0.00	0.00	-4.23	-3.10	-2.68	-2.41
TCGA-FS-A1ZZ-10A-01D-A199-08_SKCM	-2.27	0.00	-4.42	-2.36	-2.29	-2.63	-2.53	-2.83	-2.70	0.00	0.00	0.00	0.00	-2.49	0.00	-2.67	-2.46
TCGA-FS-A4F0-10A-01D-A24R-08_SKCM	-2.59	-2.65	-2.66	-2.85	-2.65	-2.64	-2.62	-2.42	-2.47	-4.51	-4.03	0.00	-4.21	-3.73	-3.10	-2.73	-2.53
TCGA-FS-A4F2-10A-01D-A24R-08_SKCM	-2.57	-3.69	-3.84	-2.66	-2.58	-2.63	-2.63	-2.51	-2.68	-4.23	-3.49	-3.58	0.00	-3.69	0.00	-2.47	-2.57
TCGA-FS-A4F4-10B-01D-A25O-08_SKCM	-2.58	-2.75	-2.75	-2.91	-2.49	-2.57	-2.59	-2.66	-2.75	-3.38	-2.78	-2.60	0.00	-2.71	0.00	-2.77	-2.53
TCGA-FS-A4F5-10B-01D-A25O-08_SKCM	-2.50	-2.56	-2.68	0.00	-2.56	-2.62	-2.51	-2.50	-2.59	-3.19	-2.94	0.00	-2.67	-2.57	-2.94	-4.34	-2.45
TCGA-FS-A4F8-10B-01D-A25O-08_SKCM	-2.48	-2.62	-2.64	-2.85	-2.64	-2.58	-2.51	-2.48	-2.48	0.00	0.00	0.00	0.00	0.00	-2.98	-2.79	-2.43
TCGA-FS-A4F9-10A-01D-A24R-08_SKCM	-2.60	-2.64	-2.68	-3.79	-2.64	-2.71	-2.65	-2.49	-2.56	-4.57	-2.86	-2.72	-3.87	-3.97	-3.09	-2.78	-2.63
TCGA-FS-A4FB-10B-01D-A25O-08_SKCM	-2.53	0.00	0.00	-2.74	-2.53	-2.56	-2.57	-2.50	-2.61	-3.24	-2.88	0.00	-2.75	-2.67	-3.03	0.00	-2.48
TCGA-FS-A4FC-10A-01D-A24R-08_SKCM	-2.55	0.00	-4.48	-2.75	-2.59	-2.58	-2.62	-2.53	-2.51	0.00	0.00	-4.18	0.00	-4.00	-3.05	-2.72	-2.52
TCGA-FS-A4FD-10B-01D-A25O-08_SKCM	-2.50	-2.70	-2.67	-2.83	-2.67	-2.66	-2.61	-2.76	-2.64	0.00	-2.94	0.00	-2.76	-2.57	0.00	-2.57	-2.42
TCGA-FT-A3EE-10A-01D-A202-08_BLCA	-2.61	-2.61	-2.60	0.00	-2.73	-2.69	-2.62	-2.61	-2.71	-3.39	-2.82	-2.72	-2.79	-2.64	0.00	-2.78	-2.57
TCGA-FT-A61P-10A-01D-A30H-08_BLCA	-2.43	-2.65	-2.61	-2.73	-2.58	-2.63	-2.50	-2.47	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.37
TCGA-FU-A23K-10A-01D-A16O-08_CESC	-2.53	0.00	0.00	-2.91	-2.58	-2.58	-2.58	-2.50	-2.62	-3.38	-2.90	0.00	-2.85	-4.63	0.00	-2.53	-2.56
TCGA-FU-A23L-10A-01D-A16O-08_CESC	-2.45	0.00	-4.55	-2.59	-2.50	-2.55	-2.55	-2.52	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.43
TCGA-FU-A2QG-10A-01D-A18J-09_CESC	-2.74	-4.47	0.00	-2.96	-2.45	-2.46	-2.43	-2.53	-2.43	0.00	0.00	-4.47	0.00	-3.87	0.00	-2.39	-2.59
TCGA-FU-A3HY-10A-01D-A21Q-09_CESC	-2.86	-2.54	-2.54	0.00	-2.67	-2.71	-2.50	-2.52	-2.41	-4.53	-2.91	-2.78	-4.23	-4.23	0.00	-2.39	-2.57
TCGA-FU-A3HZ-10A-01D-A20U-09_CESC	-2.71	-2.73	-2.72	-3.04	-2.70	-2.64	-2.45	-2.46	-2.31	0.00	-3.82	-4.42	-4.12	-3.94	-2.92	-2.72	-2.56
TCGA-FU-A3NI-10A-01D-A21Q-09_CESC	-2.88	-2.79	-2.73	-3.44	-2.54	-2.57	-2.53	-2.56	-2.49	0.00	-2.86	-2.80	0.00	0.00	-3.07	-2.74	-2.59
TCGA-FU-A3TQ-10A-01D-A22X-09_CESC	-2.77	-4.45	0.00	-2.98	-2.48	-2.51	-2.54	-2.44	-2.36	0.00	-3.98	-4.45	0.00	-4.45	0.00	-2.44	-2.54
TCGA-FU-A3TX-10A-01D-A22X-09_CESC	-2.88	-2.75	-2.82	-3.25	-2.73	-2.78	-2.53	-2.57	-2.64	-3.38	-2.90	-2.73	0.00	-2.71	0.00	-2.74	-2.60
TCGA-FU-A3WB-10A-01D-A22X-09_CESC	-2.85	-2.68	-2.78	-3.31	-2.45	-2.59	-2.54	-2.57	-2.49	0.00	-2.96	-2.84	0.00	0.00	-2.97	-2.79	-2.64
TCGA-FU-A3YQ-10A-01D-A22X-09_CESC	-2.85	0.00	0.00	-3.37	-2.58	-2.56	-2.49	-2.57	-2.66	-3.31	-2.74	0.00	-2.80	-2.71	0.00	-2.69	-2.61
TCGA-FU-A40J-10A-01D-A243-09_CESC	-2.77	-2.80	-2.79	-3.28	-2.73	-2.59	-2.46	-2.48	-2.33	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.56
TCGA-FU-A57G-10A-01D-A26G-09_CESC	-2.80	-3.33	-3.58	-2.99	-2.58	-2.62	-2.56	-2.61	-2.48	-4.24	-3.69	-3.76	-3.84	-3.54	0.00	-2.65	-2.69
TCGA-FU-A5XV-10A-01D-A28E-09_CESC	-2.82	0.00	-4.14	-2.95	-2.50	-2.49	-2.47	-2.59	-2.32	0.00	0.00	0.00	0.00	0.00	0.00	-2.48	-2.54
TCGA-FV-A2QQ-10B-01D-A22F-10_LIHC	-2.51	-2.68	-2.60	-3.01	-2.84	-2.64	-2.43	-2.43	-2.27	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.40
TCGA-FV-A3I1-10A-01D-A22F-10_LIHC	-2.36	-2.34	-2.42	0.00	0.00	0.00	-2.40	-2.50	-2.27	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.33
TCGA-FV-A3R3-10A-01D-A22F-10_LIHC	-2.34	0.00	0.00	-2.57	-2.47	-2.46	-2.36	-2.47	-2.33	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.32
TCGA-FV-A495-10A-01D-A25V-10_LIHC	-2.29	-2.57	-2.60	-2.85	-2.65	-2.59	-2.27	-2.42	-2.27	0.00	0.00	0.00	-4.23	0.00	-2.95	-2.51	-2.26
TCGA-FV-A496-10A-01D-A25V-10_LIHC	-2.39	0.00	0.00	-2.71	-2.39	-2.33	-2.33	-2.45	0.00	-3.18	-2.59	-2.60	-2.53	-2.43	0.00	0.00	-2.45
TCGA-FV-A4ZQ-10A-01D-A25V-10_LIHC	-2.37	-2.59	-2.59	-2.82	-2.39	-2.40	-2.34	-2.54	-2.34	0.00	-2.77	-2.49	-3.77	0.00	-2.73	0.00	-2.37
TCGA-FW-A3I3-10A-01D-A21A-08_SKCM	-2.36	-2.70	-2.65	-2.79	-2.63	-2.68	-2.59	-2.59	-2.49	0.00	-4.51	0.00	0.00	-4.51	-2.91	-4.21	-2.45
TCGA-FW-A3R5-10A-01D-A23B-08_SKCM	-2.67	-2.83	-2.84	-3.03	-2.60	-2.72	-2.77	-2.61	-2.86	-3.27	-2.81	-2.73	-4.39	-2.80	0.00	-2.79	-2.70
TCGA-FW-A3TU-10A-01D-A23B-08_SKCM	-2.55	0.00	-4.06	-2.82	-2.59	-2.58	-2.54	-2.46	-2.60	0.00	0.00	0.00	-4.53	0.00	-2.94	-2.64	-2.57
TCGA-FW-A3TV-10A-01D-A23B-08_SKCM	-2.44	-2.61	-2.62	-2.79	-2.61	-2.65	-2.62	-2.69	-2.65	0.00	-2.83	0.00	-2.72	-2.55	0.00	-2.71	-2.39
TCGA-FW-A5DX-10A-01D-A27N-08_SKCM	-2.37	-2.72	-2.65	-2.88	-2.59	-2.64	-2.56	-2.44	-2.54	0.00	0.00	-4.43	0.00	0.00	0.00	-2.56	-2.47
TCGA-FX-A2QS-10A-01D-A21Q-09_SARC	-2.77	-4.45	-4.45	-2.94	-2.59	-2.53	-2.51	-2.55	-2.45	0.00	-4.45	-3.97	0.00	-4.45	0.00	-2.57	-2.64
TCGA-FX-A3NJ-10A-01D-A21Q-09_SARC	-2.75	0.00	0.00	-2.92	-2.55	-2.49	-2.45	-2.60	-2.39	0.00	0.00	-4.20	0.00	0.00	0.00	-2.52	-2.58
TCGA-FX-A3NK-10A-01D-A21Q-09_SARC	-2.65	-4.18	-4.48	-3.05	-2.57	-2.53	-2.51	-2.47	-2.47	0.00	0.00	-4.48	0.00	-4.18	0.00	-2.51	-2.59
TCGA-FX-A3RE-10A-01D-A22A-09_SARC	-2.84	-2.82	-2.85	-3.23	-2.48	-2.58	-2.54	-2.59	-2.46	-4.49	-2.89	-2.68	-4.01	-4.19	0.00	-2.61	-2.61
TCGA-FX-A3TO-10A-01D-A22A-09_SARC	-2.72	0.00	0.00	-2.99	-2.63	-2.60	-2.53	-2.61	-2.70	-3.43	-3.04	-4.50	-2.76	-2.86	0.00	-2.78	-2.61
TCGA-FX-A48G-10A-01D-A24N-09_SARC	-2.85	-2.63	-2.66	-3.14	-2.61	-2.63	-2.44	-2.40	-2.37	0.00	0.00	-4.16	-3.98	0.00	-3.00	-2.73	-2.57
TCGA-FY-A2QD-10A-01D-A19M-08_THCA	-2.51	-2.75	-4.57	-2.92	-2.44	-2.54	-2.56	-2.67	-2.59	0.00	-3.04	0.00	-2.72	-4.57	0.00	-2.55	-2.40
TCGA-FY-A3BL-10A-01D-A19M-08_THCA	-2.50	-4.24	-3.94	-2.58	-2.50	-2.55	-2.57	-2.58	-2.69	-3.31	-2.91	-3.70	-2.75	-2.66	0.00	-2.76	-2.39
TCGA-FY-A3I4-10A-01D-A21A-08_THCA	-2.47	-4.10	-4.40	-2.54	-2.48	-2.49	-2.52	-2.60	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.37
TCGA-FY-A3I5-10A-01D-A21Z-08_THCA	-2.58	-2.71	0.00	-2.89	-2.44	-2.55	-2.62	-2.62	-2.70	-3.33	-2.89	0.00	-2.75	-2.65	0.00	-2.72	-2.47
TCGA-FY-A3NM-10A-01D-A21A-08_THCA	-2.55	0.00	-4.47	-2.52	-2.56	-2.47	-2.57	-2.44	-2.43	0.00	-4.47	-4.47	0.00	-3.99	-2.96	-2.70	-2.53
TCGA-FY-A3NN-10A-01D-A21A-08_THCA	-2.55	0.00	0.00	-2.59	-2.53	-2.60	-2.61	-2.59	-2.67	-3.55	-2.92	0.00	-2.92	-2.63	-3.10	0.00	-2.49
TCGA-FY-A3NP-10A-01D-A21A-08_THCA	-2.53	-2.57	-2.60	0.00	-2.61	-2.67	-2.62	-2.53	-2.59	0.00	-2.86	-2.66	0.00	-4.22	-3.04	-2.71	-2.53
TCGA-FY-A3ON-10A-01D-A21Z-08_THCA	-2.51	0.00	0.00	-2.73	-2.51	-2.52	-2.57	-2.47	-2.51	0.00	0.00	0.00	0.00	-4.46	-2.99	-2.70	-2.47
TCGA-FY-A3R6-10A-01D-A21Z-08_THCA	-2.46	-4.47	0.00	-2.67	-2.47	-2.48	-2.54	-2.57	-2.41	0.00	0.00	0.00	0.00	-4.47	0.00	-2.57	-2.49
TCGA-FY-A3R7-10A-01D-A21Z-08_THCA	-2.49	-4.43	0.00	-2.52	-2.46	-2.50	-2.55	-2.52	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.33	-2.36
TCGA-FY-A3R8-10A-01D-A21Z-08_THCA	-2.50	0.00	0.00	-2.66	-2.48	-2.52	-2.55	-2.58	-2.38	0.00	0.00	0.00	0.00	-4.46	0.00	-2.54	-2.44
TCGA-FY-A3R9-10A-01D-A21Z-08_THCA	-2.57	-2.72	-2.71	-2.92	-2.44	-2.60	-2.62	-2.52	-2.47	0.00	-2.88	-2.65	0.00	-4.55	0.00	-2.45	-2.56
TCGA-FY-A3RA-10A-01D-A21Z-08_THCA	-2.55	-2.67	-2.62	0.00	-2.61	-2.62	-2.60	-2.59	-2.83	-3.40	-2.64	-2.62	-2.92	-2.69	0.00	-2.75	-2.53
TCGA-FY-A3TY-10A-01D-A22Z-08_THCA	-2.48	-2.78	-2.76	-2.87	-2.45	-2.54	-2.52	-2.63	-2.67	-3.36	-2.72	-2.51	0.00	-2.72	0.00	-2.84	-2.41
TCGA-FY-A3W9-10A-01D-A22D-08_THCA	-2.51	0.00	-4.44	-2.55	-2.51	-2.48	-2.53	-2.58	-2.46	0.00	0.00	0.00	-4.44	-4.44	0.00	-2.54	-2.42
TCGA-FY-A3WA-10A-01D-A22D-08_THCA	-2.52	0.00	-4.12	-2.57	-2.54	-2.54	-2.52	-2.58	-2.43	0.00	0.00	0.00	0.00	-4.42	0.00	-2.56	-2.40
TCGA-FY-A3YR-10A-01D-A22Z-08_THCA	-2.48	-2.70	-2.65	-2.79	-2.62	-2.61	-2.49	-2.41	-2.48	0.00	0.00	0.00	0.00	-4.78	-2.99	-2.70	-2.44
TCGA-FY-A40K-10A-01D-A23K-08_THCA	-2.60	-2.68	-2.67	-2.83	-2.64	-2.71	-2.62	-2.54	-2.48	-4.22	0.00	-4.52	0.00	-4.22	0.00	-2.62	-2.54
TCGA-FY-A40L-10A-01D-A23K-08_THCA	-2.40	-2.70	-2.63	-2.80	-2.65	-2.59	-2.47	-2.52	-2.37	0.00	0.00	0.00	0.00	0.00	0.00	-2.44	-2.31
TCGA-FY-A40M-10A-01D-A23K-08_THCA	-2.64	-2.76	-2.74	-2.96	-2.54	-2.69	-2.65	-2.68	-2.70	-3.32	-2.74	-2.64	-3.97	-2.75	0.00	-2.86	-2.63
TCGA-FY-A40N-10A-01D-A23K-08_THCA	-2.50	0.00	0.00	-2.82	-2.62	-2.65	-2.61	-2.49	-2.72	-3.37	-2.83	0.00	-2.79	-2.74	-3.12	-4.27	-2.59
TCGA-FY-A4B0-10A-01D-A23U-08_THCA	-2.53	-4.42	-3.72	-2.57	-2.53	-2.60	-2.56	-2.45	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.53
TCGA-FY-A4B3-10A-01D-A23U-08_THCA	-2.51	-3.77	0.00	-2.66	-2.50	-2.52	-2.52	-2.46	-2.44	-3.90	-4.38	-3.90	-3.68	-4.38	-2.96	-2.64	-2.46
TCGA-FY-A4B4-10A-01D-A23U-08_THCA	-2.44	-2.74	-2.72	-2.86	-2.39	-2.52	-2.51	-2.57	-2.44	0.00	-2.97	-2.69	0.00	0.00	0.00	-2.51	-2.40
TCGA-G2-A2EC-10A-01D-A17V-08_BLCA	-2.44	-2.71	-3.83	-2.79	-2.65	-2.69	-2.66	-2.76	-2.76	0.00	-2.90	-4.06	-2.76	-2.66	0.00	-2.68	-2.32
TCGA-G2-A2EF-10A-01D-A18F-08_BLCA	-2.55	-2.78	-2.71	-2.97	-2.55	-2.62	-2.68	-2.57	-2.82	-3.48	-2.71	-2.68	0.00	-2.71	0.00	-2.82	-2.57
TCGA-G2-A2EJ-10A-01D-A17V-08_BLCA	-2.58	-2.67	-2.66	-4.74	-2.82	-2.82	-2.53	-2.48	-2.61	-3.46	-3.06	-2.74	-4.74	-4.74	-3.06	0.00	-2.47
TCGA-G2-A2EK-10A-01D-A18F-08_BLCA	-2.60	-2.67	-2.64	-4.53	-2.61	-2.62	-2.64	-2.56	-2.56	0.00	-2.70	-2.59	0.00	0.00	-2.99	-2.73	-2.57
TCGA-G2-A2EL-10A-01D-A18F-08_BLCA	-2.50	-2.63	-2.63	-2.84	-2.64	-2.68	-2.60	-2.60	-2.55	0.00	0.00	-4.49	0.00	0.00	-2.97	-2.72	-2.50
TCGA-G2-A3IB-10A-01D-A20D-08_BLCA	-2.54	0.00	0.00	-2.69	-2.41	-2.56	-2.57	-2.57	-2.44	0.00	-4.10	0.00	0.00	0.00	-3.12	-2.67	-2.45
TCGA-G2-A3IE-10A-01D-A20D-08_BLCA	-2.52	0.00	-4.44	-2.53	-2.47	-2.54	-2.53	-2.51	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.49
TCGA-G2-A3VY-10A-01D-A22Z-08_BLCA	-2.53	-2.79	0.00	-2.65	-2.56	-2.62	-2.65	-2.65	-2.74	-3.20	-2.73	0.00	-2.68	-2.56	0.00	-2.75	-2.43
TCGA-G3-A25S-10A-01D-A16V-10_LIHC	-2.58	-4.19	0.00	-2.53	-2.54	-2.53	-2.44	-2.64	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.42
TCGA-G3-A25T-10A-01D-A16V-10_LIHC	-2.53	0.00	0.00	-2.66	-2.57	-2.41	-2.40	-2.61	0.00	-3.33	-2.64	-2.80	-3.03	-2.43	0.00	0.00	-2.41
TCGA-G3-A25U-10A-01D-A16V-10_LIHC	-2.51	0.00	0.00	-2.69	-2.71	-2.61	-2.42	-2.57	-2.68	-3.07	-2.90	-2.98	0.00	-2.83	-3.46	0.00	-2.36
TCGA-G3-A25V-10A-01D-A16V-10_LIHC	-2.64	-2.84	-2.79	-2.93	-2.70	-2.53	-2.47	-2.52	-2.53	0.00	-3.03	-2.93	0.00	0.00	0.00	-2.74	-2.44
TCGA-G3-A25Y-10A-01D-A16V-10_LIHC	-2.50	0.00	0.00	-2.64	-2.56	-2.67	-2.35	-2.68	0.00	-3.07	-2.74	-2.89	-3.21	-2.52	0.00	0.00	-2.39
TCGA-G3-A25Z-10A-01D-A16V-10_LIHC	-2.52	-2.83	-2.75	-2.96	-2.83	-2.92	-2.44	-2.66	-2.70	-3.35	-3.05	0.00	-2.99	-2.76	0.00	-2.75	-2.47
TCGA-G3-A3CG-10A-01D-A20W-10_LIHC	-2.45	-2.63	-2.59	-3.03	-2.33	-2.38	-2.31	-2.42	-2.49	-3.48	-2.65	-2.60	-2.66	-2.59	0.00	-2.86	-2.39
TCGA-G3-A3CI-10A-01D-A20W-10_LIHC	-2.40	-2.44	-2.48	-2.78	-2.52	-2.49	-2.25	-2.33	-2.27	0.00	0.00	0.00	0.00	0.00	-2.99	-2.65	-2.36
TCGA-G3-A3CJ-10A-01D-A20W-10_LIHC	-2.41	0.00	0.00	-2.67	-2.25	-2.27	-2.32	-2.30	-2.34	0.00	0.00	0.00	0.00	0.00	-2.90	-2.63	-2.34
TCGA-G3-A3CK-10A-01D-A20W-10_LIHC	-2.35	-4.35	0.00	-2.56	-2.44	-2.39	-2.33	-2.37	-2.31	0.00	0.00	0.00	0.00	0.00	-2.91	-2.67	-2.38
TCGA-G3-A5SI-10A-01D-A27I-10_LIHC	-2.46	0.00	-4.34	-2.54	-2.43	-2.34	-2.30	-2.44	-4.34	-3.13	-2.60	0.00	-2.42	-2.32	0.00	-4.03	-2.42
TCGA-G3-A5SJ-10A-01D-A27I-10_LIHC	-2.46	0.00	0.00	-2.58	-2.47	-2.38	-2.40	-2.41	-2.60	-3.54	-2.90	-2.54	0.00	-2.46	0.00	-2.53	-2.41

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-G3-A5SK-10A-01D-A27I-10_LIHC	-2.43	0.00	0.00	-2.39	-2.43	-2.24	-2.31	-2.44	-2.30	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.40
TCGA-G3-A5SL-10A-01D-A27I-10_LIHC	-2.41	-2.53	-2.71	-2.72	-2.53	-2.51	-2.32	-2.41	-2.32	0.00	0.00	0.00	0.00	0.00	-2.91	-2.51	-2.35
TCGA-G3-A5SM-10A-01D-A28X-10_LIHC	-2.49	-2.53	-2.57	-2.78	-2.35	-2.37	-2.29	-2.46	-2.42	0.00	-2.89	-2.52	0.00	0.00	0.00	-2.36	-2.44
TCGA-G4-6293-10A-01D-1719-10_COAD	-2.38	0.00	0.00	-2.63	-2.39	-2.42	-2.31	-2.48	-2.32	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.38
TCGA-G4-6294-10A-01D-1771-10_COAD	-2.58	0.00	0.00	-2.64	-2.63	-2.55	-2.41	-2.71	-2.71	-3.28	-2.96	0.00	-2.96	-2.83	0.00	-2.91	-2.44
TCGA-G4-6295-10A-01D-1719-10_COAD	-2.62	-2.80	-2.86	-3.07	-2.50	-2.62	-2.50	-2.75	-2.70	-3.34	-2.85	-2.66	0.00	-2.72	0.00	-2.95	-2.51
TCGA-G4-6297-10A-01D-1719-10_COAD	-2.57	0.00	0.00	-2.74	-2.40	-2.38	-2.39	-2.55	-2.53	-3.32	-2.96	0.00	-2.69	-2.66	0.00	-3.07	-2.41
TCGA-G4-6298-10A-01D-1719-10_COAD	-2.38	-2.74	-2.74	-2.90	-2.68	-2.64	-2.51	-2.74	-2.56	0.00	-2.84	0.00	-2.76	-2.56	-3.34	0.00	-2.18
TCGA-G4-6299-10A-01D-1771-10_COAD	-2.46	0.00	0.00	-2.66	-2.61	-2.63	-2.47	-2.51	-2.43	0.00	0.00	0.00	0.00	0.00	-3.32	-2.82	-2.45
TCGA-G4-6302-10A-01D-1719-10_COAD	-2.53	-2.58	-2.56	-2.87	-2.60	-2.60	-2.29	-2.55	-2.32	0.00	0.00	0.00	0.00	0.00	-3.06	-2.74	-2.35
TCGA-G4-6303-10A-01D-1771-10_COAD	-2.48	-4.07	0.00	-2.74	-2.57	-2.48	-2.46	-2.62	-2.52	0.00	0.00	0.00	0.00	0.00	-3.14	-2.86	-2.43
TCGA-G4-6304-10A-01D-1924-10_COAD	-2.67	0.00	0.00	-2.77	-2.81	-2.67	-2.58	-2.64	-2.85	-3.43	-3.09	0.00	-3.18	-2.88	0.00	-2.93	-2.54
TCGA-G4-6306-10A-01D-1771-10_COAD	-2.63	-2.85	-2.91	-2.96	-2.72	-2.68	-2.52	-2.69	-2.69	-3.23	-2.85	-2.80	0.00	-2.74	0.00	-2.89	-2.55
TCGA-G4-6307-10A-01D-1720-10_COAD	-2.50	-2.74	-2.73	-2.96	-2.44	-2.55	-2.57	-2.60	-2.44	0.00	-2.95	-2.74	0.00	0.00	-3.13	-2.86	-2.52
TCGA-G4-6309-10A-01D-1835-10_COAD	-2.46	0.00	-2.78	-2.68	-2.68	-2.71	-2.51	-2.63	-2.56	0.00	-2.90	0.00	-2.71	-2.73	0.00	0.00	-2.58
TCGA-G4-6310-10A-01D-1720-10_COAD	-2.48	-2.67	-2.68	-2.95	-2.72	-2.70	-2.40	-2.52	-2.28	0.00	0.00	0.00	0.00	-4.22	-3.14	-2.83	-2.37
TCGA-G4-6314-10A-01D-1720-10_COAD	-2.55	-2.75	-2.67	-3.09	-2.44	-2.52	-2.39	-2.59	-2.34	0.00	-3.02	-2.77	0.00	0.00	0.00	-2.61	-2.40
TCGA-G4-6315-10A-01D-1720-10_COAD	-2.55	-2.76	-2.63	-3.01	-2.58	-2.53	-2.38	-2.51	-2.37	0.00	-3.04	-2.72	-4.58	0.00	-3.10	-2.88	-2.43
TCGA-G4-6317-10A-01D-1720-10_COAD	-2.47	-4.60	-4.13	-2.75	-2.46	-2.41	-2.35	-2.50	-2.26	0.00	0.00	0.00	0.00	-4.60	0.00	-2.60	-2.35
TCGA-G4-6320-10A-01D-1720-10_COAD	-2.51	0.00	0.00	-2.78	-2.45	-2.47	-2.40	-2.57	-2.52	-3.29	-2.93	0.00	-2.77	-2.71	0.00	-3.00	-2.40
TCGA-G4-6321-10A-01D-1720-10_COAD	-2.50	0.00	0.00	-2.84	-2.43	-2.47	-2.49	-2.47	-2.59	-3.34	-2.82	0.00	-2.77	-2.74	0.00	-3.01	-2.39
TCGA-G4-6323-10A-01D-1720-10_COAD	-2.58	0.00	-4.50	-2.78	-2.47	-2.40	-2.36	-2.52	-2.31	0.00	0.00	0.00	-3.80	-4.02	-3.27	-3.07	-2.31
TCGA-G4-6586-10A-01D-1771-10_COAD	-2.52	0.00	0.00	-2.69	-2.61	-2.52	-2.50	-2.59	-2.76	-3.27	-3.14	0.00	-2.90	-2.71	0.00	-2.85	-2.52
TCGA-G4-6588-10A-01D-1771-10_COAD	-2.48	-2.74	-2.71	-2.91	-2.82	-2.77	-2.44	-2.62	-2.39	0.00	0.00	0.00	0.00	0.00	-2.86	0.00	-2.45
TCGA-G4-6626-10A-01D-1771-10_COAD	-2.62	-2.90	-2.73	-3.02	-2.62	-2.59	-2.58	-2.79	-3.00	-3.45	-2.87	-2.64	0.00	-2.80	-3.22	0.00	-2.51
TCGA-G4-6628-10A-01D-1835-10_COAD	-2.68	-2.87	-2.69	-2.92	-2.65	-2.64	-2.63	-2.87	-2.75	-3.45	-2.88	-2.71	0.00	-2.85	0.00	-3.00	-2.54
TCGA-G5-6233-10A-01D-1733-10_READ	-2.53	-2.78	-2.81	-3.20	-2.54	-2.61	-2.52	-2.64	-2.43	0.00	-3.05	-2.92	0.00	0.00	-3.46	-3.08	-2.48
TCGA-G5-6235-10A-01D-1733-10_READ	-2.51	0.00	0.00	-2.88	-2.57	-2.55	-2.44	-2.64	-2.72	-3.28	-2.98	0.00	-2.92	-2.77	-3.42	-4.42	-2.48
TCGA-G5-6572-10A-01D-1826-10_READ	-2.51	-2.97	-2.83	-2.73	-2.80	-2.79	-2.44	-2.54	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.42
TCGA-G5-6641-10A-01D-1826-10_READ	-2.54	-2.78	-2.72	-2.88	-2.96	-2.96	-2.49	-2.62	-2.52	0.00	0.00	0.00	0.00	0.00	-3.40	-2.82	-2.50
TCGA-G7-6789-10A-01D-1962-08_KIRP	-2.51	-4.63	0.00	-2.74	-2.57	-2.61	-2.65	-2.47	-2.50	0.00	0.00	0.00	0.00	-4.16	-3.19	-2.73	-2.50
TCGA-G7-6790-10A-01D-1962-08_KIRP	-2.62	-2.86	-2.79	-2.96	-2.55	-2.70	-2.67	-2.66	-2.81	-3.50	-2.73	-2.62	-4.73	-2.77	0.00	-2.86	-2.58
TCGA-G7-6792-10A-01D-1962-08_KIRP	-2.59	0.00	-4.70	-2.64	-2.52	-2.62	-2.64	-2.49	-2.52	0.00	0.00	0.00	-4.70	-4.40	-3.15	-2.76	-2.52
TCGA-G7-6793-10A-01D-1962-08_KIRP	-2.59	0.00	-4.19	-2.83	-2.61	-2.63	-2.70	-2.66	-2.73	-3.37	-2.90	-4.67	-2.79	-2.75	0.00	-2.76	-2.57
TCGA-G7-6795-10A-01D-1962-08_KIRP	-2.59	0.00	-4.67	-2.80	-2.56	-2.66	-2.66	-2.73	-2.83	-3.37	-2.90	-4.67	-2.80	-2.73	0.00	-2.79	-2.51
TCGA-G7-6796-10A-01D-1962-08_KIRP	-2.41	-2.75	-2.76	-2.88	-2.68	-2.73	-2.68	-2.47	-2.55	0.00	-4.64	0.00	-4.64	0.00	-3.10	-2.73	-2.47
TCGA-G7-6797-10A-01D-1962-08_KIRP	-2.66	0.00	0.00	-2.91	-2.57	-2.63	-2.70	-2.60	-2.76	-3.42	-2.82	-2.71	-4.78	-2.85	0.00	-2.90	-2.64
TCGA-G7-7501-10A-01D-2201-08_KIRP	-2.54	0.00	0.00	-2.73	-2.51	-2.55	-2.57	-2.50	-2.48	0.00	0.00	-4.50	0.00	-4.50	0.00	-2.37	-2.52
TCGA-G7-7502-10A-01D-2201-08_KIRP	-2.49	0.00	0.00	-2.72	-2.60	-2.55	-2.55	-2.61	-2.56	0.00	-4.49	0.00	0.00	0.00	-2.89	0.00	-2.46
TCGA-G7-A4TM-10B-01D-A31X-10_KIRP	-2.35	0.00	0.00	-2.62	-2.35	-2.33	-2.29	-2.44	-2.37	0.00	0.00	0.00	0.00	0.00	0.00	-2.94	-2.38
TCGA-G9-6329-10A-01D-1961-08_PRAD	-2.52	-2.74	-2.74	-2.95	-2.71	-2.73	-2.57	-2.66	-2.67	-3.39	-2.92	-4.62	-2.84	-2.70	0.00	-2.74	-2.49
TCGA-G9-6332-10A-01D-1786-08_PRAD	-2.52	-2.72	-2.68	-2.77	-2.64	-2.63	-2.60	-2.61	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.48
TCGA-G9-6333-10A-01D-1961-08_PRAD	-2.49	0.00	-4.61	-2.71	-2.53	-2.55	-2.56	-2.50	-2.63	0.00	0.00	-4.30	0.00	-4.61	0.00	-2.45	-2.43
TCGA-G9-6336-10A-01D-1786-08_PRAD	-2.58	-2.86	-2.76	-2.96	-2.54	-2.66	-2.66	-2.70	-4.28	-3.25	-2.62	-2.79	-2.71	-2.60	0.00	-4.28	-2.60
TCGA-G9-6338-10A-01D-1961-08_PRAD	-2.42	-2.83	-2.81	-2.96	-2.51	-2.62	-2.63	-2.59	-2.59	0.00	-2.99	-2.76	0.00	-4.20	-3.25	-2.80	-2.47
TCGA-G9-6339-10A-01D-A30X-08_PRAD	-2.58	0.00	-4.54	-2.77	-2.61	-2.66	-2.63	-2.57	-2.53	0.00	0.00	0.00	0.00	0.00	-3.06	-2.74	-2.59
TCGA-G9-6342-10A-01D-1961-08_PRAD	-2.47	-2.75	-2.68	-2.88	-2.66	-2.68	-2.58	-2.52	-2.52	0.00	-4.61	-4.61	0.00	-4.31	0.00	-2.63	-2.47
TCGA-G9-6343-10A-01D-1961-08_PRAD	-2.42	0.00	0.00	-2.79	-2.60	-2.59	-2.61	-2.54	-2.73	-3.36	-2.90	0.00	-2.79	-2.70	-3.08	-4.34	-2.48
TCGA-G9-6347-10A-01D-A31J-08_PRAD	-2.59	0.00	0.00	-2.77	-2.58	-2.55	-2.60	-2.56	-2.69	-3.25	-2.81	-4.45	-2.72	-2.64	-3.02	0.00	-2.54
TCGA-G9-6348-10A-01D-1786-08_PRAD	-2.59	-4.58	0.00	-2.82	-2.61	-2.63	-2.68	-2.62	-2.75	-3.20	-2.90	-4.28	-2.83	-2.77	0.00	-2.71	-2.58
TCGA-G9-6351-10A-01D-1961-08_PRAD	-2.50	0.00	0.00	-2.81	-2.54	-2.57	-2.53	-2.64	-2.81	-3.35	-2.93	0.00	-2.85	-2.66	0.00	-2.74	-2.47
TCGA-G9-6353-10A-01D-1961-08_PRAD	-2.49	-4.59	0.00	-2.72	-2.49	-2.58	-2.61	-2.48	-2.47	0.00	-4.59	0.00	0.00	-4.12	0.00	-2.59	-2.41
TCGA-G9-6354-10A-01D-A30X-08_PRAD	-2.64	0.00	0.00	-2.81	-2.69	-2.68	-2.66	-2.68	-2.81	-3.37	-3.00	-2.76	0.00	-2.74	-3.15	0.00	-2.57
TCGA-G9-6356-10A-01D-1786-08_PRAD	-2.63	-2.85	-2.75	-2.94	-2.56	-2.68	-2.64	-2.58	-2.80	-3.58	-2.76	-2.80	-2.92	-2.74	0.00	-2.82	-2.60
TCGA-G9-6361-10A-01D-1961-08_PRAD	-2.44	0.00	-4.60	-2.68	-2.56	-2.58	-2.63	-2.54	-2.60	0.00	0.00	-4.60	0.00	0.00	0.00	-2.46	-2.45
TCGA-G9-6362-10A-01D-1786-08_PRAD	-2.59	-2.60	-2.64	-4.25	-2.72	-2.74	-2.61	-2.63	-2.55	-4.55	-2.89	-2.76	0.00	0.00	0.00	-2.47	-2.53
TCGA-G9-6363-10A-01D-1786-08_PRAD	-2.54	-2.78	-2.77	-2.87	-2.70	-2.71	-2.63	-2.53	-2.71	-3.38	-2.85	0.00	-2.80	-2.74	-3.08	-4.56	-2.51
TCGA-G9-6364-10A-01D-1786-08_PRAD	-2.55	0.00	-4.51	-2.61	-2.57	-2.59	-2.60	-2.50	-2.52	0.00	0.00	0.00	0.00	-4.51	0.00	-2.47	-2.51
TCGA-G9-6365-10A-01D-1786-08_PRAD	-2.59	-2.70	-2.62	-2.84	-2.67	-2.70	-2.59	-2.42	-2.47	0.00	-4.48	0.00	0.00	0.00	0.00	-2.44	-2.56
TCGA-G9-6366-10A-01D-2115-08_PRAD	-2.51	0.00	0.00	-2.51	-2.55	-2.51	-2.51	-2.55	-2.45	0.00	0.00	-4.05	0.00	-3.87	-3.05	-2.66	-2.41
TCGA-G9-6367-10A-01D-1786-08_PRAD	-2.61	-4.23	-4.53	-2.64	-2.57	-2.55	-2.64	-2.45	-2.51	0.00	0.00	-4.23	0.00	-4.53	-3.17	-2.76	-2.56
TCGA-G9-6369-10A-01D-1961-08_PRAD	-2.45	0.00	-4.61	-2.70	-2.53	-2.56	-2.51	-2.50	-2.48	0.00	0.00	0.00	0.00	-4.61	-3.09	-2.73	-2.37
TCGA-G9-6370-10A-01D-1786-08_PRAD	-2.58	-2.71	-2.76	-2.92	-2.54	-2.62	-2.65	-2.58	-2.56	0.00	-2.89	-2.77	0.00	0.00	0.00	-2.48	-2.55
TCGA-G9-6371-10A-01D-1786-08_PRAD	-2.63	-2.74	-2.79	-2.89	-2.55	-2.64	-2.66	-2.55	-2.74	-3.47	-2.80	-2.66	0.00	-2.67	0.00	-2.74	-2.56
TCGA-G9-6373-10A-01D-1786-08_PRAD	-2.58	0.00	-4.66	-2.85	-2.58	-2.66	-2.62	-2.69	-2.71	-3.43	-2.87	0.00	-2.84	-2.77	0.00	-2.79	-2.56
TCGA-G9-6377-10A-01D-1961-08_PRAD	-2.59	-2.80	-2.76	-2.94	-2.62	-2.64	-2.66	-2.64	-2.81	-3.68	-2.76	-2.80	-2.83	-2.78	0.00	-2.80	-2.56
TCGA-G9-6378-10A-01D-1786-08_PRAD	-2.60	-2.77	-2.76	-2.92	-2.56	-2.61	-2.63	-2.64	-2.72	-3.45	-2.77	-2.76	-2.76	-2.77	0.00	-4.26	-2.62
TCGA-G9-6379-10A-01D-A31J-08_PRAD	-2.51	0.00	0.00	-2.71	-2.52	-2.51	-2.58	-2.57	-2.50	0.00	0.00	0.00	0.00	0.00	-3.01	-2.63	-2.50
TCGA-G9-6384-10A-01D-1786-08_PRAD	-2.54	-4.50	-4.50	-2.76	-2.53	-2.59	-2.60	-2.47	-2.54	0.00	0.00	0.00	0.00	0.00	-3.01	-2.70	-2.47
TCGA-G9-6385-10A-01D-1786-08_PRAD	-2.55	-2.65	-2.63	-4.56	-2.73	-2.75	-2.64	-2.64	-4.26	-3.13	-2.61	-2.63	0.00	-2.61	0.00	0.00	-2.47
TCGA-G9-6494-10A-01D-1786-08_PRAD	-2.63	-2.79	-2.80	-2.95	-2.56	-2.64	-2.71	-2.67	-2.72	-3.32	-2.81	-2.69	-4.62	-2.75	0.00	-2.82	-2.61
TCGA-G9-6496-10A-01D-1786-08_PRAD	-2.52	-4.48	-4.48	-2.56	-2.58	-2.62	-2.61	-2.45	-2.49	0.00	-4.48	0.00	0.00	-4.48	0.00	-2.50	-2.49
TCGA-G9-6498-10A-01D-A30X-08_PRAD	-2.62	0.00	0.00	-2.85	-2.61	-2.62	-2.63	-2.69	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.64	-2.54
TCGA-G9-6499-10A-01D-1961-08_PRAD	-2.52	-2.80	-2.75	-2.87	-2.73	-2.72	-2.56	-2.61	-4.64	-3.32	-2.74	0.00	-2.64	-2.53	0.00	0.00	-2.50
TCGA-G9-7510-10A-01D-2260-08_PRAD	-2.50	-2.61	-2.66	-2.80	-2.54	-2.59	-2.50	-2.54	-2.48	0.00	0.00	0.00	0.00	0.00	-2.95	-2.66	-2.35
TCGA-G9-7519-10A-01D-2260-08_PRAD	-2.51	-2.57	-2.52	-4.12	-3.95	0.00	-2.49	-2.48	-2.54	-3.34	-2.92	-2.64	0.00	-2.54	-2.98	0.00	-2.40
TCGA-G9-7521-10A-01D-2260-08_PRAD	-2.53	-2.63	-2.65	0.00	-2.52	-2.57	-2.56	-2.67	-2.52	0.00	-2.71	-2.61	-4.47	-3.99	0.00	-2.51	-2.48
TCGA-G9-7522-10A-01D-2260-08_PRAD	-2.47	0.00	0.00	-2.81	-2.50	-2.53	-2.60	-2.60	-2.62	-3.24	-2.87	0.00	-2.75	-2.65	-3.11	0.00	-2.46
TCGA-G9-7523-10A-01D-2260-08_PRAD	-2.59	-2.71	-2.72	-2.92	-2.46	-2.63	-2.61	-2.55	-2.46	0.00	-2.94	-2.70	0.00	0.00	0.00	-2.43	-2.55
TCGA-G9-7525-10A-01D-2260-08_PRAD	-2.55	0.00	-4.49	-2.51	-2.53	-2.56	-2.54	-2.50	-2.48	0.00	0.00	0.00	-4.49	-4.49	-2.97	-2.66	-2.48
TCGA-GC-A3BM-10A-01D-A22Z-08_BLCA	-2.44	-2.72	-2.65	-2.81	-2.57	-2.68	-2.46	-2.47	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.40	-2.38
TCGA-GC-A3I6-10A-01D-A20D-08_BLCA	-2.49	-4.43	0.00	-2.49	-2.44	-2.49	-2.54	-2.60	-2.47	0.00	0.00	-4.43	0.00	-4.43	0.00	-2.52	-2.41
TCGA-GC-A3OO-10C-01D-A22Z-08_BLCA	-2.48	-2.66	-2.74	-2.89	-2.42	-2.54	-2.51	-2.51	-2.46	0.00	-2.98	-2.69	0.00	0.00	-3.23	-2.80	-2.42
TCGA-GC-A3RB-10A-01D-A21Z-08_BLCA	-2.47	-4.14	0.00	-2.52	-2.47	-2.49	-2.53	-2.56	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.37	-2.37
TCGA-GC-A3RC-10B-01D-A22Z-08_BLCA	-2.52	0.00	0.00	-2.71	-2.50	-2.51	-2.55	-2.57	-2.71	-3.29	-2.91	0.00	-2.78	-2.64	0.00	-2.70	-2.43
TCGA-GC-A3RD-10B-01D-A22Z-08_BLCA	-2.47	-2.69	-2.68	-2.91	-2.65	-2.66	-2.57	-2.58	-2.62	-3.44	-2.96	0.00	-2.73	-2.66	0.00	-2.79	-2.38
TCGA-GC-A3WC-10A-01D-A22Z-08_BLCA	-2.51	-2.77	-2.79	-2.89	-2.44	-2.52	-2.54	-2.59	-2.51	0.00	-2.99	-2.78	0.00	0.00	0.00	-2.51	-2.45
TCGA-GC-A3YS-10A-01D-A23K-08_BLCA	-2.51	-4.76	-4.76	-2.81	-2.44	-2.51	-2.57	-2.57	-2.78	-3.29	-2.79	-2.76	-2.82	-2.74	0.00	-2.86	-2.54
TCGA-GC-A4ZW-10A-01D-A26K-08_BLCA	-2.36	-4.11	-3.71	-2.54	-2.45	-2.49	-2.45	-2.61	-2.50	0.00	-3.81	-3.71	0.00	-3.81	0.00	-2.51	-2.41
TCGA-GC-A6I1-10A-01D-A31J-08_BLCA	-2.58	0.00	-4.57	-2.76	-2.51	-2.54	-2.55	-2.60	-2.63	-3.32	-2.94	0.00	-2.79	-2.67	0.00	-2.80	-2.46
TCGA-GC-A6I3-10A-01D-A31J-08_BLCA	-2.37	-2.42	-2.54	0.00	0.00	0.00	0.00	-4.42	0.00	0.00	-2.56	0.00	-2.43	-2.40	0.00	0.00	-2.39
TCGA-GD-A2C5-10A-01D-A17V-08_BLCA	-2.47	0.00	-4.41	-2.63	-2.51	-2.60	-2.54	-2.58	-2.80	-3.36	-2.97	0.00	-2.80	-2.72	0.00	-2.78	-2.52
TCGA-GD-A3OP-10A-01D-A21Z-08_BLCA	-2.51	-2.70	-2.67	-2.77	-2.61	-2.60	-2.57	-2.46	-2.43	0.00	-4.02	0.00	0.00	-4.49	-3.05	-2.67	-2.48
TCGA-GD-A3OQ-10A-01D-A21Z-08_BLCA	-2.54	-4.54	0.00	-2.82	-2.58	-2.57	-2.57	-2.63	-2.70	-3.34	-2.86	-4.54	-2.82	-2.59	0.00	-2.70	-2.49
TCGA-GD-A3OS-10A-01D-A21Z-08_BLCA	-2.52	0.00	0.00	-2.58	-2.50	-2.54	-2.54	-2.47	-2.44	0.00	0.00	0.00	0.00	-4.19	0.00	-2.32	-2.46
TCGA-GD-A6C6-10A-01D-A31J-08_BLCA	-2.54	-2.72	-2.69	-2.92	-2.65	-2.74	-2.58	-2.57	-2.68	-3.33	-2.94	0.00	-2.76	-2.69	-3.13	0.00	-2.57

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-GD-A76B-10A-01D-A329-08_BLCA	-2.60	-2.74	-2.76	-2.98	-2.47	-2.58	-2.64	-2.63	-2.68	-3.59	-2.82	-2.79	-2.96	-2.65	-3.24	0.00	-2.55
TCGA-GE-A2C6-10A-01D-A16O-08_THCA	-2.58	-2.78	-2.75	-2.95	-2.51	-2.68	-2.64	-2.61	-2.63	0.00	-2.95	-2.73	0.00	0.00	-3.07	-2.76	-2.60
TCGA-GF-A2C7-10A-01D-A199-08_SKCM	-2.43	-4.54	-4.06	-2.56	-2.45	-2.55	-2.51	-2.48	-2.50	-4.54	0.00	-4.54	0.00	-4.54	0.00	-2.41	-2.38
TCGA-GF-A3OT-10A-01D-A23B-08_SKCM	-2.58	-2.76	-2.75	-2.85	-2.67	-2.71	-2.62	-2.49	-2.60	0.00	0.00	-4.55	0.00	-4.55	-3.06	-2.72	-2.55
TCGA-GF-A4EO-10A-01D-A24R-08_SKCM	-2.60	-2.67	-2.67	-2.85	-2.67	-2.67	-2.65	-2.51	-2.52	0.00	-4.19	-4.02	-4.49	0.00	-3.00	-2.69	-2.52
TCGA-GF-A6C8-10A-01D-A30X-08_SKCM	-2.68	0.00	-4.29	-2.70	-2.57	-2.71	-2.73	-2.68	-2.77	-3.55	-3.11	0.00	-2.84	-2.79	-3.25	0.00	-2.57
TCGA-GF-A6C9-10A-01D-A30X-08_SKCM	-2.45	-2.60	-2.63	-4.22	0.00	-4.52	-2.65	-2.58	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.53
TCGA-GF-A769-10A-01D-A32N-08_SKCM	-2.57	-2.57	-2.55	0.00	0.00	0.00	-2.55	-2.56	-2.49	0.00	0.00	0.00	0.00	0.00	-2.89	0.00	-2.52
TCGA-GJ-A6C0-10A-01D-A30V-10_LIHC	-2.43	-4.08	-4.08	-2.51	-2.40	-2.39	-2.35	-2.38	-2.27	0.00	0.00	0.00	0.00	0.00	-3.08	-2.60	-2.35
TCGA-GL-6846-10A-01D-1962-08_KIRP	-2.59	-2.78	-2.77	-2.99	-2.57	-2.60	-2.64	-2.55	-2.66	0.00	-2.90	-2.77	0.00	0.00	0.00	-2.55	-2.58
TCGA-GL-7773-10A-01D-2136-08_KIRP	-2.53	-2.64	-2.59	-3.67	-2.64	-2.67	-2.59	-2.58	-2.52	-4.51	-2.80	-2.67	-3.91	-4.21	0.00	-2.54	-2.48
TCGA-GL-7966-10A-01D-2201-08_KIRP	-2.51	0.00	-4.20	-2.78	-2.54	-2.55	-2.52	-2.43	-2.45	0.00	0.00	0.00	0.00	-4.50	0.00	-2.42	-2.50
TCGA-GL-8500-10A-01D-2396-08_KIRP	-2.67	-2.77	-2.74	-2.90	-2.50	-2.65	-2.67	-2.61	-2.56	-4.59	-2.93	-2.76	-4.11	-3.81	0.00	-2.48	-2.62
TCGA-GL-A4EM-10A-01D-A25F-10_KIRP	-2.36	0.00	0.00	-2.53	-2.36	-2.29	-2.30	-2.32	-2.30	0.00	0.00	0.00	0.00	-4.33	0.00	-2.30	-2.26
TCGA-GL-A59R-10A-01D-A26P-10_KIRP	-2.39	0.00	-4.33	-2.57	-2.44	-2.40	-2.37	-2.31	-2.61	-3.43	-2.81	0.00	-2.67	-2.50	0.00	-2.67	-2.36
TCGA-GL-A59T-10A-01D-A28G-10_KIRP	-2.30	-2.52	-2.52	-2.79	-2.56	-2.43	-2.31	-2.24	-2.32	0.00	0.00	0.00	0.00	0.00	-2.87	-2.47	-2.38
TCGA-GM-A2DA-10C-01D-A18P-09_BRCA	-2.85	-2.57	-2.56	-4.59	0.00	-4.59	-2.53	-2.60	-2.49	0.00	0.00	0.00	0.00	0.00	-2.83	0.00	-2.63
TCGA-GM-A2DB-10C-01D-A18P-09_BRCA	-2.95	-2.74	-2.82	-3.11	-2.78	-2.81	-2.57	-2.60	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.72
TCGA-GM-A2DC-10C-01D-A18P-09_BRCA	-2.88	0.00	0.00	-2.72	-2.58	-2.57	-2.52	-2.55	-2.54	0.00	0.00	-4.45	0.00	0.00	-3.04	-2.80	-2.65
TCGA-GM-A2DD-10C-01D-A17W-09_BRCA	-3.03	-2.89	-2.91	-3.17	-2.65	-2.72	-2.77	-2.74	-2.74	0.00	-3.05	-2.85	0.00	0.00	-3.19	-2.97	-2.87
TCGA-GM-A2DF-10C-01D-A17W-09_BRCA	-2.89	0.00	0.00	-2.79	-2.54	-2.65	-2.58	-2.71	-2.63	0.00	0.00	0.00	0.00	0.00	-3.00	-2.85	-2.74
TCGA-GM-A2DH-10C-01D-A17W-09_BRCA	-2.91	-4.50	-4.81	-3.01	-2.72	-2.70	-2.64	-2.76	-2.79	-3.41	-2.95	-4.81	-2.85	-2.81	0.00	-2.89	-2.83
TCGA-GM-A2DK-10C-01D-A17W-09_BRCA	-2.92	0.00	0.00	-2.78	-2.62	-2.62	-2.57	-2.61	-2.57	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.67
TCGA-GM-A2DL-10C-01D-A18P-09_BRCA	-2.98	0.00	0.00	-2.81	-2.68	-2.63	-2.56	-2.64	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.65	-2.79
TCGA-GM-A2DM-10C-01D-A17W-09_BRCA	-2.99	-2.83	-2.83	-3.14	-2.61	-2.74	-2.69	-2.72	-2.88	-3.35	-2.72	-2.85	-2.82	-2.87	-3.24	-4.43	-2.87
TCGA-GM-A2DN-10C-01D-A17W-09_BRCA	-2.96	-2.72	-2.78	-3.08	-2.82	-2.80	-2.65	-2.61	-2.65	0.00	0.00	0.00	0.00	0.00	-3.16	-2.90	-2.76
TCGA-GM-A2DO-10D-01D-A18P-09_BRCA	-3.08	0.00	-2.84	-3.11	-2.60	-2.69	-2.62	-2.74	-2.68	-4.26	-2.87	0.00	-2.85	-4.73	-2.91	0.00	-2.77
TCGA-GM-A3NW-10A-01D-A22A-09_BRCA	-2.75	-2.65	-2.60	-3.26	-2.66	-2.68	-2.42	-2.55	-2.43	0.00	-4.16	0.00	-4.47	0.00	-2.96	-2.76	-2.55
TCGA-GM-A3NY-10A-01D-A21Q-09_BRCA	-2.71	-4.55	-4.07	-3.21	-2.54	-2.57	-2.50	-2.54	-2.33	0.00	-4.55	0.00	-3.95	-4.55	-3.06	-2.84	-2.56
TCGA-GM-A3XG-10A-01D-A243-09_BRCA	-2.70	-3.64	-4.12	-3.04	-2.44	-2.58	-2.45	-2.54	-2.33	0.00	0.00	-4.12	-4.12	-4.42	-2.97	-2.82	-2.61
TCGA-GM-A3XL-10A-01D-A22X-09_BRCA	-2.68	-2.67	-2.61	-3.18	-2.64	-2.69	-2.40	-2.55	-2.35	-4.35	0.00	0.00	0.00	-3.88	-2.67	-3.88	-2.53
TCGA-GM-A3XN-10A-01D-A22X-09_BRCA	-2.84	-2.77	-2.74	-3.20	-2.55	-2.61	-2.56	-2.65	-2.49	-4.54	-2.91	-2.74	-3.84	-4.24	0.00	-2.64	-2.69
TCGA-GM-A4E0-10A-01D-A25Q-09_BRCA	-2.89	-2.64	-2.66	-4.08	-3.64	-3.54	-2.64	-2.56	-2.67	-3.45	-2.94	-3.91	-2.83	-2.79	0.00	-2.85	-2.66
TCGA-GM-A5PV-10A-01D-A28E-09_BRCA	-2.70	-4.38	-4.08	-3.08	-2.51	-2.49	-2.47	-2.53	-2.41	0.00	-4.38	0.00	0.00	0.00	0.00	-2.54	-2.53
TCGA-GM-A5PX-10A-01D-A28E-09_BRCA	-2.88	-2.62	-2.62	0.00	-2.63	-2.64	-2.60	-2.60	-2.74	-3.45	-2.64	-2.63	0.00	-2.77	0.00	-2.92	-2.72
TCGA-GN-A261-10A-01D-A199-08_SKCM	-2.62	-2.71	-2.76	-2.88	-2.51	-2.66	-2.62	-2.55	-2.51	0.00	-2.90	-2.68	0.00	-4.51	0.00	-2.49	-2.58
TCGA-GN-A262-10A-01D-A198-08_SKCM	-2.48	-2.57	-2.52	-4.48	-4.48	-4.48	-2.58	-2.44	-2.61	-3.31	-2.89	0.00	-2.73	-2.62	-3.03	0.00	-2.49
TCGA-GN-A263-10A-01D-A198-08_SKCM	-2.55	-2.81	-2.64	-2.90	-2.78	-2.81	-2.65	-2.47	-2.78	-3.13	-2.69	0.00	-2.74	-2.74	0.00	-2.81	-2.54
TCGA-GN-A264-10A-01D-A198-08_SKCM	-2.36	0.00	0.00	-2.53	-2.40	-2.56	-2.51	-2.69	-2.64	0.00	0.00	0.00	0.00	-2.53	0.00	-2.61	-2.48
TCGA-GN-A265-10A-01D-A199-08_SKCM	-2.55	0.00	0.00	-2.81	-2.55	-2.55	-2.55	-2.51	-2.59	0.00	0.00	-4.56	0.00	-4.56	0.00	-2.50	-2.44
TCGA-GN-A266-10A-01D-A199-08_SKCM	-2.51	-2.75	-2.79	-2.95	-2.56	-2.62	-2.69	-2.49	-2.56	0.00	-2.82	-2.80	0.00	0.00	0.00	-2.44	-2.57
TCGA-GN-A267-10A-01D-A198-08_SKCM	-2.49	-4.50	0.00	-2.57	-2.53	-2.60	-2.60	-2.53	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.45
TCGA-GN-A268-10A-01D-A198-08_SKCM	-2.48	-2.71	-2.82	-2.87	-2.66	-2.66	-2.59	-2.55	-2.76	-3.62	-2.88	0.00	-2.85	-2.72	-3.00	0.00	-2.42
TCGA-GN-A269-10A-01D-A19A-08_SKCM	-2.45	0.00	0.00	-2.61	-2.45	-2.55	-2.50	-2.52	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.40
TCGA-GN-A26A-10A-01D-A19A-08_SKCM	-2.29	-2.70	-2.70	-2.77	-2.67	-2.69	-2.53	-2.46	-2.43	0.00	0.00	0.00	0.00	0.00	-3.18	-2.71	-2.40
TCGA-GN-A26C-10A-01D-A19A-08_SKCM	-2.36	-2.79	-2.68	-2.72	-2.67	-2.66	-2.48	-2.57	-2.45	0.00	-4.11	0.00	0.00	0.00	-3.20	-2.78	-2.36
TCGA-GN-A26D-10A-01D-A19A-08_SKCM	-2.49	0.00	0.00	-2.71	-2.50	-2.52	-2.57	-2.50	-2.48	0.00	0.00	0.00	0.00	-4.12	0.00	-2.44	-2.47
TCGA-GN-A4U3-10F-01D-A32N-08_SKCM	-2.61	0.00	0.00	-2.63	-2.54	-2.67	-2.62	-2.61	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.64	-2.58
TCGA-GN-A4U4-10B-01D-A32N-08_SKCM	-2.60	0.00	0.00	-2.98	-2.69	-2.69	-2.66	-2.68	-2.72	-3.40	-2.93	0.00	-2.83	-2.76	0.00	-2.78	-2.56
TCGA-GN-A4U5-10B-01D-A32N-08_SKCM	-2.63	0.00	0.00	-2.84	-2.57	-2.56	-2.64	-2.68	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.51
TCGA-GN-A4U7-10B-01D-A32N-08_SKCM	-2.59	-2.59	-2.64	-4.59	-2.69	-2.73	-2.63	-2.63	-2.60	0.00	-2.91	-2.72	0.00	-4.59	-3.04	0.00	-2.54
TCGA-GN-A4U8-10B-01D-A32N-08_SKCM	-2.55	0.00	-4.21	-2.74	-2.49	-2.58	-2.57	-2.52	-2.47	0.00	0.00	0.00	0.00	-4.51	-3.10	-2.72	-2.48
TCGA-GN-A4U9-10B-01D-A32N-08_SKCM	-2.67	-2.83	-2.78	-3.05	-2.61	-2.69	-2.76	-2.75	-2.78	-3.50	-2.74	-2.79	-2.86	-2.77	0.00	-2.82	-2.62
TCGA-GR-A4D4-10A-01D-A31X-10_DLBC	-2.39	0.00	0.00	-2.48	-2.35	-2.32	-2.31	-2.38	-2.34	0.00	0.00	0.00	0.00	-4.08	0.00	-4.08	-2.34
TCGA-GR-A4D5-10A-01D-A31X-10_DLBC	-2.52	0.00	-4.12	-2.63	-2.37	-2.36	-2.34	-2.43	-2.59	-3.52	-2.70	0.00	-2.56	-2.64	0.00	-2.60	-2.42
TCGA-GR-A4D6-10A-01D-A31X-10_DLBC	-2.37	-4.11	0.00	-2.60	-2.58	-2.34	-2.38	-2.42	-2.48	-3.41	-2.83	0.00	-2.77	-2.55	0.00	-4.11	-2.35
TCGA-GR-A4D9-10A-01D-A31X-10_DLBC	-2.33	-2.48	-2.64	-2.71	-2.71	-2.56	-2.29	-2.33	-2.26	0.00	0.00	0.00	0.00	0.00	0.00	-2.37	-2.33
TCGA-GU-A42P-10A-01D-A23U-08_BLCA	-2.52	-3.94	-4.24	-2.75	-2.50	-2.67	-2.64	-2.68	-2.73	-3.31	-2.68	-2.74	-2.81	-2.75	0.00	-2.76	-2.61
TCGA-GU-A42Q-10A-01D-A23U-08_BLCA	-2.51	-2.49	-2.50	-3.75	-3.75	-3.35	-2.54	-2.56	-2.59	-3.12	-2.94	-4.35	-2.67	-2.61	0.00	-2.81	-2.50
TCGA-GU-A42R-10A-01D-A23K-08_BLCA	-2.53	-3.73	-3.93	-2.75	-2.71	-2.73	-2.72	-2.57	-2.75	-3.33	-2.93	0.00	-2.79	-2.78	-3.11	-3.93	-2.65
TCGA-GU-A762-10A-01D-A339-08_BLCA	-2.41	0.00	0.00	-2.82	-2.47	-2.51	-2.56	-2.55	-2.69	-3.31	-2.95	0.00	-2.70	-2.64	0.00	-2.74	-2.44
TCGA-GU-A763-10A-01D-A329-08_BLCA	-2.43	-2.77	-2.71	-2.72	-2.55	-2.59	-2.46	-2.47	-2.42	0.00	0.00	0.00	0.00	0.00	-3.02	-2.73	-2.39
TCGA-GU-A766-10A-01D-A329-08_BLCA	-2.42	0.00	0.00	-2.58	-2.46	-2.48	-2.48	-2.63	-2.50	0.00	0.00	-4.49	-4.49	0.00	-2.94	0.00	-2.41
TCGA-GU-A767-10A-01D-A329-08_BLCA	-2.50	-2.66	-2.64	-2.77	-2.64	-2.60	-2.49	-2.61	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.60	-2.40
TCGA-GV-A3JV-10B-01D-A21Z-08_BLCA	-2.51	0.00	0.00	-2.66	-2.48	-2.48	-2.48	-2.58	-2.56	0.00	-4.48	0.00	0.00	-4.48	0.00	-2.54	-2.40
TCGA-GV-A3JW-10A-01D-A20D-08_BLCA	-2.60	-2.66	-2.61	-4.54	-2.68	-2.71	-2.61	-2.53	-2.67	-3.26	-2.73	-2.59	0.00	-2.62	0.00	-2.79	-2.54
TCGA-GV-A3JX-10A-01D-A20D-08_BLCA	-2.51	-2.71	-2.69	-2.84	-2.57	-2.64	-2.52	-2.41	-2.42	0.00	-4.17	0.00	0.00	0.00	-2.95	-2.62	-2.39
TCGA-GV-A3JZ-10A-01D-A21A-08_BLCA	-2.47	0.00	0.00	-2.72	-2.44	-2.50	-2.55	-2.56	-2.42	0.00	0.00	0.00	0.00	-4.40	0.00	-2.36	-2.46
TCGA-GV-A3QF-10A-01D-A22Z-08_BLCA	-2.47	-4.60	-4.30	-2.58	-2.49	-2.46	-2.48	-2.46	-2.44	0.00	0.00	-4.60	0.00	0.00	0.00	-2.52	-2.38
TCGA-GV-A3QG-10A-01D-A21Z-08_BLCA	-2.52	-2.63	-2.65	-2.76	-2.54	-2.61	-2.57	-2.48	-2.51	0.00	0.00	0.00	0.00	-4.50	0.00	-2.50	-2.48
TCGA-GV-A3QH-10A-01D-A21Z-08_BLCA	-2.46	0.00	-4.43	-2.69	-2.50	-2.48	-2.50	-2.48	-2.41	0.00	0.00	0.00	0.00	0.00	-2.91	-2.65	-2.35
TCGA-GV-A3QI-10A-01D-A21Z-08_BLCA	-2.56	-4.56	-4.56	-2.77	-2.55	-2.56	-2.63	-2.64	-2.65	-3.26	-2.86	0.00	-2.76	-2.68	0.00	-2.73	-2.47
TCGA-GV-A3QK-10A-01D-A23K-08_BLCA	-2.56	-2.65	-2.61	-2.81	-2.65	-2.63	-2.54	-2.44	-2.55	0.00	-4.47	0.00	0.00	-4.47	-2.90	-4.00	-2.51
TCGA-GV-A40E-10A-01D-A23K-08_BLCA	-2.43	-2.65	-2.62	-2.83	-2.60	-2.58	-2.68	-2.72	-2.69	0.00	-2.81	0.00	-2.72	-2.59	0.00	-2.68	-2.36
TCGA-GV-A40G-10A-01D-A23K-08_BLCA	-2.52	-4.23	-3.63	-2.58	-2.58	-2.57	-2.59	-2.49	-2.63	0.00	-4.23	0.00	-3.76	-3.93	0.00	-2.41	-2.50
TCGA-GV-A6ZA-10A-01D-A339-08_BLCA	-2.49	-2.74	-2.68	-2.86	-2.80	-2.73	-2.60	-2.58	-2.67	-3.41	-2.95	0.00	-2.72	-2.63	-3.25	0.00	-2.46
TCGA-H2-A26U-10A-01D-A16O-08_THCA	-2.44	-2.72	-2.61	-2.82	-2.63	-2.72	-2.56	-2.50	-2.48	0.00	0.00	0.00	0.00	-4.12	-3.04	-2.74	-2.42
TCGA-H2-A2K9-10A-01D-A17V-08_THCA	-2.55	-2.70	-2.66	-2.84	-2.66	-2.72	-2.58	-2.53	-2.54	0.00	0.00	0.00	-4.61	-4.31	0.00	-2.46	-2.49
TCGA-H2-A3RH-10A-01D-A21Z-08_THCA	-2.36	0.00	0.00	-2.70	-2.47	-2.43	-2.51	-2.55	-2.43	0.00	-4.14	-3.97	0.00	-4.44	0.00	-2.53	-2.42
TCGA-H2-A3RI-10A-01D-A21Z-08_THCA	-2.54	-2.64	-2.62	-2.76	-2.63	-2.58	-2.67	-2.69	-2.62	0.00	-2.86	0.00	-2.74	-2.61	0.00	-2.70	-2.43
TCGA-H2-A421-10A-01D-A23K-08_THCA	-2.57	-4.24	-3.94	-2.72	-2.54	-2.56	-2.61	-2.54	-2.50	-4.54	-4.54	0.00	-4.06	-3.43	-3.04	-2.78	-2.56
TCGA-H2-A422-10A-01D-A23K-08_THCA	-2.31	-2.69	-2.65	-2.72	-2.58	-2.55	-2.45	-2.46	-2.38	0.00	0.00	0.00	0.00	0.00	-3.02	-2.72	-2.33
TCGA-H4-A2HO-10A-01D-A17V-08_BLCA	-2.54	-2.58	-2.57	-4.10	-4.10	-3.80	-2.60	-2.46	-2.48	-4.58	-3.98	-3.80	-4.10	-3.98	-3.05	-2.65	-2.47
TCGA-H4-A2HQ-10A-01D-A17V-08_BLCA	-2.56	-2.74	-2.73	-2.91	-2.69	-2.69	-2.63	-2.51	-2.49	0.00	0.00	-4.64	0.00	0.00	0.00	-2.48	-2.54
TCGA-H5-A2HR-10A-01D-A17W-09_UCEC	-2.85	-2.70	-2.70	-3.40	-2.52	-2.55	-2.51	-2.54	-2.36	0.00	-2.83	0.00	-2.68	0.00	0.00	-2.83	-2.81
TCGA-H6-8124-10A-01D-2396-08_PAAD	-2.52	-2.63	-2.60	-4.15	-4.45	-4.15	-2.62	-2.54	-2.63	-3.31	-2.73	0.00	-2.74	-2.65	0.00	-2.60	-2.57
TCGA-H6-A45N-10A-01D-A26I-08_PAAD	-2.43	0.00	0.00	-2.62	-2.42	-2.44	-2.44	-2.56	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.34
TCGA-H7-7774-10A-01D-2078-08_HNSC	-2.50	-2.61	-2.63	-2.76	-2.60	-2.61	-2.52	-2.52	-2.44	0.00	-4.37	-3.59	0.00	-4.37	-2.88	0.00	-2.45
TCGA-H7-8501-10A-01D-2394-08_HNSC	-2.62	-2.78	-2.73	-2.92	-2.54	-2.64	-2.65	-2.58	-2.55	0.00	-2.82	-2.79	0.00	0.00	0.00	-2.49	-2.59
TCGA-H7-8502-10A-01D-2394-08_HNSC	-2.64	-2.81	-2.77	-2.94	-2.57	-2.63	-2.69	-2.53	-2.54	0.00	-2.84	-2.77	0.00	0.00	0.00	-2.54	-2.59
TCGA-H7-A6C4-10A-01D-A30H-08_HNSC	-2.50	-2.51	-2.52	0.00	-2.70	-2.67	-2.50	-2.54	-2.39	0.00	-2.92	-2.68	0.00	-4.65	0.00	-2.52	-2.38
TCGA-H7-A6C5-10A-01D-A30H-08_HNSC	-2.56	-2.62	-2.57	0.00	-2.56	-2.57	-2.58	-2.61	-2.70	-3.48	-2.66	-2.49	0.00	-2.69	0.00	-2.90	-2.49
TCGA-H8-A6C1-10A-01D-A32N-08_PAAD	-2.46	-2.64	-2.69	-2.81	-2.61	-2.65	-2.59	-2.53	-2.43	0.00	0.00	-4.44	0.00	0.00	0.00	-2.53	-2.45
TCGA-H9-7775-10A-01D-2115-08_PRAD	-2.47	0.00	-4.41	-2.65	-2.43	-2.45	-2.52	-2.49	-2.48	-4.41	0.00	0.00	0.00	0.00	0.00	-2.40	-2.40
TCGA-H9-A6BX-10A-01D-A30X-08_PRAD	-2.58	0.00	-4.51	-2.74	-2.55	-2.59	-2.57	-2.60	-2.63	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.56
TCGA-H9-A6BY-10A-01D-A30H-08_PRAD	-2.43	-2.63	-2.61	-2.79	-2.58	-2.60	-2.47	-2.49	-2.41	0.00	0.00	0.00	0.00	0.00	-3.00	-2.66	-2.40

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-HB-A2OT-10A-01D-A21Q-09_SARC	-2.79	-2.80	-2.82	-3.31	-2.61	-2.58	-2.58	-2.56	-2.46	0.00	-2.83	-2.87	-4.09	0.00	-3.01	-2.81	-2.65
TCGA-HB-A3L4-10A-01D-A21Q-09_SARC	-2.71	-3.92	-4.40	-2.89	-2.48	-2.50	-2.48	-2.43	-2.41	-4.40	0.00	-4.10	0.00	-3.79	0.00	-2.48	-2.52
TCGA-HB-A3YV-10A-01D-A24N-09_SARC	-2.82	-2.71	-2.72	-3.42	-2.47	-2.58	-2.49	-2.55	-2.40	0.00	-3.12	-2.78	0.00	-4.42	0.00	-2.57	-2.57
TCGA-HB-A43Z-10A-01D-A24N-09_SARC	-2.68	0.00	-4.03	-2.96	-2.49	-2.50	-2.50	-2.56	-2.41	0.00	-4.20	-4.50	0.00	0.00	0.00	-2.55	-2.56
TCGA-HB-A5W3-10A-01D-A29N-09_SARC	-2.83	-3.98	-3.98	-3.01	-2.60	-2.58	-2.55	-2.56	-2.66	-3.50	-2.85	-3.98	-2.78	-2.76	0.00	-2.77	-2.60
TCGA-HC-7075-10A-01D-1961-08_PRAD	-2.55	-4.58	0.00	-2.78	-2.53	-2.57	-2.60	-2.53	-2.54	0.00	0.00	0.00	0.00	-4.58	-3.09	-2.80	-2.50
TCGA-HC-7077-10A-01D-1961-08_PRAD	-2.45	-2.49	-2.45	-4.07	0.00	-4.55	-2.61	-2.70	-2.56	0.00	-2.80	0.00	-2.71	-2.61	-3.15	-4.55	-2.36
TCGA-HC-7078-10A-01D-2115-08_PRAD	-2.40	-2.66	-2.66	-2.81	-2.63	-2.70	-2.52	-2.65	-2.73	-3.27	-2.92	0.00	-2.82	-2.62	0.00	-2.71	-2.43
TCGA-HC-7079-10A-01D-1961-08_PRAD	-2.48	0.00	-4.58	-2.70	-2.48	-2.53	-2.53	-2.57	-2.50	0.00	0.00	0.00	0.00	-4.58	0.00	-2.55	-2.40
TCGA-HC-7080-10A-01D-1961-08_PRAD	-2.44	0.00	-4.30	-2.65	-2.48	-2.49	-2.53	-2.55	-2.54	0.00	-4.60	0.00	0.00	-4.60	0.00	-2.48	-2.40
TCGA-HC-7081-10A-01D-1962-08_PRAD	-2.49	0.00	0.00	-2.59	-2.55	-2.58	-2.63	-2.52	-2.50	0.00	0.00	0.00	0.00	0.00	-3.09	-2.74	-2.44
TCGA-HC-7209-10A-01D-2115-08_PRAD	-2.51	0.00	0.00	-2.65	-2.48	-2.50	-2.49	-2.46	-2.50	0.00	0.00	0.00	0.00	-4.42	0.00	-2.36	-2.42
TCGA-HC-7210-10A-01D-2115-08_PRAD	-2.59	-2.72	-2.71	-2.85	-2.67	-2.71	-2.64	-2.52	-2.57	0.00	0.00	-4.56	-4.56	-4.56	-2.99	-2.64	-2.52
TCGA-HC-7212-10A-01D-2115-08_PRAD	-2.47	0.00	0.00	-2.59	-2.50	-2.50	-2.55	-2.50	-2.49	0.00	-4.44	-4.44	0.00	-4.44	0.00	-2.52	-2.44
TCGA-HC-7213-10A-01D-2115-08_PRAD	-2.46	-2.67	-2.64	-2.80	-2.58	-2.62	-2.53	-2.38	-2.41	0.00	0.00	0.00	0.00	-4.46	-3.06	-2.63	-2.43
TCGA-HC-7230-10A-01D-2115-08_PRAD	-2.41	-4.38	-4.38	-2.53	-2.51	-2.48	-2.48	-2.49	-2.43	0.00	-4.08	0.00	0.00	-4.38	-3.12	-2.68	-2.37
TCGA-HC-7231-10A-01D-2115-08_PRAD	-2.53	0.00	0.00	-2.72	-2.51	-2.55	-2.61	-2.59	-2.63	-3.34	-2.90	0.00	-2.85	-2.66	-2.99	-4.54	-2.44
TCGA-HC-7232-10A-01D-2115-08_PRAD	-2.40	-2.69	-2.74	-2.83	-2.69	-2.70	-2.55	-2.51	-2.65	-3.25	-2.84	0.00	-2.79	-2.68	-3.08	0.00	-2.52
TCGA-HC-7233-10A-01D-2115-08_PRAD	-2.52	0.00	0.00	-2.87	-2.56	-2.55	-2.60	-2.55	-2.65	-3.18	-2.86	-2.74	0.00	-2.67	0.00	-2.70	-2.44
TCGA-HC-7736-10A-01D-2115-08_PRAD	-2.69	-2.81	-2.79	-3.00	-2.56	-2.73	-2.68	-2.58	-2.80	-3.18	-2.75	-2.86	-2.84	-2.78	-3.14	-4.21	-2.66
TCGA-HC-7738-10A-01D-2115-08_PRAD	-2.59	-2.84	-2.81	-2.79	-2.65	-2.65	-2.64	-2.61	-2.49	-4.52	-4.52	0.00	0.00	0.00	0.00	-2.65	-2.53
TCGA-HC-7740-10A-01D-2115-08_PRAD	-2.62	-2.63	-2.58	0.00	-2.69	-2.74	-2.75	-2.74	-4.08	-3.22	-2.62	-2.76	-2.67	-2.56	0.00	0.00	-2.56
TCGA-HC-7742-10A-01D-2115-08_PRAD	-2.57	-2.76	-2.71	-2.90	-2.49	-2.63	-2.67	-2.71	-2.81	-3.42	-2.72	-2.58	0.00	-2.69	0.00	-2.84	-2.53
TCGA-HC-7744-10A-01D-2115-08_PRAD	-2.51	-4.52	-4.05	-2.70	-2.53	-2.54	-2.59	-2.63	-2.72	-3.32	-2.81	0.00	-2.80	-2.66	0.00	-2.71	-2.46
TCGA-HC-7745-10A-01D-2115-08_PRAD	-2.45	0.00	0.00	-2.56	-2.37	-2.47	-2.55	-2.62	-2.39	0.00	0.00	0.00	0.00	-4.17	-3.10	-2.68	-2.41
TCGA-HC-7747-10A-01D-2115-08_PRAD	-2.33	0.00	-4.53	-2.69	-2.44	-2.59	-2.54	-2.56	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.47
TCGA-HC-7748-10A-01D-2115-08_PRAD	-2.58	-3.97	-4.09	-2.82	-2.61	-2.59	-2.63	-2.49	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.43	-2.50
TCGA-HC-7749-10A-01D-2115-08_PRAD	-2.47	-4.48	0.00	-2.54	-2.53	-2.55	-2.55	-2.60	-2.64	-3.25	-2.80	0.00	-2.78	-2.59	-3.02	0.00	-2.45
TCGA-HC-7750-10A-01D-2115-08_PRAD	-2.51	-4.47	0.00	-2.69	-2.46	-2.51	-2.61	-2.69	-2.63	-3.22	-2.80	0.00	-2.77	-2.63	0.00	-2.74	-2.43
TCGA-HC-7752-10A-01D-2115-08_PRAD	-2.44	0.00	0.00	-2.66	-2.47	-2.47	-2.52	-2.45	-2.45	0.00	0.00	0.00	0.00	-4.47	-3.02	-2.66	-2.44
TCGA-HC-7817-10A-01D-A29Q-08_PRAD	-2.52	-2.69	-2.69	-2.97	-2.45	-2.57	-2.58	-2.53	-2.56	0.00	-2.89	-2.75	0.00	0.00	-3.06	-2.78	-2.45
TCGA-HC-7818-10A-01D-2115-08_PRAD	-2.47	0.00	0.00	-2.81	-2.57	-2.58	-2.56	-2.61	-2.64	-3.23	-2.90	0.00	-2.77	-2.64	0.00	-2.68	-2.45
TCGA-HC-7819-10A-01D-2115-08_PRAD	-2.47	-2.66	-2.71	-2.76	-2.61	-2.63	-2.55	-2.63	-2.51	0.00	0.00	0.00	0.00	-4.41	0.00	-2.54	-2.43
TCGA-HC-7820-10A-01D-2115-08_PRAD	-2.48	0.00	0.00	-2.68	-2.47	-2.55	-2.48	-2.53	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.44
TCGA-HC-7821-10A-01D-2115-08_PRAD	-2.50	0.00	0.00	-2.68	-2.54	-2.55	-2.72	-2.55	-2.64	-3.39	-2.85	0.00	-2.71	-2.68	0.00	-2.65	-2.49
TCGA-HC-8213-10A-01D-A29Q-08_PRAD	-2.43	0.00	-4.57	-2.71	-2.45	-2.44	-2.50	-2.48	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.44	-2.42
TCGA-HC-8216-10A-01D-A29Q-08_PRAD	-2.39	0.00	0.00	-2.55	-2.46	-2.51	-2.54	-2.55	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.38
TCGA-HC-8256-10A-01D-2260-08_PRAD	-2.57	-2.60	-2.66	0.00	-2.68	-2.66	-2.63	-2.67	-2.65	-3.32	-2.76	-2.65	-2.83	-2.63	0.00	-2.69	-2.38
TCGA-HC-8257-10A-01D-2260-08_PRAD	-2.63	-2.73	-2.73	-2.87	-2.50	-2.64	-2.65	-2.57	-2.62	0.00	-2.90	-2.68	0.00	-4.60	0.00	-2.46	-2.59
TCGA-HC-8258-10A-01D-2260-08_PRAD	-2.52	-2.71	-2.63	-2.81	-2.53	-2.56	-2.52	-2.47	-2.39	0.00	0.00	0.00	0.00	-4.40	-2.91	-2.58	-2.43
TCGA-HC-8259-10A-01D-2260-08_PRAD	-2.56	-2.61	-2.62	0.00	-2.56	-2.53	-2.57	-2.56	-2.69	-3.33	-2.67	-2.59	-2.88	-2.66	-3.17	0.00	-2.54
TCGA-HC-8260-10A-01D-2260-08_PRAD	-2.40	0.00	0.00	-2.50	-2.39	-2.43	-2.47	-2.35	-2.41	0.00	0.00	0.00	0.00	0.00	-2.88	0.00	-2.47
TCGA-HC-8261-10A-01D-2260-08_PRAD	-2.61	0.00	-4.50	-2.78	-2.43	-2.55	-2.57	-2.47	-2.52	-3.24	-2.96	-2.72	0.00	0.00	0.00	-2.50	-2.52
TCGA-HC-8262-10A-01D-2260-08_PRAD	-2.67	-2.67	-2.66	0.00	-2.64	-2.68	-2.64	-2.52	-2.65	-3.37	-2.80	-2.65	0.00	0.00	-3.09	-4.12	-2.60
TCGA-HC-8264-10A-01D-2395-08_PRAD	-2.49	-2.65	-2.69	-2.83	-2.64	-2.66	-2.61	-2.56	-2.55	0.00	0.00	0.00	0.00	0.00	-2.96	-3.82	-2.49
TCGA-HC-8265-10A-01D-2260-08_PRAD	-2.36	-2.38	-2.37	0.00	-4.00	-3.83	-4.31	-4.31	0.00	0.00	-2.46	0.00	-2.45	-2.33	0.00	0.00	-2.34
TCGA-HC-8266-10A-01D-2260-08_PRAD	-2.46	-2.62	-2.57	-4.51	-2.60	-2.67	-2.60	-2.54	-2.50	0.00	-2.93	-2.62	0.00	-4.51	-2.97	-2.69	-2.43
TCGA-HC-A48F-10A-01D-A25A-08_PRAD	-2.61	-2.65	-2.59	-4.29	-2.70	-2.70	-2.68	-2.55	-2.62	0.00	-2.88	-2.76	-4.59	-4.11	-3.04	-2.72	-2.61
TCGA-HC-A4ZV-10A-01D-A26K-08_PRAD	-2.53	0.00	0.00	-2.70	-2.55	-2.56	-2.59	-2.43	-2.46	0.00	0.00	0.00	0.00	0.00	-3.10	-2.73	-2.48
TCGA-HC-A631-10A-01D-A29Q-08_PRAD	-2.48	0.00	-4.63	-2.71	-2.46	-2.55	-2.57	-2.55	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.48	-2.39
TCGA-HC-A632-10A-01D-A29Q-08_PRAD	-2.50	-2.74	-2.63	-2.82	-2.63	-2.68	-2.66	-2.74	-2.63	0.00	-2.88	0.00	-2.71	-2.60	0.00	-2.69	-2.40
TCGA-HC-A6AL-10A-01D-A30H-08_PRAD	-2.52	0.00	0.00	-2.57	-2.45	-2.52	-2.58	-2.59	-2.71	-3.58	-2.95	0.00	-2.68	-2.68	0.00	-2.73	-2.39
TCGA-HC-A6AN-10A-01D-A30H-08_PRAD	-2.44	0.00	-4.63	-2.66	-2.38	-2.45	-2.49	-2.53	-2.42	0.00	0.00	0.00	0.00	0.00	-3.02	-2.66	-2.38
TCGA-HC-A6AO-10A-01D-A30H-08_PRAD	-2.42	0.00	0.00	-2.66	-2.44	-2.45	-2.49	-2.48	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.38	-2.36
TCGA-HC-A6AP-10A-01D-A30H-08_PRAD	-2.51	-2.72	-2.78	-2.89	-2.51	-2.56	-2.59	-2.58	-2.67	-3.51	-2.71	-2.74	-2.81	-2.77	-3.15	0.00	-2.46
TCGA-HC-A6AQ-10A-01D-A30H-08_PRAD	-2.48	-2.71	0.00	-2.89	-2.43	-2.51	-2.52	-2.56	-2.61	-3.43	-2.89	0.00	-2.74	-2.62	0.00	-2.75	-2.43
TCGA-HC-A6AS-10A-01D-A30H-08_PRAD	-2.47	0.00	0.00	-2.59	-2.48	-2.49	-2.52	-2.60	-2.66	-3.67	-2.93	0.00	-2.68	-2.63	0.00	-2.79	-2.39
TCGA-HC-A6HX-10A-01D-A31J-08_PRAD	-2.45	0.00	0.00	-2.67	-2.50	-2.52	-2.49	-2.51	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.43
TCGA-HC-A6HY-10A-01D-A31J-08_PRAD	-2.57	-2.82	-2.70	-2.95	-2.71	-2.71	-2.61	-2.53	-2.65	-3.32	-2.87	0.00	-2.71	-2.65	-3.09	-4.52	-2.54
TCGA-HC-A76W-10A-01D-A33W-08_PRAD	-2.48	0.00	-4.43	-2.55	-2.57	-2.53	-2.57	-2.48	-2.51	0.00	0.00	0.00	0.00	0.00	0.00	-2.64	-2.48
TCGA-HC-A76X-10A-01D-A33W-08_PRAD	-2.45	0.00	0.00	-2.65	-2.58	-2.64	-2.61	-2.54	-2.65	-3.32	-2.91	0.00	-2.74	-2.67	-3.14	0.00	-2.51
TCGA-HD-7229-10A-01D-2013-08_HNSC	-2.52	-2.67	-2.66	-2.84	-2.67	-2.69	-2.57	-2.60	-2.47	0.00	0.00	0.00	0.00	0.00	-2.96	0.00	-2.42
TCGA-HD-7753-10A-01D-2078-08_HNSC	-2.52	-4.40	0.00	-2.70	-2.51	-2.55	-2.52	-2.47	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.45
TCGA-HD-7754-10A-01D-2078-08_HNSC	-2.52	-2.62	-2.64	-2.78	-2.67	-2.61	-2.54	-2.58	-2.56	-4.42	0.00	0.00	-3.94	-3.94	0.00	-2.56	-2.46
TCGA-HD-7831-10A-01D-2129-08_HNSC	-2.59	-2.64	-2.63	-4.53	-2.67	-2.68	-2.67	-2.59	-2.56	0.00	-2.88	-2.71	-3.93	-3.83	-3.04	-2.69	-2.54
TCGA-HD-7832-10A-01D-2129-08_HNSC	-2.48	-2.71	-2.73	-2.83	-2.47	-2.61	-2.67	-2.63	-2.58	0.00	-2.86	-2.70	0.00	-3.79	-3.09	-2.73	-2.54
TCGA-HD-7917-10A-01D-2229-08_HNSC	-2.53	0.00	0.00	-2.61	-2.57	-2.53	-2.56	-2.52	-2.63	-3.38	-2.92	0.00	-2.73	-2.64	-3.10	0.00	-2.49
TCGA-HD-8224-10A-01D-2394-08_HNSC	-2.55	-2.67	-2.64	-2.80	-2.64	-2.65	-2.58	-2.48	-2.56	-4.45	-4.45	-3.85	0.00	-4.15	-3.02	-2.67	-2.48
TCGA-HD-8314-10A-01D-2394-08_HNSC	-2.43	-2.68	-2.64	-2.81	-2.64	-2.61	-2.57	-2.47	-2.52	0.00	0.00	0.00	0.00	0.00	-3.08	-2.69	-2.49
TCGA-HD-8634-10A-01D-2394-08_HNSC	-2.59	-2.71	-2.74	-2.87	-2.64	-2.71	-2.63	-2.54	-2.69	-3.25	-2.94	-2.74	0.00	-2.70	-3.03	-3.85	-2.57
TCGA-HD-8635-10A-01D-2394-08_HNSC	-2.58	-2.73	-2.74	-2.95	-2.70	-2.75	-2.63	-2.58	-2.69	-3.26	-2.86	0.00	-2.76	-2.72	0.00	-2.81	-2.57
TCGA-HD-A4C1-10A-02D-A24F-08_HNSC	-2.47	0.00	0.00	-2.56	-2.48	-2.48	-2.48	-2.53	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.40
TCGA-HD-A6HZ-10A-01D-A31J-08_HNSC	-2.46	-2.66	-2.59	-2.78	-2.65	-2.67	-2.49	-2.50	-2.49	0.00	0.00	0.00	0.00	-4.38	-2.91	-2.75	-2.43
TCGA-HD-A6I0-10A-01D-A31J-08_HNSC	-2.40	0.00	0.00	-2.57	-2.51	-2.57	-2.57	-2.48	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.48
TCGA-HE-7128-10A-01D-1962-08_KIRP	-2.64	0.00	-4.73	-2.86	-2.65	-2.54	-2.58	-2.55	-2.59	-3.48	-2.94	-4.73	-2.82	-4.73	0.00	-2.66	-2.62
TCGA-HE-7129-10A-01D-1962-08_KIRP	-2.43	-4.33	0.00	-2.60	-2.62	-2.56	-2.54	-2.47	-2.50	0.00	0.00	0.00	0.00	-4.63	0.00	-2.47	-2.51
TCGA-HE-7130-10A-01D-1962-08_KIRP	-2.59	-2.74	-4.69	-2.97	-2.51	-2.62	-2.69	-2.66	-2.78	-3.55	-2.87	-4.69	-2.82	-2.75	0.00	-2.85	-2.48
TCGA-HE-A5NF-10A-01D-A26P-10_KIRP	-2.32	-2.34	-2.57	-2.66	-2.65	-2.40	-2.23	-2.32	-2.27	0.00	0.00	0.00	0.00	0.00	-2.87	-2.47	-2.35
TCGA-HE-A5NH-10A-01D-A26P-10_KIRP	-2.38	0.00	0.00	-2.47	-2.39	-2.24	-2.23	-2.31	-2.30	0.00	0.00	0.00	0.00	0.00	0.00	-2.30	-2.37
TCGA-HE-A5NI-10A-01D-A26P-10_KIRP	-2.47	-2.55	-2.57	-2.80	-2.47	-2.33	-2.37	-2.50	-2.57	-3.76	-2.60	-2.64	-2.74	-2.53	0.00	-2.60	-2.44
TCGA-HE-A5NJ-10A-01D-A26P-10_KIRP	-2.37	0.00	-4.25	-2.37	-2.31	-2.26	-2.29	-2.41	-2.34	-4.25	0.00	-4.25	0.00	0.00	0.00	-2.30	-2.35
TCGA-HE-A5NK-10A-01D-A26P-10_KIRP	-2.53	-2.72	-2.69	-2.85	-2.39	-2.42	-2.36	-2.49	-2.60	-3.30	-2.60	-2.60	-2.67	-2.60	0.00	-2.60	-2.47
TCGA-HE-A5NL-10A-01D-A26P-10_KIRP	-2.40	0.00	-4.29	-2.61	-2.42	-2.33	-2.33	-2.33	-2.26	0.00	0.00	0.00	0.00	-4.29	0.00	-2.25	-2.39
TCGA-HF-7131-10A-01D-2053-08_STAD	-2.54	-2.58	-2.66	0.00	-2.63	-2.67	-2.61	-2.60	-2.72	-3.21	-2.72	-2.67	-2.85	-2.69	-2.96	0.00	-2.53
TCGA-HF-7132-10A-01D-2053-08_STAD	-2.56	0.00	-2.69	-2.78	-2.43	-2.50	-2.56	-2.52	-2.55	0.00	-2.94	0.00	-2.74	0.00	-3.03	-2.69	-2.42
TCGA-HF-7133-10A-01D-2053-08_STAD	-2.52	-2.77	-2.69	-2.83	-2.42	-2.54	-2.58	-2.57	-2.52	-4.50	-2.83	-2.69	-4.50	-4.02	-3.12	-2.71	-2.48
TCGA-HF-7134-10A-01D-2053-08_STAD	-2.56	-2.72	-2.71	-2.78	-2.43	-2.56	-2.59	-2.58	-2.45	0.00	-2.92	-2.71	0.00	-4.02	-3.00	-2.74	-2.52
TCGA-HF-7136-10A-01D-2053-08_STAD	-2.49	-2.63	-2.68	-2.79	-2.61	-2.63	-2.49	-2.46	-2.41	0.00	0.00	-4.11	0.00	-3.94	-2.95	-2.71	-2.42
TCGA-HF-A5NB-10A-01D-A31J-08_STAD	-2.43	-2.61	-2.56	-2.72	-2.58	-4.39	-2.59	-2.60	-2.51	0.00	0.00	0.00	0.00	-2.54	-2.91	0.00	-2.44
TCGA-HG-A2PA-10B-01D-A20U-09_CESC	-2.87	-2.79	-2.80	-3.20	-2.50	-2.66	-2.55	-2.62	-2.39	0.00	-2.88	-2.89	0.00	-4.10	-3.09	-2.95	-2.69
TCGA-HI-7168-10A-01D-2115-08_PRAD	-2.63	-2.80	-2.80	-2.95	-2.54	-2.70	-2.69	-2.56	-2.80	-3.39	-2.75	-2.64	0.00	-2.71	0.00	-2.77	-2.59
TCGA-HI-7169-10A-01D-2115-08_PRAD	-2.52	-2.71	-2.68	-2.81	-2.61	-2.61	-2.57	-2.44	-2.45	-4.48	0.00	0.00	0.00	-3.87	0.00	-2.37	-2.40
TCGA-HI-7170-10A-01D-2115-08_PRAD	-2.46	-2.71	-2.78	-2.80	-2.68	-2.68	-2.56	-2.59	-2.65	-3.23	-2.82	0.00	-2.72	-2.65	0.00	-2.70	-2.48
TCGA-HI-7171-10A-01D-2115-08_PRAD	-2.50	0.00	-4.14	-2.64	-2.46	-2.45	-2.58	-2.52	-2.45	0.00	0.00	0.00	0.00	0.00	-2.99	-2.61	-2.41
TCGA-HJ-7597-10A-01D-2201-08_STAD	-2.42	0.00	0.00	-2.54	-2.50	-2.52	-2.54	-2.63	-2.64	-3.20	-3.10	0.00	-2.86	-2.66	-3.07	0.00	-2.44
TCGA-HL-7533-10A-01D-2229-08_HNSC	-2.40	0.00	-4.42	-2.60	-2.42	-2.38	-2.49	-2.58	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.38

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-HM-A3JJ-10A-01D-A21Q-09_CESC	-2.71	-4.20	-4.50	-3.04	-2.46	-2.47	-2.41	-2.51	-2.40	0.00	0.00	-4.20	0.00	0.00	-2.94	-2.74	-2.52
TCGA-HM-A3JK-10A-01D-A21Q-09_CESC	-2.77	0.00	0.00	-2.93	-2.40	-2.45	-2.37	-2.52	-2.38	0.00	0.00	0.00	0.00	-4.43	0.00	-2.50	-2.51
TCGA-HM-A4S6-10A-01D-A26G-09_CESC	-2.88	-3.82	-3.62	-3.07	-2.55	-2.64	-2.58	-2.53	-2.66	-3.48	-3.04	-3.74	-2.80	-2.84	0.00	-2.77	-2.65
TCGA-HN-A2NL-10A-01D-A18P-09_BRCA	-3.11	-2.88	-2.93	-3.13	-2.69	-2.75	-2.74	-2.77	-2.95	-3.43	-2.75	-2.90	-2.94	-2.93	0.00	-3.04	-2.83
TCGA-HN-A2OB-10B-01D-A27P-09_BRCA	-2.79	-4.14	0.00	-2.86	-2.50	-2.51	-2.48	-2.53	-2.50	0.00	-4.14	-4.14	0.00	0.00	0.00	-2.56	-2.53
TCGA-HP-A5MZ-10A-01D-A27I-10_LIHC	-2.41	-2.54	-2.60	-2.77	-2.36	-2.34	-2.34	-2.41	-2.36	0.00	-3.04	-2.56	-4.27	-4.27	0.00	-2.52	-2.37
TCGA-HP-A5N0-10A-01D-A28X-10_LIHC	-2.40	-2.50	-2.56	-2.81	-2.55	-2.45	-2.25	-2.29	-2.28	0.00	0.00	-4.27	0.00	0.00	0.00	-2.29	-2.47
TCGA-HQ-A2OE-10A-01D-A202-08_BLCA	-2.46	0.00	0.00	-2.59	-2.48	-2.48	-2.55	-2.53	-2.42	0.00	-4.41	0.00	-4.41	-4.41	-3.05	-2.75	-2.48
TCGA-HQ-A2OF-10B-01D-A26K-08_BLCA	-2.46	-4.36	-4.06	-2.53	-2.46	-2.44	-2.45	-2.54	-2.42	0.00	-3.89	-4.36	0.00	-4.36	0.00	-2.54	-2.37
TCGA-HQ-A5ND-10A-01D-A26K-08_BLCA	-2.42	0.00	0.00	-2.57	-2.46	-2.45	-2.48	-2.53	-2.42	0.00	0.00	-4.63	0.00	0.00	-2.83	-3.86	-2.35
TCGA-HQ-A5NE-10A-01D-A289-08_BLCA	-2.39	0.00	0.00	-2.64	-2.50	-2.55	-2.53	-2.42	-2.43	0.00	0.00	0.00	0.00	-4.56	-2.99	-2.72	-2.46
TCGA-HR-A2OG-10A-01D-A199-08_SKCM	-2.50	-2.78	-2.72	-3.03	-2.74	-2.77	-2.59	-2.52	-2.44	0.00	0.00	-4.35	-4.35	0.00	-3.03	-2.80	-2.38
TCGA-HR-A2OH-10A-01D-A199-08_SKCM	-2.38	-2.70	-2.65	-2.76	-2.70	-2.64	-2.57	-2.70	-2.65	0.00	-2.85	-4.10	-2.73	-2.59	0.00	-2.76	-2.37
TCGA-HR-A5NC-10A-01D-A27N-08_SKCM	-2.54	-2.67	-2.65	-2.82	-2.60	-2.62	-2.57	-2.63	-2.55	0.00	0.00	0.00	0.00	0.00	-2.90	-4.47	-2.45
TCGA-HS-A5N7-10A-01D-A26G-09_SARC	-2.83	-2.66	-2.74	-3.28	-2.73	-2.72	-2.51	-2.57	-2.44	-4.09	0.00	0.00	-4.39	-4.09	-2.92	-2.79	-2.54
TCGA-HS-A5N8-10A-01D-A26G-09_SARC	-2.76	-3.93	-3.76	-2.95	-2.59	-2.57	-2.51	-2.59	-2.44	-4.23	-4.06	0.00	-3.69	-3.69	0.00	-2.56	-2.68
TCGA-HS-A5N9-10A-01D-A26G-09_SARC	-2.77	-2.71	-2.72	-3.23	-2.73	-2.75	-2.58	-2.54	-2.41	-4.51	-4.51	0.00	-4.03	-4.21	-2.97	-2.88	-2.62
TCGA-HT-7467-10A-01D-2024-08_LGG	-2.51	-2.66	-2.63	-2.86	-2.72	-2.68	-2.53	-2.58	-2.51	0.00	0.00	0.00	0.00	-4.46	-2.86	-3.68	-2.50
TCGA-HT-7468-10A-01D-2024-08_LGG	-2.64	-2.69	-2.69	-2.90	-2.48	-2.64	-2.61	-2.61	-2.59	0.00	-2.93	-2.72	0.00	-4.50	0.00	-2.60	-2.50
TCGA-HT-7469-10B-01D-2253-08_LGG	-2.50	-2.62	-2.74	-2.78	-2.61	-2.64	-2.49	-2.40	-2.42	0.00	-4.46	-4.46	-4.16	-4.46	-2.98	-2.66	-2.46
TCGA-HT-7470-10A-01D-2086-08_LGG	-2.47	0.00	-4.42	-2.54	-2.53	-2.54	-2.55	-2.48	-2.42	0.00	0.00	0.00	0.00	-4.42	0.00	-2.53	-2.47
TCGA-HT-7471-10B-01D-2253-08_LGG	-2.58	-2.71	-2.74	-2.82	-2.45	-2.52	-2.58	-2.70	-2.56	0.00	-2.96	-2.70	0.00	0.00	0.00	-2.54	-2.48
TCGA-HT-7472-10A-01D-2024-08_LGG	-2.47	-2.52	-2.48	0.00	-4.39	-4.39	-2.48	-2.49	-2.41	-4.39	-4.39	-3.69	-3.91	-4.09	0.00	-2.47	-2.36
TCGA-HT-7473-10A-01D-2024-08_LGG	-2.58	-4.25	0.00	-2.83	-2.61	-2.62	-2.57	-2.55	-2.68	-3.19	-2.88	-4.55	-2.84	-2.68	-3.23	0.00	-2.55
TCGA-HT-7474-10A-01D-2024-08_LGG	-2.42	-2.60	-2.58	0.00	-2.65	-2.64	-2.57	-2.60	-2.53	-4.47	-2.91	-2.69	-4.17	-4.17	0.00	-2.62	-2.48
TCGA-HT-7475-10A-01D-2024-08_LGG	-2.46	-3.71	-4.01	-2.71	-2.50	-2.59	-2.55	-2.50	-2.44	-4.48	0.00	-4.48	0.00	-4.18	-3.05	-2.74	-2.48
TCGA-HT-7476-10A-01D-2024-08_LGG	-2.50	-3.97	-4.14	-2.73	-2.49	-2.56	-2.56	-2.56	-2.44	0.00	0.00	0.00	-4.44	-4.44	0.00	-2.55	-2.47
TCGA-HT-7477-10A-01D-A289-08_LGG	-2.62	-2.62	-2.64	-4.54	-2.62	-2.64	-2.64	-2.57	-2.55	0.00	-2.71	-2.61	0.00	0.00	0.00	-2.67	-2.58
TCGA-HT-7478-10A-01D-2024-08_LGG	-2.49	-3.79	-4.19	-2.63	-2.52	-2.53	-2.57	-2.48	-2.45	0.00	0.00	-4.49	0.00	0.00	-3.00	-2.73	-2.46
TCGA-HT-7479-10A-01D-2024-08_LGG	-2.56	-4.51	-3.67	-2.61	-2.55	-2.54	-2.56	-2.50	-2.62	0.00	-4.51	-3.91	-4.51	-4.51	0.00	-2.46	-2.45
TCGA-HT-7480-10A-01D-2086-08_LGG	-2.55	-2.70	-2.81	-2.84	-2.44	-2.61	-2.61	-2.61	-2.52	-4.50	-2.83	-2.73	0.00	0.00	-3.14	-2.73	-2.50
TCGA-HT-7481-10A-01D-2024-08_LGG	-2.44	-4.22	0.00	-2.77	-2.55	-2.57	-2.63	-2.63	-2.72	-3.32	-2.85	0.00	-2.79	-2.69	0.00	-2.68	-2.54
TCGA-HT-7482-10A-01D-2024-08_LGG	-2.53	-2.63	-2.66	-2.86	-2.56	-2.62	-2.54	-2.54	-2.50	-4.46	0.00	-3.86	0.00	0.00	-2.98	-2.73	-2.41
TCGA-HT-7483-10A-01D-2024-08_LGG	-2.52	0.00	-4.03	-2.59	-2.51	-2.55	-2.56	-2.54	-2.49	0.00	-4.51	-4.21	0.00	0.00	0.00	-2.40	-2.48
TCGA-HT-7485-10A-01D-2024-08_LGG	-2.61	-2.74	-2.71	-2.91	-2.50	-2.65	-2.64	-2.52	-2.53	0.00	-2.97	-2.72	-4.55	-4.25	0.00	-2.49	-2.55
TCGA-HT-7601-10A-01D-2086-08_LGG	-2.50	-2.65	-2.63	-2.73	-2.62	-2.66	-2.54	-2.52	-2.47	0.00	-4.43	0.00	0.00	0.00	-2.98	-2.64	-2.42
TCGA-HT-7602-10A-01D-2086-08_LGG	-2.49	-4.46	0.00	-2.75	-2.50	-2.52	-2.51	-2.44	-2.44	0.00	0.00	0.00	-4.46	-4.46	-3.03	-2.67	-2.48
TCGA-HT-7603-10A-01D-2086-08_LGG	-2.40	0.00	0.00	-2.54	-2.48	-2.50	-2.56	-2.48	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.35	-2.45
TCGA-HT-7604-10A-01D-2086-08_LGG	-2.56	-4.54	-2.71	-2.83	-2.39	-2.58	-2.64	-2.58	-2.66	-3.22	-2.78	0.00	-2.70	-2.69	-3.09	-4.54	-2.52
TCGA-HT-7605-10A-01D-2086-08_LGG	-2.48	0.00	0.00	-2.49	-2.52	-2.53	-2.55	-2.45	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.37	-2.52
TCGA-HT-7606-10A-01D-2086-08_LGG	-2.50	0.00	0.00	-2.61	-2.43	-2.41	-2.43	-2.66	-2.40	0.00	0.00	-4.28	0.00	-3.98	0.00	-2.46	-2.34
TCGA-HT-7607-10A-01D-2086-08_LGG	-2.50	-2.63	-2.68	-2.81	-2.63	-2.54	-2.57	-2.47	-2.42	0.00	0.00	0.00	0.00	-4.47	-2.96	-2.61	-2.46
TCGA-HT-7608-10A-01D-2086-08_LGG	-2.46	-2.71	-2.64	-2.81	-2.56	-2.60	-2.46	-2.47	-2.46	0.00	0.00	0.00	-4.42	0.00	0.00	-2.33	-2.41
TCGA-HT-7609-10A-01D-2086-08_LGG	-2.61	-2.63	-2.66	0.00	-2.65	-2.64	-2.62	-2.67	-2.75	-3.11	-2.72	-2.66	-2.86	-2.75	0.00	-2.80	-2.56
TCGA-HT-7610-10A-01D-2086-08_LGG	-2.37	-2.62	-2.64	-2.81	-2.60	-2.62	-2.50	-2.48	-2.46	0.00	0.00	0.00	0.00	-4.11	-2.98	-2.64	-2.43
TCGA-HT-7611-10B-01D-2396-08_LGG	-2.67	-2.73	-2.65	-3.85	-2.65	-2.65	-2.68	-2.73	-2.79	-3.37	-2.68	-2.72	-2.82	-2.77	0.00	-2.83	-2.66
TCGA-HT-7616-10A-01D-2253-08_LGG	-2.43	-2.66	-2.68	-2.73	-2.60	-2.60	-2.53	-2.49	-2.42	0.00	0.00	0.00	0.00	0.00	-2.96	-2.58	-2.42
TCGA-HT-7620-10A-01D-2253-08_LGG	-2.50	-2.68	-2.73	-2.74	-2.44	-2.63	-2.68	-2.68	-2.53	0.00	-2.78	-2.73	0.00	-2.56	-3.02	-4.13	-2.56
TCGA-HT-7676-10B-01D-2396-08_LGG	-2.66	-2.80	-2.79	-2.96	-2.55	-2.65	-2.71	-2.59	-2.72	-3.34	-2.77	-2.68	0.00	-2.74	-3.14	-4.00	-2.60
TCGA-HT-7677-10A-01D-2253-08_LGG	-2.54	-4.26	-4.56	-2.59	-2.55	-2.62	-2.43	-2.39	-2.50	-3.36	-4.26	-4.26	0.00	-4.26	-3.03	-2.75	-2.49
TCGA-HT-7680-10A-01D-2253-08_LGG	-2.53	-2.73	-2.76	-2.81	-2.67	-2.65	-2.59	-2.58	-2.68	-3.27	-2.83	0.00	-2.85	-2.66	0.00	-2.74	-2.55
TCGA-HT-7681-10C-01D-2396-08_LGG	-2.60	0.00	-4.03	-2.77	-2.58	-2.64	-2.66	-2.55	-2.49	0.00	-3.91	-4.51	-3.73	-4.21	0.00	-2.62	-2.54
TCGA-HT-7684-10A-01D-2253-08_LGG	-2.53	-2.79	-2.87	-2.92	-2.49	-2.58	-2.63	-2.59	-2.84	-3.22	-2.72	-2.65	-2.96	-2.75	0.00	-2.84	-2.59
TCGA-HT-7686-10A-01D-2253-08_LGG	-2.56	0.00	0.00	-2.54	-2.50	-2.50	-2.56	-2.48	-2.40	0.00	0.00	0.00	0.00	0.00	-2.95	-2.60	-2.43
TCGA-HT-7687-10A-01D-2253-08_LGG	-2.30	-2.51	-2.49	-4.39	-4.39	-4.09	-2.46	-2.46	-2.43	0.00	0.00	0.00	0.00	0.00	-2.81	-4.39	-2.37
TCGA-HT-7688-10A-01D-2253-08_LGG	-2.44	0.00	0.00	-2.54	-2.54	-2.56	-2.55	-2.60	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.46
TCGA-HT-7689-10A-01D-2253-08_LGG	-2.49	-2.70	0.00	-2.86	-2.52	-2.49	-2.59	-2.67	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.44
TCGA-HT-7690-10A-01D-2253-08_LGG	-2.48	0.00	0.00	-2.57	-2.58	-2.65	-2.57	-2.60	-2.84	-3.07	-2.93	-2.80	0.00	-2.82	0.00	-2.71	-2.48
TCGA-HT-7691-10A-01D-2253-08_LGG	-2.55	0.00	0.00	-2.73	-2.53	-2.50	-2.61	-2.61	-2.61	-3.32	-2.88	0.00	-2.84	-2.64	0.00	-2.80	-2.53
TCGA-HT-7692-10A-01D-2253-08_LGG	-2.59	-2.82	-2.76	-2.81	-2.43	-2.57	-2.58	-2.63	-2.66	-3.23	-2.73	-2.61	0.00	-2.68	-2.98	0.00	-2.57
TCGA-HT-7693-10A-01D-2253-08_LGG	-2.57	0.00	-2.71	-2.84	-2.54	-2.56	-2.64	-2.48	-2.51	0.00	-2.80	0.00	-2.84	-4.26	-3.02	-2.72	-2.50
TCGA-HT-7694-10A-01D-2253-08_LGG	-2.55	0.00	0.00	-2.50	-2.50	-2.48	-2.51	-2.49	-2.53	0.00	0.00	0.00	0.00	-4.41	0.00	-2.38	-2.40
TCGA-HT-7695-10A-01D-2253-08_LGG	-2.47	-2.74	-2.67	-2.78	-2.65	-2.65	-2.52	-2.53	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.37	-2.43
TCGA-HT-7854-10A-01D-2253-08_LGG	-2.48	0.00	0.00	-2.54	-2.46	-2.47	-2.59	-2.63	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.40
TCGA-HT-7855-10A-01D-2396-08_LGG	-2.63	-3.97	-3.97	-2.84	-2.64	-2.65	-2.67	-2.66	-2.77	-3.25	-2.84	-4.28	-2.77	-2.72	0.00	-2.77	-2.55
TCGA-HT-7856-10A-01D-2396-08_LGG	-2.41	-2.62	-2.64	-2.75	-2.60	-2.60	-2.50	-2.40	-2.41	0.00	0.00	0.00	0.00	-4.64	-2.97	-2.66	-2.39
TCGA-HT-7857-10A-01D-2396-08_LGG	-2.61	-2.70	-2.75	-2.94	-2.70	-2.65	-2.62	-2.56	-2.61	0.00	-4.51	-3.91	0.00	0.00	0.00	-2.53	-2.58
TCGA-HT-7858-10A-01D-2396-08_LGG	-2.62	-2.60	-2.71	-4.55	-2.69	-2.71	-2.69	-2.54	-2.70	-3.32	-2.84	0.00	-2.74	-2.67	-3.05	-3.77	-2.59
TCGA-HT-7860-10A-01D-2396-08_LGG	-2.47	0.00	-4.06	-2.78	-2.51	-2.63	-2.63	-2.51	-2.47	0.00	-4.54	0.00	0.00	0.00	-3.08	-2.68	-2.52
TCGA-HT-7873-10A-01D-2396-08_LGG	-2.57	-3.79	-3.88	-2.60	-2.57	-2.57	-2.63	-2.47	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.40	-2.51
TCGA-HT-7874-10A-01D-2396-08_LGG	-2.54	-3.54	-3.84	-2.64	-2.54	-2.58	-2.58	-2.59	-2.54	0.00	-3.84	-3.74	0.00	0.00	0.00	-2.57	-2.50
TCGA-HT-7875-10A-01D-2396-08_LGG	-2.58	-2.82	-2.81	-2.97	-2.55	-2.70	-2.76	-2.59	-2.84	-3.22	-2.70	-2.75	-2.87	-2.84	0.00	-2.84	-2.64
TCGA-HT-7877-10A-01D-2396-08_LGG	-2.61	-2.64	-2.65	-3.86	-2.68	-2.69	-2.66	-2.62	-2.63	0.00	-2.82	-2.76	-4.56	-4.26	0.00	-2.67	-2.58
TCGA-HT-7879-10A-01D-2396-08_LGG	-2.61	-2.60	-2.66	-4.55	-2.63	-2.69	-2.64	-2.58	-2.52	-4.55	-2.94	-2.68	-3.77	-3.64	0.00	-2.46	-2.40
TCGA-HT-7880-10A-01D-2396-08_LGG	-2.59	-3.90	-4.03	-2.72	-2.57	-2.57	-2.58	-2.59	-2.57	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.48
TCGA-HT-7881-10A-01D-2396-08_LGG	-2.64	-2.78	-2.76	-2.89	-2.54	-2.66	-2.72	-2.58	-2.59	0.00	-2.95	-3.80	-2.78	0.00	0.00	-2.58	-2.62
TCGA-HT-7882-10A-01D-2396-08_LGG	-2.65	-2.68	-2.74	-2.88	-2.74	-2.72	-2.67	-2.54	-2.72	-3.21	-2.91	-3.80	-2.79	-2.72	-3.03	0.00	-2.59
TCGA-HT-7884-10A-01D-2396-08_LGG	-2.56	-2.68	-2.69	-2.88	-2.66	-2.65	-2.59	-2.49	-2.60	0.00	-4.03	-3.91	0.00	-3.73	0.00	-2.40	-2.50
TCGA-HT-7902-10A-01D-2396-08_LGG	-2.66	-2.79	-2.74	-2.97	-2.53	-2.65	-2.68	-2.58	-2.64	-4.30	-2.87	-2.77	-3.56	-3.76	-3.09	-2.76	-2.62
TCGA-HT-8010-10A-01D-2396-08_LGG	-2.40	-2.65	-2.66	-2.78	-2.60	-2.68	-2.59	-2.42	-2.46	0.00	0.00	-3.84	-4.44	0.00	-3.06	-2.75	-2.46
TCGA-HT-8011-10A-01D-2396-08_LGG	-2.57	-3.90	-4.03	-2.62	-2.55	-2.60	-2.59	-2.61	-2.51	0.00	0.00	0.00	-4.51	-4.20	0.00	-2.46	-2.53
TCGA-HT-8012-10A-01D-2396-08_LGG	-2.58	-2.57	-2.57	-4.03	-4.20	-4.03	-2.63	-2.62	-2.65	-3.30	-2.74	-2.72	-4.50	-2.65	0.00	-2.69	-2.53
TCGA-HT-8013-10A-01D-2396-08_LGG	-2.49	-2.49	-2.49	0.00	-2.64	-2.67	-2.50	-2.64	-2.50	0.00	-2.89	-2.64	0.00	0.00	0.00	-2.57	-2.39
TCGA-HT-8015-10A-01D-A289-08_LGG	-2.53	0.00	0.00	-2.80	-2.58	-2.59	-2.55	-2.47	-2.61	0.00	0.00	-4.51	0.00	0.00	0.00	-2.40	-2.51
TCGA-HT-8018-10A-01D-2396-08_LGG	-2.55	-3.50	-3.60	-2.79	-2.58	-2.58	-2.59	-2.51	-2.47	0.00	0.00	0.00	0.00	-4.50	0.00	-2.43	-2.51
TCGA-HT-8019-10A-01D-2396-08_LGG	-2.59	-2.70	-2.72	-2.88	-2.67	-2.67	-2.59	-2.54	-2.57	-4.50	-4.20	-4.03	0.00	-3.80	-3.06	-2.70	-2.55
TCGA-HT-8104-10A-01D-2396-08_LGG	-2.54	-2.61	-2.64	-2.88	-2.62	-2.64	-2.61	-2.65	-2.56	-4.50	0.00	0.00	-4.50	-4.50	0.00	-2.59	-2.53
TCGA-HT-8105-10A-01D-2396-08_LGG	-2.68	-2.66	-2.67	-4.32	-2.64	-2.68	-2.70	-2.61	-2.73	-3.34	-2.68	-2.70	-2.82	-2.75	-3.17	-4.14	-2.63
TCGA-HT-8106-10A-01D-2396-08_LGG	-2.43	-4.62	-4.62	-2.66	-2.45	-2.48	-2.48	-2.57	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.36
TCGA-HT-8107-10A-01D-2396-08_LGG	-2.65	-3.97	-3.79	-2.72	-2.60	-2.66	-2.67	-2.62	-2.65	-3.29	-2.91	-2.75	-4.27	-2.66	0.00	-2.82	-2.59
TCGA-HT-8108-10A-01D-2396-08_LGG	-2.62	-2.77	-2.75	-2.92	-2.51	-2.66	-2.67	-2.61	-2.64	0.00	-2.86	-2.79	0.00	-4.11	0.00	-2.52	-2.60
TCGA-HT-8109-10A-01D-2396-08_LGG	-2.60	-3.91	-3.81	-2.83	-2.58	-2.61	-2.63	-2.61	-2.54	0.00	-3.73	-3.81	0.00	0.00	-2.96	0.00	-2.51
TCGA-HT-8110-10A-01D-2396-08_LGG	-2.59	-2.72	-2.70	-2.90	-2.46	-2.63	-2.72	-2.70	-3.83	-3.38	-2.64	-2.70	-2.70	-2.67	0.00	-4.05	-2.60
TCGA-HT-8111-10A-01D-2396-08_LGG	-2.63	-4.08	-4.56	-2.78	-2.49	-2.63	-2.66	-2.63	-2.75	-3.26	-2.93	-4.26	-2.80	-2.69	0.00	-2.74	-2.59
TCGA-HT-8113-10A-01D-2396-08_LGG	-2.50	0.00	0.00	-2.61	-2.38	-2.39	-2.55	-2.58	-2.49	0.00	0.00	-4.67	0.00	0.00	0.00	-2.55	-2.43
TCGA-HT-8114-10A-01D-2396-08_LGG	-2.53	-4.22	-3.61	-2.80	-2.55	-2.62	-2.59	-2.60	-2.46	0.00	-4.04	0.00	-4.22	-4.04	0.00	-2.60	-2.58

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-HT-8558-10A-01D-2396-08_LGG	-2.65	-2.76	-2.78	-3.01	-2.55	-2.65	-2.73	-2.67	-2.66	0.00	-2.88	-2.73	0.00	0.00	-3.01	-4.30	-2.60
TCGA-HT-8563-10A-01D-2396-08_LGG	-2.68	-2.78	-2.78	-2.89	-2.56	-2.66	-2.70	-2.61	-2.63	0.00	-2.83	-2.78	0.00	-4.60	-3.11	-2.85	-2.61
TCGA-HT-8564-10A-01D-2396-08_LGG	-2.59	-2.72	-2.65	-2.93	-2.63	-2.66	-2.58	-2.50	-2.60	0.00	0.00	0.00	-3.83	-3.83	-3.00	-2.78	-2.55
TCGA-HT-A4DS-10A-01D-A26K-08_LGG	-2.39	0.00	0.00	-2.66	-2.45	-2.45	-2.45	-2.52	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.44	-2.32
TCGA-HT-A4DV-10A-01D-A26K-08_LGG	-2.46	-2.50	-2.47	0.00	-4.04	-3.56	-2.41	-2.52	-2.53	-3.26	-2.79	-3.86	-2.70	-2.60	-2.96	-3.86	-2.38
TCGA-HT-A5R5-10A-01D-A289-08_LGG	-2.53	0.00	0.00	-2.77	-2.49	-2.52	-2.60	-2.46	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.48
TCGA-HT-A5R7-10A-01D-A289-08_LGG	-2.52	-2.77	-2.76	-2.92	-2.50	-2.67	-2.64	-2.69	-2.74	-3.25	-2.73	-2.76	-2.80	-2.74	0.00	-2.80	-2.58
TCGA-HT-A5R9-10A-01D-A289-08_LGG	-2.58	0.00	0.00	-2.62	-2.56	-2.54	-2.60	-2.61	-2.72	-3.41	-2.90	0.00	-2.76	-2.59	0.00	-2.78	-2.53
TCGA-HT-A5RA-10A-01D-A289-08_LGG	-2.49	-2.81	-2.72	-2.98	-2.50	-2.71	-2.65	-2.49	-2.53	-3.37	-2.95	-2.77	0.00	0.00	-3.13	-2.83	-2.58
TCGA-HT-A5RB-10A-01D-A289-08_LGG	-2.58	-2.71	-2.68	-2.91	-2.65	-2.64	-2.58	-2.62	-4.03	-3.17	-2.70	0.00	-2.60	-2.56	0.00	0.00	-2.51
TCGA-HT-A5RC-10A-01D-A289-08_LGG	-2.55	-2.64	-2.67	-2.84	-2.43	-2.63	-2.66	-2.74	-2.59	0.00	-2.83	-2.69	0.00	-2.63	0.00	-2.72	-2.58
TCGA-HT-A614-10A-01D-A29Q-08_LGG	-2.48	0.00	-4.59	-2.69	-2.47	-2.52	-2.50	-2.54	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.42
TCGA-HT-A615-10A-01D-A29Q-08_LGG	-2.53	-2.66	-2.67	-2.86	-2.46	-2.57	-2.61	-2.60	-2.60	0.00	-2.95	-2.71	0.00	0.00	0.00	-2.62	-2.46
TCGA-HT-A616-10A-01D-A29Q-08_LGG	-2.36	-2.68	-2.61	-2.91	-2.76	-2.68	-2.60	-2.61	-2.59	-3.32	-2.80	0.00	-2.80	-2.66	-3.10	0.00	-2.45
TCGA-HT-A617-10A-01D-A29Q-08_LGG	-2.40	0.00	0.00	-2.59	-2.49	-2.50	-2.53	-2.57	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.40
TCGA-HT-A618-10A-01D-A29Q-08_LGG	-2.49	-2.62	-2.67	-2.84	-2.59	-2.61	-2.52	-2.45	-2.42	0.00	0.00	0.00	0.00	0.00	-3.01	-2.68	-2.40
TCGA-HT-A619-10A-01D-A29Q-08_LGG	-2.49	-2.68	-2.67	-2.75	-2.63	-2.62	-2.53	-2.53	-2.46	0.00	0.00	0.00	0.00	0.00	-2.87	0.00	-2.40
TCGA-HT-A61A-10A-01D-A29Q-08_LGG	-2.41	0.00	0.00	-2.67	-2.50	-2.54	-2.52	-2.58	-2.45	0.00	-4.63	0.00	0.00	-4.63	-3.05	-2.72	-2.40
TCGA-HT-A61B-10A-01D-A29Q-08_LGG	-2.45	-2.73	-2.68	-2.94	-2.69	-2.68	-2.55	-2.59	-2.66	-3.38	-2.87	0.00	-2.74	-2.62	0.00	-2.71	-2.42
TCGA-HT-A61C-10A-01D-A29Q-08_LGG	-2.41	-2.45	-2.44	0.00	0.00	0.00	-2.44	-2.39	-2.41	0.00	0.00	0.00	0.00	-4.56	-2.92	-2.64	-2.35
TCGA-HT-A74H-10A-01D-A329-08_LGG	-2.47	0.00	0.00	-2.57	-2.47	-2.54	-2.48	-2.55	-2.45	0.00	0.00	0.00	0.00	0.00	-3.03	-2.81	-2.41
TCGA-HT-A74J-10A-01D-A329-08_LGG	-2.56	-2.71	-2.73	-2.92	-2.54	-2.62	-2.62	-2.62	-2.73	-3.36	-2.74	-2.76	-2.75	-2.68	0.00	-2.82	-2.55
TCGA-HT-A74K-10A-01D-A329-08_LGG	-2.54	0.00	0.00	-2.76	-2.53	-2.54	-2.54	-2.56	-2.63	-3.28	-2.97	-2.67	0.00	-2.64	-3.20	0.00	-2.52
TCGA-HT-A74L-10A-01D-A329-08_LGG	-2.49	0.00	0.00	-2.58	-2.49	-2.52	-2.51	-2.56	-2.42	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.44
TCGA-HT-A74O-10A-01D-A329-08_LGG	-2.39	-4.36	0.00	-2.53	-2.45	-2.48	-2.53	-2.55	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.41
TCGA-HU-8238-10A-01D-2341-08_STAD	-2.40	0.00	0.00	-2.61	-2.59	-2.56	-2.58	-2.49	-2.46	0.00	0.00	0.00	0.00	0.00	-3.02	-2.72	-2.47
TCGA-HU-8243-10A-01D-2341-08_STAD	-2.61	0.00	-4.32	-2.80	-2.56	-2.59	-2.57	-2.54	-2.67	-3.21	-2.87	0.00	-2.75	-2.75	-3.10	0.00	-2.54
TCGA-HU-8244-10A-01D-2341-08_STAD	-2.58	-4.60	-4.60	-2.81	-2.53	-2.63	-2.58	-2.56	-2.70	-3.26	-2.96	-4.30	-2.77	-2.66	-3.08	-4.12	-2.55
TCGA-HU-8245-10A-01D-2341-08_STAD	-2.60	-2.71	-2.73	-2.87	-2.71	-2.72	-2.63	-2.57	-2.66	-3.22	-2.84	0.00	-2.79	-2.76	-3.04	0.00	-2.50
TCGA-HU-8249-10A-01D-2341-08_STAD	-2.52	0.00	0.00	-2.74	-2.53	-2.54	-2.50	-2.60	-2.49	0.00	0.00	0.00	0.00	0.00	-2.88	0.00	-2.43
TCGA-HU-8602-10A-01D-2394-08_STAD	-2.58	-4.19	-4.19	-2.78	-2.54	-2.55	-2.62	-2.56	-2.70	-3.31	-2.85	-3.89	-2.75	-2.62	-3.06	0.00	-2.50
TCGA-HU-8604-10A-01D-2394-08_STAD	-2.46	-3.73	-3.91	-2.57	-2.60	-2.62	-2.61	-2.55	-2.54	0.00	-4.51	0.00	0.00	-4.51	-2.91	-3.73	-2.51
TCGA-HU-8608-10A-01D-2394-08_STAD	-2.62	-2.68	-2.72	-2.89	-2.68	-2.62	-2.61	-2.51	-2.57	0.00	0.00	-3.89	-4.49	0.00	-3.03	-2.74	-2.51
TCGA-HU-8610-10A-01D-2394-08_STAD	-2.53	0.00	0.00	-2.69	-2.55	-2.57	-2.54	-2.59	-2.53	0.00	0.00	0.00	0.00	0.00	-2.90	0.00	-2.53
TCGA-HU-A4G2-10A-01D-A25E-08_STAD	-2.54	0.00	-4.50	-2.75	-2.55	-2.64	-2.60	-2.62	-2.59	0.00	0.00	0.00	0.00	-4.50	-2.93	-4.50	-2.52
TCGA-HU-A4G3-10A-01D-A24F-08_STAD	-2.62	-3.81	-4.03	-2.82	-2.62	-2.61	-2.68	-2.51	-2.70	-3.46	-2.86	-3.60	-2.81	-2.73	-3.03	-3.66	-2.59
TCGA-HU-A4G6-10A-01D-A24F-08_STAD	-2.60	0.00	0.00	-2.61	-2.58	-2.60	-2.63	-2.49	-2.47	0.00	0.00	0.00	0.00	0.00	-3.01	-2.73	-2.58
TCGA-HU-A4G8-10A-01D-A25E-08_STAD	-2.65	0.00	0.00	-2.88	-2.67	-2.62	-2.62	-2.62	-2.68	-3.47	-2.92	-2.74	-4.59	0.00	0.00	-2.55	-2.64
TCGA-HU-A4G9-10A-01D-A24F-08_STAD	-2.57	-3.94	-3.72	-2.75	-2.56	-2.57	-2.55	-2.55	-2.54	0.00	0.00	0.00	0.00	0.00	-3.01	-2.78	-2.49
TCGA-HU-A4GC-10A-01D-A25E-08_STAD	-2.55	0.00	0.00	-2.70	-2.53	-2.63	-2.58	-2.54	-2.47	0.00	0.00	0.00	0.00	-4.52	-3.00	-2.72	-2.56
TCGA-HU-A4GD-10A-01D-A25E-08_STAD	-2.54	-4.49	0.00	-2.77	-2.51	-2.57	-2.60	-2.49	-2.54	0.00	-4.49	0.00	0.00	0.00	-3.02	-2.73	-2.53
TCGA-HU-A4GF-10A-01D-A24F-08_STAD	-2.48	-4.40	0.00	-2.76	-2.50	-2.55	-2.54	-2.50	-2.53	0.00	0.00	0.00	0.00	0.00	-2.97	-2.74	-2.42
TCGA-HU-A4GH-10A-01D-A24F-08_STAD	-2.61	0.00	0.00	-2.85	-2.62	-2.61	-2.63	-2.62	-2.66	-3.35	-2.79	0.00	-2.78	-2.66	0.00	-2.74	-2.60
TCGA-HU-A4GJ-10A-01D-A25E-08_STAD	-2.57	0.00	0.00	-2.76	-2.55	-2.58	-2.60	-2.47	-2.46	0.00	0.00	0.00	0.00	0.00	-2.98	-2.67	-2.53
TCGA-HU-A4GN-10A-01D-A25E-08_STAD	-2.58	0.00	-4.54	-2.76	-2.55	-2.68	-2.59	-2.56	-2.65	-3.24	-2.91	-2.72	0.00	-2.66	0.00	-2.72	-2.49
TCGA-HU-A4GP-10A-01D-A25E-08_STAD	-2.43	-4.49	-4.19	-2.63	-2.54	-2.58	-2.60	-2.58	-2.60	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.55
TCGA-HU-A4GQ-10A-01D-A25E-08_STAD	-2.61	0.00	-3.77	-2.77	-2.59	-2.61	-2.63	-2.56	-2.66	-3.27	-2.83	-2.73	0.00	-2.74	-3.10	-4.55	-2.50
TCGA-HU-A4GT-10A-01D-A25E-08_STAD	-2.43	-4.23	-4.23	-2.60	-2.62	-2.58	-2.59	-2.64	-3.69	-3.13	-2.71	0.00	-2.63	-2.57	0.00	0.00	-2.55
TCGA-HU-A4GU-10A-01D-A25E-08_STAD	-2.54	-2.72	-2.72	-2.92	-2.61	-2.66	-2.58	-2.50	-2.45	-4.54	-4.54	0.00	0.00	-4.24	0.00	-2.54	-2.51
TCGA-HU-A4GX-10A-01D-A25E-08_STAD	-2.44	-4.14	-4.14	-2.69	-2.47	-2.52	-2.54	-2.52	-2.48	0.00	0.00	0.00	0.00	0.00	-2.86	-3.96	-2.46
TCGA-HU-A4GY-10A-01D-A24F-08_STAD	-2.53	0.00	0.00	-2.71	-2.54	-2.54	-2.55	-2.48	-2.52	0.00	0.00	-4.40	0.00	-4.40	-2.93	-2.67	-2.47
TCGA-HU-A4H2-10A-01D-A25E-08_STAD	-2.53	0.00	0.00	-2.83	-2.55	-2.60	-2.57	-2.59	-2.59	0.00	0.00	0.00	0.00	0.00	-2.93	-4.50	-2.50
TCGA-HU-A4H3-10A-01D-A25E-08_STAD	-2.46	-4.43	0.00	-2.67	-2.45	-2.51	-2.53	-2.48	-2.56	-4.43	-4.43	-4.43	0.00	-4.13	-3.01	-3.83	-2.41
TCGA-HU-A4H6-10A-01D-A25E-08_STAD	-2.47	0.00	-4.12	-2.68	-2.46	-2.46	-2.49	-2.51	-2.58	0.00	-3.95	-4.42	0.00	0.00	-2.93	-3.95	-2.39
TCGA-HU-A4H8-10A-01D-A25E-08_STAD	-2.59	-2.77	-2.74	-2.86	-2.49	-2.63	-2.60	-2.61	-2.56	0.00	-2.94	-2.75	0.00	0.00	-3.10	-2.68	-2.50
TCGA-HU-A4HB-10A-01D-A25E-08_STAD	-2.58	0.00	0.00	-2.75	-2.61	-2.56	-2.59	-2.45	-2.51	0.00	0.00	0.00	0.00	-4.57	-2.94	-2.69	-2.46
TCGA-HU-A4HD-10A-01D-A25E-08_STAD	-2.55	0.00	0.00	-2.77	-2.55	-2.56	-2.66	-2.60	-2.55	0.00	0.00	0.00	0.00	-4.50	-2.94	0.00	-2.51
TCGA-HV-A5A3-10A-01D-A26I-08_PAAD	-2.48	-4.43	-4.43	-2.59	-2.45	-2.54	-2.53	-2.62	-2.69	-3.32	-2.90	-3.48	-2.70	-2.66	0.00	-2.72	-2.44
TCGA-HV-A5A4-10A-01D-A26I-08_PAAD	-2.43	-4.42	-3.82	-2.61	-2.46	-2.45	-2.52	-2.54	-2.60	-3.30	-3.04	-3.82	-2.84	-2.67	-3.08	-3.72	-2.42
TCGA-HV-A5A5-10A-01D-A26I-08_PAAD	-2.45	0.00	-4.39	-2.67	-2.48	-2.43	-2.50	-2.49	-2.38	0.00	-4.09	0.00	-4.09	-3.43	-3.01	-2.70	-2.39
TCGA-HV-A5A6-10A-01D-A26I-08_PAAD	-2.45	0.00	0.00	-2.67	-2.45	-2.52	-2.53	-2.60	-2.72	-3.19	-2.89	-2.70	-3.92	-2.65	0.00	-2.71	-2.43
TCGA-HV-A7OL-10A-01D-A33W-08_PAAD	-2.51	0.00	-4.41	-2.69	-2.52	-2.51	-2.54	-2.49	-2.48	0.00	0.00	0.00	0.00	0.00	-2.99	-2.72	-2.49
TCGA-HV-A7OP-10A-01D-A33W-08_PAAD	-2.57	0.00	0.00	-2.76	-2.54	-2.55	-2.61	-2.58	-2.64	-3.47	-2.88	0.00	-2.76	-2.67	0.00	-2.84	-2.52
TCGA-HW-7486-10A-01D-2024-08_LGG	-2.50	-4.48	-4.18	-2.70	-2.45	-2.51	-2.48	-2.56	-2.41	0.00	0.00	0.00	0.00	-4.48	0.00	-2.56	-2.37
TCGA-HW-7487-10A-01D-2024-08_LGG	-2.50	-4.15	-3.75	-2.73	-2.48	-2.51	-2.53	-2.52	-2.49	0.00	-4.45	-4.45	0.00	0.00	0.00	-2.55	-2.49
TCGA-HW-7489-10A-01D-2024-08_LGG	-2.52	-2.70	-2.65	-2.83	-2.56	-2.60	-2.58	-2.44	-2.40	0.00	0.00	-4.16	-4.16	0.00	-3.12	-2.70	-2.44
TCGA-HW-7490-10A-01D-2024-08_LGG	-2.54	-2.70	-2.68	-2.93	-2.68	-2.67	-2.65	-2.52	-2.67	-3.38	-2.86	0.00	-2.75	-2.65	-3.11	-4.52	-2.55
TCGA-HW-7491-10A-01D-2024-08_LGG	-2.43	-2.67	-2.63	-2.89	-2.54	-2.72	-2.51	-2.48	-2.39	0.00	-4.01	-4.49	0.00	-4.49	0.00	-2.48	-2.34
TCGA-HW-7493-10A-01D-2024-08_LGG	-2.51	0.00	-4.48	-2.72	-2.51	-2.55	-2.51	-2.53	-2.55	0.00	-4.18	0.00	-3.88	-4.00	0.00	-2.53	-2.50
TCGA-HW-7495-10A-01D-2024-08_LGG	-2.48	-4.45	-4.45	-2.76	-2.48	-2.52	-2.55	-2.54	-2.47	0.00	-4.45	0.00	-4.45	-4.15	0.00	-2.57	-2.45
TCGA-HW-8319-10A-01D-2396-08_LGG	-2.59	-3.81	-4.21	-2.76	-2.60	-2.55	-2.65	-2.47	-2.47	-4.21	-4.03	0.00	-3.91	-3.61	-3.01	-2.71	-2.51
TCGA-HW-8320-10A-01D-2396-08_LGG	-2.56	-2.77	-2.68	-2.91	-2.66	-2.75	-2.63	-2.48	-2.48	0.00	0.00	-4.50	0.00	-4.50	-2.96	-2.66	-2.57
TCGA-HW-8321-10A-01D-2396-08_LGG	-2.65	0.00	-3.76	-2.80	-2.61	-2.65	-2.63	-2.59	-2.67	-3.26	-2.84	0.00	-2.78	-2.70	-3.06	0.00	-2.57
TCGA-HW-8322-10A-01D-2396-08_LGG	-2.55	-2.66	-2.64	-2.86	-2.67	-2.66	-2.57	-2.50	-2.61	0.00	0.00	-4.22	0.00	0.00	-3.02	-2.66	-2.54
TCGA-HW-A5KJ-10A-01D-A27N-08_LGG	-2.42	0.00	0.00	-2.53	-2.47	-2.49	-2.51	-2.52	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.46
TCGA-HW-A5KK-10A-01D-A27N-08_LGG	-2.50	-2.74	-2.75	-2.98	-2.52	-2.56	-2.61	-2.54	-2.76	-3.59	-2.73	-2.65	0.00	-2.71	-3.11	0.00	-2.53
TCGA-HW-A5KL-10A-01D-A27N-08_LGG	-2.49	0.00	0.00	-2.53	-2.47	-2.48	-2.55	-2.48	-2.54	0.00	0.00	0.00	0.00	0.00	0.00	-2.38	-2.41
TCGA-HW-A5KM-10A-01D-A27N-08_LGG	-2.54	-2.72	-2.66	-2.87	-2.66	-2.69	-2.54	-2.60	-4.57	-3.23	-2.73	0.00	-2.64	-2.54	0.00	0.00	-2.46
TCGA-HZ-7920-10B-01D-2201-08_PAAD	-2.60	-2.80	-2.76	-2.91	-2.53	-2.66	-2.66	-2.57	-2.53	0.00	-2.87	0.00	-2.86	0.00	0.00	-2.48	-2.53
TCGA-HZ-8001-10A-01D-2201-08_PAAD	-2.63	-2.79	-2.82	-2.90	-2.49	-2.64	-2.65	-2.52	-2.54	0.00	-2.90	-2.79	0.00	-4.55	0.00	-2.53	-2.54
TCGA-HZ-8002-10A-01D-2201-08_PAAD	-2.56	-2.72	-2.69	-2.90	-2.69	-2.65	-2.67	-2.74	-3.76	-3.31	-2.66	-3.84	-2.65	-2.58	0.00	-4.54	-2.52
TCGA-HZ-8003-10A-01D-2201-08_PAAD	-2.48	-2.53	-2.47	-3.94	-3.72	-4.11	-2.52	-2.46	-2.51	-4.42	0.00	-4.11	-4.42	-4.42	-2.86	-2.65	-2.46
TCGA-HZ-8005-10A-01D-2201-08_PAAD	-2.33	0.00	-4.10	-2.79	-2.56	-2.56	-2.61	-2.61	-2.52	0.00	-4.40	0.00	-4.40	-2.52	0.00	-2.59	-2.41
TCGA-HZ-8315-10A-01D-2396-08_PAAD	-2.46	-2.64	-2.65	-2.76	-2.63	-2.58	-2.66	-2.64	-2.59	0.00	-2.78	0.00	-2.74	-2.60	0.00	-2.68	-2.43
TCGA-HZ-8317-10A-01D-2396-08_PAAD	-2.53	-3.94	-4.41	-2.57	-2.50	-2.53	-2.55	-2.55	-2.46	0.00	-4.41	-4.41	0.00	0.00	0.00	-2.58	-2.47
TCGA-HZ-8519-10A-01D-2396-08_PAAD	-2.67	-2.87	-2.74	-2.98	-2.55	-2.70	-2.70	-2.68	-2.80	-3.39	-2.75	-2.75	-2.76	-2.71	0.00	-2.78	-2.62
TCGA-HZ-8636-10A-01D-2396-08_PAAD	-2.46	-2.69	-2.60	-2.84	-2.60	-2.68	-2.60	-2.59	-2.46	0.00	0.00	-3.69	0.00	0.00	0.00	-2.54	-2.48
TCGA-HZ-8637-10A-01D-2396-08_PAAD	-2.49	0.00	-4.54	-2.69	-2.52	-2.55	-2.58	-2.48	-2.53	0.00	0.00	0.00	0.00	-4.54	0.00	-2.42	-2.45
TCGA-HZ-8638-10A-01D-2396-08_PAAD	-2.56	-2.67	-2.63	-2.89	-2.64	-2.65	-2.53	-2.48	-2.50	0.00	-4.41	0.00	-4.41	-4.11	-3.11	-2.75	-2.50
TCGA-HZ-A49G-10A-01D-A26I-08_PAAD	-2.44	-2.71	-2.65	-2.87	-2.43	-2.52	-2.50	-2.50	-2.44	-4.15	-2.95	-2.76	0.00	-3.76	-3.09	-2.70	-2.46
TCGA-HZ-A49H-10A-01D-A26I-08_PAAD	-2.49	0.00	0.00	-2.61	-2.44	-2.38	-2.48	-2.51	-2.40	0.00	-4.14	0.00	0.00	-4.14	0.00	-2.40	-2.44
TCGA-HZ-A49I-10A-01D-A26I-08_PAAD	-2.37	-2.68	-2.63	-2.79	-2.58	-2.60	-2.52	-2.47	-2.36	0.00	0.00	0.00	0.00	-4.79	-2.92	-2.65	-2.42
TCGA-HZ-A4BH-10A-01D-A26I-08_PAAD	-2.44	0.00	-4.17	-2.59	-2.52	-2.53	-2.53	-2.56	-2.64	-3.36	-2.90	0.00	-2.73	-2.61	0.00	-2.65	-2.47
TCGA-HZ-A4BK-10A-01D-A26I-08_PAAD	-2.39	-2.45	-2.47	0.00	-3.63	-3.55	-2.44	-2.50	-2.39	-4.33	-4.33	-4.03	0.00	-4.33	-2.77	-3.63	-2.32
TCGA-HZ-A77O-10A-01D-A33W-08_PAAD	-2.59	0.00	0.00	-2.88	-2.59	-2.57	-2.57	-2.57	-2.82	-3.26	-2.96	0.00	-2.74	-2.66	0.00	-2.74	-2.53
TCGA-HZ-A77P-10A-01D-A33W-08_PAAD	-2.49	-2.66	-2.60	-2.82	-2.66	-2.58	-2.57	-2.43	-2.43	0.00	0.00	0.00	-4.39	0.00	-2.91	-2.68	-2.48

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-IA-A40U-10A-01D-A25F-10_KIRP	-2.64	-2.49	-2.47	-3.98	-2.51	-2.46	-2.44	-2.49	-2.64	-3.42	-2.43	-2.52	-2.61	-2.59	0.00	-2.65	-2.56
TCGA-IA-A40X-10A-01D-A25F-10_KIRP	-2.44	-2.54	-2.66	-2.83	-2.42	-2.37	-2.30	-2.44	-2.33	0.00	-3.04	-2.72	0.00	0.00	-3.00	-2.75	-2.37
TCGA-IA-A40Y-10A-01D-A25F-10_KIRP	-2.41	-2.52	-2.51	-2.77	-2.52	-2.46	-2.32	-2.28	-2.20	0.00	0.00	0.00	0.00	0.00	-2.87	-2.54	-2.30
TCGA-IB-7645-10A-01D-2201-08_PAAD	-2.47	-2.68	-2.68	-2.83	-2.61	-2.64	-2.56	-2.54	-2.52	0.00	-4.47	-4.47	0.00	-4.47	-2.83	-3.87	-2.46
TCGA-IB-7890-10A-01D-2201-08_PAAD	-2.58	-2.72	-2.69	-2.88	-2.66	-2.70	-2.64	-2.57	-2.45	0.00	-4.52	-4.52	-4.52	-4.52	-3.00	-2.67	-2.55
TCGA-IB-7891-10A-01D-2201-08_PAAD	-2.52	-3.88	-4.48	-2.54	-2.54	-2.57	-2.58	-2.55	-2.56	0.00	0.00	-4.48	0.00	-4.48	0.00	-2.51	-2.52
TCGA-IB-7893-10A-01D-2201-08_PAAD	-2.56	-2.69	-2.66	-2.88	-2.65	-2.64	-2.60	-2.56	-2.46	0.00	-4.17	-3.87	-3.87	-4.00	0.00	-2.59	-2.48
TCGA-IB-7897-10A-01D-2201-08_PAAD	-2.54	-4.48	-4.18	-2.54	-2.56	-2.56	-2.57	-2.42	-2.46	0.00	0.00	0.00	0.00	-4.48	0.00	-2.41	-2.49
TCGA-IB-8126-10A-01D-2396-08_PAAD	-2.59	0.00	-4.46	-2.77	-2.55	-2.59	-2.63	-2.66	-2.64	-3.38	-2.85	-3.86	-2.73	-2.67	0.00	-2.77	-2.53
TCGA-IB-8127-10A-01D-2396-08_PAAD	-2.56	-2.67	-2.63	-2.82	-2.60	-2.66	-2.55	-2.48	-2.46	0.00	0.00	0.00	-4.44	0.00	0.00	-2.41	-2.50
TCGA-IB-A5SO-10A-01D-A32N-08_PAAD	-2.60	-2.80	-2.74	-2.92	-2.49	-2.61	-2.65	-2.59	-2.77	-3.39	-2.69	-2.63	0.00	-2.68	0.00	-2.84	-2.55
TCGA-IB-A5SP-10A-01D-A32N-08_PAAD	-2.39	-2.66	-2.64	-2.91	-2.59	-2.62	-2.68	-2.74	-2.62	0.00	-2.86	-2.74	0.00	-2.64	-2.95	0.00	-2.51
TCGA-IB-A5SQ-10A-01D-A32N-08_PAAD	-2.48	-2.69	-2.61	-2.85	-2.69	-2.63	-2.55	-2.44	-2.42	0.00	0.00	0.00	0.00	0.00	-2.93	-2.72	-2.40
TCGA-IB-A5SS-10A-01D-A32N-08_PAAD	-2.53	-2.74	-2.71	-2.81	-2.63	-2.61	-2.61	-2.47	-2.51	0.00	0.00	0.00	0.00	0.00	-2.97	-2.69	-2.47
TCGA-IB-A5ST-10A-01D-A32N-08_PAAD	-2.43	0.00	0.00	-2.77	-2.56	-2.61	-2.64	-2.50	-2.74	-3.28	-2.83	0.00	-2.78	-2.71	0.00	-2.70	-2.54
TCGA-IB-A6UF-10A-01D-A33W-08_PAAD	-2.59	-2.62	-2.63	0.00	-2.61	-2.60	-2.65	-2.58	-2.62	0.00	-2.81	-2.65	0.00	0.00	0.00	-2.48	-2.57
TCGA-IB-A6UG-10A-01D-A33W-08_PAAD	-2.40	0.00	0.00	-2.72	-2.55	-2.55	-2.55	-2.48	-2.47	0.00	-4.42	0.00	0.00	0.00	-2.97	-2.71	-2.50
TCGA-IE-A4EH-10A-01D-A24N-09_SARC	-2.89	-4.21	-4.51	-3.03	-2.59	-2.55	-2.54	-2.53	-2.56	-3.30	-2.94	-4.21	-2.77	-2.75	0.00	-2.86	-2.59
TCGA-IE-A4EI-10A-01D-A24N-09_SARC	-2.76	-3.99	0.00	-3.01	-2.48	-2.50	-2.50	-2.51	-2.34	0.00	-4.47	-4.47	-3.99	-4.47	-2.85	-2.76	-2.57
TCGA-IE-A4EJ-10A-01D-A24N-09_SARC	-2.77	-2.69	-2.67	-3.45	-2.53	-2.58	-2.50	-2.53	-2.48	0.00	-2.70	-2.69	0.00	0.00	-3.05	-2.86	-2.74
TCGA-IE-A4EK-10A-01D-A24N-09_SARC	-2.75	-4.20	-3.90	-2.94	-2.50	-2.53	-2.48	-2.39	-2.39	0.00	0.00	-4.02	-4.50	-4.02	0.00	-2.48	-2.63
TCGA-IE-A6BZ-10A-01D-A307-09_SARC	-2.85	-4.68	0.00	-2.91	-2.53	-2.57	-2.48	-2.61	-2.42	0.00	0.00	0.00	0.00	0.00	-2.81	0.00	-2.64
TCGA-IH-A3EA-10A-01D-A20D-08_SKCM	-2.48	-2.63	-2.70	-2.79	-2.67	-2.68	-2.51	-2.62	-2.71	-3.34	-2.79	0.00	-2.75	-2.63	0.00	-2.68	-2.48
TCGA-IK-7675-10A-01D-2086-08_LGG	-2.58	-2.80	-2.76	-2.84	-2.51	-2.61	-2.60	-2.62	-2.60	0.00	-2.87	-2.71	0.00	0.00	0.00	-2.49	-2.52
TCGA-IK-8125-10A-01D-2253-08_LGG	-2.44	-2.67	-2.77	0.00	-2.55	-2.60	-2.71	-2.66	-2.66	-3.34	-2.64	-2.71	-2.88	-2.72	-3.17	0.00	-2.52
TCGA-IM-A3EB-10A-01D-A202-08_THCA	-2.54	-2.79	-2.72	-2.90	-2.49	-2.62	-2.60	-2.57	-2.49	0.00	-2.95	-2.76	0.00	-4.24	0.00	-2.46	-2.54
TCGA-IM-A3ED-10A-01D-A202-08_THCA	-2.53	0.00	0.00	-2.70	-2.52	-2.63	-2.56	-2.50	-2.53	0.00	0.00	0.00	0.00	0.00	-3.01	-2.68	-2.57
TCGA-IM-A3U2-10A-01D-A22D-08_THCA	-2.49	0.00	0.00	-2.71	-2.53	-2.52	-2.55	-2.59	-2.44	0.00	0.00	-4.48	0.00	-4.01	0.00	-2.55	-2.48
TCGA-IM-A3U3-10A-01D-A22D-08_THCA	-2.57	-2.71	-2.79	-2.89	-2.45	-2.59	-2.56	-2.57	-2.45	0.00	-2.93	-2.67	0.00	0.00	-3.02	-2.73	-2.50
TCGA-IM-A41Y-10A-01D-A23U-08_THCA	-2.54	-3.92	-4.39	-2.58	-2.42	-2.57	-2.53	-2.58	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.52
TCGA-IM-A41Z-10A-01D-A23K-08_THCA	-2.63	-2.80	-2.76	-2.93	-2.56	-2.69	-2.74	-2.68	-2.78	-3.40	-2.77	-2.67	-3.86	-2.72	0.00	-2.82	-2.57
TCGA-IM-A420-10A-01D-A23K-08_THCA	-2.66	-2.72	-2.72	-2.89	-2.64	-2.73	-2.66	-2.49	-2.53	-4.61	-4.61	-4.31	0.00	-4.61	0.00	-2.45	-2.57
TCGA-IM-A4EB-10A-01D-A25A-08_THCA	-2.51	-4.06	-3.88	-2.83	-2.55	-2.58	-2.58	-2.48	-2.52	0.00	0.00	0.00	0.00	0.00	-2.95	-2.67	-2.52
TCGA-IN-7806-10A-01D-2053-08_STAD	-2.45	0.00	0.00	-2.48	-2.46	-2.46	-2.50	-2.50	-2.45	0.00	-4.40	0.00	0.00	-4.40	0.00	-2.48	-2.37
TCGA-IN-7808-10A-01D-2201-08_STAD	-2.44	0.00	0.00	-2.71	-2.46	-2.54	-2.61	-2.57	-2.76	-3.25	-2.79	-2.84	-2.97	-2.72	0.00	-2.85	-2.54
TCGA-IN-8462-10A-01D-2341-08_STAD	-2.51	-2.70	-2.69	-2.89	-2.65	-2.67	-2.60	-2.58	-2.51	0.00	0.00	0.00	0.00	0.00	-3.05	-2.63	-2.51
TCGA-IN-8663-10A-01D-2394-08_STAD	-2.54	-2.48	-2.52	-3.73	-4.12	-4.12	-2.51	-2.53	-2.45	-4.42	-3.95	0.00	-4.12	-3.82	0.00	-2.53	-2.43
TCGA-IN-A6RI-10A-01D-A32N-08_STAD	-2.60	0.00	0.00	-2.61	-2.61	-2.64	-2.62	-2.65	-2.57	0.00	0.00	0.00	0.00	-4.60	0.00	-2.55	-2.53
TCGA-IN-A6RJ-10A-21D-A33W-08_STAD	-2.51	0.00	-4.47	-2.69	-2.49	-2.52	-2.52	-2.54	-2.52	0.00	0.00	0.00	0.00	-4.47	-2.95	-2.74	-2.49
TCGA-IN-A6RL-10A-01D-A32N-08_STAD	-2.70	-2.78	-2.77	-4.42	-2.62	-2.70	-2.71	-2.76	0.00	-3.38	-2.76	-2.80	-2.77	-2.76	0.00	0.00	-2.68
TCGA-IN-A6RN-10A-01D-A33W-08_STAD	-2.51	0.00	0.00	-2.72	-2.52	-2.57	-2.55	-2.47	-2.46	0.00	0.00	0.00	0.00	0.00	-3.07	-2.69	-2.44
TCGA-IN-A6RO-10A-01D-A33W-08_STAD	-2.45	0.00	-4.53	-2.78	-2.54	-2.55	-2.52	-2.51	-2.53	-3.35	0.00	0.00	0.00	0.00	0.00	-2.56	-2.46
TCGA-IN-A6RP-10A-01D-A33W-08_STAD	-2.52	0.00	0.00	-2.76	-2.58	-2.62	-2.59	-2.54	-2.64	-3.35	-2.89	-2.78	0.00	-2.70	-3.13	0.00	-2.57
TCGA-IN-A6RR-10A-01D-A32N-08_STAD	-2.63	-2.89	-2.82	-3.04	-2.59	-2.71	-2.76	-2.74	-2.76	-3.48	-2.74	-2.80	-2.88	-2.76	0.00	-2.81	-2.64
TCGA-IP-7968-10A-01D-2201-08_STAD	-2.51	0.00	0.00	-2.76	-2.46	-2.48	-2.53	-2.49	-2.39	0.00	0.00	0.00	0.00	0.00	-3.06	-2.73	-2.40
TCGA-IQ-7630-10A-01D-2078-08_HNSC	-2.59	-2.78	-2.71	-2.91	-2.53	-2.64	-2.67	-2.61	-2.73	-3.41	-2.73	-2.73	-2.81	-2.72	0.00	-2.79	-2.56
TCGA-IQ-7631-10A-01D-2078-08_HNSC	-2.54	-3.75	-4.45	-2.68	-2.45	-2.51	-2.54	-2.63	-2.60	-3.37	-2.96	-3.97	-2.76	-2.65	0.00	-2.79	-2.47
TCGA-IQ-7632-10A-01D-2078-08_HNSC	-2.57	-4.16	-2.70	-2.80	-2.42	-2.53	-2.57	-2.62	-2.48	0.00	-2.90	0.00	-2.75	-3.69	-2.93	0.00	-2.44
TCGA-IQ-A61E-10A-01D-A30H-08_HNSC	-2.43	0.00	-4.65	-2.67	-2.42	-2.45	-2.49	-2.44	-2.42	0.00	0.00	0.00	0.00	0.00	-3.00	-2.74	-2.39
TCGA-IQ-A61G-10A-01D-A30H-08_HNSC	-2.42	-2.76	0.00	-2.93	-2.43	-2.49	-2.50	-2.50	-2.65	-3.30	-2.91	0.00	-2.82	-2.64	-3.06	0.00	-2.39
TCGA-IQ-A61H-10A-01D-A30H-08_HNSC	-2.37	0.00	0.00	-2.66	-2.44	-2.47	-2.49	-2.40	-2.37	0.00	0.00	0.00	-4.71	-4.71	-2.97	-2.67	-2.40
TCGA-IQ-A61I-10A-01D-A30H-08_HNSC	-2.41	0.00	0.00	-2.58	-2.48	-2.51	-2.47	-2.44	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.40
TCGA-IQ-A61J-10A-01D-A30H-08_HNSC	-2.46	0.00	-4.70	-2.90	-2.49	-2.52	-2.54	-2.54	-2.68	-3.38	-2.97	0.00	-2.67	-2.71	0.00	-2.86	-2.43
TCGA-IQ-A61K-10A-01D-A30H-08_HNSC	-2.50	-2.70	-2.72	-2.82	-2.43	-2.53	-2.53	-2.58	-2.58	0.00	-2.93	-2.65	0.00	0.00	0.00	-2.51	-2.42
TCGA-IQ-A61L-10A-01D-A30H-08_HNSC	-2.54	-2.55	-2.71	0.00	-2.68	-2.69	-2.71	-2.77	-4.42	-3.44	-2.59	-2.69	-2.59	-2.49	0.00	0.00	-2.48
TCGA-IQ-A61O-10A-01D-A30H-08_HNSC	-2.48	0.00	-4.69	-2.52	-2.45	-2.47	-2.47	-2.47	-2.42	0.00	0.00	0.00	0.00	0.00	-3.01	-2.72	-2.40
TCGA-IR-A3L7-10A-01D-A20U-09_CESC	-2.76	-2.69	-2.81	-3.42	-2.76	-2.72	-2.43	-2.44	-2.37	-3.42	-4.46	-4.46	-4.46	-4.16	0.00	-2.49	-2.62
TCGA-IR-A3LA-10A-01D-A22X-09_CESC	-2.72	0.00	0.00	-3.05	-2.49	-2.53	-2.51	-2.50	-2.66	-3.41	-2.84	0.00	-2.71	-2.69	-2.93	-3.89	-2.62
TCGA-IR-A3LB-10A-01D-A243-09_CESC	-2.90	0.00	-4.53	-3.04	-2.55	-2.49	-2.53	-2.61	-2.64	-3.45	-2.74	0.00	-2.73	-2.69	0.00	-2.73	-2.64
TCGA-IR-A3LC-10A-01D-A20U-09_CESC	-2.72	-2.59	-2.71	-3.38	-2.66	-2.71	-2.42	-2.42	-2.39	0.00	-3.90	-4.38	-4.38	-4.08	0.00	-2.44	-2.53
TCGA-IR-A3LF-10A-01D-A22X-09_CESC	-2.68	0.00	-4.52	-2.99	-2.52	-2.49	-2.46	-2.46	-2.33	0.00	-4.52	-4.52	0.00	0.00	0.00	-2.38	-2.54
TCGA-IR-A3LH-10A-01D-A20U-09_CESC	-2.86	-2.80	-2.80	-3.45	-2.58	-2.57	-2.58	-2.72	-2.68	-3.58	-2.68	-2.86	-2.80	-2.82	-3.04	-4.49	-2.65
TCGA-IR-A3LI-10A-01D-A20U-09_CESC	-2.74	-4.43	-4.13	-2.99	-2.52	-2.52	-2.49	-2.46	-2.41	-4.43	-4.13	-4.43	0.00	-4.43	0.00	-2.47	-2.56
TCGA-IR-A3LK-10A-01D-A20U-09_CESC	-2.67	-2.51	-2.54	-4.47	-3.99	-3.99	-2.47	-2.44	-2.55	-3.35	-2.78	0.00	-2.66	-2.64	-2.86	-3.99	-2.60
TCGA-IR-A3LL-10A-01D-A20U-09_CESC	-2.81	-4.04	-4.04	-3.02	-2.47	-2.52	-2.47	-2.52	-2.72	-3.43	-2.68	-4.51	-2.73	-2.77	0.00	-2.74	-2.62
TCGA-IS-A3K6-10A-01D-A21Q-09_SARC	-2.70	-2.62	-2.67	-3.29	-2.63	-2.66	-2.36	-2.55	-2.37	0.00	0.00	0.00	-4.37	-4.07	0.00	-2.53	-2.56
TCGA-IS-A3K7-10A-01D-A21Q-09_SARC	-2.79	-2.64	-2.65	-3.16	-2.68	-2.63	-2.45	-2.47	-2.40	0.00	0.00	0.00	-4.41	0.00	0.00	-2.48	-2.48
TCGA-IS-A3K8-10A-01D-A21Q-09_SARC	-2.90	0.00	-4.43	-3.01	-2.49	-2.48	-2.47	-2.54	-2.42	0.00	-4.43	0.00	0.00	0.00	-2.90	-2.76	-2.54
TCGA-IS-A3KA-10A-01D-A21Q-09_SARC	-2.87	-2.81	-2.92	-3.31	-2.54	-2.59	-2.62	-2.56	-2.67	-3.49	-2.69	-2.63	-4.26	-2.75	-3.09	-4.56	-2.75
TCGA-IW-A3M4-10B-01D-A21Q-09_SARC	-2.88	-2.74	-2.82	-3.34	-2.57	-2.60	-2.62	-2.68	-2.76	-3.44	-2.63	-2.75	-2.76	-2.75	0.00	-2.81	-2.69
TCGA-IW-A3M5-10A-01D-A21Q-09_SARC	-2.72	-4.14	-4.44	-3.08	-2.50	-2.51	-2.44	-2.53	-2.37	0.00	0.00	0.00	0.00	0.00	-3.01	-2.77	-2.58
TCGA-IW-A3M6-10A-01D-A21Q-09_SARC	-2.79	-4.57	0.00	-3.21	-2.61	-2.56	-2.63	-2.59	-2.68	-3.45	-2.85	0.00	-2.81	-2.70	0.00	-2.82	-2.69
TCGA-IZ-8195-10A-01D-2396-08_KIRP	-2.57	-4.54	-4.54	-2.61	-2.60	-2.63	-2.62	-2.49	-2.50	0.00	-4.24	-4.24	0.00	0.00	0.00	-2.46	-2.55
TCGA-IZ-8196-10A-01D-2396-08_KIRP	-2.58	-4.52	0.00	-2.80	-2.60	-2.60	-2.67	-2.57	-2.64	0.00	-4.52	0.00	-4.52	0.00	0.00	-2.39	-2.56
TCGA-IZ-A6M8-10A-01D-A31X-10_KIRP	-2.37	-2.54	-2.71	-2.62	-2.68	-2.58	-2.31	-2.46	-2.31	0.00	0.00	0.00	0.00	0.00	-2.68	0.00	-2.37
TCGA-IZ-A6M9-10A-01D-A31X-10_KIRP	-2.42	0.00	0.00	-2.58	-2.44	-2.37	-2.38	-2.39	-2.57	-3.47	-2.81	0.00	-2.68	-2.68	-3.09	-3.87	-2.45
TCGA-J1-A4AH-10A-01D-A24F-08_LUSC	-2.58	0.00	-4.18	-2.81	-2.57	-2.57	-2.59	-2.63	-2.68	-3.25	-2.86	0.00	-2.73	-2.71	0.00	-2.75	-2.55
TCGA-J2-8192-10A-01D-2238-08_LUAD	-2.42	-2.69	-2.69	-2.82	-2.60	-2.68	-2.56	-2.52	-2.65	-3.39	-2.91	-4.53	-2.79	-2.65	-3.01	0.00	-2.50
TCGA-J2-8194-10A-01D-2238-08_LUAD	-2.40	-4.44	-4.44	-2.71	-2.50	-2.44	-2.52	-2.56	-2.48	0.00	0.00	0.00	-4.44	0.00	-3.01	-2.60	-2.42
TCGA-J2-A4AD-10A-01D-A24F-08_LUAD	-2.57	-2.63	-2.67	-2.82	-2.63	-2.67	-2.59	-2.58	-2.53	0.00	0.00	0.00	0.00	-4.46	-2.89	-4.46	-2.52
TCGA-J2-A4AE-10A-01D-A24F-08_LUAD	-2.52	0.00	0.00	-2.71	-2.52	-2.54	-2.57	-2.55	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.50
TCGA-J2-A4AG-10A-01D-A24F-08_LUAD	-2.65	-2.76	-2.80	-2.95	-2.56	-2.68	-2.72	-2.56	-2.84	-3.35	-2.69	-2.73	-4.58	-2.77	0.00	-2.77	-2.68
TCGA-J4-8198-10A-01D-2260-08_PRAD	-2.63	-2.81	-2.79	-2.90	-2.53	-2.56	-2.63	-2.67	-2.71	-3.35	-2.70	-2.78	-2.81	-2.67	0.00	-2.75	-2.59
TCGA-J4-8200-10A-01D-A29Q-08_PRAD	-2.57	-2.51	-2.77	-2.95	-2.52	-2.60	-2.63	-2.60	-2.71	-3.26	-2.77	-2.79	-2.75	-2.65	0.00	-2.87	-2.53
TCGA-J4-A67K-10A-01D-A30H-08_PRAD	-2.41	-4.62	0.00	-2.66	-2.43	-2.46	-2.47	-2.52	-2.38	0.00	0.00	0.00	0.00	0.00	-3.00	-2.68	-2.34
TCGA-J4-A67L-10A-01D-A30H-08_PRAD	-2.42	-2.71	-2.62	-2.80	-2.62	-2.62	-2.48	-2.50	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.42	-2.37
TCGA-J4-A67M-10A-01D-A30H-08_PRAD	-2.46	-2.68	-2.61	-2.79	-2.57	-2.66	-2.51	-2.48	-2.40	0.00	0.00	0.00	0.00	-4.63	0.00	-2.39	-2.41
TCGA-J4-A67N-10A-01D-A30H-08_PRAD	-2.44	0.00	-4.66	-2.66	-2.48	-2.51	-2.59	-2.55	-2.65	-3.45	-2.94	0.00	-2.73	-2.65	0.00	-2.84	-2.47
TCGA-J4-A67O-10A-01D-A30H-08_PRAD	-2.46	0.00	-4.60	-2.56	-2.45	-2.47	-2.49	-2.48	-2.43	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.40
TCGA-J4-A67Q-10A-01D-A30H-08_PRAD	-2.58	-2.77	-2.74	0.00	-2.50	-2.59	-2.52	-2.60	-2.85	-3.49	-2.81	-2.56	0.00	-2.70	0.00	-2.82	-2.44
TCGA-J4-A67R-10A-01D-A30H-08_PRAD	-2.46	0.00	0.00	-2.66	-2.43	-2.47	-2.50	-2.54	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.39
TCGA-J4-A67S-10A-01D-A30H-08_PRAD	-2.42	-2.67	-2.65	-2.87	-2.62	-2.61	-2.49	-2.52	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.39
TCGA-J4-A67T-10A-01D-A30X-08_PRAD	-2.66	-2.78	-2.80	-3.00	-2.76	-2.80	-2.69	-2.64	-2.75	-3.60	-2.98	0.00	-2.84	-2.75	-3.16	0.00	-2.60
TCGA-J4-A6G1-10A-01D-A30X-08_PRAD	-2.60	0.00	-4.55	-2.85	-2.58	-2.62	-2.69	-2.65	-2.74	-3.40	-3.03	0.00	-2.86	-2.71	-3.22	0.00	-2.58
TCGA-J4-A6G3-10A-01D-A30X-08_PRAD	-2.45	0.00	0.00	-2.68	-2.54	-2.60	-2.66	-2.61	-2.49	0.00	0.00	0.00	-4.23	0.00	0.00	-2.56	-2.54
TCGA-J4-A6M7-10A-01D-A31J-08_PRAD	-2.50	-4.42	0.00	-2.67	-2.50	-2.54	-2.61	-2.59	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.44

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-J7-6720-10A-01D-2136-08_KIRP	-2.58	-2.73	-2.70	-2.88	-2.73	-2.64	-2.55	-2.53	-2.67	-3.30	-2.93	0.00	-2.78	-2.68	-2.97	-3.93	-2.51
TCGA-J7-8537-10A-01D-2396-08_KIRP	-2.59	-2.63	-2.59	-3.90	-3.50	-3.72	-2.63	-2.55	-2.66	-3.20	-2.86	-2.63	0.00	-2.62	0.00	-2.68	-2.56
TCGA-J8-A3NZ-10A-01D-A21A-08_THCA	-2.46	-2.73	-2.71	-2.74	-2.67	-2.60	-2.57	-2.56	-2.49	0.00	0.00	0.00	0.00	-4.44	-3.00	-2.62	-2.44
TCGA-J8-A3O0-10A-01D-A21A-08_THCA	-2.54	0.00	0.00	-2.60	-2.53	-2.54	-2.58	-2.66	-2.70	-3.34	-2.86	0.00	-2.86	-2.69	0.00	-2.68	-2.37
TCGA-J8-A3O1-10A-01D-A21A-08_THCA	-2.53	-2.66	-2.78	-2.71	-2.60	-2.61	-2.52	-2.55	-2.42	0.00	0.00	0.00	0.00	-4.43	-2.79	0.00	-2.37
TCGA-J8-A3O2-10A-01D-A23K-08_THCA	-2.52	0.00	0.00	-2.56	-2.49	-2.53	-2.43	-2.50	0.00	-2.99	-2.75	0.00	-2.58	-2.50	0.00	0.00	-2.38
TCGA-J8-A3YD-10A-01D-A22Z-08_THCA	-2.47	-4.35	-4.35	-2.56	-2.48	-2.48	-2.46	-2.53	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.49
TCGA-J8-A3YE-10A-01D-A23K-08_THCA	-2.57	-4.21	-3.67	-2.79	-2.54	-2.64	-2.55	-2.39	-2.48	-4.51	0.00	0.00	0.00	0.00	-3.01	-2.67	-2.55
TCGA-J8-A3YF-10A-01D-A23K-08_THCA	-2.46	-2.68	0.00	-2.88	-2.39	-2.49	-2.51	-2.58	-2.72	-3.27	-2.90	0.00	-2.75	-2.63	0.00	-2.75	-2.37
TCGA-J8-A3YG-10A-01D-A22Z-08_THCA	-2.50	0.00	0.00	-2.58	-2.49	-2.49	-2.52	-2.39	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.40
TCGA-J8-A3YH-10A-01D-A22Z-08_THCA	-2.35	0.00	0.00	-2.71	-2.51	-2.50	-2.53	-2.55	-2.51	0.00	0.00	0.00	0.00	-4.35	-2.81	0.00	-2.41
TCGA-J8-A42S-10A-01D-A23K-08_THCA	-2.63	-2.73	-2.74	-2.91	-2.74	-2.74	-2.66	-2.67	-2.76	-3.25	-2.86	-3.77	-2.79	-2.70	0.00	-2.76	-2.64
TCGA-J8-A4HW-10A-01D-A25A-08_THCA	-2.57	-2.64	-2.61	-4.48	-2.62	-2.62	-2.62	-2.59	-4.00	-3.14	-2.59	-2.58	-4.18	-2.64	0.00	0.00	-2.58
TCGA-J8-A4HY-10A-01D-A25A-08_THCA	-2.48	0.00	-4.73	-2.65	-2.43	-2.50	-2.52	-2.60	-2.74	-3.23	-2.76	-2.78	-2.82	-2.70	0.00	-2.91	-2.48
TCGA-J9-A52B-10A-01D-A26K-08_PRAD	-2.31	0.00	0.00	-2.67	-2.38	-2.49	-2.48	-2.55	-2.47	-4.05	0.00	0.00	-4.35	-3.57	0.00	-2.49	-2.37
TCGA-J9-A52C-10A-01D-A26K-08_PRAD	-2.53	0.00	-4.44	-2.87	-2.45	-2.51	-2.58	-2.61	-2.66	-3.33	-3.01	-4.44	-2.78	-2.63	0.00	-2.69	-2.45
TCGA-J9-A52D-10A-01D-A29Q-08_PRAD	-2.50	0.00	0.00	-2.93	-2.55	-2.52	-2.56	-2.59	-2.71	-3.34	-2.94	0.00	-2.77	-2.67	0.00	-2.77	-2.49
TCGA-J9-A52E-10A-01D-A26K-08_PRAD	-2.56	-2.76	-2.67	-2.94	-2.44	-2.52	-2.57	-2.55	-2.51	0.00	-3.05	-2.70	-4.17	0.00	0.00	-2.53	-2.46
TCGA-JL-A3YW-10B-01D-A23C-09_BRCA	-2.88	-2.59	-2.56	-4.30	-2.62	-2.59	-2.55	-2.62	-2.57	0.00	-2.74	-2.58	-4.30	-4.00	-3.07	-2.90	-2.65
TCGA-JL-A3YX-10A-01D-A22X-09_BRCA	-2.89	-2.77	-2.87	-3.43	-2.66	-2.63	-2.63	-2.56	-2.65	-3.46	-2.73	-2.79	-2.85	-2.83	-3.19	-4.13	-2.73
TCGA-JV-A5VE-10A-01D-A29N-09_SARC	-2.82	-2.71	-2.68	-3.16	-2.75	-2.63	-2.41	-2.52	-2.43	0.00	-4.44	-4.44	-4.44	-4.44	0.00	-2.57	-2.60
TCGA-JV-A5VF-10A-01D-A29N-09_SARC	-2.84	-2.75	-2.80	-3.26	-2.57	-2.59	-2.58	-2.65	-2.55	-4.58	-2.96	-2.73	0.00	0.00	0.00	-2.53	-2.66
TCGA-JW-A5VG-10A-01D-A28E-09_CESC	-2.80	-2.65	-2.78	-3.37	-2.49	-2.45	-2.46	-2.58	-2.47	0.00	-2.89	-2.65	0.00	0.00	-2.74	-4.52	-2.56
TCGA-JW-A5VH-10A-01D-A28E-09_CESC	-2.67	-2.63	-2.68	-3.43	-2.62	-2.66	-2.34	-2.52	-2.35	0.00	-4.21	0.00	-4.51	0.00	0.00	-2.53	-2.56
TCGA-JW-A5VI-10A-01D-A28E-09_CESC	-2.72	-4.54	0.00	-3.01	-2.49	-2.43	-2.41	-2.50	-2.34	0.00	0.00	0.00	0.00	0.00	-2.63	0.00	-2.52
TCGA-JW-A5VJ-10A-01D-A28E-09_CESC	-2.82	-4.55	0.00	-3.10	-2.47	-2.53	-2.43	-2.55	-2.62	-3.55	-2.80	-4.25	-2.71	-2.69	0.00	-2.77	-2.54
TCGA-JW-A5VK-10A-01D-A28E-09_CESC	-2.77	-2.60	-2.69	-3.24	-2.67	-2.67	-2.44	-2.47	-2.35	0.00	-4.54	-4.54	0.00	0.00	0.00	-2.45	-2.55
TCGA-JW-A5VL-10A-01D-A28E-09_CESC	-2.68	-4.16	-4.46	-3.03	-2.54	-2.49	-2.46	-2.54	-2.40	0.00	0.00	0.00	0.00	-4.46	-2.72	-4.46	-2.50
TCGA-JX-A3PZ-10A-01D-A21Q-09_CESC	-2.79	0.00	0.00	-2.96	-2.51	-2.46	-2.46	-2.50	-2.31	0.00	0.00	0.00	0.00	0.00	-2.87	-2.72	-2.51
TCGA-JX-A3Q0-10A-01D-A21Q-09_CESC	-2.72	-4.51	-4.03	-3.02	-2.49	-2.49	-2.45	-2.48	-2.34	0.00	-4.03	-4.51	0.00	-4.51	-3.00	-2.65	-2.53
TCGA-JX-A3Q8-10A-01D-A21Q-09_CESC	-2.79	-4.51	-4.51	-2.95	-2.47	-2.50	-2.42	-2.52	-2.41	0.00	-4.21	-4.04	0.00	0.00	-2.80	0.00	-2.51
TCGA-JX-A5QV-10A-01D-A28E-09_CESC	-2.90	-2.83	-2.89	-3.48	-2.55	-2.60	-2.53	-2.63	-2.69	-3.55	-2.68	-2.87	-2.87	-2.80	0.00	-2.82	-2.68
TCGA-K1-A3PN-10A-01D-A22A-09_SARC	-2.83	0.00	-4.35	-2.89	-2.47	-2.48	-2.39	-2.52	-2.39	0.00	-4.35	0.00	0.00	0.00	0.00	-2.54	-2.56
TCGA-K1-A3PO-10A-01D-A21Q-09_SARC	-2.88	-4.00	-4.48	-3.20	-2.67	-2.53	-2.54	-2.51	-2.69	-3.64	-2.90	-2.76	0.00	-2.77	0.00	-2.77	-2.59
TCGA-K1-A42W-10A-01D-A24N-09_SARC	-2.91	-4.27	0.00	-3.23	-2.53	-2.56	-2.58	-2.61	-3.97	-3.27	-2.70	-2.96	-2.71	-2.64	0.00	0.00	-2.74
TCGA-K4-A3WS-10A-01D-A22Z-08_BLCA	-2.44	-2.48	-2.47	-4.66	0.00	-4.66	-2.49	-2.43	-2.57	-3.38	-2.87	0.00	-2.70	-2.62	0.00	-2.71	-2.42
TCGA-K4-A3WU-10A-01D-A23K-08_BLCA	-2.53	-2.73	-2.71	-2.78	-2.62	-2.68	-2.62	-2.56	-2.53	0.00	0.00	-4.46	0.00	0.00	-3.00	-2.67	-2.49
TCGA-K4-A3WV-10A-01D-A22Z-08_BLCA	-2.39	-2.40	-2.42	0.00	0.00	0.00	-2.44	-2.48	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.47	-2.32
TCGA-K4-A4AB-10A-01D-A289-08_BLCA	-2.48	0.00	0.00	-2.56	-2.47	-2.45	-2.49	-2.53	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.41
TCGA-K4-A4AC-10A-01D-A26K-08_BLCA	-2.53	-2.61	-2.59	-2.96	-2.52	-2.61	-2.57	-2.47	-2.44	0.00	-3.08	-2.78	0.00	0.00	0.00	-2.56	-2.51
TCGA-K4-A54R-10A-01D-A26K-08_BLCA	-2.44	-2.60	-2.62	-2.80	-2.57	-2.58	-2.49	-2.50	-2.44	0.00	-4.40	0.00	0.00	0.00	-2.89	-2.61	-2.37
TCGA-K4-A5RH-10A-01D-A30H-08_BLCA	-2.52	0.00	-4.74	-2.57	-2.50	-2.53	-2.46	-2.39	-2.45	-3.34	0.00	0.00	-4.74	0.00	-3.07	-2.83	-2.45
TCGA-K4-A5RI-10A-01D-A289-08_BLCA	-2.50	-2.61	-2.58	0.00	-2.67	-2.72	-2.62	-2.50	-2.46	0.00	-2.85	-2.72	0.00	-4.59	-3.05	-2.72	-2.40
TCGA-K4-A5RJ-10A-01D-A289-08_BLCA	-2.60	-2.69	-2.60	0.00	-2.62	-2.63	-2.65	-2.56	-2.74	-3.47	-2.69	-2.59	-2.89	-2.74	0.00	-2.80	-2.51
TCGA-K4-A6FZ-10A-01D-A31J-08_BLCA	-2.53	0.00	-4.08	-2.74	-2.51	-2.55	-2.53	-2.46	-2.46	0.00	0.00	0.00	0.00	-4.55	-3.02	-2.75	-2.48
TCGA-K4-A6MB-10A-01D-A31J-08_BLCA	-2.47	0.00	0.00	-2.67	-2.54	-2.55	-2.52	-2.45	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.45	-2.43
TCGA-K6-A3WQ-10A-01D-A22A-09_UCEC	-2.82	-2.82	-2.74	-3.39	-2.59	-2.78	-2.44	-2.58	-2.50	0.00	-4.00	-4.30	-4.00	-3.82	0.00	-2.53	-2.60
TCGA-K7-A5RF-10B-01D-A28X-10_LIHC	-2.56	-2.59	-2.71	-2.93	-2.49	-2.39	-2.26	-2.36	-2.51	-3.61	-3.03	-2.59	0.00	0.00	-2.90	-2.56	-2.54
TCGA-K7-A5RG-10A-01D-A28X-10_LIHC	-2.44	-2.49	-2.59	-2.87	-2.36	-2.32	-2.33	-2.39	-2.34	0.00	-2.65	-2.55	0.00	0.00	-2.82	-2.54	-2.54
TCGA-K7-A6G5-10A-01D-A30V-10_LIHC	-2.35	-2.63	-2.68	-2.85	-2.61	-2.63	-2.29	-2.44	-2.58	-3.33	-2.80	0.00	-2.85	-2.65	-2.95	0.00	-2.50
TCGA-KB-A6F5-10A-01D-A33W-08_STAD	-2.60	-2.74	-2.74	-2.85	-2.53	-2.64	-2.62	-2.68	-2.74	-3.31	-2.71	-2.67	0.00	-2.77	0.00	-2.78	-2.54
TCGA-KB-A6F7-10A-01D-A32N-08_STAD	-2.60	0.00	0.00	-2.91	-2.65	-2.68	-2.68	-2.69	-2.72	-3.36	-2.86	0.00	-2.82	-2.80	0.00	-2.83	-2.60
TCGA-KC-A4BL-10A-01D-A25A-08_PRAD	-2.52	0.00	-2.65	-2.81	-2.67	-2.61	-2.62	-2.72	-2.58	0.00	-2.71	0.00	-2.73	-2.56	0.00	-2.73	-2.48
TCGA-KC-A4BN-10A-01D-A25A-08_PRAD	-2.60	-2.70	-2.69	-2.95	-2.51	-2.67	-2.67	-2.60	-2.60	0.00	-2.91	-2.72	0.00	-4.58	-2.96	-4.58	-2.61
TCGA-KC-A4BO-10A-01D-A25A-08_PRAD	-2.54	0.00	-4.48	-2.60	-2.45	-2.55	-2.57	-2.49	-2.50	-4.48	0.00	-4.48	0.00	-4.17	-3.03	-2.79	-2.47
TCGA-KC-A4BR-10A-01D-A25A-08_PRAD	-2.59	-2.78	-2.81	-2.95	-2.55	-2.63	-2.59	-2.68	-2.59	0.00	-2.83	-2.78	-4.68	0.00	0.00	-2.50	-2.53
TCGA-KC-A4BV-10A-01D-A26K-08_PRAD	-2.40	-2.66	-2.58	-2.88	-2.57	-2.61	-2.60	-2.70	-2.51	0.00	-2.82	0.00	-2.74	-2.60	0.00	-2.68	-2.41
TCGA-KC-A7F3-10A-01D-A33W-08_PRAD	-2.50	0.00	0.00	-2.74	-2.46	-2.48	-2.58	-2.45	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.49
TCGA-KC-A7F5-10A-01D-A33W-08_PRAD	-2.57	-4.22	-4.52	-2.57	-2.54	-2.57	-2.63	-2.45	-2.51	0.00	0.00	-3.92	-4.52	-4.22	-3.09	-2.75	-2.46
TCGA-KC-A7F6-10A-01D-A33W-08_PRAD	-2.59	-2.64	-2.62	-3.26	-2.64	-2.70	-2.62	-2.54	-2.70	-3.31	-2.77	-2.65	-3.51	-2.71	0.00	-2.76	-2.58
TCGA-KC-A7FA-10A-01D-A33W-08_PRAD	-2.56	0.00	0.00	-2.79	-2.58	-2.56	-2.57	-2.53	-2.44	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.50
TCGA-KC-A7FD-10A-01D-A33W-08_PRAD	-2.59	-2.72	-2.66	-2.86	-2.46	-2.56	-2.59	-2.66	-2.57	0.00	-2.94	-2.71	0.00	0.00	0.00	-2.62	-2.52
TCGA-KC-A7FE-10A-01D-A33W-08_PRAD	-2.54	0.00	0.00	-2.77	-2.55	-2.54	-2.62	-2.67	-2.65	-3.34	-2.87	0.00	-2.77	-2.66	0.00	-2.73	-2.48
TCGA-KD-A5QS-10A-01D-A27P-09_SARC	-2.67	-4.30	-3.82	-2.84	-2.41	-2.58	-2.62	-2.65	-2.45	0.00	-4.30	-4.00	-4.30	-2.64	0.00	-2.63	-2.74
TCGA-KD-A5QT-10A-01D-A27P-09_SARC	-2.76	0.00	0.00	-3.06	-2.54	-2.55	-2.53	-2.58	-2.67	-3.42	-2.85	-4.53	-2.76	-2.79	-2.95	-4.53	-2.58
TCGA-KD-A5QU-10A-01D-A27P-09_SARC	-2.75	-4.46	0.00	-2.90	-2.50	-2.49	-2.48	-2.49	-2.34	0.00	0.00	0.00	0.00	-4.46	0.00	-2.46	-2.53
TCGA-KF-A41W-10A-01D-A24N-09_SARC	-2.70	-2.74	-2.67	-3.21	-2.76	-2.63	-2.44	-2.49	-2.44	0.00	-4.44	0.00	0.00	-4.44	0.00	-2.41	-2.59
TCGA-KJ-A3U4-10A-01D-A22A-09_UCEC	-2.85	-2.69	-2.73	-3.32	-2.74	-2.69	-2.54	-2.55	-2.41	0.00	-4.25	-4.25	-4.08	-4.25	-2.98	-2.79	-2.64
TCGA-KM-8438-10A-01D-2311-10_KICH	-2.36	-2.60	-2.56	-2.95	-2.66	-2.65	-2.57	-2.73	-2.42	0.00	-2.84	0.00	-2.84	-2.46	0.00	-2.65	-2.22
TCGA-KM-8439-10A-01D-2311-10_KICH	-2.44	-2.48	-2.71	-4.32	-2.75	-2.81	-2.45	-2.53	0.00	-3.09	-2.57	0.00	-2.58	-2.45	0.00	0.00	-2.43
TCGA-KM-8440-10A-01D-2311-10_KICH	-2.48	-4.33	0.00	-2.64	-2.54	-2.27	-2.49	-2.52	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-2.43
TCGA-KM-8441-10A-01D-2311-10_KICH	-2.38	0.00	0.00	-2.60	-2.27	-2.58	-2.43	-2.50	-2.32	0.00	0.00	0.00	0.00	-2.51	0.00	-4.16	-2.46
TCGA-KM-8442-10A-01D-2311-10_KICH	-2.44	0.00	0.00	-2.62	-2.46	-2.38	-2.34	-2.45	-2.26	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.33
TCGA-KM-8443-10A-01D-2311-10_KICH	-2.42	0.00	0.00	-2.58	-2.52	-2.39	-2.35	-2.45	-2.29	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.38
TCGA-KM-8476-10A-01D-2311-10_KICH	-2.35	0.00	0.00	-2.67	-2.47	-2.47	-2.32	-2.45	-2.24	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.32
TCGA-KM-8477-10A-01D-2311-10_KICH	-2.40	-2.43	-2.37	-4.17	0.00	0.00	-2.33	-2.47	-2.45	-3.26	-3.02	0.00	-2.72	-2.64	0.00	-2.75	-2.31
TCGA-KM-8639-10A-01D-2397-10_KICH	-2.31	0.00	0.00	-2.73	-2.34	-2.30	-2.33	-2.40	-2.29	0.00	0.00	0.00	0.00	0.00	0.00	-2.26	-2.38
TCGA-KP-A3VZ-10A-01D-A22A-09_UCEC	-2.75	-2.55	-2.56	0.00	-4.49	-4.19	-2.58	-2.57	-2.57	-3.19	-2.72	-4.49	-2.67	-2.73	0.00	-2.67	-2.58
TCGA-KP-A3W0-10A-01D-A22A-09_UCEC	-2.70	-4.35	-4.35	-2.91	-2.39	-2.51	-2.57	-2.55	-2.49	0.00	0.00	-4.35	0.00	-2.55	-2.73	0.00	-2.65
TCGA-KP-A3W1-10A-01D-A22A-09_UCEC	-2.73	-2.72	-2.77	-3.11	-2.72	-2.79	-2.49	-2.46	-2.48	0.00	-4.59	0.00	0.00	-4.59	-3.02	-2.75	-2.54
TCGA-KP-A3W3-10A-01D-A22A-09_UCEC	-2.81	-4.43	-4.43	-3.07	-2.56	-2.63	-2.53	-2.61	-2.81	-3.23	-2.99	0.00	-2.76	-2.82	-3.13	0.00	-2.66
TCGA-KP-A3W4-10A-01D-A22A-09_UCEC	-2.81	-2.70	-2.77	-3.13	-2.61	-2.51	-2.51	-2.59	-2.46	0.00	-4.55	0.00	-4.25	-3.94	-3.02	-2.73	-2.64
TCGA-KQ-A41N-10D-01D-A339-08_BLCA	-2.59	0.00	-2.70	-2.91	-2.42	-2.58	-2.57	-2.62	-2.54	0.00	-2.95	0.00	-2.73	0.00	-2.93	0.00	-2.48
TCGA-KQ-A41P-10F-01D-A339-08_BLCA	-2.54	0.00	0.00	-2.82	-2.48	-2.49	-2.54	-2.54	-2.54	0.00	0.00	-4.43	0.00	0.00	0.00	-2.42	-2.45
TCGA-KQ-A41Q-10D-01D-A339-08_BLCA	-2.54	-2.52	-2.52	0.00	-2.63	-2.66	-2.55	-2.60	-2.45	0.00	-2.93	-2.69	0.00	0.00	0.00	-2.62	-2.47
TCGA-KQ-A41S-10C-01D-A339-08_BLCA	-2.53	-2.56	-2.53	0.00	0.00	0.00	-2.53	-2.51	-2.64	-3.31	-2.78	-2.62	0.00	-2.62	-2.91	0.00	-2.49
TCGA-KT-A74X-10A-01D-A329-08_LGG	-2.35	-2.63	-2.63	-2.77	-2.61	-2.58	-2.53	-2.59	-2.38	0.00	0.00	0.00	0.00	0.00	0.00	-2.55	-2.45
TCGA-KU-A66S-10A-01D-A30H-08_HNSC	-2.41	-4.58	0.00	-2.54	-2.38	-2.52	-2.53	-2.59	-2.51	0.00	-4.58	0.00	0.00	-2.47	0.00	-2.57	-2.41
TCGA-KU-A66T-10A-01D-A30H-08_HNSC	-2.55	-2.80	-2.72	-2.94	-2.50	-2.56	-2.57	-2.55	-2.69	-3.53	-2.73	-2.72	-2.71	-2.69	0.00	-2.86	-2.46
TCGA-KU-A6H7-10A-01D-A31J-08_HNSC	-2.55	0.00	0.00	-2.60	-2.49	-2.61	-2.59	-2.61	-2.49	0.00	0.00	0.00	0.00	-4.46	-3.08	-2.67	-2.49
TCGA-KV-A6GD-10A-01D-A31X-10_KIRP	-2.50	0.00	0.00	-2.47	-2.46	-2.32	-2.31	-2.40	-2.30	0.00	0.00	0.00	0.00	0.00	-3.07	-2.62	-2.46
TCGA-KV-A6GE-10A-01D-A31X-10_KIRP	-2.34	-2.57	-2.54	-2.97	-2.91	-2.63	-2.27	-2.42	-2.28	-4.11	0.00	0.00	0.00	-3.81	0.00	-2.40	-2.41
TCGA-L3-A4E7-10A-01D-A25A-08_LUSC	-2.66	-2.64	-2.61	-4.08	-2.78	-2.79	-2.69	-2.65	-3.78	-3.24	-2.64	-2.59	-2.75	-2.64	0.00	-3.96	-2.59
TCGA-L3-A524-10A-01D-A25L-08_LUSC	-2.57	-3.68	-3.75	-2.58	-2.57	-2.57	-2.61	-2.51	-2.44	0.00	0.00	0.00	-3.75	-3.83	0.00	-2.59	-2.50
TCGA-L4-A4E5-10A-01D-A24P-08_LUAD	-2.61	-2.77	-2.72	-2.89	-2.68	-2.71	-2.63	-2.53	-2.73	-3.30	-2.85	0.00	-2.74	-2.77	0.00	-2.83	-2.59
TCGA-L4-A4E6-10A-01D-A24F-08_LUAD	-2.59	-2.66	-2.61	0.00	-2.58	-2.65	-2.58	-2.66	-2.53	-3.41	-2.86	-2.64	-4.64	-4.64	0.00	-2.63	-2.51

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-L6-A4EP-10A-01D-A25A-08_THCA	-2.52	0.00	0.00	-2.72	-2.56	-2.53	-2.53	-2.56	-2.52	0.00	-4.25	0.00	0.00	0.00	0.00	-2.57	-2.46
TCGA-L6-A4EQ-10A-01D-A25A-08_THCA	-2.40	0.00	0.00	-2.57	-2.45	-2.47	-2.49	-2.59	-2.58	-3.36	-2.95	0.00	-2.75	-2.57	0.00	-2.85	-2.38
TCGA-L6-A4ET-10A-01D-A25A-08_THCA	-2.64	-2.74	-2.79	-2.97	-2.56	-2.65	-2.69	-2.59	-2.53	0.00	-2.88	-2.84	-3.88	-3.88	-3.23	-2.74	-2.60
TCGA-L6-A4EU-10A-01D-A25A-08_THCA	-2.64	-2.77	-2.73	-2.96	-2.50	-2.66	-2.68	-2.54	-2.55	0.00	-2.93	-2.79	0.00	0.00	-3.15	-2.86	-2.63
TCGA-L9-A443-10A-01D-A24F-08_LUAD	-2.43	0.00	-4.50	-2.77	-2.56	-2.58	-2.58	-2.42	-2.48	0.00	0.00	0.00	-4.50	-4.50	-3.07	-2.69	-2.53
TCGA-L9-A444-10A-01D-A24F-08_LUAD	-2.66	-2.74	-2.75	-2.91	-2.54	-2.69	-2.70	-2.57	-2.74	-3.54	-2.73	-2.78	-2.80	-2.74	0.00	-2.82	-2.64
TCGA-LA-A446-10A-01D-A25A-08_LUSC	-2.61	-4.04	-4.04	-2.76	-2.58	-2.58	-2.61	-2.58	-2.69	-3.40	-2.84	-4.21	-2.75	-2.68	0.00	-2.77	-2.50
TCGA-LB-A7SX-10A-01D-A33W-08_PAAD	-2.54	0.00	0.00	-2.60	-2.57	-2.55	-2.53	-2.58	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.49
TCGA-LC-A66R-10A-01D-A30H-08_BLCA	-2.46	-2.52	-2.49	-4.72	-2.63	-2.63	-2.73	-2.79	-2.68	0.00	-2.64	-2.64	-2.74	-2.63	0.00	-2.68	-2.43
TCGA-LD-A66U-10A-01D-A31U-09_BRCA	-2.93	-2.75	-2.75	-3.69	-2.46	-2.50	-2.52	-2.56	-2.62	-3.52	-2.62	-2.76	-2.69	-2.71	0.00	-2.86	-2.59
TCGA-LG-A6GG-10A-01D-A30V-10_LIHC	-2.40	-2.52	-2.66	-2.89	-2.63	-2.53	-2.35	-2.42	-2.34	0.00	0.00	0.00	0.00	0.00	-2.89	-2.60	-2.45
TCGA-LI-A67I-10A-01D-A307-09_SARC	-2.85	-2.70	-2.75	-3.28	-2.72	-2.73	-2.60	-2.51	-2.45	0.00	0.00	-4.73	0.00	0.00	-2.96	-2.81	-2.71
TCGA-LL-A440-10A-01D-A243-09_BRCA	-2.65	-4.33	-4.33	-3.07	-2.50	-2.56	-2.44	-2.56	-2.46	0.00	-3.73	-3.85	0.00	0.00	0.00	-2.65	-2.57
TCGA-LL-A441-10A-01D-A243-09_BRCA	-2.82	-2.67	-2.72	-3.41	-2.49	-2.52	-2.49	-2.46	-2.39	0.00	-2.97	-2.86	-4.36	-4.06	-2.97	0.00	-2.75
TCGA-LL-A50Y-10A-01D-A25Q-09_BRCA	-2.74	-4.49	-3.79	-3.03	-2.50	-2.52	-2.52	-2.58	-2.45	-4.49	-4.49	-4.01	0.00	-4.01	-2.97	-2.78	-2.58
TCGA-LL-A5YL-10A-01D-A29N-09_BRCA	-2.90	-2.76	-2.72	-3.38	-2.73	-2.69	-2.49	-2.53	-2.62	-3.60	-2.88	0.00	-2.77	-2.73	-2.88	-4.02	-2.64
TCGA-LL-A5YM-10A-01D-A28E-09_BRCA	-2.82	-2.64	-2.66	-3.11	-2.68	-2.76	-2.45	-2.46	-2.41	0.00	0.00	0.00	0.00	0.00	-2.96	-2.80	-2.60
TCGA-LL-A5YN-10A-01D-A28E-09_BRCA	-2.75	-4.17	-4.00	-2.98	-2.48	-2.52	-2.50	-2.49	-2.35	0.00	-4.48	0.00	0.00	0.00	-2.87	-2.69	-2.56
TCGA-LL-A5YO-10A-01D-A28E-09_BRCA	-2.74	-2.63	-2.65	-3.23	-2.68	-2.64	-2.60	-2.73	-2.51	0.00	-2.81	0.00	-2.65	-2.61	0.00	-2.68	-2.56
TCGA-LL-A5YP-10A-01D-A28E-09_BRCA	-2.71	-4.41	-4.41	-3.09	-2.52	-2.46	-2.45	-2.53	-2.46	0.00	0.00	0.00	0.00	0.00	-2.67	0.00	-2.53
TCGA-LL-A6FP-10A-01D-A31U-09_BRCA	-2.82	0.00	-4.44	-2.87	-2.50	-2.46	-2.39	-2.47	-2.33	-4.44	0.00	0.00	-4.13	-3.83	0.00	-2.38	-2.58
TCGA-LL-A6FQ-10A-01D-A31U-09_BRCA	-3.01	0.00	0.00	-2.98	-2.51	-2.48	-2.52	-2.58	-2.50	-3.54	-2.84	0.00	-2.77	-2.76	0.00	-2.73	-2.61
TCGA-LL-A6FR-10B-01D-A31U-09_BRCA	-3.03	0.00	-4.46	-3.10	-2.51	-2.49	-2.47	-2.58	-2.58	-3.46	-2.92	-2.66	0.00	-2.74	0.00	-2.78	-2.54
TCGA-LP-A4AU-10A-01D-A243-09_CESC	-2.87	0.00	0.00	-2.97	-2.51	-2.50	-2.49	-2.55	-2.33	0.00	-4.43	0.00	-4.13	-4.43	0.00	-2.52	-2.50
TCGA-LP-A4AV-10A-01D-A243-09_CESC	-2.75	-4.40	-4.40	-3.04	-2.49	-2.41	-2.46	-2.57	-2.36	0.00	-4.40	0.00	-4.40	0.00	-2.86	-2.62	-2.52
TCGA-LP-A4AW-10A-01D-A243-09_CESC	-2.73	-4.18	-4.48	-3.14	-2.51	-2.48	-2.47	-2.49	-2.34	0.00	0.00	0.00	-4.48	-4.48	-2.91	-2.70	-2.58
TCGA-LP-A4AX-10A-01D-A243-09_CESC	-2.87	-2.81	-2.88	-3.24	-2.51	-2.61	-2.47	-2.45	-2.56	-3.44	-2.89	-2.73	-4.28	0.00	-2.97	-2.92	-2.64
TCGA-LP-A5U2-10A-01D-A28E-09_CESC	-2.68	-2.72	-2.77	-3.53	-2.50	-2.53	-2.46	-2.59	-2.42	0.00	-2.82	-2.73	0.00	0.00	-2.77	0.00	-2.64
TCGA-LP-A5U3-10A-01D-A28E-09_CESC	-2.71	0.00	-4.47	-3.02	-2.48	-2.40	-2.40	-2.43	-2.37	0.00	0.00	0.00	-4.17	0.00	0.00	-2.55	-2.43
TCGA-LQ-A4E4-10A-01D-A25Q-09_BRCA	-2.80	-2.54	-2.62	-4.05	-2.74	-2.74	-2.55	-2.58	-2.51	-4.22	-2.94	-2.82	-4.05	-3.68	0.00	-2.70	-2.59
TCGA-LT-A5Z6-10A-01D-A289-08_BLCA	-2.61	-2.74	-2.75	-2.97	-2.70	-2.68	-2.57	-2.59	-2.75	-3.43	-2.93	0.00	-2.87	-2.61	0.00	-2.73	-2.47
TCGA-M7-A71Y-10A-01D-A329-08_PRAD	-2.46	0.00	-4.44	-2.67	-2.42	-2.50	-2.48	-2.58	-2.42	0.00	0.00	0.00	0.00	-4.44	0.00	-2.58	-2.47
TCGA-M7-A71Z-10A-01D-A329-08_PRAD	-2.57	0.00	-4.26	-2.75	-2.53	-2.57	-2.59	-2.64	-2.70	-3.39	-2.92	0.00	-2.72	-2.65	0.00	-2.87	-2.51
TCGA-M7-A720-10A-01D-A329-08_PRAD	-2.52	-4.51	0.00	-2.59	-2.48	-2.57	-2.61	-2.54	-2.70	-3.34	-3.00	0.00	-2.80	-2.66	0.00	-2.83	-2.46
TCGA-M7-A721-10A-01D-A329-08_PRAD	-2.58	-2.72	-2.69	-2.86	-2.68	-2.72	-2.71	-2.73	-2.73	0.00	-2.84	0.00	-2.80	-2.70	0.00	-2.75	-2.53
TCGA-M7-A723-10A-01D-A329-08_PRAD	-2.69	-2.83	-2.81	-3.00	-2.62	-2.76	-2.74	-2.65	-2.85	-3.43	-2.78	-2.80	-2.85	-2.87	0.00	-2.84	-2.57
TCGA-M7-A724-10A-01D-A329-08_PRAD	-2.47	0.00	0.00	-2.76	-2.52	-2.54	-2.52	-2.68	-2.69	-3.40	-3.02	0.00	-2.71	-2.63	0.00	-2.80	-2.42
TCGA-M7-A725-10A-01D-A329-08_PRAD	-2.66	-2.81	-2.79	-3.01	-2.56	-2.72	-2.79	-2.62	-2.59	0.00	-2.93	-2.81	0.00	-4.71	-3.15	-2.84	-2.65
TCGA-M8-A5N4-10A-01D-A26I-08_PAAD	-2.47	-2.71	-2.65	-2.88	-2.40	-2.50	-2.48	-2.59	-2.48	0.00	-2.90	-2.74	0.00	-4.41	-2.90	-3.81	-2.48
TCGA-MB-A5Y8-10A-01D-A29N-09_SARC	-2.88	-4.10	-4.40	-3.12	-2.55	-2.53	-2.46	-2.60	-2.43	0.00	0.00	0.00	-4.40	0.00	0.00	-2.53	-2.61
TCGA-MB-A5Y9-10A-01D-A29N-09_SARC	-2.89	-2.81	-2.69	-3.33	-2.92	-2.74	-2.51	-2.60	-2.70	-3.30	-2.73	0.00	-2.60	-2.78	0.00	-2.99	-2.63
TCGA-MB-A5YA-10A-01D-A29N-09_SARC	-2.79	-2.64	-2.76	-3.35	-2.66	-2.74	-2.54	-2.52	-2.60	-3.44	-2.88	-4.10	-2.70	-2.71	0.00	-2.82	-2.63
TCGA-MF-A522-10A-01D-A25L-08_LUSC	-2.66	-2.71	-2.71	-2.96	-2.54	-2.68	-2.63	-2.67	-2.53	0.00	-2.86	-2.82	-4.58	-4.58	0.00	-2.64	-2.60
TCGA-MH-A55W-10A-01D-A26P-10_KIRP	-2.37	0.00	0.00	-2.54	-2.43	-2.22	-2.31	-2.42	-2.36	0.00	0.00	0.00	0.00	0.00	-2.72	0.00	-2.34
TCGA-MH-A55Z-10A-01D-A26P-10_KIRP	-2.45	0.00	-2.53	0.00	-2.58	-2.28	-2.30	-2.33	-2.36	0.00	-2.81	0.00	-2.61	-4.30	-2.81	-2.47	-2.40
TCGA-MH-A560-10A-01D-A26P-10_KIRP	-2.36	0.00	-4.29	-2.61	-2.30	-2.27	-2.30	-2.32	-2.20	0.00	-3.99	0.00	0.00	-3.99	0.00	-2.32	-2.41
TCGA-MH-A561-10A-01D-A26P-10_KIRP	-2.47	0.00	0.00	-2.48	-2.47	-2.28	-2.30	-2.42	-2.59	-3.55	-2.82	0.00	-2.70	-2.48	-2.82	0.00	-2.39
TCGA-MH-A562-10A-01D-A26P-10_KIRP	-2.48	-2.60	-2.65	-2.78	-2.44	-2.35	-2.38	-2.46	-2.44	0.00	-2.76	-2.59	-4.36	-4.36	-2.66	-3.89	-2.50
TCGA-MJ-A68H-10A-01D-A307-09_SARC	-2.95	-2.79	-2.82	-3.25	-2.55	-2.61	-2.63	-2.56	-2.50	0.00	-2.95	-2.84	0.00	0.00	0.00	-2.52	-2.73
TCGA-MJ-A68J-10A-01D-A307-09_SARC	-3.00	-2.85	-2.75	0.00	-2.59	-2.73	-2.70	-2.56	-2.59	0.00	-2.80	-4.85	-2.67	0.00	-3.03	-2.87	-2.83
TCGA-MK-A4N6-10A-01D-A25A-08_THCA	-2.53	0.00	0.00	-2.80	-2.69	-2.60	-2.69	-2.47	-2.73	-3.27	-2.85	0.00	-2.84	-2.70	-3.00	0.00	-2.56
TCGA-MK-A4N7-10A-01D-A25A-08_THCA	-2.60	0.00	-4.01	-2.76	-2.64	-2.60	-2.70	-2.53	-2.65	-3.28	-2.86	-4.49	-2.77	-2.71	-3.02	0.00	-2.60
TCGA-MK-A4N9-10A-01D-A25A-08_THCA	-2.58	-2.68	-2.69	-2.93	-2.75	-2.72	-2.64	-2.55	-2.73	-3.37	-2.86	0.00	-2.77	-2.72	-2.96	-3.85	-2.56
TCGA-MM-A563-10A-01D-A25V-10_KIRC	-2.37	0.00	-4.36	-2.64	-2.36	-2.32	-2.31	-2.43	-2.27	0.00	0.00	0.00	-4.36	0.00	-3.00	-2.55	-2.31
TCGA-MM-A564-10A-01D-A25V-10_KIRC	-2.35	-2.36	-2.29	0.00	-3.81	-3.69	-2.32	-2.52	-2.47	-3.29	-2.80	0.00	-2.54	-2.50	0.00	-2.50	-2.31
TCGA-MN-A4N1-10A-01D-A24P-08_LUAD	-2.59	-4.02	-3.72	-2.78	-2.59	-2.56	-2.61	-2.59	-2.56	-4.50	-4.50	-4.50	-4.50	-4.20	0.00	-2.59	-2.51
TCGA-MN-A4N4-10A-01D-A24P-08_LUAD	-2.62	-4.23	-3.83	-2.78	-2.56	-2.64	-2.63	-2.65	-2.53	0.00	0.00	0.00	-4.53	-4.53	0.00	-2.63	-2.56
TCGA-MN-A4N5-10A-01D-A24P-08_LUAD	-2.44	-4.05	-3.83	-2.91	-2.65	-2.65	-2.67	-2.42	-2.53	0.00	-4.23	0.00	-3.83	-4.05	-3.04	-2.69	-2.60
TCGA-MO-A47P-10A-01D-A24N-09_SARC	-2.85	-2.70	-2.75	-3.33	-2.74	-2.72	-2.51	-2.60	-2.61	-3.54	-2.88	-4.24	-2.85	-2.70	-2.98	-3.94	-2.59
TCGA-MO-A47R-10A-01D-A24N-09_SARC	-2.77	-3.94	-3.94	-2.90	-2.50	-2.48	-2.50	-2.50	-2.43	0.00	0.00	-4.12	0.00	0.00	-2.95	-2.76	-2.59
TCGA-MP-A4SV-10A-01D-A24P-08_LUAD	-2.61	-2.57	-2.58	-3.48	-3.58	-3.70	-2.58	-2.63	-2.61	-3.18	-2.80	-4.48	-2.67	-2.68	0.00	-2.68	-2.52
TCGA-MP-A4SW-10A-01D-A24P-08_LUAD	-2.66	-4.06	-3.94	-2.68	-2.63	-2.64	-2.65	-2.71	-2.72	-3.36	-2.88	-4.24	-2.76	-2.73	0.00	-2.78	-2.64
TCGA-MP-A4SY-10A-01D-A24P-08_LUAD	-2.68	-2.77	-2.82	-2.94	-2.54	-2.67	-2.69	-2.47	-2.56	0.00	-2.90	-2.77	-4.10	-4.28	-3.12	-2.85	-2.61
TCGA-MP-A4T2-10A-01D-A24P-08_LUAD	-2.48	0.00	0.00	-2.83	-2.42	-2.55	-2.56	-2.59	-2.77	-3.26	-2.97	-4.58	-2.71	-2.64	0.00	-2.76	-2.43
TCGA-MP-A4T4-10A-01D-A25L-08_LUAD	-2.57	-4.54	-4.06	-2.74	-2.56	-2.55	-2.59	-2.60	-2.56	0.00	-4.06	0.00	-4.24	-3.50	0.00	-2.58	-2.51
TCGA-MP-A4T6-10A-01D-A25L-08_LUAD	-2.49	-2.59	-2.55	-3.93	-3.54	-4.54	-2.59	-2.56	-2.66	-3.46	-2.83	0.00	-2.76	-2.67	-3.09	-3.58	-2.55
TCGA-MP-A4T7-10A-01D-A24P-08_LUAD	-2.40	-4.45	-4.45	-2.74	-2.55	-2.54	-2.54	-2.58	-2.54	0.00	0.00	-3.75	0.00	0.00	-3.04	-2.65	-2.50
TCGA-MP-A4T8-10A-01D-A24P-08_LUAD	-2.60	-2.65	-2.64	-3.93	-2.66	-2.74	-2.60	-2.60	-2.68	-3.36	-2.70	-2.70	-2.80	-2.72	-3.07	-3.63	-2.60
TCGA-MP-A4T9-10A-01D-A24P-08_LUAD	-2.53	-2.63	-2.64	-2.87	-2.69	-2.64	-2.57	-2.53	-2.53	0.00	0.00	0.00	-4.20	0.00	-2.98	-2.72	-2.50
TCGA-MP-A4TA-10A-01D-A24P-08_LUAD	-2.62	0.00	-4.55	-2.76	-2.62	-2.65	-2.59	-2.67	-2.64	-3.40	-2.95	0.00	-2.75	-2.68	0.00	-2.79	-2.55
TCGA-MP-A4TC-10A-01D-A24P-08_LUAD	-2.53	-2.77	-2.74	-2.94	-2.54	-2.69	-2.71	-2.61	-2.78	-3.40	-2.72	-2.77	-2.80	-2.77	0.00	-2.86	-2.60
TCGA-MP-A4TD-10A-01D-A25L-08_LUAD	-2.55	0.00	-4.54	-2.62	-2.50	-2.51	-2.53	-2.56	-2.67	-3.27	-2.84	0.00	-2.70	-2.65	0.00	-2.77	-2.42
TCGA-MP-A4TE-10A-01D-A25L-08_LUAD	-2.59	-2.75	-2.68	-2.93	-2.69	-2.73	-2.65	-2.52	-2.69	-3.49	-2.95	0.00	-2.73	-2.73	0.00	-2.77	-2.56
TCGA-MP-A4TF-10A-01D-A25L-08_LUAD	-2.67	-2.66	-2.64	-4.15	-2.77	-2.75	-2.69	-2.62	-2.74	-3.23	-2.72	-2.80	-2.88	-2.82	0.00	-2.80	-2.60
TCGA-MP-A4TH-10A-01D-A25L-08_LUAD	-2.54	-2.69	-2.68	-2.86	-2.64	-2.69	-2.55	-2.52	-2.47	0.00	0.00	0.00	-3.76	-3.84	-3.07	-2.68	-2.50
TCGA-MP-A4TI-10A-01D-A24P-08_LUAD	-2.58	-3.74	-3.51	-2.62	-2.59	-2.63	-2.58	-2.64	-2.70	-3.25	-2.89	0.00	-2.80	-2.69	0.00	-2.72	-2.58
TCGA-MP-A4TJ-10A-01D-A25L-08_LUAD	-2.60	-2.65	-2.61	-4.14	-2.73	-2.76	-2.68	-2.60	-2.76	-3.41	-2.73	-2.72	-4.62	-2.77	-3.14	-3.84	-2.59
TCGA-MP-A4TK-10A-01D-A24P-08_LUAD	-2.55	-2.63	-2.67	-2.79	-2.62	-2.68	-2.61	-2.50	-2.44	-4.50	0.00	0.00	0.00	0.00	-3.14	-2.71	-2.51
TCGA-MP-A5C7-10A-01D-A25L-08_LUAD	-2.56	-2.55	-2.57	-4.52	-4.04	-3.92	-2.57	-2.51	-2.67	-3.24	-2.82	-4.52	-2.70	-2.64	-3.03	-3.82	-2.49
TCGA-MR-A520-10A-01D-A25V-10_LIHC	-2.37	-4.37	-3.77	-2.70	-2.41	-2.38	-2.27	-2.50	-2.56	-3.47	-2.82	0.00	-2.65	-2.57	-2.94	0.00	-2.37
TCGA-MS-A51U-10A-01D-A25Q-09_BRCA	-2.87	-3.78	-3.86	-3.06	-2.53	-2.54	-2.53	-2.53	-2.37	0.00	0.00	-4.25	-4.25	-4.08	-3.05	-2.78	-2.56
TCGA-MT-A51W-10A-01D-A25Y-08_HNSC	-2.46	0.00	0.00	-2.67	-2.53	-2.61	-2.60	-2.51	-2.52	0.00	-4.53	0.00	-4.53	-4.53	-3.01	-2.76	-2.55
TCGA-MT-A51X-10A-01D-A25Y-08_HNSC	-2.57	-2.66	-2.71	-2.88	-2.67	-2.78	-2.71	-2.74	-2.67	0.00	-2.86	-2.74	0.00	-2.63	0.00	-2.73	-2.47
TCGA-MT-A67A-10A-01D-A30H-08_HNSC	-2.36	-2.65	-2.63	-2.80	-2.60	-2.66	-2.50	-2.48	-2.43	0.00	0.00	0.00	0.00	0.00	-3.02	-2.68	-2.34
TCGA-MT-A67D-10A-01D-A30H-08_HNSC	-2.41	-2.66	-2.64	0.00	-2.59	-2.63	-2.63	-2.71	-4.63	-3.33	-2.61	-4.63	-2.53	-2.45	0.00	-4.63	-2.35
TCGA-MT-A67F-10A-01D-A30H-08_HNSC	-2.45	0.00	0.00	-2.65	-2.48	-2.51	-2.47	-2.60	-2.42	0.00	0.00	0.00	0.00	-4.69	0.00	-2.48	-2.38
TCGA-MT-A67G-10A-01D-A30H-08_HNSC	-2.51	0.00	-2.71	0.00	-2.43	-2.54	-2.54	-2.53	-2.68	-3.50	-2.77	0.00	-2.60	-2.67	-3.12	0.00	-2.47
TCGA-MU-A51Y-10A-01D-A26G-09_CESC	-2.77	-4.17	-3.69	-3.04	-2.62	-2.65	-2.56	-2.58	-2.43	-4.47	-4.47	-4.47	0.00	-3.99	-3.13	-2.74	-2.57
TCGA-MV-A51V-10A-01D-A26K-08_BLCA	-2.55	-2.80	-2.72	-2.87	-2.48	-2.54	-2.62	-2.57	-2.76	-3.35	-2.74	-2.60	0.00	-2.71	0.00	-2.69	-2.53
TCGA-MW-A4EC-10A-01D-A25V-10_KIRC	-2.42	-2.64	-2.57	-2.89	-2.34	-2.36	-2.35	-2.41	-2.31	0.00	-2.84	-2.58	0.00	0.00	0.00	-2.30	-2.35
TCGA-MX-A5UG-10A-01D-A31J-08_STAD	-2.58	0.00	0.00	-2.72	-2.55	-2.62	-2.56	-2.54	-2.62	-3.30	-2.81	0.00	-2.72	-2.63	-3.00	0.00	-2.54
TCGA-MX-A5UJ-10A-01D-A31J-08_STAD	-2.60	-2.74	-2.71	-2.96	-2.50	-2.56	-2.64	-2.55	-2.50	0.00	-2.89	-2.71	0.00	0.00	0.00	-2.48	-2.57
TCGA-MX-A663-10A-01D-A31J-08_STAD	-2.55	0.00	-4.43	-2.77	-2.49	-2.52	-2.56	-2.50	-2.41	0.00	0.00	0.00	-4.43	-4.43	0.00	-2.39	-2.50
TCGA-MX-A666-10A-01D-A31J-08_STAD	-2.59	-2.74	-2.75	-2.87	-2.64	-2.70	-2.59	-2.52	-2.64	-3.26	-2.93	0.00	-2.77	-2.63	-3.03	0.00	-2.54
TCGA-MY-A5BD-10A-01D-A26G-09_CESC	-2.80	-2.76	-2.84	-3.16	-2.71	-2.68	-2.58	-2.68	-2.49	-4.46	-4.16	-4.46	-4.16	-4.16	-2.81	-3.76	-2.64
TCGA-MY-A5BE-10A-01D-A26G-09_CESC	-2.76	-3.75	-3.67	-3.05	-2.51	-2.57	-2.41	-2.41	-2.47	-4.45	-3.67	0.00	-4.45	-3.67	0.00	-2.76	-2.73

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-MY-A5BF-10A-01D-A26G-09_CESC	-2.87	-2.63	-2.66	-4.02	-2.81	-2.75	-2.67	-2.73	-3.54	-3.34	-2.55	-2.64	-2.85	-2.65	0.00	-3.92	-2.72
TCGA-MZ-A6I9-10A-01D-A31J-08_HNSC	-2.59	-2.81	-2.76	-2.95	-2.51	-2.62	-2.60	-2.45	-2.58	-3.37	-3.04	-2.78	0.00	0.00	-3.16	-2.86	-2.56
TCGA-NC-A5HD-10A-01D-A26K-08_LUSC	-2.50	0.00	-3.95	-2.72	-2.50	-2.54	-2.51	-2.49	-2.54	0.00	0.00	0.00	0.00	-4.43	0.00	-2.36	-2.42
TCGA-NC-A5HE-10A-01D-A26K-08_LUSC	-2.53	0.00	0.00	-2.74	-2.53	-2.55	-2.53	-2.54	-2.69	-3.53	-2.89	0.00	-2.76	-2.68	0.00	-2.64	-2.46
TCGA-NC-A5HF-10A-01D-A26K-08_LUSC	-2.48	0.00	0.00	-2.52	-2.46	-2.50	-2.50	-2.42	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.46
TCGA-NC-A5HG-10A-01D-A26K-08_LUSC	-2.48	0.00	0.00	-2.72	-2.50	-2.52	-2.56	-2.51	-2.50	0.00	0.00	-4.47	0.00	-4.47	-3.02	-2.61	-2.51
TCGA-NC-A5HH-10A-01D-A26K-08_LUSC	-2.48	0.00	-4.19	-2.59	-2.53	-2.53	-2.53	-2.45	-2.48	0.00	-4.49	-4.19	0.00	-4.49	0.00	-2.40	-2.46
TCGA-NC-A5HI-10A-01D-A26K-08_LUSC	-2.46	-2.67	-2.69	-2.83	-2.66	-2.63	-2.51	-2.43	-2.48	-4.44	-3.96	0.00	-4.44	0.00	0.00	-2.47	-2.40
TCGA-NC-A5HJ-10A-01D-A26K-08_LUSC	-2.50	0.00	-4.45	-2.57	-2.46	-2.54	-2.56	-2.58	-2.51	0.00	-4.45	0.00	-4.45	-3.97	-2.78	0.00	-2.45
TCGA-NC-A5HK-10A-01D-A26K-08_LUSC	-2.59	0.00	-4.21	-2.64	-2.52	-2.58	-2.47	-2.47	-2.47	-3.34	0.00	0.00	0.00	-4.51	0.00	-2.61	-2.44
TCGA-NC-A5HL-10A-01D-A26K-08_LUSC	-2.41	-2.62	-2.65	-2.80	-2.60	-2.54	-2.53	-2.52	-2.46	0.00	-4.43	0.00	0.00	0.00	-2.80	-4.12	-2.41
TCGA-NC-A5HM-10A-01D-A26K-08_LUSC	-2.48	-4.17	-4.17	-2.69	-2.50	-2.48	-2.50	-2.48	-2.47	-4.17	-4.47	-4.47	-4.17	-4.17	-2.96	-2.73	-2.45
TCGA-NC-A5HN-10A-01D-A26K-08_LUSC	-2.55	-2.77	-2.71	-2.95	-2.48	-2.60	-2.57	-2.54	-2.52	0.00	-2.94	-2.69	-4.48	0.00	-2.99	-2.70	-2.49
TCGA-NC-A5HO-10A-01D-A26K-08_LUSC	-2.43	0.00	0.00	-2.62	-2.51	-2.54	-2.59	-2.51	-2.42	0.00	0.00	0.00	0.00	-4.16	-2.96	-2.75	-2.46
TCGA-NC-A5HP-10A-01D-A26K-08_LUSC	-2.50	-4.45	-4.45	-2.67	-2.54	-2.54	-2.54	-2.57	-2.59	0.00	-4.45	0.00	-4.15	-4.15	0.00	-2.50	-2.45
TCGA-NC-A5HQ-10A-01D-A26K-08_LUSC	-2.47	-2.72	-2.72	-2.87	-2.47	-2.58	-2.57	-2.52	-2.65	-3.40	-2.76	-2.78	-2.72	-2.66	0.00	-2.74	-2.49
TCGA-NC-A5HR-10A-01D-A26K-08_LUSC	-2.47	-2.62	-2.68	-2.89	-2.61	-2.66	-2.72	-2.76	-3.77	-3.16	-2.65	-3.77	-2.57	-2.46	0.00	-3.77	-2.43
TCGA-NC-A5HT-10A-01D-A26K-08_LUSC	-2.49	-2.60	-2.71	-2.82	-2.65	-2.70	-2.56	-2.43	-2.44	0.00	0.00	0.00	-4.18	0.00	-3.01	-2.73	-2.50
TCGA-NH-A50T-10A-01D-A28G-10_COAD	-2.42	-4.31	-4.00	-2.51	-2.34	-2.32	-2.28	-2.37	-2.37	0.00	-4.00	0.00	0.00	-4.31	-2.83	-2.55	-2.40
TCGA-NH-A50V-10A-01D-A28G-10_COAD	-2.46	-2.44	-2.65	-2.81	-2.56	-2.49	-2.26	-2.38	-2.64	-3.47	-2.63	0.00	-2.56	-2.49	-2.80	-4.24	-2.45
TCGA-NI-A4U2-10A-01D-A28X-10_LIHC	-2.35	-3.96	-3.78	-2.92	-2.41	-2.27	-2.26	-2.29	-2.29	0.00	-4.26	-3.66	0.00	0.00	0.00	-2.21	-2.40
TCGA-NJ-A4YF-10A-01D-A25L-08_LUAD	-2.55	0.00	-3.92	-2.61	-2.51	-2.54	-2.54	-2.51	-2.62	0.00	-4.22	0.00	-4.22	-3.56	0.00	-2.68	-2.50
TCGA-NJ-A4YG-10A-01D-A25L-08_LUAD	-2.45	0.00	-4.58	-2.72	-2.54	-2.52	-2.58	-2.52	-2.65	-3.33	-2.89	0.00	-2.83	-2.65	0.00	-2.70	-2.49
TCGA-NJ-A4YI-10A-01D-A25L-08_LUAD	-2.57	-4.27	-3.53	-2.67	-2.60	-2.60	-2.65	-2.62	-2.69	-3.49	-2.89	-4.57	-2.72	-2.66	0.00	-2.71	-2.54
TCGA-NJ-A4YP-10A-01D-A25L-08_LUAD	-2.55	-2.56	-2.53	-3.81	-3.61	-3.73	-2.57	-2.59	-2.67	-3.39	-2.84	0.00	-2.71	-2.63	0.00	-2.72	-2.52
TCGA-NJ-A4YQ-10A-01D-A25L-08_LUAD	-2.56	-4.39	-4.21	-2.88	-2.51	-2.66	-2.66	-2.59	-2.59	-3.27	-2.77	-2.84	-2.90	-2.84	0.00	-2.88	-2.68
TCGA-NJ-A55A-10A-01D-A25L-08_LUAD	-2.45	0.00	0.00	-2.69	-2.55	-2.55	-2.61	-2.48	-2.44	0.00	-4.52	-4.52	-4.52	0.00	-3.12	-2.71	-2.50
TCGA-NJ-A55O-10A-01D-A25L-08_LUAD	-2.64	0.00	0.00	-2.75	-2.59	-2.58	-2.63	-2.60	-2.63	0.00	-4.24	-4.54	-4.54	-3.84	0.00	-2.65	-2.58
TCGA-NJ-A55R-10A-01D-A25L-08_LUAD	-2.66	-2.77	-2.73	-2.97	-2.53	-2.68	-2.68	-2.59	-2.75	-3.37	-2.72	-2.77	-2.81	-2.75	0.00	-2.83	-2.60
TCGA-NK-A5CR-10A-01D-A26K-08_LUSC	-2.53	-2.70	-2.71	-2.84	-2.64	-2.65	-2.59	-2.55	-2.68	-3.53	-2.89	-2.69	0.00	-2.65	0.00	-2.76	-2.51
TCGA-NK-A5CT-10A-01D-A26K-08_LUSC	-2.56	-2.70	-2.67	-2.89	-2.65	-2.66	-2.56	-2.55	-2.69	-3.32	-2.84	0.00	-2.70	-2.70	-3.04	-4.07	-2.50
TCGA-NK-A5CX-10A-01D-A26K-08_LUSC	-2.56	-2.71	-2.69	-2.91	-2.70	-2.67	-2.59	-2.55	-2.68	-3.33	-2.85	0.00	-2.77	-2.72	-3.04	-3.83	-2.57
TCGA-NK-A5D1-10A-01D-A26K-08_LUSC	-2.59	-4.52	0.00	-2.77	-2.56	-2.60	-2.59	-2.62	-2.72	-3.44	-2.87	0.00	-2.85	-2.67	0.00	-2.75	-2.50
TCGA-O1-A52J-10A-01D-A25L-08_LUAD	-2.53	-4.18	-3.64	-2.78	-2.55	-2.58	-2.60	-2.44	-2.48	0.00	-4.49	-4.01	0.00	-4.49	-3.07	-2.71	-2.51
TCGA-O2-A52N-10A-01D-A26K-08_LUSC	-2.52	-2.74	-2.70	-2.92	-2.64	-2.71	-2.56	-2.59	-2.67	-3.36	-2.90	0.00	-2.72	-2.66	0.00	-2.83	-2.49
TCGA-O2-A52Q-10A-01D-A26K-08_LUSC	-2.64	-2.72	-2.77	-2.93	-2.53	-2.63	-2.67	-2.55	-2.53	0.00	-3.00	-2.83	0.00	0.00	-3.08	-2.77	-2.61
TCGA-O2-A52S-10A-01D-A25L-08_LUSC	-2.57	-2.76	-2.74	-2.95	-2.66	-2.74	-2.58	-2.56	-2.67	-3.38	-2.92	-4.08	-2.76	-2.65	-2.99	-4.25	-2.57
TCGA-O2-A52V-10A-01D-A25L-08_LUSC	-2.57	-4.20	-4.02	-2.75	-2.52	-2.55	-2.55	-2.52	-2.54	0.00	0.00	-4.50	0.00	0.00	-2.91	-4.50	-2.46
TCGA-O2-A52W-10A-01D-A26K-08_LUSC	-2.41	-2.66	-2.58	-2.93	-2.58	-2.55	-2.45	-2.51	-2.48	0.00	-4.06	-3.89	-4.36	-3.46	-2.80	0.00	-2.43
TCGA-O2-A5IB-10A-01D-A27N-08_LUSC	-2.38	0.00	0.00	-2.74	-2.49	-2.56	-2.56	-2.48	-2.46	0.00	0.00	0.00	0.00	0.00	-3.01	-2.70	-2.49
TCGA-OD-A75X-10A-01D-A32N-08_SKCM	-2.63	-2.79	-2.74	-2.97	-2.73	-2.79	-2.67	-2.65	-2.71	-3.45	-2.83	-4.63	-2.74	-2.75	0.00	-2.75	-2.55
TCGA-OE-A75W-10A-01D-A32N-08_PAAD	-2.50	0.00	0.00	-2.70	-2.49	-2.48	-2.58	-2.45	-2.49	0.00	0.00	0.00	-4.41	0.00	-3.01	-2.65	-2.46
TCGA-OK-A5Q2-10A-01D-A27P-09_BRCA	-2.86	-4.40	0.00	-3.04	-2.43	-2.53	-2.46	-2.47	-2.41	0.00	0.00	0.00	0.00	-4.10	-2.66	-4.10	-2.57
TCGA-OL-A5D6-10A-01D-A27P-09_BRCA	-2.89	0.00	-4.42	-2.98	-2.51	-2.50	-2.43	-2.52	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.54
TCGA-OL-A5D7-10A-01D-A27P-09_BRCA	-2.91	-2.66	-2.91	-3.35	-2.51	-2.61	-2.56	-2.59	-2.48	0.00	-2.90	-2.80	0.00	0.00	-2.84	0.00	-2.64
TCGA-OL-A5D8-10A-01D-A27P-09_BRCA	-2.75	-3.83	-4.14	-2.93	-2.51	-2.54	-2.46	-2.45	-2.39	-4.44	-3.96	-4.44	-4.44	0.00	-2.92	-2.80	-2.63
TCGA-OL-A5DA-10A-01D-A27P-09_BRCA	-2.92	-2.61	-2.69	0.00	-2.68	-2.62	-2.65	-2.69	-2.74	-3.52	-2.65	-2.58	0.00	-2.81	0.00	-2.94	-2.76
TCGA-OL-A5RU-10A-01D-A28E-09_BRCA	-2.77	0.00	-2.75	-3.27	-2.49	-2.57	-2.58	-2.50	-2.45	0.00	-2.88	0.00	-2.77	0.00	-2.89	-2.85	-2.64
TCGA-OL-A5RV-10A-01D-A28E-09_BRCA	-2.76	0.00	-2.51	0.00	-2.66	-2.66	-2.53	-2.55	-2.52	0.00	-2.90	-4.49	-2.72	0.00	-2.75	-4.01	-2.63
TCGA-OL-A5RW-10A-01D-A28E-09_BRCA	-2.75	0.00	-4.34	-2.80	-2.38	-2.47	-2.42	-2.43	-2.40	0.00	-4.34	0.00	0.00	0.00	-2.96	0.00	-2.73
TCGA-OL-A5RX-10A-01D-A28E-09_BRCA	-2.78	-2.54	-2.63	-4.50	-2.57	-2.57	-2.60	-2.61	-2.51	0.00	-2.69	-2.78	-2.78	-4.50	-3.09	-2.88	-2.63
TCGA-OL-A5RY-10A-01D-A28E-09_BRCA	-2.73	-2.66	-2.70	-3.14	-2.67	-2.69	-2.65	-2.74	-2.57	0.00	-2.86	0.00	-2.69	-2.65	0.00	-2.76	-2.57
TCGA-OL-A5RZ-10A-01D-A28E-09_BRCA	-2.83	-3.95	-4.43	-2.95	-2.43	-2.54	-2.44	-2.54	-2.39	0.00	0.00	0.00	0.00	0.00	-2.69	0.00	-2.55
TCGA-OL-A5S0-10A-01D-A28E-09_BRCA	-2.69	-2.44	-2.51	0.00	0.00	0.00	-2.46	-2.58	-2.35	0.00	0.00	0.00	0.00	0.00	-2.68	0.00	-2.58
TCGA-OL-A66H-10A-01D-A29N-09_BRCA	-2.98	-2.72	-2.80	-3.33	-2.50	-2.58	-2.59	-2.60	-2.49	0.00	-2.90	0.00	-2.81	0.00	0.00	-2.66	-2.68
TCGA-OL-A66I-10A-01D-A29N-09_BRCA	-2.83	-2.75	-2.74	-3.36	-2.50	-2.56	-2.51	-2.65	-2.49	0.00	-2.92	-2.72	-4.50	0.00	0.00	-2.52	-2.68
TCGA-OL-A66J-10A-01D-A29N-09_BRCA	-2.72	-2.67	-2.78	-3.21	-2.65	-2.68	-2.52	-2.46	-2.53	0.00	-4.57	0.00	0.00	0.00	0.00	-2.62	-2.66
TCGA-OL-A66K-10A-01D-A29N-09_BRCA	-2.84	-2.76	-4.55	-3.38	-2.50	-2.56	-2.59	-2.59	-4.25	-3.21	-2.70	0.00	-2.61	-2.59	0.00	0.00	-2.54
TCGA-OL-A66L-10A-01D-A31U-09_BRCA	-2.88	0.00	-4.38	-2.90	-2.48	-2.36	-2.41	-2.51	-2.28	0.00	0.00	0.00	0.00	0.00	0.00	-2.53	-2.50
TCGA-OL-A66N-10A-01D-A31U-09_BRCA	-2.92	-2.62	-2.74	-3.28	-2.72	-2.70	-2.49	-2.57	-2.65	-3.37	-2.75	-2.69	0.00	-2.67	0.00	-2.74	-2.57
TCGA-OL-A66O-10A-01D-A31U-09_BRCA	-2.87	-2.66	-2.77	-3.32	-2.67	-2.33	-2.42	-2.48	-2.29	0.00	-4.43	0.00	-4.43	0.00	-3.02	-2.71	-2.48
TCGA-OL-A66P-10A-01D-A31U-09_BRCA	-3.04	-2.76	0.00	-3.14	-2.58	-2.57	-2.50	-2.53	-2.39	-3.43	-2.72	-2.61	0.00	0.00	-2.90	-2.83	-2.67
TCGA-OR-A5J1-10A-01D-A29L-10_ACC	-2.44	0.00	0.00	-2.58	-2.38	-2.28	-2.30	-2.40	-2.66	-3.35	-2.83	0.00	-2.58	-2.51	-2.80	0.00	-2.44
TCGA-OR-A5J2-10A-01D-A29L-10_ACC	-2.39	0.00	-4.25	-2.52	-2.27	-2.25	-2.27	-2.32	-2.40	0.00	0.00	0.00	-3.77	0.00	-2.74	-2.43	-2.34
TCGA-OR-A5J3-10A-01D-A29L-10_ACC	-2.33	-2.58	-2.55	-2.89	-2.35	-2.35	-2.32	-2.43	-2.35	0.00	-2.76	-2.46	0.00	0.00	0.00	-2.34	-2.41
TCGA-OR-A5J4-10A-01D-A29L-10_ACC	-2.37	-4.22	-4.22	-2.43	-2.35	-2.25	-2.26	-2.29	-2.31	0.00	-4.22	-3.92	0.00	0.00	0.00	-2.27	-2.43
TCGA-OR-A5J7-10A-01D-A29L-10_ACC	-2.47	-2.54	-2.63	-2.86	-2.32	-2.40	-2.36	-2.45	-2.63	-3.45	-2.52	-2.58	-2.55	-2.55	-2.94	0.00	-2.45
TCGA-OR-A5J8-10A-01D-A29L-10_ACC	-2.42	-2.51	-2.58	-3.00	-2.38	-2.32	-2.34	-2.47	-2.68	-4.00	-2.63	-2.41	0.00	-2.51	0.00	-2.79	-2.49
TCGA-OR-A5J9-10A-01D-A29L-10_ACC	-2.49	0.00	0.00	-2.67	-2.28	-2.32	-2.30	-2.34	-2.35	-3.79	-2.84	-2.62	0.00	0.00	-2.90	-2.51	-2.51
TCGA-OR-A5JA-10A-01D-A29L-10_ACC	-2.38	0.00	-3.75	-2.50	-2.42	-2.26	-2.26	-2.34	-2.30	0.00	-4.23	-3.63	-4.23	-3.75	0.00	-2.34	-2.39
TCGA-OR-A5JB-10A-01D-A29L-10_ACC	-2.54	-2.55	-2.52	-2.91	-2.31	-2.38	-2.38	-2.54	-4.29	-3.38	-2.38	-2.62	-2.46	-2.35	0.00	0.00	-2.51
TCGA-OR-A5JD-10B-01D-A29L-10_ACC	-2.36	-2.43	-2.49	-2.90	-2.43	-2.39	-2.26	-2.23	-2.25	0.00	0.00	0.00	0.00	0.00	0.00	-2.22	-2.38
TCGA-OR-A5JE-10A-01D-A29L-10_ACC	-2.50	-2.55	-2.51	-2.89	-2.35	-2.30	-2.37	-2.33	-2.35	0.00	-2.75	-2.53	0.00	0.00	-2.83	-2.62	-2.39
TCGA-OR-A5JF-10A-01D-A29L-10_ACC	-2.42	-3.99	0.00	-2.61	-2.34	-2.32	-2.35	-2.46	-2.65	-3.60	-2.82	0.00	-2.59	-2.56	-2.97	0.00	-2.41
TCGA-OR-A5JG-10A-01D-A29L-10_ACC	-2.29	-2.47	-2.49	-2.69	-2.43	-2.34	-2.26	-2.33	-2.29	0.00	-3.92	0.00	-3.44	0.00	0.00	-2.55	-2.34
TCGA-OR-A5JH-10A-01D-A30A-10_ACC	-2.37	-2.46	-2.56	-2.82	-2.55	-2.44	-2.45	-2.51	0.00	-3.33	-2.48	0.00	-2.35	-2.24	0.00	0.00	-2.37
TCGA-OR-A5JI-10A-01D-A29L-10_ACC	-2.50	-2.53	-2.63	-2.78	-2.37	-2.33	-2.30	-2.30	-2.58	-3.71	-2.49	-2.36	0.00	-2.47	0.00	-2.69	-2.43
TCGA-OR-A5JJ-10A-01D-A29L-10_ACC	-2.38	0.00	-4.24	-2.46	-2.36	-2.30	-2.28	-2.30	-2.47	-3.47	-2.73	-4.24	-2.60	-2.37	0.00	-2.58	-2.41
TCGA-OR-A5JK-10A-01D-A29L-10_ACC	-2.36	-3.77	-3.95	-2.51	-2.37	-2.33	-2.25	-2.36	-2.28	0.00	0.00	0.00	-4.25	0.00	-2.82	-2.44	-2.35
TCGA-OR-A5JL-10A-01D-A29L-10_ACC	-2.38	-2.49	-2.50	-2.81	-2.58	-2.47	-2.26	-2.40	-2.57	-3.64	-2.79	0.00	-2.48	-2.48	0.00	-2.50	-2.36
TCGA-OR-A5JM-10B-01D-A29L-10_ACC	-2.29	-2.51	-2.56	-2.78	-2.56	-2.43	-2.32	-2.39	-2.53	-3.49	-2.64	0.00	-2.60	-2.44	0.00	-2.48	-2.44
TCGA-OR-A5JO-10A-01D-A29L-10_ACC	-2.32	-4.18	0.00	-2.54	-2.28	-2.25	-2.22	-2.33	-2.30	0.00	0.00	0.00	0.00	-4.18	0.00	-2.25	-2.37
TCGA-OR-A5JP-10A-01D-A29L-10_ACC	-2.36	0.00	-4.19	-2.60	-2.31	-2.20	-2.23	-2.37	-2.37	-3.89	-4.19	-4.19	-3.71	-4.19	-2.73	-2.41	-2.37
TCGA-OR-A5JQ-10A-01D-A29L-10_ACC	-2.40	-2.52	-2.60	-2.88	-2.28	-2.35	-2.43	-2.50	-2.72	-3.69	-2.51	-2.57	-2.53	-2.47	0.00	-2.70	-2.48
TCGA-OR-A5JR-10A-01D-A29L-10_ACC	-2.43	-2.54	0.00	-2.90	-2.39	-2.31	-2.38	-2.36	-2.51	-3.42	-2.86	0.00	-2.66	-2.55	-2.98	-4.26	-2.55
TCGA-OR-A5JS-10A-01D-A29L-10_ACC	-2.42	-2.40	-2.57	-2.88	-2.54	-2.41	-2.24	-2.35	-2.30	0.00	0.00	0.00	-4.22	-3.75	0.00	-2.27	-2.43
TCGA-OR-A5JT-10A-01D-A29L-10_ACC	-2.34	-2.60	-2.52	-2.82	-2.72	-2.47	-2.33	-2.33	-2.61	0.00	-2.82	-4.21	-2.61	-2.49	0.00	-2.54	-2.38
TCGA-OR-A5JU-10A-01D-A30A-10_ACC	-2.25	-2.58	-2.60	-2.72	-2.58	-2.39	-2.29	-2.28	-2.28	0.00	0.00	0.00	-3.72	-4.20	-2.80	-2.52	-2.36
TCGA-OR-A5JV-10A-01D-A29L-10_ACC	-2.44	-2.67	-2.57	-2.78	-2.43	-2.32	-2.28	-2.31	-2.65	-3.37	-2.68	-2.47	-4.21	-2.50	0.00	-2.68	-2.44
TCGA-OR-A5JW-10A-01D-A29L-10_ACC	-2.43	-2.57	-2.58	-2.80	-2.34	-2.32	-2.30	-2.30	-2.35	0.00	-2.88	-2.70	0.00	-4.28	0.00	-2.28	-2.40
TCGA-OR-A5JX-10B-01D-A29L-10_ACC	-2.42	-2.61	-2.57	-2.87	-2.41	-2.31	-2.33	-2.42	-2.59	-3.36	-2.57	-2.62	-2.56	-2.52	-2.93	-4.36	-2.46
TCGA-OR-A5JY-10A-01D-A29L-10_ACC	-2.24	-2.42	-2.49	-2.70	-2.44	-2.37	-2.38	-2.58	-2.44	0.00	-2.69	-4.24	-2.47	-2.40	0.00	-2.39	-2.36
TCGA-OR-A5JZ-10A-01D-A29L-10_ACC	-2.43	-2.31	-2.29	-4.23	-2.57	-2.55	-2.28	-2.39	-2.39	0.00	-2.78	-2.66	0.00	-3.93	-2.62	-3.93	-2.49
TCGA-OR-A5K0-10B-01D-A29L-10_ACC	-2.30	0.00	-3.94	-2.66	-2.36	-2.21	-2.29	-2.38	-2.31	0.00	0.00	0.00	0.00	0.00	-2.81	-2.47	-2.31
TCGA-OR-A5K1-10A-01D-A29L-10_ACC	-2.34	-2.47	-2.48	-2.84	-2.63	-2.41	-2.30	-2.40	-2.50	-3.27	-2.68	0.00	-2.58	-2.48	0.00	-2.49	-2.42
TCGA-OR-A5K2-10B-01D-A29L-10_ACC	-2.37	0.00	0.00	-2.58	-2.32	-2.24	-2.23	-2.37	-2.26	-4.20	-3.90	0.00	-3.90	-4.20	0.00	-2.24	-2.38

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-OR-A5K3-10A-01D-A29L-10_ACC	-2.40	0.00	-4.26	-2.65	-2.27	-2.29	-2.29	-2.45	-4.26	-3.48	-2.47	0.00	-2.34	-2.31	0.00	-3.65	-2.41
TCGA-OR-A5K4-10A-01D-A29L-10_ACC	-2.31	-4.28	-4.28	-2.63	-2.36	-2.21	-2.27	-2.23	-2.30	0.00	0.00	0.00	0.00	0.00	0.00	-2.23	-2.38
TCGA-OR-A5K5-10A-01D-A29L-10_ACC	-2.34	-2.41	-2.49	-2.75	-2.69	-2.43	-2.23	-2.25	-2.24	0.00	0.00	0.00	0.00	0.00	0.00	-2.17	-2.41
TCGA-OR-A5K6-10A-01D-A29L-10_ACC	-2.33	-2.48	-2.51	-2.84	-2.57	-2.43	-2.21	-2.35	-2.31	0.00	0.00	0.00	0.00	-3.67	-2.62	0.00	-2.33
TCGA-OR-A5K8-10A-01D-A29L-10_ACC	-2.43	-4.26	0.00	-2.65	-2.38	-2.27	-2.27	-2.37	-2.59	-3.56	-2.78	0.00	-2.59	-2.46	-2.94	0.00	-2.43
TCGA-OR-A5KP-10A-01D-A30A-10_ACC	-2.38	-2.55	-2.50	-2.74	-2.69	-2.43	-2.28	-2.34	-2.27	0.00	-4.15	0.00	0.00	0.00	-2.77	-2.48	-2.36
TCGA-OR-A5KQ-10A-01D-A30A-10_ACC	-2.36	-3.89	0.00	-2.62	-2.34	-2.33	-2.29	-2.40	-2.35	0.00	0.00	0.00	-3.72	-4.20	0.00	-2.29	-2.40
TCGA-OR-A5KS-10A-01D-A30A-10_ACC	-2.39	-2.56	-2.58	-2.65	-2.65	-2.45	-2.33	-2.31	-2.57	-3.39	-2.67	0.00	-2.58	-2.48	0.00	-2.51	-2.41
TCGA-OR-A5KT-10A-01D-A29L-10_ACC	-2.29	-2.22	-2.26	-4.19	0.00	-3.89	-2.23	-2.22	-2.22	0.00	0.00	0.00	0.00	0.00	0.00	-2.21	-2.31
TCGA-OR-A5KU-10A-01D-A29L-10_ACC	-2.38	0.00	-4.21	-2.57	-2.34	-2.23	-2.28	-2.30	-2.26	0.00	0.00	0.00	0.00	0.00	0.00	-2.24	-2.37
TCGA-OR-A5KV-10A-01D-A29L-10_ACC	-2.41	-2.52	-3.73	-2.87	-2.31	-2.34	-2.31	-2.39	-2.60	-3.38	-2.82	0.00	-2.57	-2.53	0.00	-2.57	-2.44
TCGA-OR-A5KW-10A-01D-A29L-10_ACC	-2.32	-2.43	-2.63	-2.73	-2.54	-2.50	-2.25	-2.32	-2.30	0.00	0.00	0.00	-4.21	-4.21	-2.93	-2.59	-2.41
TCGA-OR-A5KX-10A-01D-A29L-10_ACC	-2.38	0.00	0.00	-2.64	-2.34	-2.30	-2.25	-2.41	-2.34	-4.28	0.00	0.00	-4.28	-3.80	0.00	-2.31	-2.42
TCGA-OR-A5KY-10A-01D-A29L-10_ACC	-2.36	0.00	0.00	-2.71	-2.35	-2.36	-2.28	-2.40	-2.66	-3.52	-2.77	0.00	-2.60	-2.49	0.00	-2.62	-2.46
TCGA-OR-A5KZ-10A-01D-A29L-10_ACC	-2.29	0.00	0.00	-2.41	-2.37	-2.27	-2.22	-2.30	-2.25	0.00	0.00	0.00	0.00	0.00	-2.83	-2.60	-2.44
TCGA-OR-A5L1-10A-01D-A30A-10_ACC	-2.38	0.00	-4.21	-2.60	-2.36	-2.29	-2.37	-2.32	-2.32	0.00	0.00	0.00	0.00	0.00	0.00	-2.22	-2.38
TCGA-OR-A5L2-10A-01D-A30A-10_ACC	-2.40	0.00	0.00	-2.60	-2.42	-2.26	-2.30	-2.39	-2.51	-3.56	-2.88	0.00	-2.68	-2.51	-2.95	-4.26	-2.46
TCGA-OR-A5L3-10A-01D-A29L-10_ACC	-2.38	0.00	-4.12	-2.50	-2.29	-2.27	-2.30	-2.38	-2.29	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.38
TCGA-OR-A5L4-10A-01D-A29L-10_ACC	-2.37	-2.40	-2.56	-2.69	-2.64	-2.37	-2.21	-2.40	-2.33	0.00	-4.23	0.00	0.00	-3.76	-2.87	-2.45	-2.39
TCGA-OR-A5L6-10C-01D-A29L-10_ACC	-2.28	-2.47	-2.47	-2.77	-2.62	-2.39	-2.24	-2.32	-2.28	0.00	0.00	0.00	-4.23	-3.93	-2.91	-2.64	-2.37
TCGA-OR-A5L8-10A-01D-A29L-10_ACC	-2.35	-2.49	-2.49	-2.87	-2.57	-2.42	-2.23	-2.41	-2.50	-3.79	-2.79	0.00	-2.53	-2.49	0.00	-2.64	-2.38
TCGA-OR-A5L9-10B-01D-A29L-10_ACC	-2.29	0.00	0.00	-2.43	-2.35	-2.22	-2.25	-2.29	-2.31	0.00	0.00	0.00	0.00	0.00	0.00	-2.21	-2.31
TCGA-OR-A5LA-10A-01D-A29L-10_ACC	-2.26	0.00	0.00	-2.50	-2.28	-2.29	-2.26	-2.29	-2.30	0.00	0.00	0.00	0.00	0.00	-2.86	-2.53	-2.38
TCGA-OR-A5LB-10A-01D-A29L-10_ACC	-2.36	-2.50	-2.45	-2.80	-2.50	-2.39	-2.21	-2.32	-2.39	0.00	0.00	0.00	0.00	0.00	0.00	-2.27	-2.41
TCGA-OR-A5LC-10A-01D-A29L-10_ACC	-2.34	-2.41	-2.58	-2.76	-2.55	-2.42	-2.22	-2.36	-2.26	0.00	0.00	0.00	0.00	0.00	-2.81	-2.43	-2.41
TCGA-OR-A5LD-10A-01D-A29L-10_ACC	-2.45	-2.53	-2.64	-2.81	-2.39	-2.35	-2.38	-2.40	-2.69	-3.29	-2.62	-2.37	0.00	-2.52	-2.94	-4.33	-2.43
TCGA-OR-A5LE-10A-01D-A29L-10_ACC	-2.44	-2.58	-2.61	-2.95	-2.33	-2.32	-2.37	-2.48	-2.63	-3.48	-2.58	-2.41	0.00	-2.54	0.00	-2.62	-2.46
TCGA-OR-A5LF-10A-01D-A30A-10_ACC	-2.44	-2.44	-2.45	-4.29	-2.44	-2.34	-2.33	-2.36	-2.39	0.00	-2.53	-2.36	0.00	-4.29	0.00	-2.30	-2.47
TCGA-OR-A5LG-10A-01D-A29L-10_ACC	-2.36	-4.24	-3.94	-2.59	-2.33	-2.27	-2.35	-2.45	-2.40	0.00	-3.94	0.00	0.00	-4.24	0.00	-2.32	-2.39
TCGA-OR-A5LH-10A-01D-A29L-10_ACC	-2.38	-2.58	-2.59	-2.89	-2.54	-2.49	-2.33	-2.29	-2.55	-3.41	-2.65	0.00	-2.61	-2.43	0.00	-2.51	-2.38
TCGA-OR-A5LI-10A-01D-A30A-10_ACC	-2.46	-2.60	-2.68	-2.73	-2.41	-2.32	-2.32	-2.35	-2.65	-3.47	-2.52	-2.38	-3.95	-2.55	-2.95	-3.95	-2.47
TCGA-OR-A5LJ-10A-01D-A29L-10_ACC	-2.43	-2.40	-2.45	-4.02	-2.68	-2.42	-2.37	-2.39	-2.53	-4.02	-2.42	-2.52	-2.61	-2.59	-2.83	-4.32	-2.45
TCGA-OR-A5LK-10A-01D-A29L-10_ACC	-2.38	-4.24	0.00	-2.59	-2.36	-2.29	-2.29	-2.33	-2.36	0.00	-4.24	0.00	0.00	-3.93	0.00	-2.21	-2.37
TCGA-OR-A5LL-10A-01D-A29L-10_ACC	-2.36	-2.65	-2.59	-2.80	-2.37	-2.34	-2.42	-2.36	-2.34	0.00	-2.87	-2.66	0.00	0.00	0.00	-2.31	-2.42
TCGA-OR-A5LN-10A-01D-A29L-10_ACC	-2.37	-2.50	-2.57	-2.88	-2.41	-2.35	-2.38	-2.37	-2.33	0.00	-2.83	-2.47	-4.29	0.00	-2.79	-2.65	-2.41
TCGA-OR-A5LO-10A-01D-A29L-10_ACC	-2.46	-2.46	-2.63	-2.79	-2.39	-2.31	-2.41	-2.44	-2.67	-3.31	-2.63	-2.63	-2.76	-2.55	0.00	-2.67	-2.48
TCGA-OR-A5LP-10A-01D-A29L-10_ACC	-2.37	-2.32	-2.33	0.00	-2.63	-2.52	-2.35	-2.33	-2.24	0.00	-2.73	-2.51	0.00	0.00	-2.79	-2.49	-2.45
TCGA-OR-A5LR-10A-01D-A29L-10_ACC	-2.40	-2.33	-2.35	0.00	-2.70	-2.38	-2.30	-2.40	-2.27	0.00	-2.64	-2.51	0.00	0.00	-2.79	-2.59	-2.40
TCGA-OR-A5LS-10A-01D-A29L-10_ACC	-2.38	0.00	-4.30	-2.62	-2.43	-2.28	-2.36	-2.45	-2.59	-3.34	-2.83	0.00	-2.54	-2.50	-2.90	-4.00	-2.48
TCGA-OR-A5LT-10A-01D-A29L-10_ACC	-2.40	0.00	-4.00	-2.64	-2.36	-2.26	-2.24	-2.24	-2.34	0.00	0.00	0.00	-4.00	-3.82	0.00	-2.20	-2.38
TCGA-OU-A5PI-10A-01D-A29L-10_ACC	-2.42	-2.61	-2.63	-2.94	-2.40	-2.30	-2.26	-2.25	-2.50	-3.50	-2.93	-2.56	0.00	-4.04	-2.94	-2.74	-2.48
TCGA-OX-A56R-10A-01D-A33W-08_GBM	-2.53	0.00	0.00	-2.75	-2.56	-2.53	-2.61	-2.53	-2.74	-3.37	-2.85	0.00	-2.76	-2.66	0.00	-2.68	-2.51
TCGA-P5-A5ET-10A-01D-A27N-08_LGG	-2.69	-2.76	-2.62	-2.88	-2.77	-2.78	-2.58	-2.54	-2.73	-3.24	-2.75	0.00	-2.63	-2.73	0.00	-2.80	-2.57
TCGA-P5-A5EU-10A-01D-A27N-08_LGG	-2.48	-2.58	-2.49	0.00	-4.55	0.00	-2.54	-2.46	-2.68	-3.27	-2.84	0.00	-2.71	-2.64	0.00	-2.75	-2.51
TCGA-P5-A5EV-10A-01D-A27N-08_LGG	-2.58	-2.76	-2.76	-2.96	-2.45	-2.61	-2.67	-2.60	-2.73	-3.52	-2.73	-2.79	-2.84	-2.67	0.00	-2.81	-2.56
TCGA-P5-A5EW-10A-01D-A27N-08_LGG	-2.49	-2.74	-2.71	-2.91	-2.46	-2.60	-2.56	-2.53	-2.55	0.00	-2.93	-2.74	0.00	0.00	-3.07	-2.83	-2.51
TCGA-P5-A5EX-10A-01D-A289-08_LGG	-2.51	0.00	0.00	-2.52	-2.47	-2.56	-2.54	-2.58	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.54	-2.48
TCGA-P5-A5EY-10A-01D-A27N-08_LGG	-2.46	-2.68	-2.72	-2.88	-2.62	-2.61	-2.53	-2.51	-2.48	0.00	0.00	0.00	0.00	-4.56	-2.97	-2.68	-2.40
TCGA-P5-A5EZ-10A-01D-A27N-08_LGG	-2.44	-2.76	-2.70	-2.61	-2.51	-2.70	-2.52	-2.52	-2.47	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.47
TCGA-P5-A5F0-10A-01D-A289-08_LGG	-2.64	-2.79	-2.74	-2.92	-2.54	-2.64	-2.63	-2.53	-2.58	-3.42	-3.00	-2.77	0.00	0.00	-3.09	-2.82	-2.62
TCGA-P5-A5F1-10A-01D-A289-08_LGG	-2.65	-2.80	-2.77	-2.92	-2.55	-2.66	-2.67	-2.51	-2.77	-3.24	-2.78	-2.67	0.00	-2.71	-3.19	0.00	-2.60
TCGA-P5-A5F2-10A-01D-A289-08_LGG	-2.62	0.00	-4.55	-2.62	-2.59	-2.59	-2.65	-2.56	-2.71	-3.29	-2.93	-2.76	0.00	-2.67	0.00	-2.74	-2.56
TCGA-P5-A5F4-10A-01D-A289-08_LGG	-2.57	-2.57	-2.53	0.00	0.00	0.00	-2.58	-2.57	-2.66	-3.21	-2.79	0.00	-2.67	-2.65	0.00	-2.70	-2.50
TCGA-P5-A5F6-10A-01D-A289-08_LGG	-2.51	0.00	-4.44	-2.53	-2.46	-2.54	-2.57	-2.60	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.58	-2.45
TCGA-P5-A72U-10A-01D-A329-08_LGG	-2.47	-2.70	-2.69	-2.88	-2.68	-2.66	-2.55	-2.55	-2.65	-3.32	-3.02	-4.40	-2.69	-2.61	0.00	-2.74	-2.47
TCGA-P5-A72W-10A-01D-A329-08_LGG	-2.47	0.00	-4.49	-2.72	-2.43	-2.50	-2.53	-2.53	-2.41	0.00	0.00	0.00	0.00	-3.89	0.00	-2.61	-2.39
TCGA-P5-A72X-10A-01D-A329-08_LGG	-2.54	-2.75	-2.71	-2.88	-2.44	-2.60	-2.58	-2.49	-2.59	0.00	-3.03	-2.71	0.00	-4.47	0.00	-2.63	-2.53
TCGA-P5-A72Z-10A-01D-A329-08_LGG	-2.51	0.00	-4.13	-2.57	-2.52	-2.52	-2.58	-2.60	0.00	-3.13	-2.69	-2.66	-2.67	-2.54	0.00	0.00	-2.49
TCGA-P5-A730-10A-01D-A329-08_LGG	-2.52	-4.41	0.00	-2.59	-2.51	-2.52	-2.53	-2.48	-2.50	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.44
TCGA-P5-A731-10A-01D-A329-08_LGG	-2.51	-2.74	-2.74	-2.90	-2.63	-2.59	-2.56	-2.48	-2.62	-3.19	-2.92	-2.69	0.00	-2.65	-3.14	0.00	-2.51
TCGA-P5-A733-10A-01D-A329-08_LGG	-2.48	-2.70	-2.64	-2.58	-2.55	-2.61	-2.46	-2.50	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.62	-2.45
TCGA-P5-A735-10A-01D-A329-08_LGG	-2.51	0.00	-4.45	-2.75	-2.54	-2.57	-2.64	-2.64	0.00	-3.13	-2.68	0.00	-2.59	-2.49	0.00	0.00	-2.46
TCGA-P5-A736-10A-01D-A329-08_LGG	-2.57	-2.63	-2.63	0.00	-2.60	-2.63	-2.64	-2.59	-2.70	-3.40	-2.63	-2.62	-2.78	-2.70	0.00	0.00	-2.55
TCGA-P5-A737-10A-01D-A329-08_LGG	-2.48	0.00	0.00	-2.70	-2.46	-2.49	-2.49	-2.53	-2.52	0.00	0.00	0.00	0.00	-4.37	0.00	-2.54	-2.43
TCGA-P5-A77W-10A-01D-A329-08_LGG	-2.51	0.00	-4.46	-2.53	-2.49	-2.49	-2.51	-2.50	-2.41	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.49
TCGA-P5-A77X-10A-01D-A329-08_LGG	-2.52	0.00	0.00	-2.63	-2.53	-2.57	-2.57	-2.61	-2.62	-3.38	-2.99	-2.63	0.00	-2.63	0.00	-2.69	-2.49
TCGA-P5-A780-10A-01D-A329-08_LGG	-2.61	-2.79	-2.77	-2.95	-2.50	-2.61	-2.64	-2.74	-2.70	-3.41	-2.74	-2.69	-2.81	-2.67	0.00	-2.82	-2.60
TCGA-P5-A781-10A-01D-A329-08_LGG	-2.45	-2.64	-2.65	-2.86	-2.61	-2.61	-2.47	-2.52	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.49	-2.40
TCGA-P6-A5OF-10A-01D-A29L-10_ACC	-2.39	-4.33	-4.33	-2.64	-2.43	-2.26	-2.22	-2.35	-2.59	-3.86	-2.83	-4.03	-2.59	-2.51	-2.93	-4.33	-2.46
TCGA-P6-A5OG-10A-01D-A29L-10_ACC	-2.49	-2.62	-2.59	-2.88	-2.39	-2.32	-2.31	-2.50	-2.59	-3.83	-2.56	-2.48	-2.62	-2.55	0.00	-2.52	-2.43
TCGA-PA-A5YG-10A-01D-A29L-10_ACC	-2.40	-2.54	-2.64	-2.87	-2.58	-2.53	-2.30	-2.36	-2.64	-3.25	-2.71	0.00	-2.53	-2.46	0.00	-2.51	-2.37
TCGA-PC-A5DK-10A-01D-A27P-09_SARC	-2.85	-2.74	-2.81	-3.38	-2.58	-2.60	-2.64	-2.56	-2.76	-3.58	-2.70	-2.62	-4.66	-2.80	-2.97	-4.18	-2.71
TCGA-PC-A5DL-10A-01D-A26G-09_SARC	-2.85	-3.79	-4.09	-2.99	-2.52	-2.54	-2.51	-2.47	-2.45	0.00	-4.09	0.00	-4.39	-3.91	-2.99	-2.82	-2.56
TCGA-PC-A5DM-10A-01D-A27P-09_SARC	-2.77	0.00	-4.54	-3.00	-2.57	-2.51	-2.49	-2.46	-2.41	0.00	-4.54	0.00	-4.24	0.00	-2.96	-2.73	-2.65
TCGA-PC-A5DN-10A-01D-A27P-09_SARC	-2.67	0.00	-4.58	-2.97	-2.52	-2.52	-2.52	-2.51	-2.44	0.00	0.00	0.00	-4.11	-4.28	0.00	-2.48	-2.60
TCGA-PC-A5DO-10A-01D-A26G-09_SARC	-2.82	-3.69	-3.61	-2.93	-2.54	-2.56	-2.49	-2.52	-2.43	0.00	0.00	0.00	-3.91	-4.09	-2.96	-2.87	-2.58
TCGA-PC-A5DP-10A-01D-A26G-09_SARC	-2.88	-3.74	-4.14	-2.98	-2.53	-2.51	-2.53	-2.57	-2.46	0.00	-4.14	0.00	-3.84	-4.44	0.00	-2.52	-2.59
TCGA-PD-A5DF-10A-01D-A27I-10_LIHC	-2.37	0.00	-3.76	-2.60	-2.44	-2.35	-2.35	-2.46	-2.61	-3.46	-2.84	0.00	-2.60	-2.52	-2.96	-3.76	-2.42
TCGA-PE-A5DC-10A-01D-A27P-09_BRCA	-2.80	0.00	-4.10	-2.91	-2.47	-2.48	-2.49	-2.46	-2.45	0.00	-4.40	0.00	0.00	0.00	0.00	-2.49	-2.62
TCGA-PE-A5DD-10A-01D-A27P-09_BRCA	-2.85	-2.72	-2.74	-3.22	-2.46	-2.59	-2.56	-2.54	-2.54	0.00	-2.92	-2.79	0.00	0.00	0.00	-2.49	-2.72
TCGA-PE-A5DE-10A-01D-A27P-09_BRCA	-2.74	-2.56	-2.58	-4.48	-2.71	-2.68	-2.53	-2.55	-2.70	-3.48	-2.59	-2.78	-2.69	-2.75	-3.02	0.00	-2.60
TCGA-PG-A5BC-10A-01D-A27P-09_UCEC	-2.79	0.00	-4.58	-3.24	-2.65	-2.48	-2.66	-2.51	-2.71	-3.47	-2.74	0.00	-2.76	-2.76	-3.05	-4.28	-2.71
TCGA-PG-A6IB-10A-01D-A31U-09_UCEC	-2.90	-2.64	-2.66	-3.23	-2.62	-2.73	-2.44	-2.47	-2.30	0.00	0.00	0.00	0.00	-4.35	-2.87	-2.72	-2.42
TCGA-PJ-A5Z8-10A-01D-A28G-10_KIRP	-2.41	-2.63	-2.59	-2.91	-2.64	-2.55	-2.25	-2.27	-2.56	-3.44	-2.69	0.00	-2.69	-2.53	0.00	-2.51	-2.44
TCGA-PJ-A5Z9-10A-01D-A28G-10_KIRP	-2.36	-4.28	0.00	-2.60	-2.34	-2.26	-2.25	-2.36	-2.21	0.00	-3.98	0.00	-3.98	-4.28	0.00	-2.30	-2.44
TCGA-PK-A5H8-10A-01D-A29L-10_ACC	-2.34	-2.39	-2.56	-2.73	-2.59	-2.45	-2.26	-2.39	-2.28	0.00	0.00	0.00	-4.28	-4.28	-2.66	0.00	-2.41
TCGA-PK-A5H9-10A-01D-A29L-10_ACC	-2.35	0.00	-3.93	-2.50	-2.41	-2.28	-2.22	-2.31	-2.50	-3.63	-2.77	-4.23	-2.56	-2.45	0.00	-2.67	-2.44
TCGA-PK-A5HA-10A-01D-A29L-10_ACC	-2.38	0.00	0.00	-2.62	-2.28	-2.26	-2.29	-2.35	-2.55	-3.80	-2.70	0.00	-2.68	-2.53	0.00	-2.56	-2.40
TCGA-PQ-A6FI-10A-01D-A31J-08_BLCA	-2.53	0.00	0.00	-2.56	-2.50	-2.57	-2.55	-2.47	-2.49	0.00	0.00	0.00	0.00	0.00	0.00	-2.46	-2.46
TCGA-PQ-A6FN-10A-01D-A31J-08_BLCA	-2.45	-2.70	-2.74	-2.88	-2.64	-2.71	-2.58	-2.60	-2.69	-3.28	-3.00	-2.66	0.00	-2.65	-3.08	0.00	-2.50
TCGA-PZ-A5RE-10B-01D-A32N-08_PAAD	-2.48	0.00	0.00	-2.65	-2.48	-2.51	-2.51	-2.47	-2.55	0.00	0.00	0.00	0.00	0.00	0.00	-2.40	-2.45
TCGA-Q1-A5R1-10A-01D-A28E-09_CESC	-2.85	0.00	0.00	-2.96	-2.54	-2.50	-2.47	-2.56	-2.69	-3.45	-2.91	-2.71	0.00	-2.76	0.00	-2.80	-2.62
TCGA-Q1-A5R2-10A-01D-A28E-09_CESC	-2.78	-2.63	-2.70	-3.33	-2.70	-2.74	-2.44	-2.52	-2.56	-3.28	-2.78	0.00	-2.75	-2.69	-2.90	0.00	-2.49
TCGA-Q1-A5R3-10B-01D-A28E-09_CESC	-2.81	0.00	0.00	-3.12	-2.46	-2.46	-2.38	-2.55	-2.36	0.00	0.00	0.00	0.00	0.00	0.00	-2.50	-2.50
TCGA-Q2-A5QZ-10A-01D-A28G-10_KIRP	-2.46	-2.69	-2.56	-2.91	-2.33	-2.35	-2.40	-2.48	-2.36	0.00	-3.10	-2.68	0.00	0.00	-3.10	-2.80	-2.58
TCGA-Q3-A5QY-10A-01D-A32N-08_PAAD	-2.55	0.00	0.00	-2.65	-2.57	-2.60	-2.65	-2.54	-2.76	-3.22	-2.91	0.00	-2.76	-2.66	-3.03	0.00	-2.57

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-QB-A6FS-10A-01D-A30X-08_SKCM	-2.62	0.00	-4.51	-2.77	-2.59	-2.59	-2.61	-2.60	-2.63	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.57
TCGA-QF-A5YS-10A-01D-A31U-09_UCEC	-2.86	0.00	0.00	-3.04	-2.40	-2.50	-2.39	-2.42	-2.35	0.00	0.00	0.00	0.00	0.00	-2.92	-2.76	-2.52
TCGA-QF-A5YT-10A-01D-A31U-09_UCEC	-2.81	0.00	0.00	-2.99	-2.45	-2.46	-2.42	-2.53	-2.40	0.00	0.00	0.00	0.00	0.00	-2.68	0.00	-2.47
TCGA-QG-A5YV-10A-01D-A28G-10_COAD	-2.32	-2.44	-2.49	-2.89	-2.25	-2.27	-2.31	-2.50	-2.29	0.00	-2.62	-2.40	0.00	-4.21	-2.64	0.00	-2.61
TCGA-QG-A5YW-10A-01D-A28G-10_COAD	-2.38	0.00	0.00	-2.65	-2.26	-2.22	-2.16	-2.29	-2.31	0.00	0.00	0.00	0.00	0.00	-2.60	0.00	-2.33
TCGA-QG-A5YX-10A-01D-A28G-10_COAD	-2.44	-4.34	-4.34	-2.62	-2.31	-2.25	-2.37	-2.43	-2.39	0.00	-2.76	-2.59	-4.04	-4.04	-2.79	0.00	-2.45
TCGA-QG-A5Z1-10A-01D-A28G-10_COAD	-2.48	-2.53	-2.41	0.00	-2.47	-2.43	-2.45	-2.52	-2.81	-4.03	-2.40	-2.66	-2.41	-2.61	-3.25	0.00	-2.50
TCGA-QG-A5Z2-10A-01D-A28G-10_COAD	-2.45	-3.94	0.00	-2.54	-2.31	-2.29	-2.32	-2.49	-2.35	0.00	0.00	0.00	0.00	0.00	-2.69	0.00	-2.36
TCGA-QH-A65R-10A-01D-A31J-08_LGG	-2.49	-2.66	-2.64	-2.86	-2.62	-2.60	-2.52	-2.48	-2.48	0.00	0.00	0.00	0.00	0.00	0.00	-2.36	-2.48
TCGA-QH-A65S-10A-01D-A29Q-08_LGG	-2.55	-2.61	-2.62	0.00	-2.61	-2.61	-2.61	-2.66	-2.52	0.00	-2.75	-2.57	0.00	0.00	0.00	-2.54	-2.52
TCGA-QH-A65V-10A-01D-A29Q-08_LGG	-2.44	0.00	0.00	-2.72	-2.48	-2.53	-2.53	-2.55	-2.69	-3.37	-2.98	-2.73	0.00	-2.66	0.00	-2.77	-2.42
TCGA-QH-A65X-10D-01D-A329-08_LGG	-2.50	-4.40	0.00	-2.69	-2.46	-2.44	-2.44	-2.59	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.36
TCGA-QH-A65Z-10A-01D-A29Q-08_LGG	-2.48	0.00	0.00	-2.94	-2.53	-2.52	-2.58	-2.55	-2.72	-3.46	-2.90	0.00	-2.75	-2.65	0.00	-2.84	-2.43
TCGA-QH-A6CS-10A-01D-A31J-08_LGG	-2.54	0.00	-4.46	-2.60	-2.49	-2.57	-2.57	-2.58	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.54
TCGA-QH-A6CU-10A-01D-A31J-08_LGG	-2.61	-2.69	-2.71	-2.91	-2.52	-2.66	-2.63	-2.51	-2.55	0.00	-2.95	-2.69	0.00	-4.24	0.00	-2.46	-2.65
TCGA-QH-A6CV-10A-01D-A31J-08_LGG	-2.56	-4.49	-4.49	-2.81	-2.56	-2.42	-2.61	-2.51	-2.69	-3.32	-2.89	-2.68	0.00	-2.68	-3.00	0.00	-2.54
TCGA-QH-A6CW-10B-01D-A329-08_LGG	-2.47	-2.70	-2.64	-2.83	-2.58	-2.62	-2.48	-2.59	-2.46	0.00	0.00	-4.50	0.00	-4.50	0.00	-2.62	-2.41
TCGA-QH-A6CX-10A-01D-A329-08_LGG	-2.59	-2.76	-2.75	-2.99	-2.42	-2.51	-2.59	-2.65	-2.66	-3.23	-2.77	-2.67	-2.80	-2.67	0.00	-2.92	-2.44
TCGA-QH-A6CY-10A-01D-A329-08_LGG	-2.50	-4.52	0.00	-2.65	-2.56	-2.52	-2.54	-2.61	-2.63	-3.31	-2.88	0.00	-2.76	-2.64	0.00	-2.82	-2.44
TCGA-QH-A6CZ-10B-01D-A329-08_LGG	-2.59	-2.76	-2.72	-2.89	-2.45	-2.59	-2.62	-2.66	0.00	-3.29	-2.67	-2.59	-2.87	-2.57	0.00	0.00	-2.56
TCGA-QH-A6X3-10B-01D-A329-08_LGG	-2.67	-2.67	-2.72	-2.99	-2.49	-2.65	-2.62	-2.71	-2.70	-3.29	-2.75	-2.67	0.00	-2.74	0.00	-2.75	-2.60
TCGA-QH-A6X4-10B-01D-A329-08_LGG	-2.49	-2.77	-2.75	-2.92	-2.44	-2.54	-2.57	-2.60	-2.46	0.00	-3.03	-2.69	0.00	-4.45	0.00	-2.60	-2.44
TCGA-QH-A6X5-10B-01D-A329-08_LGG	-2.57	0.00	-4.41	-2.57	-2.54	-2.56	-2.51	-2.48	-2.43	0.00	-4.41	0.00	0.00	0.00	0.00	-2.61	-2.44
TCGA-QH-A6X8-10B-01D-A329-08_LGG	-2.46	-2.64	-2.63	-2.76	-2.59	-2.65	-2.47	-2.54	-2.52	0.00	0.00	0.00	0.00	0.00	0.00	-2.51	-2.37
TCGA-QH-A6X9-10B-01D-A329-08_LGG	-2.39	-2.68	-2.63	-2.82	-2.65	-2.63	-2.49	-2.54	-2.43	0.00	0.00	0.00	0.00	-4.43	-3.35	-2.78	-2.41
TCGA-QH-A6XA-10B-01D-A329-08_LGG	-2.42	-2.75	-2.72	-2.93	-2.43	-2.53	-2.60	-2.58	-2.50	0.00	-3.08	-2.65	0.00	0.00	-3.24	-2.87	-2.42
TCGA-QH-A6XC-10B-01D-A329-08_LGG	-2.46	-4.48	-4.18	-2.69	-2.46	-2.49	-2.56	-2.47	-2.46	0.00	0.00	0.00	0.00	0.00	0.00	-2.57	-2.35
TCGA-QK-A64Z-10A-01D-A30H-08_HNSC	-2.49	-2.53	-2.55	0.00	-2.71	-2.70	-2.56	-2.60	-2.61	-3.39	-2.75	-2.68	-2.78	-2.66	0.00	-2.76	-2.44
TCGA-QK-A652-10A-01D-A30H-08_HNSC	-2.57	-2.77	-2.78	-2.90	-2.46	-2.57	-2.54	-2.61	-2.81	-3.34	-2.68	-2.54	0.00	-2.69	0.00	-2.76	-2.48
TCGA-QK-A6IF-10A-01D-A31J-08_HNSC	-2.35	-2.61	-2.66	-2.87	-2.64	-2.64	-2.58	-2.36	-2.47	0.00	0.00	0.00	0.00	0.00	-3.08	-2.71	-2.49
TCGA-QK-A6IG-10A-01D-A31J-08_HNSC	-2.64	-2.74	-2.73	-2.92	-2.52	-2.49	-2.64	-2.57	-2.62	0.00	-2.86	-2.72	0.00	0.00	0.00	-2.49	-2.55
TCGA-QK-A6IH-10A-01D-A31J-08_HNSC	-2.51	-2.65	-2.66	-2.89	-2.64	-2.65	-2.56	-2.43	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.39	-2.44
TCGA-QK-A6II-10A-01D-A31J-08_HNSC	-2.55	-2.71	-2.74	-2.87	-2.67	-2.67	-2.56	-2.51	-2.67	-3.38	-2.92	-4.49	-2.74	-2.67	-3.09	0.00	-2.52
TCGA-QK-A6IJ-10A-01D-A31J-08_HNSC	-2.45	-2.70	-2.74	-2.86	-2.44	-2.64	-2.71	-2.71	0.00	-3.25	-2.64	-2.61	-2.67	-2.52	0.00	-4.18	-2.53
TCGA-QS-A5YQ-10A-01D-A31U-09_UCEC	-2.87	0.00	-2.79	-3.33	-2.38	-2.51	-2.50	-2.60	-2.39	0.00	-2.87	0.00	-2.77	0.00	-2.73	0.00	-2.46
TCGA-QS-A5YR-10A-01D-A31U-09_UCEC	-2.75	0.00	0.00	-2.91	-2.36	-2.44	-2.37	-2.45	-2.25	0.00	0.00	0.00	0.00	-4.35	-2.83	0.00	-2.64
TCGA-QU-A6IL-10A-01D-A31J-08_PRAD	-2.49	-2.63	-2.63	-2.77	-2.59	-2.63	-2.66	-2.66	-2.61	0.00	-2.86	-2.65	0.00	-2.60	-2.97	0.00	-2.50
TCGA-QU-A6IM-10A-01D-A31J-08_PRAD	-2.54	0.00	0.00	-2.54	-2.48	-2.51	-2.70	-2.47	-2.52	0.00	0.00	0.00	0.00	0.00	-3.08	-2.75	-2.46
TCGA-QU-A6IN-10A-01D-A31J-08_PRAD	-2.58	0.00	-4.51	-2.75	-2.61	-2.59	-2.60	-2.62	0.00	-3.21	-2.67	0.00	-2.62	-2.54	0.00	0.00	-2.53
TCGA-QU-A6IO-10A-01D-A31J-08_PRAD	-2.55	0.00	0.00	-2.76	-2.42	-2.57	-2.60	-2.42	-2.49	0.00	0.00	0.00	0.00	0.00	-3.08	-2.69	-2.52
TCGA-QU-A6IP-10A-01D-A31J-08_PRAD	-2.58	0.00	-4.48	-2.76	-2.52	-2.55	-2.55	-2.50	-2.61	0.00	0.00	0.00	0.00	0.00	0.00	-2.40	-2.46
TCGA-R3-A69X-10A-01D-A30H-08_BLCA	-2.48	-4.66	0.00	-2.68	-2.47	-2.48	-2.50	-2.50	-2.68	-3.45	-2.77	0.00	-2.77	-2.65	0.00	-2.72	-2.41
TCGA-R5-A7O7-10A-01D-A33W-08_STAD	-2.56	0.00	0.00	-2.82	-2.62	-2.60	-2.67	-2.65	-2.77	-3.26	-2.84	0.00	-2.78	-2.66	0.00	-2.73	-2.51
TCGA-R8-A6MK-10A-01D-A329-08_LGG	-2.51	-2.80	-2.69	-2.88	-2.60	-2.64	-2.50	-2.57	-2.40	0.00	0.00	-4.50	0.00	-4.20	0.00	-2.48	-2.41
TCGA-R8-A6ML-10A-01D-A329-08_LGG	-2.47	0.00	-4.38	-2.67	-2.46	-2.52	-2.48	-2.50	-2.50	0.00	0.00	0.00	0.00	0.00	-3.12	-2.70	-2.46
TCGA-R8-A6YH-10B-01D-A329-08_LGG	-2.55	0.00	0.00	-2.59	-2.42	-2.54	-2.61	-2.55	-2.65	-3.43	-2.93	0.00	-2.72	-2.66	-3.05	0.00	-2.45
TCGA-R8-A73M-10C-01D-A329-08_LGG	-2.36	-2.51	-2.50	0.00	0.00	0.00	-2.49	-2.47	-2.64	-3.36	-2.78	0.00	-2.67	-2.62	0.00	-2.74	-2.40
TCGA-RB-A7B8-10A-01D-A33W-08_PAAD	-2.61	-2.59	-2.61	0.00	-2.69	-2.77	-2.63	-2.57	-2.75	-3.42	-2.68	-2.62	0.00	-2.75	0.00	-2.80	-2.56
TCGA-RD-A7BS-10A-01D-A32N-08_STAD	-2.58	-4.30	0.00	-2.78	-2.59	-2.61	-2.60	-2.57	-2.53	0.00	0.00	0.00	0.00	0.00	-3.03	-2.71	-2.55
TCGA-RD-A7BT-10A-01D-A33W-08_STAD	-2.53	-2.71	-2.69	-2.91	-2.76	-2.70	-2.58	-2.58	-2.63	-3.39	-2.88	0.00	-2.73	-2.74	0.00	-2.80	-2.50
TCGA-RD-A7BW-10A-01D-A32N-08_STAD	-2.60	0.00	-4.62	-2.66	-2.65	-2.58	-2.68	-2.53	-2.61	0.00	0.00	0.00	0.00	0.00	-3.13	-2.75	-2.55
TCGA-RD-A7C1-10A-01D-A32N-08_STAD	-2.79	-2.82	-2.78	-4.77	-2.67	-2.69	-2.72	-2.77	0.00	-3.31	-2.69	-2.70	-2.84	-2.74	0.00	0.00	-2.64
TCGA-RN-A68Q-10A-01D-A307-09_SARC	-2.76	-2.66	-2.68	-3.23	-2.62	-2.72	-2.49	-2.66	-2.45	0.00	0.00	0.00	0.00	0.00	-2.79	0.00	-2.56
TCGA-RP-A690-10A-01D-A30X-08_SKCM	-2.63	0.00	0.00	-2.64	-2.65	-2.62	-2.63	-2.64	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.66	-2.57
TCGA-RP-A693-10A-01D-A30X-08_SKCM	-2.62	0.00	-4.55	-2.64	-2.59	-2.61	-2.64	-2.67	-2.53	0.00	0.00	0.00	0.00	0.00	0.00	-2.64	-2.58
TCGA-RP-A694-10A-01D-A30X-08_SKCM	-2.65	0.00	-4.61	-2.71	-2.62	-2.62	-2.65	-2.67	-2.57	0.00	0.00	0.00	0.00	-4.61	-3.10	-2.83	-2.61
TCGA-RP-A695-10A-01D-A30X-08_SKCM	-2.68	-2.68	-2.60	0.00	-2.76	-2.78	-2.71	-2.64	-2.56	0.00	-3.12	-2.88	0.00	0.00	0.00	-2.68	-2.65
TCGA-RQ-A68N-10A-01D-A31X-10_DLBC	-2.40	0.00	0.00	-2.57	-2.37	-2.37	-2.31	-2.42	-2.33	0.00	0.00	0.00	0.00	0.00	0.00	-2.59	-2.43
TCGA-RQ-A6JB-10A-01D-A31X-10_DLBC	-2.41	-2.55	-2.53	-2.76	-2.54	-2.78	-2.27	-2.44	-2.40	0.00	0.00	0.00	0.00	0.00	0.00	-2.52	-2.38
TCGA-RR-A6KA-10A-01D-A33W-08_GBM	-2.56	-2.74	-2.74	-2.91	-2.56	-2.63	-2.60	-2.56	-2.49	0.00	-2.91	-2.75	0.00	0.00	-3.06	-2.73	-2.52
TCGA-RR-A6KB-10A-01D-A33W-08_GBM	-2.56	-2.59	-2.60	0.00	-2.65	-2.69	-2.67	-2.71	-2.62	0.00	-2.61	-2.68	-2.72	-2.62	-3.05	0.00	-2.53
TCGA-RR-A6KC-10A-01D-A33W-08_GBM	-2.54	0.00	0.00	-2.80	-2.48	-2.64	-2.64	-2.54	-2.68	-3.27	-2.72	-2.81	-2.86	-2.76	-3.15	0.00	-2.60
TCGA-S5-A6DX-10A-01D-A31J-08_BLCA	-2.42	-2.72	-2.74	-2.85	-2.62	-2.70	-2.59	-2.45	-2.46	0.00	0.00	0.00	0.00	0.00	-3.03	-2.76	-2.47
TCGA-S9-A6TU-10A-01D-A329-08_LGG	-2.51	-2.70	-2.66	-2.75	-2.57	-2.60	-2.52	-2.46	-2.48	0.00	0.00	0.00	0.00	0.00	-3.13	-2.72	-2.46
TCGA-S9-A6TW-10A-01D-A329-08_LGG	-2.47	0.00	0.00	-2.54	-2.50	-2.53	-2.51	-2.59	0.00	-2.96	-2.72	0.00	-2.58	-2.52	0.00	0.00	-2.46
TCGA-S9-A6TX-10A-01D-A329-08_LGG	-2.54	-2.75	-2.72	-2.92	-2.49	-2.59	-2.58	-2.57	-2.45	0.00	-2.94	-2.71	0.00	0.00	-3.15	-2.80	-2.54
TCGA-S9-A6TY-10A-01D-A329-08_LGG	-2.52	0.00	0.00	-2.65	-2.55	-2.49	-2.54	-2.60	-2.63	-3.18	-2.93	0.00	-2.73	-2.65	0.00	-2.71	-2.46
TCGA-S9-A6TZ-10A-01D-A329-08_LGG	-2.52	-4.39	-4.39	-2.55	-2.47	-2.53	-2.53	-2.59	-2.64	-3.24	-2.99	0.00	-2.71	-2.62	-3.16	0.00	-2.47
TCGA-S9-A6U0-10A-01D-A329-08_LGG	-2.53	0.00	-4.45	-2.73	-2.56	-2.53	-2.55	-2.44	-2.43	0.00	0.00	0.00	0.00	0.00	-3.05	-2.71	-2.51
TCGA-S9-A6U9-10A-01D-A329-08_LGG	-2.57	0.00	-4.47	-2.63	-2.51	-2.56	-2.56	-2.50	-2.54	0.00	0.00	-4.47	0.00	0.00	-3.02	-2.67	-2.48
TCGA-SL-A6J9-10A-01D-A31U-09_UCEC	-2.84	0.00	0.00	-3.11	-2.46	-2.48	-2.40	-2.42	-2.28	0.00	0.00	0.00	0.00	0.00	-2.81	-2.72	-2.52
TCGA-SL-A6JA-10A-01D-A31U-09_UCEC	-2.88	0.00	0.00	-2.92	-2.44	-2.45	-2.44	-2.45	-2.39	0.00	0.00	0.00	0.00	0.00	-2.85	-2.76	-2.53
TCGA-SU-A7E7-10A-01D-A33W-08_PRAD	-2.46	0.00	0.00	-2.72	-2.51	-2.54	-2.51	-2.59	-2.51	0.00	0.00	0.00	0.00	0.00	-2.88	0.00	-2.43
TCGA-TM-A7C3-10A-01D-A329-08_LGG	-2.49	0.00	0.00	-2.62	-2.49	-2.54	-2.51	-2.49	-2.53	0.00	0.00	0.00	0.00	-4.14	0.00	-2.42	-2.46
TCGA-TM-A7C4-10A-01D-A329-08_LGG	-2.41	-2.68	-2.59	-2.84	-2.56	-2.58	-2.47	-2.53	-2.41	0.00	0.00	0.00	0.00	0.00	-2.97	-2.71	-2.41
TCGA-TM-A7C5-10A-01D-A329-08_LGG	-2.49	0.00	0.00	-2.62	-2.43	-2.48	-2.60	-2.47	-2.50	0.00	0.00	0.00	0.00	-4.50	-3.16	-2.91	-2.38
TCGA-TM-A7CF-10A-01D-A329-08_LGG	-2.47	0.00	0.00	-2.70	-2.46	-2.52	-2.50	-2.49	-2.47	0.00	0.00	0.00	0.00	0.00	-2.94	-2.71	-2.46
TCGA-UY-A78K-10A-01D-A339-08_BLCA	-2.55	0.00	0.00	-2.64	-2.52	-2.57	-2.53	-2.52	-2.45	0.00	0.00	0.00	0.00	0.00	0.00	-2.41	-2.49
TCGA-UY-A78L-10A-01D-A339-08_BLCA	-2.48	0.00	-4.12	-2.64	-2.46	-2.47	-2.50	-2.55	-2.56	0.00	0.00	0.00	0.00	0.00	0.00	-2.56	-2.38
TCGA-UY-A78N-10A-01D-A339-08_BLCA	-2.52	0.00	0.00	-2.70	-2.49	-2.57	-2.56	-2.60	-2.66	-3.51	-2.89	0.00	-2.85	-2.63	0.00	-2.95	-2.31
TCGA-UY-A78O-10A-01D-A339-08_BLCA	-2.67	-2.66	-2.64	0.00	-2.63	-2.63	-2.61	-2.53	-2.58	-3.37	-2.75	-2.67	0.00	-4.55	-3.19	-2.78	-2.63

Table A3 Number of KIR consensus sequence positions with minimum 10x read coverage for 2535 OKG and 5512 TCGA samples

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG00096.mapped.ILLUMINA.bwa.GBR.exome.20120522	600	332	374	0	0	0	553	559	565	0	0	0	0	0	56	87	596
HG00097.mapped.ILLUMINA.bwa.GBR.exome.20130415	635	0	0	238	430	324	477	548	327	0	0	0	0	0	25	0	556
HG00099.mapped.ILLUMINA.bwa.GBR.exome.20130415	662	0	0	349	596	423	522	579	287	93	241	0	323	148	0	28	566
HG00100.mapped.ILLUMINA.bwa.GBR.exome.20121211	753	0	0	310	602	388	528	654	392	79	582	0	358	141	0	52	579
HG00101.mapped.ILLUMINA.bwa.GBR.exome.20121211	693	0	0	386	703	470	556	639	568	0	0	0	0	0	58	100	598
HG00102.mapped.ILLUMINA.bwa.GBR.exome.20121211	694	0	0	378	597	474	553	549	556	0	0	0	0	0	0	97	593
HG00103.mapped.ILLUMINA.bwa.GBR.exome.20120522	694	0	0	385	689	458	554	549	464	0	0	0	0	0	0	106	592
HG00105.mapped.ILLUMINA.bwa.GBR.exome.20130415	607	120	0	169	502	293	479	503	270	0	71	0	265	126	0	32	562
HG00106.mapped.ILLUMINA.bwa.GBR.exome.20130415	646	0	0	336	573	359	487	542	340	0	0	0	0	0	0	46	552
HG00107.mapped.ILLUMINA.bwa.GBR.exome.20121211	695	322	365	364	581	377	556	559	564	0	0	0	0	0	0	172	597
HG00108.mapped.ILLUMINA.bwa.GBR.exome.20120522	698	285	316	343	672	425	541	643	513	101	642	541	321	149	0	64	588
HG00109.mapped.ILLUMINA.bwa.GBR.exome.20121211	703	282	315	345	657	417	544	631	446	0	0	0	0	0	38	67	584
HG00110.mapped.ILLUMINA.bwa.GBR.exome.20121211	698	278	305	344	678	336	543	633	418	101	642	523	329	157	0	61	585
HG00111.mapped.ILLUMINA.bwa.GBR.exome.20120522	701	283	315	339	633	427	542	642	442	0	0	0	0	0	0	113	587
HG00112.mapped.ILLUMINA.bwa.GBR.exome.20130415	657	0	0	296	394	356	475	555	0	92	361	0	299	170	0	0	553
HG00113.mapped.ILLUMINA.bwa.GBR.exome.20121211	698	0	0	359	665	431	544	630	533	0	0	0	0	0	0	127	589
HG00114.mapped.ILLUMINA.bwa.GBR.exome.20120522	788	0	0	379	693	477	559	562	572	0	0	0	0	0	63	94	593
HG00115.mapped.ILLUMINA.bwa.GBR.exome.20130415	664	0	0	251	398	359	465	531	250	0	216	0	236	148	0	21	560
HG00116.mapped.ILLUMINA.bwa.GBR.exome.20120522	758	256	273	293	618	288	532	663	401	75	650	574	366	140	0	90	579
HG00117.mapped.ILLUMINA.bwa.GBR.exome.20120522	750	242	262	276	506	355	530	628	467	0	0	0	0	0	0	83	577
HG00118.mapped.ILLUMINA.bwa.GBR.exome.20130415	656	0	0	342	367	362	479	537	337	0	0	0	0	0	0	37	567
HG00119.mapped.ILLUMINA.bwa.GBR.exome.20120522	688	0	0	308	605	395	530	647	410	0	0	0	0	0	23	55	575
HG00120.mapped.ILLUMINA.bwa.GBR.exome.20120522	680	243	254	279	602	358	534	635	472	0	537	509	0	0	0	98	576
HG00121.mapped.ILLUMINA.bwa.GBR.exome.20121211	785	282	299	340	665	335	540	636	536	0	591	555	0	0	45	58	591
HG00122.mapped.ILLUMINA.bwa.GBR.exome.20130415	633	148	194	201	364	311	499	591	281	93	303	354	257	122	0	20	543
HG00123.mapped.ILLUMINA.bwa.GBR.exome.20120522	686	0	0	303	601	385	528	637	376	68	607	0	361	138	0	51	579
HG00124.mapped.ILLUMINA.bwa.GBR.exome.20120522	764	0	0	307	612	393	534	647	476	0	0	0	0	0	0	121	580
HG00125.mapped.ILLUMINA.bwa.GBR.exome.20120522	692	284	328	341	640	321	537	630	450	0	0	0	0	0	0	122	589
HG00126.mapped.ILLUMINA.bwa.GBR.exome.20130415	636	133	166	199	304	297	484	544	323	0	0	0	0	0	11	39	541
HG00127.mapped.ILLUMINA.bwa.GBR.exome.20120522	593	0	0	274	583	454	550	618	456	0	0	0	0	0	33	46	588
HG00128.mapped.ILLUMINA.bwa.GBR.exome.20130415	665	0	0	263	667	376	547	643	354	99	308	436	0	0	18	35	574
HG00129.mapped.ILLUMINA.bwa.GBR.exome.20130415	632	128	194	185	578	316	461	551	347	0	88	295	0	0	9	18	548
HG00130.mapped.ILLUMINA.bwa.GBR.exome.20130415	648	0	0	244	566	426	493	554	336	0	0	0	0	0	0	51	565
HG00131.mapped.ILLUMINA.bwa.GBR.exome.20120522	754	0	0	315	616	394	532	660	487	0	0	0	0	0	61	0	579
HG00132.mapped.ILLUMINA.bwa.GBR.exome.20130415	667	0	0	329	576	375	540	558	327	0	0	0	0	0	0	69	548
HG00133.mapped.ILLUMINA.bwa.GBR.exome.20120522	692	248	258	295	620	377	534	644	455	76	653	513	304	138	0	70	578
HG00136.mapped.ILLUMINA.bwa.GBR.exome.20120522	698	291	318	351	679	337	545	642	545	0	622	575	0	0	45	89	588
HG00137.mapped.ILLUMINA.bwa.GBR.exome.20120522	697	280	283	326	616	397	541	621	528	0	0	0	0	0	28	55	588
HG00138.mapped.ILLUMINA.bwa.GBR.exome.20120522	580	294	322	0	0	0	542	634	538	0	0	0	0	0	53	64	583
HG00139.mapped.ILLUMINA.bwa.GBR.exome.20121211	698	0	0	363	679	439	544	643	537	0	0	0	0	0	0	164	590
HG00140.mapped.ILLUMINA.bwa.GBR.exome.20121211	694	280	300	334	675	326	536	648	481	99	648	512	397	153	0	61	590
HG00141.mapped.ILLUMINA.bwa.GBR.exome.20130415	654	144	208	228	414	308	506	591	328	0	0	0	0	0	14	41	568
HG00142.mapped.ILLUMINA.bwa.GBR.exome.20130415	673	0	0	259	616	417	492	542	312	0	0	0	0	150	19	1	537
HG00143.mapped.ILLUMINA.bwa.GBR.exome.20130415	641	146	145	237	327	327	511	589	338	0	0	0	0	0	12	29	567
HG00145.mapped.ILLUMINA.bwa.GBR.exome.20120522	678	246	273	291	579	290	533	657	482	0	0	0	0	0	40	83	578
HG00146.mapped.ILLUMINA.bwa.GBR.exome.20121211	683	0	0	305	607	385	534	655	376	76	607	0	298	137	0	72	577
HG00148.mapped.ILLUMINA.bwa.GBR.exome.20130415	664	154	181	217	358	319	522	560	305	0	0	0	0	0	0	72	575
HG00149.mapped.ILLUMINA.bwa.GBR.exome.20130415	627	0	0	331	595	355	501	541	341	0	0	0	0	0	7	37	550
HG00150.mapped.ILLUMINA.bwa.GBR.exome.20130415	631	134	219	206	519	336	478	584	254	87	412	496	0	151	0	29	554
HG00151.mapped.ILLUMINA.bwa.GBR.exome.20130415	618	0	0	227	448	349	490	485	297	0	0	0	0	0	0	41	539
HG00154.mapped.ILLUMINA.bwa.GBR.exome.20120522	783	0	0	360	679	435	547	638	537	0	0	0	0	0	55	74	590
HG00155.mapped.ILLUMINA.bwa.GBR.exome.20121211	688	0	0	300	612	290	522	651	486	0	0	0	0	0	29	79	577
HG00157.mapped.ILLUMINA.bwa.GBR.exome.20120522	664	246	269	183	501	273	534	640	473	0	0	0	0	0	28	64	578
HG00158.mapped.ILLUMINA.bwa.GBR.exome.20120522	687	0	0	299	600	290	530	647	459	78	608	0	357	139	21	0	573
HG00159.mapped.ILLUMINA.bwa.GBR.exome.20120522	758	0	0	306	616	400	536	654	370	79	626	501	287	135	0	66	577
HG00160.mapped.ILLUMINA.bwa.GBR.exome.20120522	675	234	250	274	552	359	531	648	397	0	0	0	0	0	15	46	574
HG00171.mapped.ILLUMINA.bwa.FIN.exome.20120522	695	0	0	362	670	437	543	629	541	0	0	0	0	0	38	77	589
HG00173.mapped.ILLUMINA.bwa.FIN.exome.20130415	649	0	0	342	609	376	517	566	291	0	372	0	304	153	11	1	560
HG00174.mapped.ILLUMINA.bwa.FIN.exome.20120522	702	0	0	362	671	435	539	644	456	0	0	0	0	0	0	130	586
HG00176.mapped.ILLUMINA.bwa.FIN.exome.20120522	760	0	0	307	604	376	533	651	470	0	0	0	0	0	0	106	577
HG00177.mapped.ILLUMINA.bwa.FIN.exome.20130415	645	0	0	240	582	358	518	573	340	0	0	0	0	0	16	25	546
HG00178.mapped.ILLUMINA.bwa.FIN.exome.20121211	792	0	0	386	711	474	557	647	539	0	543	0	449	180	42	0	598
HG00179.mapped.ILLUMINA.bwa.FIN.exome.20130415	638	0	0	260	587	361	456	512	280	0	0	0	0	158	0	42	537
HG00180.mapped.ILLUMINA.bwa.FIN.exome.20130415	637	0	0	216	537	356	505	563	324	0	0	0	0	0	7	21	551
HG00181.mapped.ILLUMINA.bwa.FIN.exome.20121211	700	0	0	406	711	472	561	662	573	86	0	0	0	0	73	109	597
HG00182.mapped.ILLUMINA.bwa.FIN.exome.20120522	790	0	0	384	699	477	554	646	558	96	543	0	451	186	0	91	593
HG00183.mapped.ILLUMINA.bwa.FIN.exome.20120522	789	333	372	278	714	386	559	567	561	97	661	584	462	191	56	0	598
HG00185.mapped.ILLUMINA.bwa.FIN.exome.20120522	788	329	364	365	711	464	562	665	572	87	543	583	0	0	57	90	600
HG00186.mapped.ILLUMINA.bwa.FIN.exome.20120522	694	0	0	378	689	472	554	556	356	81	521	0	377	184	0	83	593
HG00187.mapped.ILLUMINA.bwa.FIN.exome.20120522	698	0	0	378	703	391	554	656	577	0	0	0	0	0	63	109	600
HG00188.mapped.ILLUMINA.bwa.FIN.exome.20120522	697	0	0	378	698	474	555	654	564	0	0	0	0	0	73	1	593
HG00189.mapped.ILLUMINA.bwa.FIN.exome.20120522	600	0	0	369	692	464	548	539	0	0	541	0	449	184	0	0	591
HG00190.mapped.ILLUMINA.bwa.FIN.exome.20120522	792	325	364	363	671	366	555	646	572	0	0	0	0	0	78	0	597
HG00231.mapped.ILLUMINA.bwa.GBR.exome.20130415	663	0	0	348	629	348	513	567	333	0	0	0	0	0	0	49	572
HG00232.mapped.ILLUMINA.bwa.GBR.exome.20120522	700	287	323	338	652	424	545	649	528	0	0	0	0	0	51	76	587
HG00233.mapped.ILLUMINA.bwa.GBR.exome.20120522	599	336	374	0	675	185	556	638	456	89	654	590	0	187	0	90	596
HG00234.mapped.ILLUMINA.bwa.GBR.exome.20130415	650	0	0	231	538	352	487	543	318	0	0	0	0	0	0	64	539
HG00235.mapped.ILLUMINA.bwa.GBR.exome.20130415	636	0	0	251	519	415	463	549	279	0	0	0	0	0	0	47	529
HG00236.mapped.ILLUMINA.bwa.GBR.exome.20121211	581	304	328	0	638	163	549	643	421	99	642	539	424	160	38	0	587
HG00237.mapped.ILLUMINA.bwa.GBR.exome.20121211	694	0	0	348	668	338	545	640	536	0	0	0	0	0	36	67	585
HG00238.mapped.ILLUMINA.bwa.GBR.exome.20121211	693	0	0	367	692	476	557	660	570	0	0	0	0	0	0	164	597
HG00239.mapped.ILLUMINA.bwa.GBR.exome.20120522	683	253	259	292	590	375	532	643	391	73	581	0	297	142	0	72	580
HG00240.mapped.ILLUMINA.bwa.GBR.exome.20121211	794	0	0	391	712	478	557	658	571	0	0	0	0	0	0	172	598
HG00242.mapped.ILLUMINA.bwa.GBR.exome.20120522	689	0	0	351	622	401	535	647	490	0	0	0	0	0	32	91	578
HG00243.mapped.ILLUMINA.bwa.GBR.exome.20120522	674	263	281	0	0	0	534	660	493	0	0	0	0	0	36	88	577
HG00244.mapped.ILLUMINA.bwa.GBR.exome.20120522	761	0	0	308	611	397	533	653	417	0	0	0	0	0	0	107	579
HG00245.mapped.ILLUMINA.bwa.GBR.exome.20121211	675	251	270	295	589	286	530	650	390	79	576	0	363	135	0	63	575
HG00246.mapped.ILLUMINA.bwa.GBR.exome.20120522	779	287	314	340	642	335	540	638	538	0	0	0	0	0	43	53	589
HG00250.mapped.ILLUMINA.bwa.GBR.exome.20121211	693	0	0	354	667	431	542	622	515	0	0	0	0	0	36	61	590
HG00251.mapped.ILLUMINA.bwa.GBR.exome.20121211	697	282	310	346	672	429	546	639	405	98	640	539	412	158	0	50	584
HG00252.mapped.ILLUMINA.bwa.GBR.exome.20121211	702	0	0	362	679	442	549	637	543	0	0	0	0	0	0	137	589
HG00253.mapped.ILLUMINA.bwa.GBR.exome.20121211	693	276	296	339	666	414	531	631	434	102	636	526	337	153	0	67	580
HG00254.mapped.ILLUMINA.bwa.GBR.exome.20121211	689	290	290	338	651	329	546	647	432	101	635	0	337	167	0	66	590
HG00255.mapped.ILLUMINA.bwa.GBR.exome.20121211	681	245	264	271	581	366	530	649	450	76	603	0	298	139	0	62	579

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG00256.mapped.ILLUMINA.bwa.GBR.exome.20121211	693	0	0	358	660	427	441	592	0	100	582	496	0	161	25	0	579
HG00257.mapped.ILLUMINA.bwa.GBR.exome.20121211	700	0	0	355	675	345	537	645	541	0	0	0	0	0	48	91	587
HG00258.mapped.ILLUMINA.bwa.GBR.exome.20120522	672	247	270	284	600	279	528	643	414	0	604	566	0	0	0	113	580
HG00259.mapped.ILLUMINA.bwa.GBR.exome.20121211	784	0	0	360	676	339	536	646	548	0	0	0	0	0	63	99	594
HG00260.mapped.ILLUMINA.bwa.GBR.exome.20121211	699	290	305	337	644	325	541	637	536	0	0	0	0	0	39	74	585
HG00261.mapped.ILLUMINA.bwa.GBR.exome.20121211	574	300	330	0	0	0	542	639	541	0	0	0	0	0	47	61	584
HG00262.mapped.ILLUMINA.bwa.GBR.exome.20120522	758	254	269	298	622	288	533	657	0	86	663	581	379	144	0	0	578
HG00263.mapped.ILLUMINA.bwa.GBR.exome.20120522	698	0	0	351	677	437	545	633	453	0	0	0	0	0	0	133	586
HG00264.mapped.ILLUMINA.bwa.GBR.exome.20120522	755	241	270	279	615	284	534	649	388	73	644	579	0	138	0	66	579
HG00265.mapped.ILLUMINA.bwa.GBR.exome.20120522	664	263	279	0	543	135	530	653	480	0	590	569	0	0	20	60	579
HG00266.mapped.ILLUMINA.bwa.FIN.exome.20130415	628	0	0	239	417	356	486	548	0	0	340	0	336	169	0	0	540
HG00267.mapped.ILLUMINA.bwa.FIN.exome.20130415	655	163	281	109	529	329	505	575	350	0	0	0	0	0	0	79	564
HG00268.mapped.ILLUMINA.bwa.FIN.exome.20121211	696	0	0	359	675	431	547	640	533	0	0	0	0	0	41	76	587
HG00269.mapped.ILLUMINA.bwa.FIN.exome.20130415	660	0	0	357	599	376	538	625	352	0	0	0	0	0	19	42	558
HG00271.mapped.ILLUMINA.bwa.FIN.exome.20121211	773	0	0	356	675	347	532	644	543	0	0	0	0	0	69	0	591
HG00272.mapped.ILLUMINA.bwa.FIN.exome.20120522	665	220	239	256	543	301	518	623	393	0	0	0	0	0	31	0	569
HG00273.mapped.ILLUMINA.bwa.FIN.exome.20121211	702	280	295	349	656	308	545	639	535	0	0	0	0	0	0	119	585
HG00274.mapped.ILLUMINA.bwa.FIN.exome.20120522	786	294	313	348	679	431	549	656	550	103	599	575	0	0	46	79	588
HG00275.mapped.ILLUMINA.bwa.FIN.exome.20120522	786	0	0	360	666	431	541	644	427	100	598	0	324	159	0	58	585
HG00276.mapped.ILLUMINA.bwa.FIN.exome.20120522	699	288	317	348	681	429	547	644	535	0	615	567	0	0	72	0	590
HG00277.mapped.ILLUMINA.bwa.FIN.exome.20120522	699	0	0	360	680	449	543	643	531	0	0	0	0	0	0	130	593
HG00278.mapped.ILLUMINA.bwa.FIN.exome.20120522	700	295	317	343	658	326	545	639	541	0	0	0	0	0	73	0	593
HG00280.mapped.ILLUMINA.bwa.FIN.exome.20120522	700	0	0	360	680	424	547	644	441	101	620	0	333	163	0	73	587
HG00281.mapped.ILLUMINA.bwa.FIN.exome.20120522	702	295	309	344	641	424	548	632	453	0	0	0	0	0	43	66	591
HG00282.mapped.ILLUMINA.bwa.FIN.exome.20120522	702	277	302	341	628	326	539	641	535	0	0	0	0	0	44	61	585
HG00284.mapped.ILLUMINA.bwa.FIN.exome.20120522	697	0	0	391	677	433	545	627	531	0	0	0	0	0	23	65	589
HG00285.mapped.ILLUMINA.bwa.FIN.exome.20120522	786	289	321	342	686	326	544	655	440	102	641	576	339	163	28	0	584
HG00288.mapped.ILLUMINA.bwa.FIN.exome.20130415	701	0	0	414	718	478	560	672	577	0	0	0	0	0	72	0	594
HG00290.mapped.ILLUMINA.bwa.FIN.exome.20130415	703	0	0	391	714	480	561	675	579	104	0	0	0	0	56	104	594
HG00304.mapped.ILLUMINA.bwa.FIN.exome.20130415	663	0	0	336	648	432	546	506	523	0	0	0	0	0	0	63	579
HG00306.mapped.ILLUMINA.bwa.FIN.exome.20120522	679	0	0	292	583	380	522	618	362	0	486	0	277	135	0	46	572
HG00308.mapped.ILLUMINA.bwa.FIN.exome.20121211	680	247	265	296	590	389	534	657	484	0	0	0	0	0	35	83	577
HG00309.mapped.ILLUMINA.bwa.FIN.exome.20121211	696	273	282	326	657	419	536	629	525	0	586	557	0	0	37	51	589
HG00310.mapped.ILLUMINA.bwa.FIN.exome.20120522	788	0	0	363	688	441	549	643	551	0	0	0	0	0	0	164	591
HG00311.mapped.ILLUMINA.bwa.FIN.exome.20120522	684	0	0	298	578	381	528	627	357	64	515	0	278	137	0	51	574
HG00313.mapped.ILLUMINA.bwa.FIN.exome.20120522	691	283	285	330	672	414	537	627	421	96	643	519	314	153	0	61	587
HG00315.mapped.ILLUMINA.bwa.FIN.exome.20120522	697	0	0	357	677	445	536	639	515	99	606	0	331	163	0	75	590
HG00318.mapped.ILLUMINA.bwa.FIN.exome.20120522	697	0	0	390	671	434	540	635	447	0	0	0	0	0	0	139	591
HG00319.mapped.ILLUMINA.bwa.FIN.exome.20120522	761	300	331	0	654	152	545	623	429	100	646	524	340	164	40	1	589
HG00320.mapped.ILLUMINA.bwa.FIN.exome.20120522	701	0	0	351	679	345	542	632	531	0	0	0	0	0	0	127	588
HG00321.mapped.ILLUMINA.bwa.FIN.exome.20120522	698	289	304	218	680	316	545	642	391	100	655	583	0	158	0	74	585
HG00323.mapped.ILLUMINA.bwa.FIN.exome.20120522	697	287	313	335	678	428	541	630	527	0	591	531	0	0	0	146	591
HG00324.mapped.ILLUMINA.bwa.FIN.exome.20120522	701	282	297	335	659	327	543	620	521	0	604	520	0	0	0	92	592
HG00325.mapped.ILLUMINA.bwa.FIN.exome.20120522	697	284	310	342	672	428	545	644	533	101	576	557	0	0	48	61	581
HG00326.mapped.ILLUMINA.bwa.FIN.exome.20120522	700	288	316	344	680	331	545	642	542	0	618	564	0	0	0	129	591
HG00327.mapped.ILLUMINA.bwa.FIN.exome.20120522	700	285	297	336	651	318	541	632	403	99	559	0	329	160	0	71	586
HG00328.mapped.ILLUMINA.bwa.FIN.exome.20120522	692	276	308	324	669	321	525	602	399	97	636	542	0	148	0	64	579
HG00329.mapped.ILLUMINA.bwa.FIN.exome.20120522	697	0	0	353	672	423	496	567	0	99	588	0	329	165	0	1	574
HG00330.mapped.ILLUMINA.bwa.FIN.exome.20120522	699	0	0	365	675	429	536	640	534	0	0	0	0	0	49	76	591
HG00331.mapped.ILLUMINA.bwa.FIN.exome.20120522	696	0	0	358	670	437	542	637	545	0	0	0	0	0	35	71	589
HG00332.mapped.ILLUMINA.bwa.FIN.exome.20121211	701	0	0	351	677	428	544	642	538	0	0	0	0	0	41	68	590
HG00334.mapped.ILLUMINA.bwa.FIN.exome.20120522	699	284	284	345	670	160	509	570	411	0	585	514	0	154	0	57	578
HG00335.mapped.ILLUMINA.bwa.FIN.exome.20121211	700	292	310	347	646	322	547	638	537	0	0	0	0	0	46	81	588
HG00336.mapped.ILLUMINA.bwa.FIN.exome.20120522	699	0	0	348	672	340	542	633	512	100	596	528	0	164	31	0	585
HG00337.mapped.ILLUMINA.bwa.FIN.exome.20121211	699	0	0	350	667	430	545	644	427	104	586	0	423	154	36	0	587
HG00338.mapped.ILLUMINA.bwa.FIN.exome.20120522	692	0	0	352	665	428	541	638	389	98	581	0	323	158	0	54	584
HG00339.mapped.ILLUMINA.bwa.FIN.exome.20120522	682	0	0	355	664	421	529	619	408	99	590	0	400	154	0	58	587
HG00341.mapped.ILLUMINA.bwa.FIN.exome.20121211	697	287	306	346	646	0	517	572	403	0	0	0	0	161	0	77	575
HG00342.mapped.ILLUMINA.bwa.FIN.exome.20120522	694	282	318	343	639	322	541	649	403	102	634	0	434	165	0	58	590
HG00343.mapped.ILLUMINA.bwa.FIN.exome.20120522	695	0	0	349	669	432	546	613	426	0	0	0	0	0	0	107	585
HG00344.mapped.ILLUMINA.bwa.FIN.exome.20120522	696	0	0	353	667	433	537	608	435	99	582	0	317	157	0	69	585
HG00345.mapped.ILLUMINA.bwa.FIN.exome.20121211	701	0	0	361	671	430	538	632	454	0	0	0	0	0	0	113	588
HG00346.mapped.ILLUMINA.bwa.FIN.exome.20121211	697	0	0	355	662	437	548	621	425	103	614	0	414	160	0	87	585
HG00349.mapped.ILLUMINA.bwa.FIN.exome.20130415	613	0	0	247	591	363	486	551	320	0	0	0	0	0	14	20	542
HG00350.mapped.ILLUMINA.bwa.FIN.exome.20130415	611	0	0	255	552	369	505	536	288	0	202	337	0	142	0	25	558
HG00351.mapped.ILLUMINA.bwa.FIN.exome.20130415	664	158	162	193	393	280	515	556	326	0	0	0	0	0	14	29	551
HG00353.mapped.ILLUMINA.bwa.FIN.exome.20121211	702	281	310	339	656	327	545	642	433	101	623	0	328	158	47	0	589
HG00355.mapped.ILLUMINA.bwa.FIN.exome.20130415	511	152	115	101	277	269	460	519	301	0	0	0	0	0	13	0	533
HG00356.mapped.ILLUMINA.bwa.FIN.exome.20130415	635	135	102	189	298	240	476	500	304	0	0	0	0	0	0	48	540
HG00357.mapped.ILLUMINA.bwa.FIN.exome.20120522	678	238	245	272	598	277	528	628	470	0	570	492	0	0	0	87	580
HG00358.mapped.ILLUMINA.bwa.FIN.exome.20130415	582	0	0	251	414	361	486	495	322	0	0	0	0	0	9	32	525
HG00360.mapped.ILLUMINA.bwa.FIN.exome.20130415	629	0	0	255	543	362	472	539	277	0	137	0	212	131	12	0	560
HG00361.mapped.ILLUMINA.bwa.FIN.exome.20120522	688	28	0	310	613	388	530	655	476	0	0	0	0	0	0	120	577
HG00362.mapped.ILLUMINA.bwa.FIN.exome.20130415	534	157	216	0	375	140	477	556	307	0	127	315	0	0	26	1	560
HG00364.mapped.ILLUMINA.bwa.FIN.exome.20130415	641	166	198	302	437	341	507	575	331	0	0	0	0	0	0	70	542
HG00365.mapped.ILLUMINA.bwa.FIN.exome.20130415	661	0	0	352	583	423	517	594	307	0	253	0	289	146	21	0	585
HG00366.mapped.ILLUMINA.bwa.FIN.exome.20120522	594	250	273	0	598	138	525	627	396	0	601	571	0	0	0	59	575
HG00367.mapped.ILLUMINA.bwa.FIN.exome.20120522	677	0	0	306	600	379	534	632	384	57	564	0	292	138	0	53	576
HG00368.mapped.ILLUMINA.bwa.FIN.exome.20121211	677	0	0	297	576	360	524	629	467	0	0	0	0	0	0	74	575
HG00369.mapped.ILLUMINA.bwa.FIN.exome.20120522	680	224	258	269	604	340	529	645	470	0	520	507	0	0	0	78	576
HG00371.mapped.ILLUMINA.bwa.FIN.exome.20121211	679	218	0	275	607	378	532	636	472	0	568	480	0	0	0	71	574
HG00372.mapped.ILLUMINA.bwa.FIN.exome.20120522	667	0	0	305	601	367	521	638	407	0	0	0	0	0	0	84	580
HG00373.mapped.ILLUMINA.bwa.FIN.exome.20120522	669	244	252	267	592	360	532	648	380	77	630	569	0	137	0	53	576
HG00375.mapped.ILLUMINA.bwa.FIN.exome.20120522	700	0	0	361	681	440	542	646	541	0	0	0	0	0	0	170	586
HG00376.mapped.ILLUMINA.bwa.FIN.exome.20121211	698	283	309	342	636	420	536	622	445	0	0	0	0	0	44	64	586
HG00378.mapped.ILLUMINA.bwa.FIN.exome.20121211	700	0	0	362	680	345	539	636	523	98	593	0	407	156	0	71	589
HG00379.mapped.ILLUMINA.bwa.FIN.exome.20121211	632	230	227	251	596	327	511	620	351	66	586	492	271	132	0	39	576
HG00380.mapped.ILLUMINA.bwa.FIN.exome.20120522	649	210	228	258	562	272	520	630	468	0	563	491	0	0	8	33	569
HG00381.mapped.ILLUMINA.bwa.FIN.exome.20121211	696	0	0	360	672	428	542	630	512	0	0	0	0	0	0	90	586
HG00382.mapped.ILLUMINA.bwa.FIN.exome.20121211	691	0	0	354	670	432	536	622	437	98	577	0	319	159	0	49	588
HG00383.mapped.ILLUMINA.bwa.FIN.exome.20121211	697	0	0	351	667	432	540	622	527	0	0	0	0	0	41	53	589
HG00384.mapped.ILLUMINA.bwa.FIN.exome.20121211	678	246	261	273	542	280	531	644	402	0	0	0	0	0	24	59	575
HG00403.mapped.ILLUMINA.bwa.CHS.exome.20120522	682	0	0	299	592	384	528	631	467	0	0	0	0	0	16	45	574
HG00404.mapped.ILLUMINA.bwa.CHS.exome.20121211	688	0	0	306	602	392	532	645	485	0	0	0	0	0	24	48	579
HG00406.mapped.ILLUMINA.bwa.CHS.exome.20121211	787	0	0	358	675	439	545	645	432	101	611	545	0	165	44	0	588
HG00407.mapped.ILLUMINA.bwa.CHS.exome.20121211	690	0	0	351	664	419	532	611	524	0	0	0	0	0	55	0	587

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG00409.mapped.ILLUMINA.bwa.CHS.exome.20130415	683	0	0	309	597	387	530	646	390	73	581	0	354	133	0	59	576
HG00410.mapped.ILLUMINA.bwa.CHS.exome.20121211	686	0	0	290	596	387	534	636	470	0	0	0	0	0	37	0	578
HG00419.mapped.ILLUMINA.bwa.CHS.exome.20121211	696	0	0	353	664	436	533	610	417	101	592	502	0	158	34	0	581
HG00421.mapped.ILLUMINA.bwa.CHS.exome.20121211	699	0	0	350	660	438	537	618	532	0	0	0	0	0	37	47	583
HG00422.mapped.ILLUMINA.bwa.CHS.exome.20121211	694	0	0	358	662	422	542	632	523	0	0	0	0	0	48	64	586
HG00428.mapped.ILLUMINA.bwa.CHS.exome.20121211	697	0	0	358	676	426	539	644	539	0	0	0	0	0	0	116	591
HG00436.mapped.ILLUMINA.bwa.CHS.exome.20120522	702	0	0	361	677	438	547	648	544	0	0	0	0	0	40	81	590
HG00437.mapped.ILLUMINA.bwa.CHS.exome.20121211	697	0	0	361	668	437	536	638	534	0	0	0	0	0	54	0	581
HG00442.mapped.ILLUMINA.bwa.CHS.exome.20121211	699	0	0	355	664	435	541	636	451	0	0	0	0	0	66	0	589
HG00443.mapped.ILLUMINA.bwa.CHS.exome.20121211	695	0	0	357	665	424	542	621	414	99	565	0	308	155	0	51	584
HG00445.mapped.ILLUMINA.bwa.CHS.exome.20121211	783	0	0	353	671	434	542	625	432	101	581	528	0	159	43	0	588
HG00446.mapped.ILLUMINA.bwa.CHS.exome.20121211	694	0	0	356	672	435	544	624	532	0	0	0	0	0	38	61	585
HG00448.mapped.ILLUMINA.bwa.CHS.exome.20121211	780	0	0	349	670	439	542	621	443	0	0	0	0	0	57	0	585
HG00449.mapped.ILLUMINA.bwa.CHS.exome.20120522	699	0	0	357	672	440	545	642	537	0	0	0	0	0	62	1	590
HG00451.mapped.ILLUMINA.bwa.CHS.exome.20121211	695	288	299	339	660	431	548	653	429	101	643	509	330	157	31	0	583
HG00452.mapped.ILLUMINA.bwa.CHS.exome.20121211	701	0	0	361	678	443	548	645	527	101	631	0	432	166	0	99	589
HG00457.mapped.ILLUMINA.bwa.CHS.exome.20121211	695	0	0	343	669	433	543	607	537	0	0	0	0	0	72	1	590
HG00458.mapped.ILLUMINA.bwa.CHS.exome.20121211	700	0	0	356	662	438	542	626	525	0	0	0	0	0	69	1	589
HG00463.mapped.ILLUMINA.bwa.CHS.exome.20120522	689	0	0	356	668	438	534	633	525	0	0	0	0	0	64	0	587
HG00464.mapped.ILLUMINA.bwa.CHS.exome.20120522	701	282	310	334	628	418	547	628	0	105	641	0	417	164	0	0	585
HG00472.mapped.ILLUMINA.bwa.CHS.exome.20121211	691	0	0	354	669	425	538	629	538	0	0	0	0	0	40	64	591
HG00473.mapped.ILLUMINA.bwa.CHS.exome.20121211	702	0	0	356	675	442	544	650	438	102	622	582	0	161	46	0	589
HG00475.mapped.ILLUMINA.bwa.CHS.exome.20121211	698	0	0	343	660	434	544	623	523	0	0	0	0	0	70	0	591
HG00476.mapped.ILLUMINA.bwa.CHS.exome.20121211	701	0	0	354	674	440	545	651	515	103	603	0	331	154	45	1	592
HG00478.mapped.ILLUMINA.bwa.CHS.exome.20121211	699	282	317	342	652	412	544	635	502	103	611	531	0	158	0	73	591
HG00479.mapped.ILLUMINA.bwa.CHS.exome.20121211	693	0	0	350	668	435	547	626	450	0	0	0	0	0	58	0	580
HG00500.mapped.ILLUMINA.bwa.CHS.exome.20120522	692	0	0	356	657	432	534	631	452	0	0	0	0	0	0	91	584
HG00501.mapped.ILLUMINA.bwa.CHS.exome.20120522	695	0	0	361	683	427	539	619	535	0	0	0	0	0	0	95	584
HG00513.mapped.ILLUMINA.bwa.CHS.exome.20120522	692	0	0	349	664	435	543	642	532	0	0	0	0	0	39	67	586
HG00524.mapped.ILLUMINA.bwa.CHS.exome.20120522	699	0	0	388	679	440	546	646	545	0	0	0	0	0	0	168	593
HG00525.mapped.ILLUMINA.bwa.CHS.exome.20121211	702	0	0	355	666	439	544	636	535	0	0	0	0	0	46	82	587
HG00530.mapped.ILLUMINA.bwa.CHS.exome.20120522	699	0	0	352	665	434	543	618	525	0	0	0	0	0	37	46	587
HG00531.mapped.ILLUMINA.bwa.CHS.exome.20120522	697	0	0	358	668	436	541	642	427	98	604	535	0	160	0	70	590
HG00533.mapped.ILLUMINA.bwa.CHS.exome.20120522	693	272	315	340	619	414	531	626	432	104	602	0	323	151	0	64	586
HG00534.mapped.ILLUMINA.bwa.CHS.exome.20120522	788	293	319	345	658	426	545	629	547	0	0	0	0	0	42	73	585
HG00536.mapped.ILLUMINA.bwa.CHS.exome.20121211	701	0	0	361	673	437	550	646	433	101	623	0	418	163	49	0	588
HG00537.mapped.ILLUMINA.bwa.CHS.exome.20120522	699	0	0	362	674	438	545	647	433	101	605	0	425	157	47	2	588
HG00542.mapped.ILLUMINA.bwa.CHS.exome.20120522	701	0	0	354	672	429	540	628	505	101	581	0	411	160	0	68	587
HG00543.mapped.ILLUMINA.bwa.CHS.exome.20121211	698	0	0	356	666	434	546	635	433	99	606	0	332	161	0	82	591
HG00551.mapped.ILLUMINA.bwa.PUR.exome.20120522	757	244	268	286	592	366	534	657	491	0	0	0	0	0	38	74	580
HG00553.mapped.ILLUMINA.bwa.PUR.exome.20120522	698	0	0	404	710	483	558	654	572	0	0	0	0	0	69	112	599
HG00554.mapped.ILLUMINA.bwa.PUR.exome.20120522	793	0	0	389	705	477	555	652	570	0	0	0	0	0	61	109	597
HG00556.mapped.ILLUMINA.bwa.CHS.exome.20121211	703	0	0	357	679	441	549	658	541	0	0	0	0	0	88	0	590
HG00557.mapped.ILLUMINA.bwa.CHS.exome.20121211	698	0	0	344	661	438	526	568	0	0	0	0	0	0	42	0	571
HG00559.mapped.ILLUMINA.bwa.CHS.exome.20130415	658	0	0	355	535	434	520	594	352	0	0	0	0	0	16	42	574
HG00560.mapped.ILLUMINA.bwa.CHS.exome.20130415	666	211	258	199	609	364	514	564	338	0	324	426	0	0	6	38	552
HG00565.mapped.ILLUMINA.bwa.CHS.exome.20130415	646	151	148	223	333	290	523	562	336	0	0	0	0	0	14	0	558
HG00566.mapped.ILLUMINA.bwa.CHS.exome.20130415	648	0	0	240	531	348	466	494	271	0	0	0	0	0	17	0	540
HG00580.mapped.ILLUMINA.bwa.CHS.exome.20120522	692	286	306	341	644	393	502	479	424	0	583	518	0	156	41	0	588
HG00581.mapped.ILLUMINA.bwa.CHS.exome.20120522	694	283	300	351	674	430	553	647	453	104	588	515	0	0	47	66	586
HG00583.mapped.ILLUMINA.bwa.CHS.exome.20120522	699	0	0	350	656	431	536	634	416	96	577	0	318	161	31	0	582
HG00584.mapped.ILLUMINA.bwa.CHS.exome.20120522	701	287	308	353	636	410	542	635	540	0	0	0	0	0	36	64	590
HG00589.mapped.ILLUMINA.bwa.CHS.exome.20120522	686	269	289	333	660	417	544	627	391	97	617	584	0	154	0	66	582
HG00590.mapped.ILLUMINA.bwa.CHS.exome.20120522	701	0	0	354	674	436	540	637	537	0	0	0	0	0	39	53	589
HG00592.mapped.ILLUMINA.bwa.CHS.exome.20130415	618	0	0	328	359	404	481	558	294	0	0	0	0	0	22	1	545
HG00593.mapped.ILLUMINA.bwa.CHS.exome.20130415	611	0	0	342	412	433	521	564	327	0	0	0	0	0	13	19	555
HG00595.mapped.ILLUMINA.bwa.CHS.exome.20130415	630	0	0	250	457	430	497	552	193	0	8	0	233	139	0	19	558
HG00596.mapped.ILLUMINA.bwa.CHS.exome.20130415	642	186	141	202	464	337	490	547	316	0	0	0	0	0	17	33	552
HG00598.mapped.ILLUMINA.bwa.CHS.exome.20121211	761	243	254	284	617	391	537	659	394	81	641	564	370	132	34	1	571
HG00599.mapped.ILLUMINA.bwa.CHS.exome.20121211	682	0	0	296	607	380	533	648	449	64	607	0	363	137	31	0	574
HG00607.mapped.ILLUMINA.bwa.CHS.exome.20120522	698	0	0	357	671	433	542	638	432	102	580	526	0	163	39	0	586
HG00608.mapped.ILLUMINA.bwa.CHS.exome.20120522	699	0	0	356	668	438	541	627	419	102	620	0	327	160	34	0	591
HG00610.mapped.ILLUMINA.bwa.CHS.exome.20120522	593	250	271	0	499	138	527	637	382	70	613	494	284	134	13	1	577
HG00611.mapped.ILLUMINA.bwa.CHS.exome.20120522	669	217	240	265	590	266	526	621	362	72	610	518	0	135	14	0	571
HG00613.mapped.ILLUMINA.bwa.CHS.exome.20120522	694	0	0	358	676	434	544	627	428	101	596	537	0	163	43	0	591
HG00614.mapped.ILLUMINA.bwa.CHS.exome.20120522	692	0	0	351	671	340	533	628	431	99	579	0	401	165	29	0	586
HG00619.mapped.ILLUMINA.bwa.CHS.exome.20120522	699	0	0	358	670	438	544	638	423	101	591	570	0	157	50	0	592
HG00620.mapped.ILLUMINA.bwa.CHS.exome.20120522	692	0	0	359	666	431	545	635	439	102	628	0	324	164	50	0	585
HG00622.mapped.ILLUMINA.bwa.CHS.exome.20130415	688	0	0	304	600	383	527	640	466	0	0	0	0	0	42	1	573
HG00623.mapped.ILLUMINA.bwa.CHS.exome.20121211	677	253	234	274	511	364	532	638	386	75	578	0	354	133	0	54	578
HG00625.mapped.ILLUMINA.bwa.CHS.exome.20120522	678	0	0	288	574	380	526	621	384	0	0	0	0	0	30	0	575
HG00626.mapped.ILLUMINA.bwa.CHS.exome.20120522	678	0	0	296	597	376	525	634	390	73	516	0	288	132	21	0	575
HG00628.mapped.ILLUMINA.bwa.CHS.exome.20120522	664	0	0	282	585	284	504	631	462	0	0	0	0	0	29	0	576
HG00629.mapped.ILLUMINA.bwa.CHS.exome.20120522	688	0	0	296	607	392	532	640	470	0	0	0	0	0	36	0	575
HG00631.mapped.ILLUMINA.bwa.CHS.exome.20121211	678	243	264	287	610	371	533	658	474	71	614	571	0	0	39	0	577
HG00632.mapped.ILLUMINA.bwa.CHS.exome.20121211	685	0	0	297	607	382	533	653	477	0	0	0	0	0	29	73	576
HG00634.mapped.ILLUMINA.bwa.CHS.exome.20120522	678	0	0	294	593	368	513	623	378	74	561	0	284	134	0	49	579
HG00635.mapped.ILLUMINA.bwa.CHS.exome.20120522	666	222	244	272	587	345	527	639	396	70	513	470	0	0	27	0	574
HG00637.mapped.ILLUMINA.bwa.PUR.exome.20120522	695	0	0	399	706	473	558	566	568	0	0	0	0	0	0	204	598
HG00638.mapped.ILLUMINA.bwa.PUR.exome.20120522	795	0	0	387	711	392	553	660	473	0	0	0	0	0	0	162	596
HG00640.mapped.ILLUMINA.bwa.PUR.exome.20120522	790	332	366	364	590	468	555	657	457	0	537	0	376	184	75	4	600
HG00641.mapped.ILLUMINA.bwa.PUR.exome.20120522	763	256	278	208	532	290	535	650	490	0	0	0	0	0	36	99	583
HG00650.mapped.ILLUMINA.bwa.CHS.exome.20120522	700	0	0	358	672	442	543	641	536	0	0	0	0	0	50	79	590
HG00651.mapped.ILLUMINA.bwa.CHS.exome.20120522	704	0	0	363	682	433	544	628	548	0	0	0	0	0	43	78	587
HG00653.mapped.ILLUMINA.bwa.CHS.exome.20120522	676	305	332	0	0	0	547	632	537	0	0	0	0	0	71	1	584
HG00654.mapped.ILLUMINA.bwa.CHS.exome.20120522	697	0	0	363	668	416	540	641	540	0	0	0	0	0	80	0	590
HG00656.mapped.ILLUMINA.bwa.CHS.exome.20120522	704	0	0	361	680	428	544	632	540	0	0	0	0	0	46	65	590
HG00657.mapped.ILLUMINA.bwa.CHS.exome.20120522	699	289	314	346	641	429	481	462	0	0	0	0	0	0	0	0	578
HG00662.mapped.ILLUMINA.bwa.CHS.exome.20120522	699	0	0	357	674	439	543	637	540	0	0	0	0	0	35	75	590
HG00663.mapped.ILLUMINA.bwa.CHS.exome.20120522	702	0	0	361	675	436	544	638	431	102	610	571	0	155	41	0	587
HG00671.mapped.ILLUMINA.bwa.CHS.exome.20120522	700	269	301	342	623	417	535	616	0	103	636	0	425	159	0	0	586
HG00672.mapped.ILLUMINA.bwa.CHS.exome.20120522	697	0	0	358	665	430	539	604	516	0	0	0	0	0	0	101	585
HG00674.mapped.ILLUMINA.bwa.CHS.exome.20121211	682	248	255	285	584	367	527	651	462	74	593	0	290	137	33	0	573
HG00675.mapped.ILLUMINA.bwa.CHS.exome.20121211	683	0	0	299	606	383	534	646	476	0	0	0	0	0	44	0	581
HG00683.mapped.ILLUMINA.bwa.CHS.exome.20120522	700	0	0	353	674	438	546	638	421	99	621	563	0	162	0	63	586
HG00684.mapped.ILLUMINA.bwa.CHS.exome.20120522	780	0	0	357	671	442	544	629	431	99	631	0	331	158	43	1	590

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG00689.mapped.ILLUMINA.bwa.CHS.exome.20120522	696	0	0	353	660	429	546	641	540	0	0	0	0	0	34	53	586
HG00690.mapped.ILLUMINA.bwa.CHS.exome.20120522	697	0	0	346	666	434	546	642	514	97	622	509	0	159	37	1	589
HG00692.mapped.ILLUMINA.bwa.CHS.exome.20120522	701	0	0	364	681	434	547	635	547	0	0	0	0	0	80	0	585
HG00693.mapped.ILLUMINA.bwa.CHS.exome.20120522	778	290	300	346	641	430	531	590	524	0	571	515	0	161	36	0	590
HG00698.mapped.ILLUMINA.bwa.CHS.exome.20120522	698	0	0	359	678	443	546	639	528	0	0	0	0	0	37	85	590
HG00699.mapped.ILLUMINA.bwa.CHS.exome.20120522	701	0	0	365	673	437	550	632	458	0	0	0	0	0	72	0	592
HG00701.mapped.ILLUMINA.bwa.CHS.exome.20120522	701	0	0	358	679	445	546	625	540	0	0	0	0	0	60	0	585
HG00702.mapped.ILLUMINA.bwa.CHS.exome.20120522	694	281	303	337	647	423	531	639	538	0	0	0	0	0	0	122	591
HG00704.mapped.ILLUMINA.bwa.CHS.exome.20120522	702	0	0	359	680	434	544	643	443	103	623	514	0	160	32	0	590
HG00705.mapped.ILLUMINA.bwa.CHS.exome.20120522	698	0	0	362	677	445	548	638	541	0	0	0	0	0	70	0	590
HG00707.mapped.ILLUMINA.bwa.CHS.exome.20120522	785	303	317	337	656	426	546	628	546	0	0	0	0	0	27	84	589
HG00708.mapped.ILLUMINA.bwa.CHS.exome.20120522	698	0	0	368	689	423	544	648	439	105	610	0	421	157	34	0	592
HG00717.mapped.ILLUMINA.bwa.CHS.exome.20130415	696	0	0	371	683	453	551	645	555	0	0	0	0	0	0	105	588
HG00728.mapped.ILLUMINA.bwa.CHS.exome.20121211	685	0	0	305	603	386	533	659	472	0	0	0	0	0	31	63	578
HG00729.mapped.ILLUMINA.bwa.CHS.exome.20121211	687	0	0	293	602	391	533	648	457	76	588	0	296	139	31	0	573
HG00731.mapped.ILLUMINA.bwa.PUR.exome.20130422	752	271	291	0	612	145	540	678	506	89	653	582	73	0	58	147	582
HG00732.mapped.ILLUMINA.bwa.PUR.exome.20130422	768	0	0	0	11	67	535	662	18	88	650	0	391	142	0	3	582
HG00733.mapped.ILLUMINA.bwa.PUR.exome.20130422	687	253	269	296	611	388	536	663	480	81	618	568	52	0	33	75	575
HG00734.mapped.ILLUMINA.bwa.PUR.exome.20120522	766	0	0	0	0	0	531	551	0	0	0	0	0	0	0	0	578
HG00736.mapped.ILLUMINA.bwa.PUR.exome.20120522	675	245	260	285	588	278	531	640	393	68	632	0	294	136	0	87	579
HG00737.mapped.ILLUMINA.bwa.PUR.exome.20120522	760	263	274	301	596	385	527	647	0	78	625	0	380	140	39	0	577
HG00739.mapped.ILLUMINA.bwa.PUR.exome.20120522	745	254	267	295	588	0	519	622	461	0	0	0	0	139	33	0	575
HG00740.mapped.ILLUMINA.bwa.PUR.exome.20120522	680	234	267	276	608	278	528	644	487	0	607	513	0	0	0	115	577
HG00742.mapped.ILLUMINA.bwa.PUR.exome.20130415	570	320	353	0	602	170	550	638	403	89	617	568	0	164	41	3	584
HG00743.mapped.ILLUMINA.bwa.PUR.exome.20130415	659	294	330	204	580	424	544	628	313	82	485	0	307	165	0	46	590
HG00759.mapped.ILLUMINA.bwa.CDX.exome.20130415	792	328	372	389	711	478	561	677	486	111	668	0	462	186	68	6	596
HG00766.mapped.ILLUMINA.bwa.CDX.exome.20130415	703	0	0	399	718	478	559	668	568	108	654	0	462	182	0	121	592
HG00844.mapped.ILLUMINA.bwa.CDX.exome.20121211	695	0	0	352	671	440	545	622	435	0	0	0	0	0	58	1	586
HG00851.mapped.ILLUMINA.bwa.CDX.exome.20121211	699	277	304	343	673	427	542	627	431	100	636	526	337	156	34	0	584
HG00864.mapped.ILLUMINA.bwa.CDX.exome.20120522	701	0	0	362	663	437	541	631	531	0	0	0	0	0	0	101	585
HG00867.mapped.ILLUMINA.bwa.CDX.exome.20130415	799	0	0	396	716	475	559	673	478	106	654	0	465	186	56	3	594
HG00879.mapped.ILLUMINA.bwa.CDX.exome.20120522	697	0	0	353	669	433	545	625	451	0	0	0	0	0	53	0	584
HG00881.mapped.ILLUMINA.bwa.CDX.exome.20121211	699	0	0	355	664	436	545	621	425	102	592	537	0	168	47	0	587
HG00956.mapped.ILLUMINA.bwa.CDX.exome.20121211	673	259	288	332	661	321	529	602	392	93	633	508	316	156	0	53	571
HG00978.mapped.ILLUMINA.bwa.CDX.exome.20121211	782	285	305	338	647	425	544	636	531	0	0	0	0	0	60	0	586
HG00982.mapped.ILLUMINA.bwa.CDX.exome.20121211	698	0	0	354	665	440	542	633	425	96	597	0	333	157	30	0	580
HG01028.mapped.ILLUMINA.bwa.CDX.exome.20121211	698	0	0	362	681	436	545	650	412	101	624	0	342	164	0	86	588
HG01029.mapped.ILLUMINA.bwa.CDX.exome.20121211	697	0	0	360	678	441	547	635	433	98	616	530	0	162	0	91	592
HG01031.mapped.ILLUMINA.bwa.CDX.exome.20120522	697	0	0	354	666	421	542	629	423	97	598	0	324	157	0	67	586
HG01046.mapped.ILLUMINA.bwa.CDX.exome.20121211	696	0	0	353	656	432	537	629	418	99	581	0	410	158	34	0	572
HG01047.mapped.ILLUMINA.bwa.PUR.exome.20120522	596	260	275	0	0	0	532	649	477	0	0	0	0	0	0	140	579
HG01048.mapped.ILLUMINA.bwa.PUR.exome.20121211	693	0	0	321	649	412	537	664	498	0	0	0	0	0	41	106	583
HG01049.mapped.ILLUMINA.bwa.PUR.exome.20120522	774	262	273	300	626	387	539	659	463	77	650	581	0	140	0	107	585
HG01051.mapped.ILLUMINA.bwa.PUR.exome.20120522	695	0	0	352	665	437	541	616	527	0	0	0	0	0	0	111	586
HG01052.mapped.ILLUMINA.bwa.PUR.exome.20120522	701	0	310	344	670	330	546	636	541	0	607	0	343	0	36	72	589
HG01054.mapped.ILLUMINA.bwa.PUR.exome.20120522	761	0	0	319	630	401	537	663	494	0	0	0	0	0	0	184	583
HG01055.mapped.ILLUMINA.bwa.PUR.exome.20120522	764	0	0	355	648	395	537	666	492	0	0	0	0	0	61	0	582
HG01058.mapped.ILLUMINA.bwa.PUR.exome.20130415	670	0	0	360	652	457	531	607	438	0	0	0	0	0	0	71	584
HG01060.mapped.ILLUMINA.bwa.PUR.exome.20120522	681	281	327	0	0	0	544	618	453	0	0	0	0	0	62	0	587
HG01061.mapped.ILLUMINA.bwa.PUR.exome.20120522	694	248	294	347	675	422	527	619	534	0	582	510	0	0	0	94	583
HG01063.mapped.ILLUMINA.bwa.PUR.exome.20130415	681	273	305	313	592	444	545	629	537	0	0	0	0	0	21	40	587
HG01064.mapped.ILLUMINA.bwa.PUR.exome.20130415	677	0	0	346	635	451	552	635	525	0	0	0	0	0	32	54	583
HG01066.mapped.ILLUMINA.bwa.PUR.exome.20120522	777	0	0	316	627	409	536	668	497	0	0	0	0	0	0	169	582
HG01067.mapped.ILLUMINA.bwa.PUR.exome.20120522	758	248	272	300	614	377	536	660	479	0	543	565	0	0	0	134	579
HG01069.mapped.ILLUMINA.bwa.PUR.exome.20120522	696	0	0	359	671	431	547	641	448	0	0	0	0	0	0	137	584
HG01070.mapped.ILLUMINA.bwa.PUR.exome.20120522	696	0	0	358	662	424	540	634	450	0	0	0	0	0	43	64	588
HG01072.mapped.ILLUMINA.bwa.PUR.exome.20120522	699	0	0	349	661	436	539	628	439	0	0	0	0	0	0	123	585
HG01073.mapped.ILLUMINA.bwa.PUR.exome.20120522	594	295	315	0	0	0	509	572	0	99	632	507	315	163	0	0	588
HG01075.mapped.ILLUMINA.bwa.PUR.exome.20120522	683	246	259	283	555	380	528	638	469	0	0	0	0	0	0	110	576
HG01077.mapped.ILLUMINA.bwa.PUR.exome.20130415	679	0	0	350	647	445	539	627	448	0	0	0	0	0	46	1	586
HG01079.mapped.ILLUMINA.bwa.PUR.exome.20120522	691	0	0	305	609	390	529	651	485	0	0	0	0	0	0	133	578
HG01080.mapped.ILLUMINA.bwa.PUR.exome.20120522	688	0	0	304	614	391	533	652	385	69	587	0	297	139	0	63	579
HG01082.mapped.ILLUMINA.bwa.PUR.exome.20120522	702	291	321	352	647	327	546	640	537	0	0	0	0	0	0	116	589
HG01083.mapped.ILLUMINA.bwa.PUR.exome.20120522	698	288	308	340	665	431	544	626	409	98	630	529	403	158	0	63	588
HG01085.mapped.ILLUMINA.bwa.PUR.exome.20121211	699	290	312	345	651	427	544	638	539	0	0	0	0	0	0	139	590
HG01086.mapped.ILLUMINA.bwa.PUR.exome.20121211	783	0	0	358	674	432	543	624	527	0	0	0	0	0	0	114	586
HG01088.mapped.ILLUMINA.bwa.PUR.exome.20130415	684	0	0	328	671	367	545	636	458	0	0	0	0	0	0	79	585
HG01089.mapped.ILLUMINA.bwa.PUR.exome.20130415	575	311	352	0	603	165	554	644	446	0	455	515	0	0	30	40	588
HG01092.mapped.ILLUMINA.bwa.PUR.exome.20130415	566	271	344	0	572	164	529	625	448	0	443	0	353	0	49	1	584
HG01094.mapped.ILLUMINA.bwa.PUR.exome.20120522	693	249	267	296	588	286	533	656	488	0	0	0	0	0	62	0	579
HG01095.mapped.ILLUMINA.bwa.PUR.exome.20121211	688	0	0	288	604	383	533	649	472	0	595	567	0	0	0	67	570
HG01097.mapped.ILLUMINA.bwa.PUR.exome.20120522	688	0	0	374	694	475	555	557	566	0	0	0	0	0	0	126	596
HG01098.mapped.ILLUMINA.bwa.PUR.exome.20120522	697	326	367	358	709	467	559	641	575	0	543	557	0	0	49	80	598
HG01101.mapped.ILLUMINA.bwa.PUR.exome.20121211	688	0	0	308	612	387	531	652	491	0	0	0	0	0	0	136	576
HG01102.mapped.ILLUMINA.bwa.PUR.exome.20120522	596	259	283	0	0	0	534	647	388	76	618	0	376	138	0	73	581
HG01104.mapped.ILLUMINA.bwa.PUR.exome.20121211	698	0	0	354	669	436	541	629	435	102	608	0	323	159	42	0	586
HG01105.mapped.ILLUMINA.bwa.PUR.exome.20121211	683	284	314	340	629	408	543	617	407	99	597	529	0	159	27	0	582
HG01107.mapped.ILLUMINA.bwa.PUR.exome.20120522	702	285	303	348	678	423	547	642	535	0	596	582	0	0	33	63	590
HG01108.mapped.ILLUMINA.bwa.PUR.exome.20120522	700	0	0	356	678	437	547	650	446	0	0	0	0	0	0	117	588
HG01110.mapped.ILLUMINA.bwa.PUR.exome.20120522	757	264	276	292	643	390	539	659	488	0	624	541	0	0	30	75	580
HG01111.mapped.ILLUMINA.bwa.PUR.exome.20120522	756	254	271	304	603	384	535	664	493	0	0	0	0	0	40	95	584
HG01112.mapped.ILLUMINA.bwa.CLM.exome.20120522	695	0	0	372	713	483	562	655	576	0	0	0	0	0	0	159	598
HG01113.mapped.ILLUMINA.bwa.CLM.exome.20120522	694	0	0	388	710	474	556	652	456	95	542	0	454	185	0	70	597
HG01119.mapped.ILLUMINA.bwa.CLM.exome.20130415	797	0	0	413	718	479	561	667	582	0	0	0	0	0	0	256	596
HG01121.mapped.ILLUMINA.bwa.CLM.exome.20130415	794	113	372	373	721	472	561	673	291	112	670	98	466	185	0	6	591
HG01122.mapped.ILLUMINA.bwa.CLM.exome.20130415	794	339	377	0	705	282	560	668	577	0	631	557	132	43	54	105	593
HG01124.mapped.ILLUMINA.bwa.CLM.exome.20130415	656	0	0	247	571	330	479	467	0	0	273	0	267	173	0	0	563
HG01125.mapped.ILLUMINA.bwa.CLM.exome.20130415	658	0	0	339	598	339	519	548	342	0	0	0	0	0	9	33	547
HG01130.mapped.ILLUMINA.bwa.CLM.exome.20130415	700	333	371	391	703	475	559	675	585	0	0	0	0	0	58	123	593
HG01131.mapped.ILLUMINA.bwa.CLM.exome.20130415	799	0	0	393	714	472	559	674	582	0	0	0	0	0	57	112	593
HG01133.mapped.ILLUMINA.bwa.CLM.exome.20130415	631	0	0	255	571	344	488	555	318	0	0	0	0	0	0	53	555
HG01134.mapped.ILLUMINA.bwa.CLM.exome.20130415	644	0	0	245	484	424	491	504	269	0	309	0	239	149	13	1	550
HG01136.mapped.ILLUMINA.bwa.CLM.exome.20130415	631	0	0	245	476	360	501	536	308	0	0	0	0	0	22	0	545
HG01137.mapped.ILLUMINA.bwa.CLM.exome.20130415	655	0	0	246	587	427	512	595	291	0	320	0	291	138	9	1	567
HG01139.mapped.ILLUMINA.bwa.CLM.exome.20130415	661	0	0	225	460	421	501	566	308	0	0	0	0	0	0	64	554
HG01140.mapped.ILLUMINA.bwa.CLM.exome.20130415	640	0	0	234	497	336	498	585	276	0	12	236	0	0	0	51	555

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG01142.mapped.ILLUMINA.bwa.CLM.exome.20130415	703	0	0	391	715	472	560	677	568	106	649	0	459	187	58	2	593
HG01148.mapped.ILLUMINA.bwa.CLM.exome.20130415	646	0	0	329	559	433	489	549	319	0	0	0	0	0	17	0	564
HG01149.mapped.ILLUMINA.bwa.CLM.exome.20130415	639	231	154	107	331	309	546	610	272	98	305	0	281	157	0	31	577
HG01161.mapped.ILLUMINA.bwa.PUR.exome.20130415	664	0	0	230	616	435	539	592	300	91	447	0	342	164	0	39	579
HG01162.mapped.ILLUMINA.bwa.PUR.exome.20130415	658	0	0	347	622	454	542	608	408	89	360	0	330	164	0	38	581
HG01164.mapped.ILLUMINA.bwa.CLM.exome.20130415	592	316	361	0	684	185	554	619	450	0	622	584	0	0	0	76	590
HG01167.mapped.ILLUMINA.bwa.PUR.exome.20121211	600	262	278	0	0	0	532	661	395	77	612	0	365	138	31	2	574
HG01168.mapped.ILLUMINA.bwa.PUR.exome.20120522	756	256	280	300	598	386	537	656	409	83	622	517	0	139	36	0	582
HG01170.mapped.ILLUMINA.bwa.PUR.exome.20120522	702	0	0	356	672	430	541	640	542	0	0	0	0	0	39	71	586
HG01171.mapped.ILLUMINA.bwa.PUR.exome.20120522	689	0	0	344	659	430	542	610	523	0	0	0	0	0	27	48	586
HG01173.mapped.ILLUMINA.bwa.PUR.exome.20120522	765	302	332	0	0	0	550	628	443	101	600	514	0	161	47	0	589
HG01174.mapped.ILLUMINA.bwa.PUR.exome.20120522	681	0	0	357	659	428	543	632	515	0	0	0	0	0	0	84	589
HG01176.mapped.ILLUMINA.bwa.PUR.exome.20120522	664	249	257	278	611	284	531	645	389	75	641	578	0	136	0	67	575
HG01177.mapped.ILLUMINA.bwa.PUR.exome.20120522	683	0	0	301	612	385	532	641	481	0	0	0	0	0	46	0	577
HG01182.mapped.ILLUMINA.bwa.PUR.exome.20121211	675	254	264	289	613	380	530	648	489	0	613	562	0	0	32	50	580
HG01183.mapped.ILLUMINA.bwa.PUR.exome.20121211	680	246	271	295	593	374	533	656	394	79	606	0	368	135	36	1	576
HG01187.mapped.ILLUMINA.bwa.PUR.exome.20120522	683	0	0	312	616	394	526	650	384	75	596	0	369	137	31	0	579
HG01188.mapped.ILLUMINA.bwa.PUR.exome.20120522	755	0	0	303	612	293	523	644	485	0	0	0	0	0	0	121	580
HG01190.mapped.ILLUMINA.bwa.PUR.exome.20120522	685	0	0	303	607	377	529	639	474	0	0	0	0	0	0	98	576
HG01191.mapped.ILLUMINA.bwa.PUR.exome.20121211	599	261	275	0	555	136	533	666	490	78	604	573	0	0	30	61	577
HG01197.mapped.ILLUMINA.bwa.PUR.exome.20121211	670	250	273	295	615	380	534	647	483	0	606	571	0	0	0	102	575
HG01198.mapped.ILLUMINA.bwa.PUR.exome.20121211	686	246	260	292	587	283	531	653	474	0	0	0	0	0	0	90	575
HG01200.mapped.ILLUMINA.bwa.PUR.exome.20130415	686	0	0	337	639	448	528	609	304	93	561	0	350	156	0	32	569
HG01204.mapped.ILLUMINA.bwa.PUR.exome.20121211	675	251	268	292	613	383	532	657	483	0	607	567	0	0	28	79	576
HG01205.mapped.ILLUMINA.bwa.PUR.exome.20121211	668	259	281	0	572	138	520	638	458	0	646	580	0	137	0	76	579
HG01241.mapped.ILLUMINA.bwa.PUR.exome.20120522	599	257	276	0	0	0	0	0	0	0	630	0	398	143	0	0	577
HG01242.mapped.ILLUMINA.bwa.PUR.exome.20120522	596	235	277	0	0	359	519	624	389	0	605	0	296	138	27	0	575
HG01247.mapped.ILLUMINA.bwa.PUR.exome.20120522	690	0	0	309	618	379	532	650	476	0	0	0	0	0	0	94	579
HG01248.mapped.ILLUMINA.bwa.PUR.exome.20120522	685	0	0	308	617	385	529	640	471	0	0	0	0	0	0	113	577
HG01250.mapped.ILLUMINA.bwa.CLM.exome.20120522	703	0	0	407	711	471	556	562	471	0	0	0	0	0	0	162	598
HG01251.mapped.ILLUMINA.bwa.CLM.exome.20120522	692	320	350	278	569	369	555	644	464	0	0	0	0	0	33	68	597
HG01253.mapped.ILLUMINA.bwa.CLM.exome.20120522	791	321	364	371	684	374	560	649	578	0	0	0	0	0	0	84	598
HG01254.mapped.ILLUMINA.bwa.CLM.exome.20120522	701	0	0	399	714	484	561	655	571	0	0	0	0	0	116	0	599
HG01256.mapped.ILLUMINA.bwa.CLM.exome.20121211	680	219	233	249	484	325	528	629	377	70	492	0	284	130	0	28	575
HG01257.mapped.ILLUMINA.bwa.CLM.exome.20121211	667	230	252	275	484	276	521	620	0	83	634	0	369	138	0	0	575
HG01259.mapped.ILLUMINA.bwa.CLM.exome.20121211	666	230	254	175	566	351	516	590	384	0	547	0	296	135	0	43	572
HG01260.mapped.ILLUMINA.bwa.CLM.exome.20121211	688	243	263	284	588	363	535	647	395	74	602	0	295	138	0	67	575
HG01269.mapped.ILLUMINA.bwa.CLM.exome.20130415	703	0	0	399	723	479	562	677	586	0	0	0	0	0	82	0	597
HG01271.mapped.ILLUMINA.bwa.CLM.exome.20130415	663	105	139	230	473	398	503	573	334	0	237	349	0	0	8	26	547
HG01272.mapped.ILLUMINA.bwa.CLM.exome.20130415	652	0	0	224	557	428	496	531	244	0	136	0	226	117	15	0	551
HG01275.mapped.ILLUMINA.bwa.CLM.exome.20130415	658	0	0	254	614	359	511	598	283	83	326	0	243	146	0	33	565
HG01277.mapped.ILLUMINA.bwa.CLM.exome.20130415	646	0	0	251	562	439	519	610	303	85	279	0	253	154	0	42	563
HG01280.mapped.ILLUMINA.bwa.CLM.exome.20130415	690	335	377	0	0	0	560	673	580	0	0	0	0	0	61	100	595
HG01281.mapped.ILLUMINA.bwa.CLM.exome.20130415	796	332	368	384	723	477	562	678	579	108	654	560	0	0	0	247	596
HG01284.mapped.ILLUMINA.bwa.CLM.exome.20130415	797	326	373	385	709	387	556	669	558	106	662	0	460	184	0	120	593
HG01286.mapped.ILLUMINA.bwa.PUR.exome.20130415	578	305	329	0	0	0	550	592	246	87	332	493	0	152	0	38	578
HG01302.mapped.ILLUMINA.bwa.PUR.exome.20130415	661	291	307	194	566	406	516	451	379	0	347	0	327	165	0	40	583
HG01303.mapped.ILLUMINA.bwa.PUR.exome.20130415	692	301	318	226	598	427	505	494	302	0	417	0	339	176	0	45	583
HG01305.mapped.ILLUMINA.bwa.PUR.exome.20130415	678	289	318	312	457	416	548	607	0	97	596	0	443	174	0	0	583
HG01308.mapped.ILLUMINA.bwa.PUR.exome.20130415	693	0	0	354	644	437	545	623	533	0	0	0	0	0	50	2	582
HG01311.mapped.ILLUMINA.bwa.PUR.exome.20130415	685	298	329	318	618	172	549	633	551	0	0	0	0	0	0	108	585
HG01312.mapped.ILLUMINA.bwa.PUR.exome.20130415	660	288	315	218	579	402	549	628	408	0	556	512	0	161	36	0	581
HG01323.mapped.ILLUMINA.bwa.PUR.exome.20130415	663	0	0	354	654	447	551	613	448	0	0	0	0	0	32	42	580
HG01325.mapped.ILLUMINA.bwa.PUR.exome.20130415	671	0	0	331	661	373	540	633	304	0	537	0	359	169	0	40	588
HG01326.mapped.ILLUMINA.bwa.PUR.exome.20130415	689	306	333	232	614	432	552	633	414	87	575	0	355	167	0	49	581
HG01334.mapped.ILLUMINA.bwa.GBR.exome.20120522	689	0	0	349	663	440	543	627	526	0	0	0	0	0	40	65	587
HG01341.mapped.ILLUMINA.bwa.CLM.exome.20120522	690	0	0	289	578	367	531	647	452	0	0	0	0	0	0	96	570
HG01342.mapped.ILLUMINA.bwa.CLM.exome.20120522	596	236	247	0	514	126	526	647	426	67	634	571	326	121	0	48	571
HG01344.mapped.ILLUMINA.bwa.CLM.exome.20130415	657	0	0	247	571	425	513	543	326	0	0	0	0	0	0	50	565
HG01345.mapped.ILLUMINA.bwa.CLM.exome.20130415	641	153	228	213	581	356	500	559	0	101	428	502	273	167	0	0	544
HG01348.mapped.ILLUMINA.bwa.CLM.exome.20130415	634	129	146	105	545	312	493	567	259	0	344	321	186	143	0	21	554
HG01350.mapped.ILLUMINA.bwa.CLM.exome.20120522	695	293	309	335	676	431	542	638	444	0	608	530	0	0	39	61	587
HG01351.mapped.ILLUMINA.bwa.CLM.exome.20120522	699	0	0	351	674	427	544	631	537	0	0	0	0	0	0	132	591
HG01353.mapped.ILLUMINA.bwa.CLM.exome.20120522	678	306	327	0	657	163	541	636	542	0	611	520	0	0	42	95	586
HG01354.mapped.ILLUMINA.bwa.CLM.exome.20120522	786	0	0	352	683	335	0	0	0	0	0	0	0	164	0	0	568
HG01356.mapped.ILLUMINA.bwa.CLM.exome.20130415	626	0	0	232	445	342	468	486	302	0	0	0	0	0	10	28	557
HG01357.mapped.ILLUMINA.bwa.CLM.exome.20130415	650	137	222	209	318	301	407	391	0	0	385	0	339	172	0	0	558
HG01359.mapped.ILLUMINA.bwa.CLM.exome.20120522	672	0	0	269	567	345	522	637	426	0	0	0	0	0	0	67	561
HG01360.mapped.ILLUMINA.bwa.CLM.exome.20120522	598	333	368	0	550	181	558	557	0	0	656	553	466	185	0	0	596
HG01362.mapped.ILLUMINA.bwa.CLM.exome.20130415	597	341	379	0	0	0	560	671	578	0	0	0	0	0	68	110	597
HG01363.mapped.ILLUMINA.bwa.CLM.exome.20130415	791	344	382	0	713	186	562	672	584	0	661	590	0	0	0	276	597
HG01365.mapped.ILLUMINA.bwa.CLM.exome.20120522	694	282	303	317	640	323	541	627	412	100	613	0	320	156	0	75	588
HG01366.mapped.ILLUMINA.bwa.CLM.exome.20120522	697	273	292	334	637	420	535	625	528	0	0	0	0	0	41	69	585
HG01369.mapped.ILLUMINA.bwa.CLM.exome.20130415	703	330	360	377	714	468	557	673	577	0	648	554	0	0	49	111	594
HG01372.mapped.ILLUMINA.bwa.CLM.exome.20130415	696	327	370	383	692	471	559	667	474	103	646	0	460	186	0	107	592
HG01374.mapped.ILLUMINA.bwa.CLM.exome.20120522	695	0	0	347	657	429	539	626	516	0	0	0	0	0	58	0	584
HG01375.mapped.ILLUMINA.bwa.CLM.exome.20120522	698	0	0	352	660	439	543	640	425	98	601	0	408	158	46	0	588
HG01377.mapped.ILLUMINA.bwa.CLM.exome.20120522	692	0	0	306	611	389	532	647	483	0	0	0	0	0	40	2	578
HG01378.mapped.ILLUMINA.bwa.CLM.exome.20120522	668	0	0	293	596	382	530	625	400	0	0	0	0	0	0	72	573
HG01383.mapped.ILLUMINA.bwa.CLM.exome.20120522	653	216	236	248	524	245	528	627	380	55	510	0	282	132	14	1	568
HG01384.mapped.ILLUMINA.bwa.CLM.exome.20120522	671	229	240	188	589	277	525	637	369	0	611	479	270	135	0	37	574
HG01389.mapped.ILLUMINA.bwa.CLM.exome.20120522	699	283	0	220	679	332	546	645	445	101	630	0	428	161	0	75	590
HG01390.mapped.ILLUMINA.bwa.CLM.exome.20120522	698	294	305	333	620	418	519	575	431	0	602	531	0	151	0	53	590
HG01392.mapped.ILLUMINA.bwa.PUR.exome.20130415	796	325	364	385	718	471	560	675	580	0	652	586	0	0	76	0	593
HG01393.mapped.ILLUMINA.bwa.PUR.exome.20130415	695	324	365	375	715	383	557	662	579	0	643	555	0	0	49	91	594
HG01395.mapped.ILLUMINA.bwa.PUR.exome.20130415	799	0	0	404	716	473	561	664	574	0	0	0	0	0	0	212	594
HG01396.mapped.ILLUMINA.bwa.PUR.exome.20130415	691	330	371	374	699	467	558	652	478	0	653	0	461	187	58	1	595
HG01398.mapped.ILLUMINA.bwa.PUR.exome.20130415	662	291	325	308	509	427	553	634	544	0	0	0	0	0	30	42	584
HG01402.mapped.ILLUMINA.bwa.PUR.exome.20130415	799	0	0	397	720	471	559	669	0	108	670	0	467	192	0	0	594
HG01403.mapped.ILLUMINA.bwa.PUR.exome.20130415	700	0	0	388	720	478	561	672	589	0	0	0	0	0	60	103	593
HG01405.mapped.ILLUMINA.bwa.PUR.exome.20130415	785	337	376	0	705	184	563	672	582	0	659	593	0	0	0	238	596
HG01412.mapped.ILLUMINA.bwa.PUR.exome.20130415	703	0	0	397	714	471	559	663	578	0	0	0	0	0	0	177	591
HG01413.mapped.ILLUMINA.bwa.PUR.exome.20130415	701	329	371	384	701	463	560	670	369	105	653	590	0	187	0	104	592
HG01414.mapped.ILLUMINA.bwa.PUR.exome.20130415	702	327	365	385	699	383	555	661	366	105	643	0	382	186	0	97	596
HG01431.mapped.ILLUMINA.bwa.PUR.exome.20130415	796	329	372	385	707	469	560	671	567	104	650	0	458	186	0	124	594
HG01432.mapped.ILLUMINA.bwa.CLM.exome.20130415	703	328	374	384	710	469	562	672	574	0	0	0	0	0	0	150	594

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG01435.mapped.ILLUMINA.bwa.CLM.exome.20130415	697	0	0	388	718	471	562	651	575	0	0	0	0	0	0	202	592
HG01437.mapped.ILLUMINA.bwa.CLM.exome.20120522	658	239	247	0	494	124	524	655	446	0	562	546	0	0	22	52	572
HG01438.mapped.ILLUMINA.bwa.CLM.exome.20120522	635	219	230	230	526	250	524	631	439	0	0	0	0	0	0	112	573
HG01440.mapped.ILLUMINA.bwa.CLM.exome.20120522	631	211	219	234	508	320	529	644	0	69	620	0	348	126	0	0	573
HG01441.mapped.ILLUMINA.bwa.CLM.exome.20120522	656	216	209	241	477	310	526	640	370	0	0	0	0	0	22	52	573
HG01443.mapped.ILLUMINA.bwa.CLM.exome.20130415	701	327	367	383	700	475	561	670	564	105	663	0	455	187	58	1	593
HG01444.mapped.ILLUMINA.bwa.CLM.exome.20130415	700	332	369	382	695	466	559	674	580	0	0	0	0	0	50	100	593
HG01447.mapped.ILLUMINA.bwa.CLM.exome.20130415	700	0	0	392	717	479	560	672	583	0	0	0	0	0	66	111	591
HG01455.mapped.ILLUMINA.bwa.CLM.exome.20120522	793	0	0	385	709	478	558	568	574	0	0	0	0	0	0	166	598
HG01456.mapped.ILLUMINA.bwa.CLM.exome.20120522	599	338	0	0	691	190	557	651	564	0	0	0	0	0	0	124	593
HG01459.mapped.ILLUMINA.bwa.CLM.exome.20130415	699	0	0	385	708	467	557	663	578	0	0	0	0	0	47	82	592
HG01461.mapped.ILLUMINA.bwa.CLM.exome.20120522	577	216	249	0	550	128	529	642	446	0	615	502	338	0	16	56	573
HG01462.mapped.ILLUMINA.bwa.CLM.exome.20120522	661	222	225	255	514	329	525	636	433	0	0	0	0	0	0	102	569
HG01464.mapped.ILLUMINA.bwa.CLM.exome.20120522	595	222	248	0	580	250	532	645	456	0	628	543	342	0	32	57	574
HG01465.mapped.ILLUMINA.bwa.CLM.exome.20120522	663	224	0	171	543	246	531	640	454	0	0	0	0	0	19	53	574
HG01468.mapped.ILLUMINA.bwa.CLM.exome.20130415	586	321	347	0	521	174	556	646	417	94	628	542	364	175	45	1	585
HG01474.mapped.ILLUMINA.bwa.CLM.exome.20130415	677	306	330	326	680	358	547	633	339	90	618	530	324	177	0	46	586
HG01479.mapped.ILLUMINA.bwa.CLM.exome.20130415	681	307	319	309	623	437	550	624	411	87	558	0	346	168	30	2	582
HG01485.mapped.ILLUMINA.bwa.CLM.exome.20130415	798	0	0	399	719	472	560	665	586	0	0	0	0	0	82	0	594
HG01486.mapped.ILLUMINA.bwa.CLM.exome.20130415	799	0	0	398	723	480	562	670	587	0	0	0	0	0	78	0	596
HG01488.mapped.ILLUMINA.bwa.CLM.exome.20120522	742	0	0	268	546	356	528	641	291	61	570	0	338	117	0	43	570
HG01489.mapped.ILLUMINA.bwa.CLM.exome.20120522	672	0	0	266	573	349	526	648	366	0	0	0	0	0	18	0	557
HG01491.mapped.ILLUMINA.bwa.CLM.exome.20120522	737	0	0	268	573	348	527	643	455	0	0	0	0	0	0	92	571
HG01492.mapped.ILLUMINA.bwa.CLM.exome.20120522	731	222	234	251	555	250	520	645	295	59	577	0	275	123	21	0	571
HG01494.mapped.ILLUMINA.bwa.CLM.exome.20120522	599	333	372	0	570	183	556	637	548	0	550	590	0	181	0	83	596
HG01495.mapped.ILLUMINA.bwa.CLM.exome.20120522	700	321	358	371	696	458	555	550	555	0	538	587	0	0	72	0	597
HG01497.mapped.ILLUMINA.bwa.CLM.exome.20120522	693	320	358	221	704	378	557	660	557	0	547	587	0	0	0	158	597
HG01498.mapped.ILLUMINA.bwa.CLM.exome.20120522	700	0	0	377	697	475	555	557	453	91	537	0	453	178	0	78	600
HG01500.mapped.ILLUMINA.bwa.IBS.exome.20130415	666	214	229	234	584	324	527	607	301	82	373	505	0	152	0	8	546
HG01501.mapped.ILLUMINA.bwa.IBS.exome.20130415	617	127	88	190	255	281	519	558	0	90	365	0	319	169	0	1	546
HG01503.mapped.ILLUMINA.bwa.IBS.exome.20130415	605	109	65	80	462	248	482	537	295	0	109	335	0	0	0	20	526
HG01504.mapped.ILLUMINA.bwa.IBS.exome.20130415	610	0	0	246	399	329	470	506	312	0	0	0	0	0	0	43	549
HG01506.mapped.ILLUMINA.bwa.IBS.exome.20120522	689	0	0	360	672	437	540	628	522	0	0	0	0	0	0	109	586
HG01507.mapped.ILLUMINA.bwa.IBS.exome.20120522	698	0	0	363	678	431	533	634	527	0	0	0	0	0	0	119	584
HG01509.mapped.ILLUMINA.bwa.IBS.exome.20121211	700	0	0	358	665	440	547	639	544	0	0	0	0	0	0	137	588
HG01510.mapped.ILLUMINA.bwa.IBS.exome.20120522	699	291	296	345	647	420	545	635	0	104	633	0	437	166	0	0	586
HG01512.mapped.ILLUMINA.bwa.IBS.exome.20120522	698	0	0	357	669	434	538	627	392	102	587	0	338	152	0	75	594
HG01513.mapped.ILLUMINA.bwa.IBS.exome.20120522	780	0	0	358	673	441	547	649	531	0	0	0	0	0	0	139	587
HG01515.mapped.ILLUMINA.bwa.IBS.exome.20120522	597	332	373	0	538	179	557	565	355	0	650	583	448	183	0	93	598
HG01516.mapped.ILLUMINA.bwa.IBS.exome.20120522	601	340	372	0	0	0	559	563	479	0	0	0	0	0	0	133	597
HG01518.mapped.ILLUMINA.bwa.IBS.exome.20120522	793	327	366	368	658	373	560	563	558	0	0	0	0	0	0	160	600
HG01519.mapped.ILLUMINA.bwa.IBS.exome.20120522	700	0	0	395	708	469	556	656	575	0	0	0	0	0	60	118	602
HG01521.mapped.ILLUMINA.bwa.IBS.exome.20120522	700	342	379	0	712	188	562	678	559	94	674	594	461	185	102	0	601
HG01522.mapped.ILLUMINA.bwa.IBS.exome.20120522	789	0	0	387	707	393	554	674	573	86	636	0	457	0	0	176	601
HG01524.mapped.ILLUMINA.bwa.IBS.exome.20121211	700	288	315	348	676	338	545	650	539	0	609	532	0	0	0	172	588
HG01525.mapped.ILLUMINA.bwa.IBS.exome.20121211	692	290	306	337	651	425	538	581	431	0	595	568	0	155	0	77	588
HG01527.mapped.ILLUMINA.bwa.IBS.exome.20121211	697	0	0	351	663	431	544	636	537	0	0	0	0	0	42	70	589
HG01528.mapped.ILLUMINA.bwa.IBS.exome.20121211	699	0	0	359	669	438	544	637	533	0	0	0	0	0	0	172	586
HG01530.mapped.ILLUMINA.bwa.IBS.exome.20121211	787	0	0	362	669	445	547	642	548	0	0	0	0	0	43	85	587
HG01531.mapped.ILLUMINA.bwa.IBS.exome.20121211	702	297	320	349	689	434	546	655	543	0	640	582	0	0	45	97	589
HG01536.mapped.ILLUMINA.bwa.IBS.exome.20121211	785	289	304	344	649	339	542	649	444	103	606	0	336	165	0	89	589
HG01537.mapped.ILLUMINA.bwa.IBS.exome.20121211	784	290	318	343	657	431	548	642	539	0	0	0	0	0	0	149	589
HG01550.mapped.ILLUMINA.bwa.CLM.exome.20120522	597	339	377	0	679	188	557	653	562	99	643	595	0	187	61	0	597
HG01551.mapped.ILLUMINA.bwa.CLM.exome.20120522	701	0	0	392	719	480	561	566	581	0	0	0	0	0	0	177	597
HG01556.mapped.ILLUMINA.bwa.CLM.exome.20130415	797	326	366	382	712	465	562	674	581	0	0	0	0	0	62	116	592
HG01565.mapped.ILLUMINA.bwa.PEL.exome.20130415	676	219	197	228	621	417	538	604	360	0	357	0	348	0	26	1	565
HG01566.mapped.ILLUMINA.bwa.PEL.exome.20130415	638	168	181	226	314	319	506	592	339	0	0	0	0	0	21	0	560
HG01571.mapped.ILLUMINA.bwa.PEL.exome.20130415	622	0	0	253	516	412	458	531	298	0	0	0	0	0	16	0	568
HG01572.mapped.ILLUMINA.bwa.PEL.exome.20130415	611	0	0	330	491	408	473	544	334	0	0	0	0	0	20	1	553
HG01577.mapped.ILLUMINA.bwa.PEL.exome.20120522	697	0	0	358	678	435	547	645	527	0	0	0	0	0	64	0	589
HG01578.mapped.ILLUMINA.bwa.PEL.exome.20120522	701	288	316	111	647	160	547	640	508	103	651	523	334	163	45	0	585
HG01583.mapped.ILLUMINA.bwa.PJL.exome.20130415	568	307	348	0	504	169	540	631	441	0	529	504	0	0	0	79	580
HG01586.mapped.ILLUMINA.bwa.PJL.exome.20130415	666	0	0	342	644	434	545	501	274	82	455	0	308	149	33	2	578
HG01589.mapped.ILLUMINA.bwa.PJL.exome.20130415	694	276	288	308	628	436	548	617	384	87	513	533	0	166	0	31	578
HG01593.mapped.ILLUMINA.bwa.PJL.exome.20130415	680	284	305	211	597	398	547	600	434	0	0	0	0	0	0	73	578
HG01595.mapped.ILLUMINA.bwa.KHV.exome.20120522	698	0	0	360	680	445	545	655	545	0	0	0	0	0	58	73	591
HG01596.mapped.ILLUMINA.bwa.KHV.exome.20120522	698	0	0	355	674	436	544	639	527	0	0	0	0	0	60	0	591
HG01597.mapped.ILLUMINA.bwa.KHV.exome.20120522	683	0	0	360	665	438	541	642	539	0	0	0	0	0	39	79	585
HG01598.mapped.ILLUMINA.bwa.KHV.exome.20120522	698	0	0	354	665	428	538	625	527	0	0	0	0	0	59	1	588
HG01599.mapped.ILLUMINA.bwa.KHV.exome.20120522	696	0	0	350	665	436	543	634	539	0	0	0	0	0	51	0	582
HG01600.mapped.ILLUMINA.bwa.KHV.exome.20120522	701	0	0	348	662	433	541	630	448	0	0	0	0	0	53	0	586
HG01602.mapped.ILLUMINA.bwa.IBS.exome.20130415	527	264	288	0	463	157	545	589	344	0	352	499	0	0	12	22	553
HG01603.mapped.ILLUMINA.bwa.IBS.exome.20130415	639	0	0	247	549	360	489	539	326	0	0	0	0	0	0	35	545
HG01605.mapped.ILLUMINA.bwa.IBS.exome.20130415	646	0	0	331	454	408	497	545	266	0	220	0	222	148	0	22	562
HG01606.mapped.ILLUMINA.bwa.IBS.exome.20130415	619	0	0	327	580	340	475	575	318	0	0	0	0	0	0	57	559
HG01607.mapped.ILLUMINA.bwa.IBS.exome.20130415	629	0	0	226	540	419	474	513	275	0	48	0	192	149	0	12	521
HG01608.mapped.ILLUMINA.bwa.IBS.exome.20130415	616	112	132	205	321	247	480	517	329	0	0	0	0	0	17	0	540
HG01610.mapped.ILLUMINA.bwa.IBS.exome.20130415	639	0	0	238	472	358	506	569	257	0	262	0	264	131	0	26	558
HG01612.mapped.ILLUMINA.bwa.IBS.exome.20130415	535	118	132	167	447	335	479	527	0	93	395	470	133	167	0	0	542
HG01613.mapped.ILLUMINA.bwa.IBS.exome.20130415	675	0	0	355	645	368	495	607	298	88	362	0	319	143	0	36	571
HG01615.mapped.ILLUMINA.bwa.IBS.exome.20130415	626	0	0	323	420	309	452	424	278	0	0	0	0	0	0	35	546
HG01617.mapped.ILLUMINA.bwa.IBS.exome.20130415	643	0	0	250	482	353	481	565	316	0	0	0	0	0	0	48	528
HG01618.mapped.ILLUMINA.bwa.IBS.exome.20130415	658	220	188	211	552	433	504	550	316	0	282	315	0	0	0	65	553
HG01619.mapped.ILLUMINA.bwa.IBS.exome.20130415	652	153	223	221	410	345	507	563	267	87	281	0	281	155	0	37	555
HG01620.mapped.ILLUMINA.bwa.IBS.exome.20130415	650	0	0	340	457	365	481	557	260	87	127	0	249	163	0	32	558
HG01623.mapped.ILLUMINA.bwa.IBS.exome.20130415	673	0	0	265	509	365	496	544	337	0	0	0	0	0	12	40	570
HG01624.mapped.ILLUMINA.bwa.IBS.exome.20130415	667	151	252	175	463	348	504	562	266	0	256	0	285	152	0	23	561
HG01625.mapped.ILLUMINA.bwa.IBS.exome.20130415	641	93	112	96	326	289	471	530	310	0	0	0	0	0	0	57	543
HG01626.mapped.ILLUMINA.bwa.IBS.exome.20130415	641	0	0	224	421	362	479	508	313	0	0	0	0	0	6	48	538
HG01628.mapped.ILLUMINA.bwa.IBS.exome.20130415	651	148	168	98	320	314	513	575	348	0	0	0	0	0	17	26	557
HG01630.mapped.ILLUMINA.bwa.IBS.exome.20130415	544	243	255	0	0	0	495	543	340	0	0	0	0	0	0	69	566
HG01631.mapped.ILLUMINA.bwa.IBS.exome.20121211	697	0	0	359	666	435	544	642	414	99	592	0	329	150	0	67	586
HG01632.mapped.ILLUMINA.bwa.IBS.exome.20121211	702	293	321	350	675	433	547	646	0	105	663	585	445	169	0	0	591
HG01668.mapped.ILLUMINA.bwa.IBS.exome.20130415	643	0	0	254	591	433	514	566	321	0	0	0	0	0	0	41	564
HG01669.mapped.ILLUMINA.bwa.IBS.exome.20130415	616	0	0	213	438	353	472	525	212	0	123	0	186	98	0	21	550
HG01670.mapped.ILLUMINA.bwa.IBS.exome.20130415	620	0	0	239	378	346	476	521	310	0	0	0	0	0	14	0	550

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG01672.mapped.ILLUMINA.bwa.IBS.exome.20130415	676	0	0	250	611	364	514	566	260	0	219	0	285	140	0	21	568
HG01673.mapped.ILLUMINA.bwa.IBS.exome.20120522	696	0	0	361	671	432	545	644	541	0	0	0	0	0	43	69	582
HG01675.mapped.ILLUMINA.bwa.IBS.exome.20120522	700	0	0	361	670	427	540	649	536	0	0	0	0	0	38	70	588
HG01676.mapped.ILLUMINA.bwa.IBS.exome.20120522	696	0	0	359	673	434	540	638	538	0	0	0	0	0	56	0	585
HG01678.mapped.ILLUMINA.bwa.IBS.exome.20120522	701	289	305	345	648	419	533	616	515	0	617	0	420	156	0	82	586
HG01679.mapped.ILLUMINA.bwa.IBS.exome.20120522	695	0	0	357	679	433	542	636	412	101	612	0	332	157	0	66	586
HG01680.mapped.ILLUMINA.bwa.IBS.exome.20120522	785	0	0	357	672	433	548	638	542	0	0	0	0	0	0	150	584
HG01682.mapped.ILLUMINA.bwa.IBS.exome.20120522	698	0	0	357	674	434	542	642	538	0	0	0	0	0	41	78	585
HG01684.mapped.ILLUMINA.bwa.IBS.exome.20120522	695	0	0	357	674	436	542	632	451	0	0	0	0	0	0	138	585
HG01685.mapped.ILLUMINA.bwa.IBS.exome.20120522	699	0	0	356	678	434	541	641	532	0	0	0	0	0	0	118	587
HG01686.mapped.ILLUMINA.bwa.IBS.exome.20120522	700	287	320	339	652	428	545	610	438	0	628	573	0	163	0	82	587
HG01694.mapped.ILLUMINA.bwa.IBS.exome.20120522	697	282	321	221	672	334	545	641	516	96	631	585	0	160	0	72	588
HG01695.mapped.ILLUMINA.bwa.IBS.exome.20120522	701	295	314	347	653	428	545	646	531	0	0	0	0	0	47	69	589
HG01697.mapped.ILLUMINA.bwa.IBS.exome.20120522	778	263	285	318	619	400	540	679	506	0	0	62	41	11	0	232	584
HG01699.mapped.ILLUMINA.bwa.IBS.exome.20120522	690	245	273	284	562	381	536	645	465	73	618	0	370	138	0	73	576
HG01700.mapped.ILLUMINA.bwa.IBS.exome.20121211	699	0	0	363	677	429	545	648	532	0	0	0	0	0	0	156	590
HG01702.mapped.ILLUMINA.bwa.IBS.exome.20121211	702	284	308	340	637	416	541	638	535	0	0	0	0	0	39	70	587
HG01704.mapped.ILLUMINA.bwa.IBS.exome.20120522	760	0	0	314	622	292	526	664	476	75	618	0	371	139	0	87	579
HG01705.mapped.ILLUMINA.bwa.IBS.exome.20120522	677	260	281	296	626	389	533	660	496	0	602	569	0	0	0	107	580
HG01707.mapped.ILLUMINA.bwa.IBS.exome.20120522	690	0	0	309	616	392	531	663	494	0	0	0	0	0	39	85	581
HG01708.mapped.ILLUMINA.bwa.IBS.exome.20120522	688	0	0	316	614	295	526	658	485	0	0	0	0	0	42	84	580
HG01709.mapped.ILLUMINA.bwa.IBS.exome.20120522	675	265	284	0	620	140	537	673	491	76	643	582	0	0	50	1	577
HG01710.mapped.ILLUMINA.bwa.IBS.exome.20120522	679	257	276	296	574	291	532	660	498	0	0	0	0	0	0	171	580
HG01746.mapped.ILLUMINA.bwa.IBS.exome.20120522	759	258	273	304	622	390	534	655	460	79	647	573	372	144	0	81	580
HG01747.mapped.ILLUMINA.bwa.IBS.exome.20120522	762	0	0	353	621	397	537	651	490	0	0	0	0	0	0	169	579
HG01756.mapped.ILLUMINA.bwa.IBS.exome.20120522	699	344	386	0	703	186	564	682	570	105	671	594	470	190	92	2	600
HG01757.mapped.ILLUMINA.bwa.IBS.exome.20120522	696	0	0	386	703	478	555	653	567	0	0	0	0	0	0	138	593
HG01761.mapped.ILLUMINA.bwa.IBS.exome.20120522	792	0	0	388	710	479	558	665	0	101	665	0	467	190	0	0	593
HG01762.mapped.ILLUMINA.bwa.IBS.exome.20120522	700	333	366	374	711	385	557	663	462	98	657	594	0	183	0	111	595
HG01765.mapped.ILLUMINA.bwa.IBS.exome.20130415	795	40	0	387	709	393	549	650	570	0	0	0	0	0	0	194	590
HG01766.mapped.ILLUMINA.bwa.IBS.exome.20130415	695	321	368	374	709	379	555	662	569	0	627	556	0	0	62	0	593
HG01767.mapped.ILLUMINA.bwa.IBS.exome.20130415	700	0	0	390	718	472	559	656	576	0	0	0	0	0	0	138	592
HG01768.mapped.ILLUMINA.bwa.IBS.exome.20130415	694	0	0	393	707	473	561	665	552	104	641	0	452	187	0	104	594
HG01770.mapped.ILLUMINA.bwa.IBS.exome.20130415	629	157	155	230	384	394	493	425	331	0	0	0	0	0	0	57	566
HG01771.mapped.ILLUMINA.bwa.IBS.exome.20130415	618	136	150	92	521	300	491	516	0	0	415	444	117	156	0	0	545
HG01773.mapped.ILLUMINA.bwa.IBS.exome.20130415	655	172	235	226	583	431	514	604	277	83	439	452	292	151	0	24	561
HG01775.mapped.ILLUMINA.bwa.IBS.exome.20130415	624	0	0	253	439	322	479	535	0	84	301	0	305	179	0	0	553
HG01776.mapped.ILLUMINA.bwa.IBS.exome.20130415	613	117	107	216	281	288	488	524	325	0	0	0	0	0	8	16	529
HG01777.mapped.ILLUMINA.bwa.IBS.exome.20130415	618	158	133	222	243	327	487	577	303	0	0	0	0	0	6	31	553
HG01779.mapped.ILLUMINA.bwa.IBS.exome.20130415	643	159	170	233	560	348	511	560	271	0	404	360	280	117	0	29	555
HG01781.mapped.ILLUMINA.bwa.IBS.exome.20130415	643	150	207	223	334	289	503	566	321	0	0	0	0	0	11	29	545
HG01783.mapped.ILLUMINA.bwa.IBS.exome.20130415	651	131	197	102	297	280	498	533	313	0	0	0	0	0	12	20	547
HG01784.mapped.ILLUMINA.bwa.IBS.exome.20130415	646	124	116	202	489	336	494	566	326	0	131	406	0	0	14	20	562
HG01785.mapped.ILLUMINA.bwa.IBS.exome.20130415	677	289	332	300	674	374	551	632	448	0	551	527	0	0	31	53	581
HG01786.mapped.ILLUMINA.bwa.IBS.exome.20130415	687	0	0	354	664	445	554	514	449	0	0	0	0	0	0	68	578
HG01789.mapped.ILLUMINA.bwa.GBR.exome.20130415	625	160	200	221	567	423	504	590	297	0	409	462	288	154	0	35	544
HG01790.mapped.ILLUMINA.bwa.GBR.exome.20130415	595	124	101	218	310	287	469	580	248	0	25	0	234	136	0	17	542
HG01791.mapped.ILLUMINA.bwa.GBR.exome.20120522	699	293	313	346	654	423	544	642	546	0	0	0	0	0	44	87	586
HG01794.mapped.ILLUMINA.bwa.CDX.exome.20120522	677	304	325	0	647	160	545	633	0	105	653	528	434	165	0	0	588
HG01795.mapped.ILLUMINA.bwa.CDX.exome.20120522	696	287	316	345	682	429	546	657	540	102	625	570	0	0	60	0	588
HG01796.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	0	0	357	665	440	545	644	535	0	0	0	0	0	60	0	588
HG01797.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	0	0	355	667	339	538	639	429	100	630	0	337	160	44	0	584
HG01798.mapped.ILLUMINA.bwa.CDX.exome.20120522	697	0	0	356	671	439	545	633	542	0	0	0	0	0	45	72	583
HG01799.mapped.ILLUMINA.bwa.CDX.exome.20120522	696	291	316	346	650	426	542	639	537	0	0	0	0	0	0	105	590
HG01800.mapped.ILLUMINA.bwa.CDX.exome.20120522	702	0	0	356	672	432	539	635	440	102	592	523	0	163	0	79	581
HG01801.mapped.ILLUMINA.bwa.CDX.exome.20120522	788	0	0	356	670	440	545	650	438	103	635	0	419	156	0	86	583
HG01802.mapped.ILLUMINA.bwa.CDX.exome.20120522	698	0	0	359	664	435	546	634	444	0	0	0	0	0	60	0	588
HG01804.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	0	0	366	677	438	544	642	543	0	0	0	0	0	45	88	586
HG01805.mapped.ILLUMINA.bwa.CDX.exome.20120522	697	0	0	358	674	433	532	637	0	103	638	0	433	163	0	0	584
HG01806.mapped.ILLUMINA.bwa.CDX.exome.20120522	701	291	300	337	661	424	546	654	443	103	629	0	417	158	40	0	585
HG01807.mapped.ILLUMINA.bwa.CDX.exome.20120522	697	0	0	360	671	430	543	639	438	100	617	0	415	161	0	73	584
HG01808.mapped.ILLUMINA.bwa.CDX.exome.20120522	696	0	0	352	671	442	540	644	537	0	0	0	0	0	59	1	591
HG01809.mapped.ILLUMINA.bwa.CDX.exome.20120522	702	290	299	352	650	419	543	648	0	105	649	559	407	170	0	0	591
HG01810.mapped.ILLUMINA.bwa.CDX.exome.20120522	699	290	319	341	676	430	542	654	432	102	650	533	425	164	0	79	585
HG01811.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	284	313	344	648	429	523	607	432	0	604	0	323	162	42	0	579
HG01812.mapped.ILLUMINA.bwa.CDX.exome.20120522	697	0	0	354	669	443	542	637	531	0	0	0	0	0	38	69	588
HG01813.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	287	315	350	677	430	550	645	430	104	646	535	419	160	41	0	587
HG01815.mapped.ILLUMINA.bwa.CDX.exome.20120522	699	289	311	351	651	325	544	640	435	101	623	0	415	163	48	0	590
HG01816.mapped.ILLUMINA.bwa.CDX.exome.20120522	679	302	331	0	658	163	547	654	543	0	624	523	0	0	47	82	586
HG01817.mapped.ILLUMINA.bwa.CDX.exome.20120522	698	0	0	356	682	434	544	639	448	0	0	0	0	0	0	111	586
HG01840.mapped.ILLUMINA.bwa.KHV.exome.20120522	700	292	319	351	676	426	552	657	530	101	605	567	0	0	63	0	590
HG01841.mapped.ILLUMINA.bwa.KHV.exome.20120522	701	0	0	355	671	441	545	635	507	101	599	524	0	157	0	70	588
HG01842.mapped.ILLUMINA.bwa.KHV.exome.20120522	691	286	306	329	646	419	547	645	431	101	628	0	424	164	48	0	585
HG01843.mapped.ILLUMINA.bwa.KHV.exome.20120522	702	0	0	356	677	440	547	635	542	0	0	0	0	0	42	89	592
HG01844.mapped.ILLUMINA.bwa.KHV.exome.20120522	699	0	0	359	680	436	546	650	435	106	616	562	0	158	51	0	589
HG01845.mapped.ILLUMINA.bwa.KHV.exome.20120522	697	0	0	359	671	434	544	636	536	0	0	0	0	0	45	80	588
HG01846.mapped.ILLUMINA.bwa.KHV.exome.20120522	698	294	313	351	662	432	537	599	507	0	611	568	0	161	0	81	588
HG01847.mapped.ILLUMINA.bwa.KHV.exome.20120522	695	0	0	355	662	429	534	628	538	0	0	0	0	0	35	74	585
HG01848.mapped.ILLUMINA.bwa.KHV.exome.20120522	781	0	0	360	674	442	549	633	531	0	0	0	0	0	0	106	589
HG01849.mapped.ILLUMINA.bwa.KHV.exome.20120522	782	0	0	353	678	436	544	637	547	0	0	0	0	0	48	68	591
HG01850.mapped.ILLUMINA.bwa.KHV.exome.20120522	701	0	0	358	673	440	546	630	534	0	0	0	0	0	62	0	587
HG01851.mapped.ILLUMINA.bwa.KHV.exome.20120522	695	0	0	356	670	436	541	639	534	0	0	0	0	0	38	72	585
HG01852.mapped.ILLUMINA.bwa.KHV.exome.20120522	699	298	317	350	659	414	546	634	519	102	615	0	335	165	0	72	586
HG01853.mapped.ILLUMINA.bwa.KHV.exome.20120522	697	0	0	357	676	437	546	647	537	0	0	0	0	0	50	71	592
HG01855.mapped.ILLUMINA.bwa.KHV.exome.20120522	784	0	0	360	678	439	548	647	439	102	596	531	0	160	0	72	589
HG01857.mapped.ILLUMINA.bwa.KHV.exome.20120522	786	0	0	361	680	444	544	650	542	0	0	0	0	0	0	143	594
HG01858.mapped.ILLUMINA.bwa.KHV.exome.20120522	701	0	0	361	676	432	541	631	429	103	612	564	0	0	0	81	590
HG01859.mapped.ILLUMINA.bwa.KHV.exome.20120522	699	0	0	356	676	347	525	642	537	0	0	0	0	0	63	1	588
HG01860.mapped.ILLUMINA.bwa.KHV.exome.20121211	691	0	0	356	656	433	541	634	521	0	0	0	0	0	56	0	584
HG01861.mapped.ILLUMINA.bwa.KHV.exome.20121211	697	0	0	360	679	435	540	632	454	0	0	0	0	0	59	0	590
HG01862.mapped.ILLUMINA.bwa.KHV.exome.20120522	682	259	274	296	594	393	528	631	461	0	611	0	370	136	0	70	577
HG01863.mapped.ILLUMINA.bwa.KHV.exome.20120522	757	252	276	298	598	388	536	659	490	0	0	0	0	0	36	84	580
HG01864.mapped.ILLUMINA.bwa.KHV.exome.20120522	763	0	0	308	619	402	532	655	493	0	0	0	0	0	35	76	580
HG01865.mapped.ILLUMINA.bwa.KHV.exome.20120522	690	0	0	348	641	396	533	651	477	0	0	0	0	0	0	112	578
HG01866.mapped.ILLUMINA.bwa.KHV.exome.20120522	761	0	0	316	618	393	534	646	492	0	0	0	0	0	0	144	578
HG01867.mapped.ILLUMINA.bwa.KHV.exome.20120522	687	0	0	306	621	398	538	644	487	0	0	0	0	0	45	1	577

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG01868.mapped.ILLUMINA.bwa.KHV.exome.20120522	691	0	0	305	619	396	535	653	476	68	614	0	375	136	33	1	580
HG01869.mapped.ILLUMINA.bwa.KHV.exome.20120522	757	251	264	301	598	389	534	654	494	0	0	0	0	0	0	157	579
HG01870.mapped.ILLUMINA.bwa.KHV.exome.20120522	701	0	0	381	697	475	558	665	562	99	647	588	0	185	68	0	594
HG01871.mapped.ILLUMINA.bwa.KHV.exome.20120522	704	0	0	391	712	477	558	672	583	0	0	0	0	0	81	105	600
HG01872.mapped.ILLUMINA.bwa.KHV.exome.20120522	701	0	0	402	709	477	557	663	0	101	665	0	466	190	0	0	596
HG01873.mapped.ILLUMINA.bwa.KHV.exome.20120522	698	0	0	386	701	475	556	660	582	0	0	0	0	0	63	107	595
HG01874.mapped.ILLUMINA.bwa.KHV.exome.20120522	798	0	0	405	720	471	559	667	582	0	0	0	0	0	69	128	599
HG01878.mapped.ILLUMINA.bwa.KHV.exome.20120522	703	324	369	369	686	472	555	641	555	0	554	587	0	184	65	0	596
HG01879.mapped.ILLUMINA.bwa.ACB.exome.20120522	697	293	315	348	586	426	526	604	0	102	637	0	443	165	0	1	591
HG01880.mapped.ILLUMINA.bwa.ACB.exome.20120522	699	296	313	342	653	429	524	603	515	0	642	0	328	162	0	76	588
HG01882.mapped.ILLUMINA.bwa.ACB.exome.20121211	700	280	301	338	679	167	544	632	539	0	598	566	0	0	62	0	591
HG01883.mapped.ILLUMINA.bwa.ACB.exome.20121211	697	0	0	360	668	331	543	656	163	104	576	537	0	162	0	0	579
HG01885.mapped.ILLUMINA.bwa.ACB.exome.20120522	687	0	0	311	612	402	537	646	492	0	0	0	0	0	50	0	577
HG01886.mapped.ILLUMINA.bwa.ACB.exome.20120522	703	0	0	388	713	478	562	651	571	0	0	0	0	0	0	234	596
HG01889.mapped.ILLUMINA.bwa.ACB.exome.20130415	665	122	192	212	476	413	510	564	333	0	243	0	262	0	16	21	555
HG01890.mapped.ILLUMINA.bwa.ACB.exome.20130415	644	0	0	246	460	409	520	565	300	0	0	0	0	0	10	0	503
HG01892.mapped.ILLUMINA.bwa.PEL.exome.20120522	697	0	0	355	671	435	539	621	532	0	0	0	0	0	0	107	590
HG01893.mapped.ILLUMINA.bwa.PEL.exome.20120522	701	0	0	356	673	439	544	629	530	0	0	0	0	0	72	0	587
HG01894.mapped.ILLUMINA.bwa.ACB.exome.20130415	602	0	0	253	474	417	518	576	325	0	0	0	0	0	0	36	550
HG01896.mapped.ILLUMINA.bwa.ACB.exome.20120522	701	0	0	353	674	439	545	633	535	0	0	0	0	0	48	75	588
HG01912.mapped.ILLUMINA.bwa.ACB.exome.20130415	669	227	264	238	574	355	522	608	307	0	393	394	0	0	0	22	550
HG01914.mapped.ILLUMINA.bwa.ACB.exome.20120522	697	0	0	365	672	430	541	654	520	0	0	0	0	0	44	88	585
HG01915.mapped.ILLUMINA.bwa.ACB.exome.20120522	698	167	324	351	658	426	544	635	533	0	0	0	0	0	49	0	582
HG01917.mapped.ILLUMINA.bwa.PEL.exome.20120522	699	0	0	360	670	439	549	647	434	101	620	0	428	164	0	3	589
HG01918.mapped.ILLUMINA.bwa.PEL.exome.20120522	693	0	0	355	678	435	544	625	536	0	0	0	0	0	43	75	592
HG01920.mapped.ILLUMINA.bwa.PEL.exome.20120522	701	300	317	346	654	424	548	643	523	102	619	0	418	165	51	1	588
HG01921.mapped.ILLUMINA.bwa.PEL.exome.20120522	700	0	0	360	676	433	540	653	418	103	607	0	420	160	0	78	587
HG01923.mapped.ILLUMINA.bwa.PEL.exome.20121211	785	0	0	359	671	442	542	642	438	102	606	0	414	164	51	0	585
HG01924.mapped.ILLUMINA.bwa.PEL.exome.20121211	694	0	0	350	673	435	546	625	528	0	0	0	0	0	41	76	587
HG01926.mapped.ILLUMINA.bwa.PEL.exome.20120522	690	0	0	309	614	399	535	650	488	0	0	0	0	0	49	0	579
HG01927.mapped.ILLUMINA.bwa.PEL.exome.20120522	760	0	0	311	618	400	535	658	489	0	0	0	0	0	48	1	578
HG01932.mapped.ILLUMINA.bwa.PEL.exome.20120522	752	257	274	300	624	387	533	654	490	0	605	572	0	0	38	82	578
HG01933.mapped.ILLUMINA.bwa.PEL.exome.20120522	756	255	274	297	588	0	521	640	471	0	0	0	0	140	37	1	580
HG01935.mapped.ILLUMINA.bwa.PEL.exome.20120522	763	0	0	311	617	403	535	656	484	0	0	0	0	0	47	1	580
HG01936.mapped.ILLUMINA.bwa.PEL.exome.20120522	761	0	0	350	615	392	531	654	492	0	0	0	0	0	32	74	577
HG01938.mapped.ILLUMINA.bwa.PEL.exome.20120522	761	258	269	295	601	386	534	654	497	0	0	0	0	0	49	1	580
HG01939.mapped.ILLUMINA.bwa.PEL.exome.20120522	759	255	269	296	595	388	535	656	459	70	607	0	378	141	0	88	577
HG01941.mapped.ILLUMINA.bwa.PEL.exome.20120522	759	0	0	357	619	392	534	663	497	0	0	0	0	0	40	75	578
HG01942.mapped.ILLUMINA.bwa.PEL.exome.20120522	686	0	0	303	631	391	535	646	490	0	0	0	0	0	46	0	579
HG01944.mapped.ILLUMINA.bwa.PEL.exome.20120522	686	0	0	310	609	395	535	649	482	0	0	0	0	0	44	0	576
HG01945.mapped.ILLUMINA.bwa.PEL.exome.20120522	762	0	0	316	618	394	536	653	492	0	0	0	0	0	48	2	577
HG01947.mapped.ILLUMINA.bwa.PEL.exome.20120522	593	248	276	0	547	136	532	641	391	76	644	569	367	137	30	0	577
HG01948.mapped.ILLUMINA.bwa.PEL.exome.20120522	691	0	0	307	609	397	533	655	491	0	0	0	0	0	36	82	577
HG01950.mapped.ILLUMINA.bwa.PEL.exome.20120522	745	257	272	294	620	382	537	656	491	0	610	577	0	0	44	80	581
HG01951.mapped.ILLUMINA.bwa.PEL.exome.20120522	755	0	0	314	613	394	535	646	486	0	0	0	0	0	39	0	579
HG01953.mapped.ILLUMINA.bwa.PEL.exome.20120522	792	329	372	376	687	472	557	665	559	88	637	0	457	184	61	0	598
HG01954.mapped.ILLUMINA.bwa.PEL.exome.20120522	798	0	0	383	707	479	555	664	579	0	0	0	0	0	68	109	595
HG01956.mapped.ILLUMINA.bwa.ACB.exome.20120522	753	260	260	196	566	386	535	658	489	0	0	0	0	0	31	79	579
HG01958.mapped.ILLUMINA.bwa.ACB.exome.20120522	703	285	315	354	682	435	544	638	545	0	629	573	0	0	68	0	589
HG01961.mapped.ILLUMINA.bwa.PEL.exome.20130415	660	291	331	315	506	430	536	579	318	0	464	0	330	165	26	2	585
HG01965.mapped.ILLUMINA.bwa.PEL.exome.20130415	689	0	0	358	682	457	556	629	552	0	0	0	0	0	39	58	592
HG01967.mapped.ILLUMINA.bwa.PEL.exome.20120522	796	0	0	386	709	475	560	669	570	0	0	0	0	0	72	116	595
HG01968.mapped.ILLUMINA.bwa.PEL.exome.20120522	696	0	0	385	707	474	557	655	574	0	0	0	0	0	85	0	597
HG01970.mapped.ILLUMINA.bwa.PEL.exome.20120522	702	0	0	382	712	477	560	667	577	0	0	0	0	0	67	116	599
HG01971.mapped.ILLUMINA.bwa.PEL.exome.20120522	700	0	0	393	707	476	559	659	578	0	0	0	0	0	83	0	599
HG01973.mapped.ILLUMINA.bwa.PEL.exome.20120522	700	0	0	406	712	473	557	662	574	0	0	0	0	0	82	0	600
HG01974.mapped.ILLUMINA.bwa.PEL.exome.20120522	698	0	0	387	714	475	558	650	573	0	0	0	0	0	86	0	598
HG01976.mapped.ILLUMINA.bwa.PEL.exome.20120522	797	0	0	386	705	476	557	663	576	0	0	0	0	0	68	103	595
HG01977.mapped.ILLUMINA.bwa.PEL.exome.20120522	702	0	0	390	711	475	558	659	574	0	0	0	0	0	88	1	596
HG01979.mapped.ILLUMINA.bwa.PEL.exome.20130415	625	0	0	227	532	417	500	551	301	0	0	0	0	0	0	47	549
HG01980.mapped.ILLUMINA.bwa.PEL.exome.20130415	632	144	141	209	471	324	502	571	256	0	388	485	0	149	0	31	561
HG01982.mapped.ILLUMINA.bwa.PEL.exome.20120522	700	0	0	358	674	436	547	648	537	0	0	0	0	0	59	1	589
HG01983.mapped.ILLUMINA.bwa.PEL.exome.20120522	700	277	304	338	646	430	547	634	537	0	613	82	358	0	37	69	579
HG01985.mapped.ILLUMINA.bwa.ACB.exome.20120522	693	285	310	350	674	437	548	637	540	0	612	0	346	0	55	0	587
HG01986.mapped.ILLUMINA.bwa.ACB.exome.20120522	696	0	0	354	663	436	547	637	532	0	0	0	0	0	42	78	585
HG01988.mapped.ILLUMINA.bwa.ACB.exome.20121211	761	0	0	309	619	384	537	653	479	0	0	0	0	0	40	1	579
HG01989.mapped.ILLUMINA.bwa.ACB.exome.20121211	686	246	269	291	609	378	534	651	384	72	646	571	297	138	0	79	579
HG01990.mapped.ILLUMINA.bwa.ACB.exome.20121211	774	0	0	358	674	444	544	640	460	0	0	0	0	0	66	2	590
HG01991.mapped.ILLUMINA.bwa.PEL.exome.20130415	581	0	0	230	402	413	496	558	311	0	0	0	0	0	14	18	550
HG01992.mapped.ILLUMINA.bwa.PEL.exome.20130415	596	124	116	196	276	303	456	484	296	0	0	0	0	0	15	0	535
HG01997.mapped.ILLUMINA.bwa.PEL.exome.20130415	581	0	0	231	433	348	467	514	323	0	0	0	0	0	16	0	548
HG02002.mapped.ILLUMINA.bwa.PEL.exome.20130415	600	101	142	195	248	262	479	557	297	0	0	0	0	0	14	1	540
HG02003.mapped.ILLUMINA.bwa.PEL.exome.20130415	644	138	252	185	491	334	484	586	329	0	258	351	0	0	7	19	557
HG02006.mapped.ILLUMINA.bwa.PEL.exome.20130415	799	0	0	391	716	480	561	663	579	0	0	0	11	0	0	153	595
HG02008.mapped.ILLUMINA.bwa.PEL.exome.20130415	607	131	107	191	547	296	488	541	254	0	384	501	0	128	0	24	543
HG02009.mapped.ILLUMINA.bwa.ACB.exome.20130415	624	148	125	194	454	276	486	504	155	0	323	316	110	123	0	0	479
HG02010.mapped.ILLUMINA.bwa.ACB.exome.20130415	631	0	0	242	574	315	519	542	321	0	0	0	0	0	0	33	547
HG02012.mapped.ILLUMINA.bwa.ACB.exome.20121211	789	292	309	350	685	439	548	649	522	102	654	573	418	165	52	0	588
HG02013.mapped.ILLUMINA.bwa.ACB.exome.20120522	700	0	0	351	672	436	540	638	528	0	0	0	0	0	56	0	588
HG02014.mapped.ILLUMINA.bwa.ACB.exome.20120522	704	0	0	403	707	474	557	657	561	92	653	0	457	184	64	0	600
HG02016.mapped.ILLUMINA.bwa.KHV.exome.20130415	649	131	147	218	381	310	499	558	252	0	305	0	276	168	13	2	552
HG02017.mapped.ILLUMINA.bwa.KHV.exome.20130415	652	0	0	348	601	441	513	577	355	0	0	0	0	0	0	56	562
HG02019.mapped.ILLUMINA.bwa.KHV.exome.20130415	668	148	192	193	308	329	501	556	340	0	0	0	0	0	0	55	566
HG02020.mapped.ILLUMINA.bwa.KHV.exome.20130415	641	0	0	246	570	366	489	588	341	0	0	0	0	0	7	24	555
HG02023.mapped.ILLUMINA.bwa.KHV.exome.20120522	690	259	269	303	620	387	535	650	490	0	625	567	0	0	34	80	575
HG02024.mapped.ILLUMINA.bwa.KHV.exome.20130422	601	260	278	0	596	141	531	654	68	83	651	516	384	138	0	2	577
HG02025.mapped.ILLUMINA.bwa.KHV.exome.20130422	766	263	280	308	626	406	538	669	474	82	663	580	386	142	0	112	581
HG02026.mapped.ILLUMINA.bwa.KHV.exome.20130422	764	259	275	304	615	394	535	669	484	88	646	0	381	141	0	89	582
HG02028.mapped.ILLUMINA.bwa.KHV.exome.20120522	754	0	0	307	602	292	526	656	466	75	607	0	375	136	42	0	576
HG02029.mapped.ILLUMINA.bwa.KHV.exome.20120522	689	0	0	305	616	404	533	652	481	0	0	0	0	0	52	1	580
HG02031.mapped.ILLUMINA.bwa.KHV.exome.20121211	700	0	0	357	663	437	541	634	544	0	0	0	0	0	40	57	590
HG02032.mapped.ILLUMINA.bwa.KHV.exome.20121211	690	0	0	357	673	434	544	628	529	0	0	0	0	0	36	84	580
HG02035.mapped.ILLUMINA.bwa.KHV.exome.20130415	650	0	0	339	476	360	493	563	283	0	266	0	175	110	14	3	542
HG02040.mapped.ILLUMINA.bwa.KHV.exome.20120522	688	0	0	309	601	392	533	651	483	0	0	0	0	0	30	79	578
HG02046.mapped.ILLUMINA.bwa.KHV.exome.20120522	686	247	267	297	614	382	535	664	488	73	546	567	0	0	31	67	576
HG02047.mapped.ILLUMINA.bwa.KHV.exome.20120522	679	0	0	309	627	389	533	648	456	68	613	516	0	138	0	68	578

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02048.mapped.ILLUMINA.bwa.KHV.exome.20120522	698	0	0	388	711	479	558	666	574	0	0	0	0	0	74	107	599
HG02049.mapped.ILLUMINA.bwa.KHV.exome.20120522	701	0	0	390	707	477	558	663	579	0	0	0	0	0	96	0	600
HG02050.mapped.ILLUMINA.bwa.KHV.exome.20121211	701	0	0	362	674	429	538	645	453	0	0	0	0	0	45	75	586
HG02051.mapped.ILLUMINA.bwa.ACB.exome.20120522	689	0	294	341	668	420	543	638	528	0	591	0	350	0	42	68	586
HG02052.mapped.ILLUMINA.bwa.ACB.exome.20121211	687	0	0	307	617	389	531	654	485	0	0	0	0	0	35	61	578
HG02053.mapped.ILLUMINA.bwa.ACB.exome.20121211	700	293	323	220	682	436	547	657	522	103	656	584	339	165	0	76	590
HG02054.mapped.ILLUMINA.bwa.ACB.exome.20130415	555	0	0	228	599	425	507	558	343	0	0	0	0	0	17	0	556
HG02057.mapped.ILLUMINA.bwa.KHV.exome.20120522	702	0	0	393	714	478	562	670	576	0	0	0	0	0	78	127	601
HG02058.mapped.ILLUMINA.bwa.KHV.exome.20120522	704	327	363	375	712	474	560	666	566	84	665	592	459	187	69	2	598
HG02060.mapped.ILLUMINA.bwa.KHV.exome.20120522	698	286	316	348	651	424	546	641	536	0	0	0	0	0	46	76	590
HG02061.mapped.ILLUMINA.bwa.KHV.exome.20120522	698	295	320	357	683	431	543	649	437	102	604	0	340	161	0	79	586
HG02064.mapped.ILLUMINA.bwa.KHV.exome.20120522	697	284	310	337	678	423	543	642	0	104	668	572	431	167	0	0	585
HG02067.mapped.ILLUMINA.bwa.KHV.exome.20120522	700	290	312	341	677	426	549	663	536	104	601	540	0	0	60	0	585
HG02069.mapped.ILLUMINA.bwa.KHV.exome.20120522	791	334	375	387	699	384	558	665	562	94	556	0	470	189	77	1	600
HG02070.mapped.ILLUMINA.bwa.KHV.exome.20120522	704	333	373	371	704	389	558	657	0	104	670	0	469	191	0	1	599
HG02072.mapped.ILLUMINA.bwa.KHV.exome.20120522	796	331	368	375	684	380	558	670	577	0	0	0	0	0	0	224	599
HG02073.mapped.ILLUMINA.bwa.KHV.exome.20120522	702	0	0	391	715	478	562	665	582	0	0	0	0	0	81	122	596
HG02075.mapped.ILLUMINA.bwa.KHV.exome.20130415	657	143	177	216	383	342	525	585	305	0	0	0	0	0	16	20	575
HG02076.mapped.ILLUMINA.bwa.KHV.exome.20130415	644	0	0	252	470	407	478	560	300	0	0	0	0	0	14	15	548
HG02078.mapped.ILLUMINA.bwa.KHV.exome.20130415	649	144	136	185	368	350	481	575	277	0	126	0	242	149	0	23	556
HG02079.mapped.ILLUMINA.bwa.KHV.exome.20130415	656	0	0	335	582	418	507	567	324	0	0	0	0	0	28	0	549
HG02081.mapped.ILLUMINA.bwa.KHV.exome.20130415	618	0	0	243	591	362	478	518	321	0	0	0	0	0	14	1	555
HG02082.mapped.ILLUMINA.bwa.KHV.exome.20130415	637	159	233	178	377	321	514	565	311	0	0	0	0	0	11	31	561
HG02084.mapped.ILLUMINA.bwa.KHV.exome.20130415	643	0	0	338	507	365	495	534	0	0	367	0	285	158	0	0	556
HG02085.mapped.ILLUMINA.bwa.KHV.exome.20130415	669	0	0	258	588	433	521	578	337	0	0	0	0	0	29	0	572
HG02086.mapped.ILLUMINA.bwa.KHV.exome.20130415	572	0	0	205	410	397	391	441	172	0	138	0	143	132	0	9	535
HG02087.mapped.ILLUMINA.bwa.KHV.exome.20130415	634	0	0	342	514	357	502	584	305	0	129	0	230	129	0	18	571
HG02088.mapped.ILLUMINA.bwa.KHV.exome.20130415	648	0	0	338	585	365	487	555	309	0	0	0	0	0	32	0	554
HG02089.mapped.ILLUMINA.bwa.PEL.exome.20130415	635	145	146	231	258	277	512	576	238	85	190	0	281	142	12	0	563
HG02090.mapped.ILLUMINA.bwa.PEL.exome.20130415	639	0	0	230	456	368	458	438	327	0	0	0	0	0	0	50	539
HG02095.mapped.ILLUMINA.bwa.ACB.exome.20120522	764	0	0	307	606	394	531	626	395	0	594	0	367	140	31	1	578
HG02102.mapped.ILLUMINA.bwa.PEL.exome.20130415	796	327	367	374	704	465	558	670	568	105	654	0	459	187	56	7	591
HG02104.mapped.ILLUMINA.bwa.PEL.exome.20130415	642	138	124	102	358	300	467	547	272	0	311	0	260	149	0	38	557
HG02105.mapped.ILLUMINA.bwa.KHV.exome.20130415	587	0	0	282	514	316	459	514	304	0	0	0	0	0	4	26	544
HG02107.mapped.ILLUMINA.bwa.ACB.exome.20121211	754	0	0	306	606	384	528	647	460	67	600	0	364	133	0	72	577
HG02108.mapped.ILLUMINA.bwa.ACB.exome.20120522	747	257	129	271	570	377	533	623	455	0	596	0	361	140	33	1	576
HG02111.mapped.ILLUMINA.bwa.ACB.exome.20120522	761	249	265	294	571	331	533	654	487	0	0	0	0	0	31	67	577
HG02113.mapped.ILLUMINA.bwa.KHV.exome.20130415	679	0	0	335	608	431	502	607	260	0	298	426	0	169	0	33	562
HG02116.mapped.ILLUMINA.bwa.KHV.exome.20120522	690	0	0	306	608	386	534	659	485	0	0	0	0	0	33	60	577
HG02121.mapped.ILLUMINA.bwa.KHV.exome.20130415	666	0	0	351	607	424	540	588	323	0	0	0	0	0	16	35	563
HG02122.mapped.ILLUMINA.bwa.KHV.exome.20130415	590	128	113	183	303	301	482	483	292	0	0	0	0	0	18	0	551
HG02127.mapped.ILLUMINA.bwa.KHV.exome.20130415	665	210	126	225	604	355	533	579	287	0	426	460	258	148	11	0	563
HG02128.mapped.ILLUMINA.bwa.KHV.exome.20130415	665	0	0	263	599	445	519	569	262	94	332	0	271	156	13	0	567
HG02130.mapped.ILLUMINA.bwa.KHV.exome.20120522	697	290	296	347	646	403	548	635	539	0	0	0	0	0	36	57	589
HG02131.mapped.ILLUMINA.bwa.KHV.exome.20120522	785	288	314	346	658	430	548	643	439	103	632	581	0	161	0	83	589
HG02133.mapped.ILLUMINA.bwa.KHV.exome.20120522	699	0	0	364	671	433	543	635	545	0	0	0	0	0	45	80	585
HG02134.mapped.ILLUMINA.bwa.KHV.exome.20120522	784	0	0	365	677	438	547	643	442	102	621	0	409	164	49	1	588
HG02136.mapped.ILLUMINA.bwa.KHV.exome.20120522	698	0	0	358	666	437	542	643	538	0	0	0	0	0	40	74	586
HG02137.mapped.ILLUMINA.bwa.KHV.exome.20120522	785	0	0	358	675	432	547	634	542	0	0	0	0	0	73	0	588
HG02138.mapped.ILLUMINA.bwa.KHV.exome.20130415	654	0	0	239	606	425	503	585	265	0	165	431	0	157	0	28	552
HG02139.mapped.ILLUMINA.bwa.KHV.exome.20130415	649	0	0	246	549	428	509	567	326	0	0	0	0	0	8	23	553
HG02140.mapped.ILLUMINA.bwa.KHV.exome.20130415	642	133	171	228	334	380	514	570	346	0	0	0	0	0	16	32	561
HG02141.mapped.ILLUMINA.bwa.KHV.exome.20130415	651	0	0	240	452	345	480	541	326	0	0	0	0	0	12	25	549
HG02142.mapped.ILLUMINA.bwa.KHV.exome.20121211	701	0	0	359	678	435	539	644	534	0	0	0	0	0	0	133	591
HG02143.mapped.ILLUMINA.bwa.ACB.exome.20120522	761	0	0	297	609	398	536	646	397	75	584	0	302	135	26	0	577
HG02144.mapped.ILLUMINA.bwa.ACB.exome.20120522	676	254	264	104	614	283	531	650	479	0	640	566	319	0	37	1	578
HG02146.mapped.ILLUMINA.bwa.PEL.exome.20120522	700	0	0	355	670	437	546	643	539	0	0	0	0	0	42	89	587
HG02147.mapped.ILLUMINA.bwa.PEL.exome.20120522	697	0	0	355	675	433	541	638	532	0	0	0	0	0	60	0	587
HG02150.mapped.ILLUMINA.bwa.PEL.exome.20130415	700	0	0	392	708	472	562	674	0	111	665	0	465	187	0	2	591
HG02151.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	0	0	360	674	444	545	649	520	104	621	0	430	163	51	0	587
HG02152.mapped.ILLUMINA.bwa.CDX.exome.20130415	663	0	0	259	560	430	528	621	342	0	0	0	0	0	27	0	566
HG02153.mapped.ILLUMINA.bwa.CDX.exome.20130415	626	0	0	228	299	339	486	411	302	0	0	0	0	0	0	27	536
HG02154.mapped.ILLUMINA.bwa.CDX.exome.20130415	649	0	0	257	585	437	512	579	300	0	330	417	0	164	0	29	565
HG02155.mapped.ILLUMINA.bwa.CDX.exome.20130415	512	159	286	0	297	147	519	540	286	0	388	482	0	162	0	20	547
HG02156.mapped.ILLUMINA.bwa.CDX.exome.20130415	626	0	0	234	429	413	456	531	338	0	0	0	0	0	6	13	550
HG02164.mapped.ILLUMINA.bwa.CDX.exome.20130415	642	0	0	225	531	423	511	528	316	0	0	0	0	0	10	26	539
HG02165.mapped.ILLUMINA.bwa.CDX.exome.20130415	579	0	0	224	366	346	461	524	276	0	0	0	0	0	8	10	533
HG02166.mapped.ILLUMINA.bwa.CDX.exome.20130415	658	0	0	342	616	433	514	579	339	0	0	0	0	0	25	0	564
HG02178.mapped.ILLUMINA.bwa.CDX.exome.20130415	651	0	0	250	530	412	522	567	342	0	0	0	0	0	30	0	551
HG02179.mapped.ILLUMINA.bwa.CDX.exome.20130415	546	261	292	0	405	171	549	621	342	83	374	489	0	0	30	0	578
HG02180.mapped.ILLUMINA.bwa.CDX.exome.20130415	619	0	0	241	456	338	453	533	222	0	164	0	216	120	9	0	542
HG02181.mapped.ILLUMINA.bwa.CDX.exome.20130415	614	0	0	238	403	411	477	535	326	0	0	0	0	0	17	1	545
HG02182.mapped.ILLUMINA.bwa.CDX.exome.20130415	664	0	0	260	583	422	512	532	335	0	0	0	0	0	18	0	561
HG02184.mapped.ILLUMINA.bwa.CDX.exome.20130415	626	0	0	324	449	320	492	434	138	0	59	0	107	134	9	1	531
HG02185.mapped.ILLUMINA.bwa.CDX.exome.20130415	569	0	0	237	355	327	461	445	304	0	0	0	0	0	0	28	531
HG02186.mapped.ILLUMINA.bwa.CDX.exome.20130415	619	0	0	330	540	358	470	561	261	0	212	0	214	137	0	34	547
HG02187.mapped.ILLUMINA.bwa.CDX.exome.20130415	476	82	103	153	284	270	438	535	292	0	0	0	0	0	4	20	495
HG02188.mapped.ILLUMINA.bwa.CDX.exome.20130415	659	0	0	250	484	361	481	545	303	0	349	0	262	161	0	17	546
HG02190.mapped.ILLUMINA.bwa.CDX.exome.20130415	657	127	216	224	269	294	506	565	0	97	393	0	338	176	0	0	565
HG02215.mapped.ILLUMINA.bwa.GBR.exome.20120522	700	295	317	343	655	334	546	631	540	0	0	0	0	0	0	151	589
HG02219.mapped.ILLUMINA.bwa.IBS.exome.20130415	684	0	0	365	679	463	556	523	446	0	0	0	0	0	0	65	579
HG02220.mapped.ILLUMINA.bwa.IBS.exome.20130415	604	123	219	188	351	290	492	530	308	0	0	0	0	0	9	24	548
HG02221.mapped.ILLUMINA.bwa.IBS.exome.20130415	636	160	163	205	381	330	509	552	329	0	0	0	0	0	17	40	545
HG02223.mapped.ILLUMINA.bwa.IBS.exome.20120522	664	247	264	283	514	285	529	644	382	73	538	0	369	137	0	71	579
HG02224.mapped.ILLUMINA.bwa.IBS.exome.20120522	754	249	272	288	590	373	535	655	0	81	637	566	368	141	0	0	574
HG02230.mapped.ILLUMINA.bwa.IBS.exome.20120522	685	0	0	301	607	293	531	651	481	0	0	0	0	0	0	88	576
HG02231.mapped.ILLUMINA.bwa.IBS.exome.20120522	668	254	268	291	568	376	532	649	487	0	0	0	0	0	32	71	579
HG02232.mapped.ILLUMINA.bwa.IBS.exome.20120522	699	296	305	347	670	325	543	638	522	103	643	519	423	161	0	73	587
HG02233.mapped.ILLUMINA.bwa.IBS.exome.20120522	698	0	0	355	676	441	547	644	540	0	0	0	0	0	41	72	588
HG02235.mapped.ILLUMINA.bwa.IBS.exome.20130415	649	0	0	234	545	356	503	530	278	82	239	0	269	133	0	20	558
HG02236.mapped.ILLUMINA.bwa.IBS.exome.20130415	633	0	0	251	455	357	476	576	315	0	0	0	0	0	9	27	550
HG02238.mapped.ILLUMINA.bwa.IBS.exome.20120522	700	0	0	350	663	345	544	643	411	100	619	0	330	165	0	85	585
HG02239.mapped.ILLUMINA.bwa.IBS.exome.20120522	782	0	0	357	677	438	544	632	533	0	0	0	0	0	0	124	589
HG02250.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	283	319	346	647	420	546	643	0	105	638	542	330	165	0	0	588
HG02252.mapped.ILLUMINA.bwa.PEL.exome.20130415	797	0	0	397	721	473	559	673	585	0	0	0	0	0	71	120	596
HG02253.mapped.ILLUMINA.bwa.PEL.exome.20130415	701	0	0	393	713	471	561	667	566	106	657	0	463	189	0	107	594

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02255.mapped.ILLUMINA.bwa.ACB.exome.20130415	658	0	183	179	528	305	488	546	306	0	298	338	0	0	0	46	563
HG02256.mapped.ILLUMINA.bwa.ACB.exome.20130415	593	105	127	189	567	331	471	536	331	0	82	307	0	0	13	28	540
HG02259.mapped.ILLUMINA.bwa.PEL.exome.20121211	702	282	304	340	652	429	544	634	438	103	616	0	413	163	41	1	586
HG02260.mapped.ILLUMINA.bwa.PEL.exome.20121211	695	0	0	361	676	440	544	640	534	0	0	0	0	0	39	78	588
HG02262.mapped.ILLUMINA.bwa.PEL.exome.20130415	699	325	369	375	699	458	560	661	571	0	0	0	0	0	75	1	591
HG02265.mapped.ILLUMINA.bwa.PEL.exome.20130422	746	256	258	299	619	400	538	656	482	0	587	571	0	0	36	75	580
HG02266.mapped.ILLUMINA.bwa.PEL.exome.20130422	755	0	0	323	591	393	532	659	493	0	0	0	0	0	32	72	582
HG02271.mapped.ILLUMINA.bwa.PEL.exome.20121211	701	0	0	359	672	442	549	644	538	0	0	0	0	0	55	78	589
HG02272.mapped.ILLUMINA.bwa.PEL.exome.20130415	620	0	0	222	446	355	481	525	325	0	0	0	0	0	18	1	543
HG02274.mapped.ILLUMINA.bwa.PEL.exome.20130422	687	0	0	316	619	409	540	656	487	0	0	0	0	0	44	3	581
HG02275.mapped.ILLUMINA.bwa.PEL.exome.20130422	680	253	0	288	621	394	537	651	470	79	600	7	366	138	30	3	579
HG02277.mapped.ILLUMINA.bwa.PEL.exome.20130415	646	0	0	239	598	369	514	609	270	0	237	0	179	143	15	0	563
HG02278.mapped.ILLUMINA.bwa.PEL.exome.20130415	613	0	0	235	557	412	496	440	308	0	0	0	0	0	11	0	519
HG02281.mapped.ILLUMINA.bwa.ACB.exome.20130415	646	149	198	173	308	304	502	548	352	0	0	0	0	0	10	24	563
HG02282.mapped.ILLUMINA.bwa.ACB.exome.20130415	589	0	0	212	400	336	449	491	303	0	0	0	0	0	8	17	537
HG02283.mapped.ILLUMINA.bwa.ACB.exome.20120522	673	248	133	283	589	382	530	589	459	0	605	0	358	138	34	2	575
HG02284.mapped.ILLUMINA.bwa.ACB.exome.20121211	676	255	273	191	619	291	531	654	480	0	605	0	384	0	0	104	579
HG02285.mapped.ILLUMINA.bwa.PEL.exome.20130415	614	140	170	157	392	332	511	561	328	0	0	0	0	0	9	33	541
HG02286.mapped.ILLUMINA.bwa.PEL.exome.20130415	603	0	0	329	567	431	499	570	329	0	0	0	0	0	26	0	550
HG02291.mapped.ILLUMINA.bwa.PEL.exome.20120522	799	0	0	387	708	468	557	563	571	0	0	0	0	0	45	93	596
HG02292.mapped.ILLUMINA.bwa.PEL.exome.20120522	796	0	0	410	719	480	564	672	482	81	655	594	0	191	53	0	599
HG02298.mapped.ILLUMINA.bwa.PEL.exome.20120522	702	0	0	385	687	475	558	645	565	0	0	0	0	0	86	2	593
HG02299.mapped.ILLUMINA.bwa.PEL.exome.20120522	700	332	378	388	704	477	559	671	563	95	559	0	468	188	49	0	600
HG02301.mapped.ILLUMINA.bwa.PEL.exome.20130415	618	0	0	244	464	417	433	518	314	0	0	0	0	0	15	0	545
HG02304.mapped.ILLUMINA.bwa.PEL.exome.20130415	799	331	379	390	712	466	562	676	462	108	663	0	462	188	0	115	597
HG02307.mapped.ILLUMINA.bwa.ACB.exome.20120522	672	0	265	191	603	382	533	649	479	0	612	0	390	0	33	83	573
HG02308.mapped.ILLUMINA.bwa.ACB.exome.20120522	687	0	0	309	607	389	532	653	488	0	0	0	0	0	38	69	577
HG02309.mapped.ILLUMINA.bwa.ACB.exome.20120522	659	244	127	188	564	319	529	621	382	0	613	0	360	135	0	77	578
HG02312.mapped.ILLUMINA.bwa.PEL.exome.20130415	693	0	0	359	700	451	555	641	436	100	612	0	368	175	31	0	589
HG02314.mapped.ILLUMINA.bwa.ACB.exome.20120522	686	251	270	292	557	384	536	649	484	0	0	0	0	0	35	81	582
HG02315.mapped.ILLUMINA.bwa.ACB.exome.20120522	754	0	0	301	601	329	533	648	478	0	0	0	0	0	31	63	574
HG02317.mapped.ILLUMINA.bwa.ACB.exome.20130415	614	129	145	79	220	238	478	539	313	0	0	0	0	0	12	24	551
HG02318.mapped.ILLUMINA.bwa.ACB.exome.20130415	492	161	151	0	0	0	392	300	229	0	99	0	161	113	0	12	532
HG02322.mapped.ILLUMINA.bwa.ACB.exome.20120522	689	0	0	306	610	390	533	645	480	0	0	0	0	0	42	0	570
HG02323.mapped.ILLUMINA.bwa.ACB.exome.20120522	757	0	0	307	584	389	535	657	471	0	0	0	0	0	30	1	573
HG02325.mapped.ILLUMINA.bwa.ACB.exome.20120522	677	255	263	293	566	144	533	649	492	0	0	0	0	0	29	72	576
HG02330.mapped.ILLUMINA.bwa.ACB.exome.20120522	687	0	0	345	610	393	530	650	485	0	0	0	0	0	0	137	579
HG02332.mapped.ILLUMINA.bwa.ACB.exome.20120522	687	0	0	308	614	388	536	659	485	78	0	0	0	0	0	116	575
HG02334.mapped.ILLUMINA.bwa.ACB.exome.20120522	746	251	271	287	607	380	536	640	479	0	0	0	0	0	0	148	580
HG02337.mapped.ILLUMINA.bwa.ACB.exome.20120522	690	0	0	306	606	394	539	649	398	0	0	0	0	0	0	69	576
HG02339.mapped.ILLUMINA.bwa.ACB.exome.20120522	661	0	0	303	613	390	535	657	487	0	0	0	0	0	29	87	574
HG02343.mapped.ILLUMINA.bwa.ACB.exome.20120522	679	257	270	185	608	382	536	649	483	0	534	513	0	0	43	1	576
HG02345.mapped.ILLUMINA.bwa.PEL.exome.20130415	685	0	0	349	664	457	550	622	545	0	0	0	0	0	43	2	585
HG02348.mapped.ILLUMINA.bwa.PEL.exome.20130415	696	316	356	369	690	457	556	660	557	104	643	0	377	178	44	0	593
HG02351.mapped.ILLUMINA.bwa.CDX.exome.20120522	699	0	0	370	691	447	543	642	440	101	625	573	0	165	0	84	591
HG02353.mapped.ILLUMINA.bwa.CDX.exome.20120522	788	0	0	365	678	439	545	650	540	0	0	0	0	0	72	0	588
HG02355.mapped.ILLUMINA.bwa.CDX.exome.20120522	702	289	322	354	661	425	543	656	546	0	0	0	0	0	45	88	589
HG02356.mapped.ILLUMINA.bwa.CDX.exome.20120522	699	0	0	360	664	434	544	634	532	0	0	0	0	0	0	119	589
HG02360.mapped.ILLUMINA.bwa.CDX.exome.20120522	698	0	0	361	674	437	542	638	507	100	604	0	335	157	39	0	589
HG02363.mapped.ILLUMINA.bwa.CDX.exome.20120522	786	295	315	348	665	430	545	652	0	106	655	0	437	168	0	0	587
HG02364.mapped.ILLUMINA.bwa.CDX.exome.20120522	702	0	0	358	678	440	546	638	539	0	0	0	0	0	69	0	590
HG02367.mapped.ILLUMINA.bwa.CDX.exome.20120522	694	279	301	342	641	410	546	640	542	0	0	0	0	0	0	124	591
HG02371.mapped.ILLUMINA.bwa.CDX.exome.20120522	681	308	335	0	0	0	547	645	0	103	648	580	423	169	0	0	588
HG02372.mapped.ILLUMINA.bwa.CDX.exome.20120522	676	301	330	0	0	0	542	655	509	101	585	524	0	158	0	88	589
HG02373.mapped.ILLUMINA.bwa.CDX.exome.20120522	789	0	0	363	683	442	547	648	539	0	0	0	0	0	75	2	589
HG02374.mapped.ILLUMINA.bwa.CDX.exome.20120522	701	0	0	357	672	439	550	658	525	108	636	0	429	164	53	0	587
HG02375.mapped.ILLUMINA.bwa.CDX.exome.20120522	699	297	317	348	648	430	545	657	440	103	626	0	335	162	41	0	590
HG02377.mapped.ILLUMINA.bwa.CDX.exome.20120522	699	0	0	355	666	443	546	642	536	0	0	0	0	0	53	74	593
HG02379.mapped.ILLUMINA.bwa.CDX.exome.20120522	699	0	0	356	676	439	550	644	537	0	0	0	0	0	58	73	588
HG02380.mapped.ILLUMINA.bwa.CDX.exome.20120522	698	0	0	353	670	434	545	619	522	0	0	0	0	0	69	0	590
HG02381.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	289	313	339	655	326	546	646	435	101	626	528	0	163	0	83	586
HG02382.mapped.ILLUMINA.bwa.CDX.exome.20120522	699	0	0	357	671	423	545	644	434	101	620	0	333	164	44	0	587
HG02383.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	287	312	351	658	423	520	603	431	0	616	575	0	165	51	0	587
HG02384.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	0	0	359	671	445	545	643	531	0	0	0	0	0	72	0	587
HG02385.mapped.ILLUMINA.bwa.CDX.exome.20120522	693	0	0	357	671	440	540	632	537	0	0	0	0	0	69	0	587
HG02386.mapped.ILLUMINA.bwa.CDX.exome.20120522	702	289	315	339	681	434	543	635	536	0	618	559	0	0	0	132	589
HG02387.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	0	0	360	681	439	544	640	521	103	618	571	0	158	0	91	592
HG02388.mapped.ILLUMINA.bwa.CDX.exome.20120522	695	0	0	355	671	439	546	638	434	101	596	0	334	157	37	0	588
HG02389.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	281	300	346	682	426	546	631	427	100	640	504	322	161	41	0	586
HG02390.mapped.ILLUMINA.bwa.CDX.exome.20120522	702	0	0	360	676	420	542	650	0	103	637	0	439	169	0	1	585
HG02391.mapped.ILLUMINA.bwa.CDX.exome.20120522	677	303	333	0	0	0	547	636	544	0	0	0	0	0	0	123	587
HG02392.mapped.ILLUMINA.bwa.CDX.exome.20120522	703	0	0	358	673	437	548	641	429	101	603	524	0	158	43	1	587
HG02394.mapped.ILLUMINA.bwa.CDX.exome.20120522	698	0	0	358	677	441	545	637	532	0	0	0	0	0	32	72	586
HG02395.mapped.ILLUMINA.bwa.CDX.exome.20120522	784	0	0	359	681	441	544	644	541	0	0	0	0	0	39	58	592
HG02396.mapped.ILLUMINA.bwa.CDX.exome.20120522	700	0	0	363	678	444	544	642	536	0	0	0	0	0	63	0	586
HG02397.mapped.ILLUMINA.bwa.CDX.exome.20120522	701	290	322	338	656	407	540	633	429	101	595	0	418	165	0	79	590
HG02398.mapped.ILLUMINA.bwa.CDX.exome.20120522	788	0	0	358	668	437	547	627	448	0	0	0	0	0	54	1	591
HG02399.mapped.ILLUMINA.bwa.CDX.exome.20120522	701	294	314	346	648	425	547	644	541	0	0	0	0	0	0	160	593
HG02401.mapped.ILLUMINA.bwa.CDX.exome.20120522	698	0	0	358	674	434	539	642	436	102	624	0	332	165	0	72	588
HG02402.mapped.ILLUMINA.bwa.CDX.exome.20120522	784	0	0	363	677	436	544	644	442	102	623	0	349	167	0	75	591
HG02406.mapped.ILLUMINA.bwa.CDX.exome.20120522	703	0	0	361	688	439	548	648	0	106	653	0	440	169	0	0	590
HG02407.mapped.ILLUMINA.bwa.CDX.exome.20120522	785	289	310	348	654	425	543	656	518	102	621	0	337	161	57	0	586
HG02408.mapped.ILLUMINA.bwa.CDX.exome.20130422	681	0	0	295	594	379	529	629	463	0	0	0	0	0	26	53	571
HG02409.mapped.ILLUMINA.bwa.CDX.exome.20120522	698	0	0	360	677	432	542	642	0	103	643	538	426	166	0	0	585
HG02410.mapped.ILLUMINA.bwa.CDX.exome.20130422	684	0	0	295	589	376	529	644	461	0	0	0	0	0	22	49	574
HG02419.mapped.ILLUMINA.bwa.ACB.exome.20120522	599	250	278	0	610	141	533	636	490	0	626	515	383	0	35	0	580
HG02420.mapped.ILLUMINA.bwa.ACB.exome.20120522	683	0	265	190	615	285	535	643	396	66	633	0	400	140	36	2	575
HG02425.mapped.ILLUMINA.bwa.PEL.exome.20130422	747	248	240	281	551	371	538	644	468	75	585	0	367	140	0	79	582
HG02427.mapped.ILLUMINA.bwa.ACB.exome.20121211	686	0	0	301	605	387	532	639	475	0	0	0	0	0	26	58	574
HG02429.mapped.ILLUMINA.bwa.ACB.exome.20121211	681	0	0	307	600	379	532	638	469	0	0	0	0	0	27	61	574
HG02433.mapped.ILLUMINA.bwa.ACB.exome.20121211	689	0	0	299	607	383	532	637	459	70	612	0	364	138	0	75	579
HG02439.mapped.ILLUMINA.bwa.ACB.exome.20130415	793	0	371	234	722	469	560	670	567	0	648	0	472	0	48	2	586
HG02442.mapped.ILLUMINA.bwa.ACB.exome.20121211	689	0	0	313	610	389	533	639	472	0	0	0	0	0	43	0	577
HG02445.mapped.ILLUMINA.bwa.ACB.exome.20121211	688	0	0	298	610	401	533	640	483	0	0	0	0	0	32	70	576
HG02449.mapped.ILLUMINA.bwa.ACB.exome.20120522	703	0	0	393	711	479	559	660	576	0	0	0	0	0	150	0	600
HG02450.mapped.ILLUMINA.bwa.ACB.exome.20120522	798	333	374	226	715	477	562	657	568	0	651	0	482	0	0	134	597

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02455.mapped.ILLUMINA.bwa.ACB.exome.20130415	700	0	0	395	714	476	561	672	577	0	4	0	12	0	0	158	593
HG02461.mapped.ILLUMINA.bwa.GWD.exome.20130415	665	0	251	101	608	283	531	648	480	0	614	568	358	0	27	66	575
HG02462.mapped.ILLUMINA.bwa.GWD.exome.20130415	760	0	0	302	611	386	536	653	483	0	0	0	0	0	43	2	576
HG02464.mapped.ILLUMINA.bwa.GWD.exome.20130415	757	0	0	289	614	384	531	655	481	0	0	0	0	0	0	79	574
HG02465.mapped.ILLUMINA.bwa.GWD.exome.20130415	686	0	0	292	587	381	530	639	470	0	0	0	0	0	30	56	576
HG02470.mapped.ILLUMINA.bwa.ACB.exome.20120522	796	329	186	380	701	473	561	656	567	0	647	0	477	188	85	0	599
HG02471.mapped.ILLUMINA.bwa.ACB.exome.20120522	702	329	366	369	718	480	562	658	581	0	644	589	0	0	79	123	600
HG02476.mapped.ILLUMINA.bwa.ACB.exome.20130415	679	304	334	239	676	368	550	650	463	0	592	0	376	0	40	63	591
HG02477.mapped.ILLUMINA.bwa.ACB.exome.20130415	560	309	349	0	603	158	553	612	387	0	588	544	0	158	28	0	586
HG02479.mapped.ILLUMINA.bwa.ACB.exome.20130415	614	0	0	240	443	320	447	522	309	0	0	0	0	0	11	19	505
HG02481.mapped.ILLUMINA.bwa.ACB.exome.20130415	690	289	327	237	678	439	552	638	320	0	600	520	357	172	30	3	588
HG02484.mapped.ILLUMINA.bwa.ACB.exome.20130415	623	168	117	185	334	343	499	587	333	0	43	0	207	0	9	20	541
HG02485.mapped.ILLUMINA.bwa.ACB.exome.20130415	614	124	139	0	591	333	505	583	217	0	414	486	195	140	0	19	530
HG02489.mapped.ILLUMINA.bwa.ACB.exome.20120522	703	333	376	380	717	475	561	661	577	0	653	593	0	0	0	249	601
HG02490.mapped.ILLUMINA.bwa.PJL.exome.20121211	667	235	233	265	569	359	521	622	378	0	581	0	287	133	0	43	574
HG02491.mapped.ILLUMINA.bwa.PJL.exome.20130415	683	251	253	284	600	279	526	644	0	82	646	564	376	137	0	1	575
HG02493.mapped.ILLUMINA.bwa.PJL.exome.20130415	701	325	372	374	717	469	560	667	0	106	668	550	465	190	0	0	591
HG02494.mapped.ILLUMINA.bwa.PJL.exome.20130415	702	0	0	410	720	471	559	666	466	105	658	0	460	185	0	112	590
HG02496.mapped.ILLUMINA.bwa.ACB.exome.20130415	656	0	0	342	614	438	513	582	445	0	0	0	0	0	13	41	571
HG02497.mapped.ILLUMINA.bwa.ACB.exome.20130415	639	0	0	262	561	275	497	564	345	0	0	0	0	0	7	30	571
HG02501.mapped.ILLUMINA.bwa.ACB.exome.20130415	684	0	345	342	682	457	546	630	532	0	552	0	382	0	34	49	578
HG02502.mapped.ILLUMINA.bwa.ACB.exome.20130415	680	0	0	364	655	452	553	623	548	0	0	0	0	0	31	47	585
HG02505.mapped.ILLUMINA.bwa.ACB.exome.20130415	641	265	298	189	637	417	543	594	333	0	420	510	0	0	0	76	580
HG02508.mapped.ILLUMINA.bwa.ACB.exome.20130415	635	150	224	148	380	304	487	513	283	0	0	0	0	0	11	0	516
HG02511.mapped.ILLUMINA.bwa.ACB.exome.20130415	609	126	0	156	287	173	398	400	216	0	200	0	270	154	14	0	551
HG02512.mapped.ILLUMINA.bwa.KHV.exome.20120522	681	0	0	304	601	388	532	656	487	0	0	0	0	0	29	83	575
HG02513.mapped.ILLUMINA.bwa.KHV.exome.20120522	759	0	0	309	610	389	529	653	397	85	587	560	0	138	0	76	578
HG02521.mapped.ILLUMINA.bwa.KHV.exome.20120522	688	0	0	303	606	389	534	659	486	0	0	0	0	0	33	78	575
HG02522.mapped.ILLUMINA.bwa.KHV.exome.20120522	681	249	276	282	615	381	533	641	471	81	636	568	301	139	0	67	576
HG02536.mapped.ILLUMINA.bwa.ACB.exome.20130415	654	0	0	327	612	430	526	512	329	0	0	0	0	0	0	62	572
HG02537.mapped.ILLUMINA.bwa.ACB.exome.20130415	796	0	0	398	723	479	562	673	579	0	0	0	0	0	87	5	599
HG02541.mapped.ILLUMINA.bwa.ACB.exome.20130415	794	339	375	0	0	0	560	673	586	0	0	0	0	0	64	98	596
HG02545.mapped.ILLUMINA.bwa.ACB.exome.20130415	567	0	293	194	627	335	523	605	422	0	392	0	319	0	32	1	572
HG02546.mapped.ILLUMINA.bwa.ACB.exome.20130415	663	0	0	307	606	415	553	629	404	0	0	0	0	0	20	27	578
HG02549.mapped.ILLUMINA.bwa.ACB.exome.20130415	797	327	371	379	717	471	559	662	581	0	655	587	0	0	88	1	593
HG02554.mapped.ILLUMINA.bwa.ACB.exome.20130415	694	0	0	388	716	473	560	672	471	110	659	0	454	189	0	95	595
HG02555.mapped.ILLUMINA.bwa.ACB.exome.20130415	696	328	369	283	721	466	559	666	473	102	666	587	463	185	0	106	597
HG02557.mapped.ILLUMINA.bwa.ACB.exome.20130415	682	0	0	347	633	451	551	597	439	0	0	0	0	0	44	1	582
HG02558.mapped.ILLUMINA.bwa.ACB.exome.20130415	684	0	0	351	665	439	544	605	458	0	0	0	0	0	44	1	586
HG02561.mapped.ILLUMINA.bwa.GWD.exome.20121211	755	0	257	105	571	136	535	646	475	0	597	575	0	0	35	68	578
HG02562.mapped.ILLUMINA.bwa.GWD.exome.20130415	684	0	0	298	605	312	532	637	479	0	0	0	0	0	34	6	572
HG02568.mapped.ILLUMINA.bwa.GWD.exome.20130415	794	0	0	391	723	473	560	667	585	0	0	0	0	0	78	1	597
HG02570.mapped.ILLUMINA.bwa.GWD.exome.20130415	692	0	0	297	604	285	534	654	480	0	604	566	0	0	27	82	574
HG02571.mapped.ILLUMINA.bwa.GWD.exome.20121211	686	0	251	289	614	277	532	643	475	0	594	0	373	0	41	0	578
HG02573.mapped.ILLUMINA.bwa.GWD.exome.20130415	671	236	239	286	541	346	533	633	477	0	0	0	0	0	31	0	575
HG02574.mapped.ILLUMINA.bwa.GWD.exome.20121211	681	0	0	299	596	382	534	644	471	0	0	0	0	0	21	56	572
HG02577.mapped.ILLUMINA.bwa.ACB.exome.20130415	683	0	288	317	651	443	548	594	432	0	525	0	353	0	45	0	577
HG02580.mapped.ILLUMINA.bwa.ACB.exome.20130415	797	0	0	397	715	476	560	668	578	0	0	0	0	0	80	1	594
HG02582.mapped.ILLUMINA.bwa.GWD.exome.20130415	679	0	0	305	601	379	530	645	478	0	0	0	0	0	0	83	578
HG02583.mapped.ILLUMINA.bwa.GWD.exome.20130415	594	255	268	0	590	138	534	641	472	0	628	510	0	0	38	0	573
HG02585.mapped.ILLUMINA.bwa.GWD.exome.20121211	681	246	256	270	612	366	537	647	478	0	607	564	0	0	34	1	578
HG02586.mapped.ILLUMINA.bwa.GWD.exome.20121211	668	0	0	350	612	394	532	657	477	0	0	0	0	0	0	124	578
HG02588.mapped.ILLUMINA.bwa.GWD.exome.20130415	761	0	0	301	610	383	535	651	477	0	0	0	0	0	30	72	574
HG02589.mapped.ILLUMINA.bwa.GWD.exome.20130415	769	0	0	361	630	408	540	671	504	0	0	0	76	0	74	2	585
HG02594.mapped.ILLUMINA.bwa.GWD.exome.20121211	673	235	274	200	610	379	534	655	480	0	587	562	0	0	0	139	579
HG02595.mapped.ILLUMINA.bwa.GWD.exome.20130415	669	0	252	282	607	377	530	649	487	0	620	0	383	0	35	68	576
HG02597.mapped.ILLUMINA.bwa.PJL.exome.20130415	557	272	262	273	637	436	541	609	432	0	489	490	0	0	0	57	582
HG02600.mapped.ILLUMINA.bwa.PJL.exome.20130415	684	0	0	303	600	287	521	644	0	78	629	0	368	138	0	0	577
HG02601.mapped.ILLUMINA.bwa.PJL.exome.20121211	591	249	258	0	496	129	529	642	467	0	564	566	0	0	0	70	572
HG02603.mapped.ILLUMINA.bwa.PJL.exome.20130415	757	0	0	299	596	377	531	637	476	0	0	0	0	0	0	73	573
HG02604.mapped.ILLUMINA.bwa.PJL.exome.20121211	684	0	0	295	605	373	532	646	383	78	585	0	364	134	27	0	577
HG02610.mapped.ILLUMINA.bwa.GWD.exome.20121211	600	241	267	293	606	375	535	650	485	0	613	0	382	0	35	73	575
HG02611.mapped.ILLUMINA.bwa.GWD.exome.20130415	595	255	270	0	592	139	528	642	466	0	632	572	0	0	32	52	574
HG02613.mapped.ILLUMINA.bwa.GWD.exome.20130415	690	0	257	283	578	375	535	645	388	77	607	0	292	137	33	0	573
HG02614.mapped.ILLUMINA.bwa.GWD.exome.20121211	660	0	0	295	595	387	531	635	468	0	0	0	0	0	32	0	577
HG02620.mapped.ILLUMINA.bwa.GWD.exome.20130415	688	0	0	299	613	383	532	657	473	72	0	0	0	0	30	58	573
HG02621.mapped.ILLUMINA.bwa.GWD.exome.20130415	681	250	128	275	583	369	525	627	392	0	581	0	278	137	23	2	573
HG02623.mapped.ILLUMINA.bwa.GWD.exome.20121211	758	0	0	303	613	392	535	641	487	0	0	0	0	0	28	67	575
HG02624.mapped.ILLUMINA.bwa.GWD.exome.20130415	685	0	263	292	631	383	536	654	482	0	606	0	385	0	32	79	577
HG02628.mapped.ILLUMINA.bwa.GWD.exome.20121211	684	0	0	274	613	373	531	656	387	80	594	0	282	131	32	1	574
HG02629.mapped.ILLUMINA.bwa.GWD.exome.20130415	671	241	259	183	600	381	533	642	470	0	588	516	0	0	48	1	575
HG02634.mapped.ILLUMINA.bwa.GWD.exome.20121211	757	0	0	306	608	378	534	639	482	0	0	0	0	0	0	122	577
HG02635.mapped.ILLUMINA.bwa.GWD.exome.20121211	683	0	0	295	605	377	532	653	472	0	0	0	0	0	29	68	576
HG02642.mapped.ILLUMINA.bwa.GWD.exome.20130415	755	252	256	277	590	370	533	655	490	0	0	0	0	0	34	63	570
HG02643.mapped.ILLUMINA.bwa.GWD.exome.20130415	673	0	0	244	555	317	526	609	452	0	500	488	0	0	29	0	575
HG02645.mapped.ILLUMINA.bwa.GWD.exome.20121211	685	0	0	275	609	379	537	641	474	0	598	515	0	0	41	0	575
HG02646.mapped.ILLUMINA.bwa.GWD.exome.20130415	675	244	236	279	595	368	533	649	471	0	530	505	0	0	20	50	574
HG02648.mapped.ILLUMINA.bwa.PJL.exome.20130415	797	0	0	397	721	467	561	672	579	0	0	0	0	0	0	209	596
HG02649.mapped.ILLUMINA.bwa.PJL.exome.20130415	702	0	0	390	713	478	558	669	563	104	656	0	461	185	0	109	595
HG02651.mapped.ILLUMINA.bwa.PJL.exome.20130415	703	333	372	387	711	475	553	658	571	0	654	0	460	188	58	2	593
HG02652.mapped.ILLUMINA.bwa.PJL.exome.20130415	693	339	374	0	708	186	559	653	571	0	677	592	459	187	0	119	595
HG02654.mapped.ILLUMINA.bwa.PJL.exome.20121211	689	0	0	297	608	382	530	651	0	79	624	0	378	139	0	1	571
HG02655.mapped.ILLUMINA.bwa.PJL.exome.20121211	681	238	0	285	582	359	520	614	0	72	622	0	370	140	0	1	576
HG02657.mapped.ILLUMINA.bwa.PJL.exome.20121211	669	231	243	276	602	366	528	642	472	0	568	555	0	0	21	55	575
HG02658.mapped.ILLUMINA.bwa.PJL.exome.20130415	668	230	246	269	509	368	531	650	309	67	520	0	359	131	0	52	575
HG02660.mapped.ILLUMINA.bwa.PJL.exome.20121211	594	253	253	0	589	136	531	626	385	75	640	572	354	132	20	0	577
HG02661.mapped.ILLUMINA.bwa.PJL.exome.20130415	684	0	0	299	610	381	529	646	473	0	0	0	0	0	0	86	575
HG02666.mapped.ILLUMINA.bwa.PJL.exome.20130415	745	0	252	273	599	142	532	649	469	0	530	0	304	0	34	1	574
HG02667.mapped.ILLUMINA.bwa.GWD.exome.20121211	681	0	0	304	596	387	532	645	474	0	0	0	0	0	38	0	572
HG02675.mapped.ILLUMINA.bwa.GWD.exome.20130415	689	247	248	281	601	369	529	656	474	0	599	564	0	0	31	62	575
HG02676.mapped.ILLUMINA.bwa.GWD.exome.20130415	685	0	0	298	599	381	534	642	470	0	0	0	0	0	37	1	576
HG02678.mapped.ILLUMINA.bwa.GWD.exome.20130415	679	0	0	303	602	381	530	641	477	0	0	0	0	0	37	0	574
HG02679.mapped.ILLUMINA.bwa.GWD.exome.20130415	673	241	252	280	582	280	532	653	474	0	0	0	0	0	31	55	576
HG02681.mapped.ILLUMINA.bwa.PJL.exome.20130415	691	0	0	391	712	468	560	670	465	106	651	0	388	181	0	92	595
HG02682.mapped.ILLUMINA.bwa.PJL.exome.20130415	699	321	365	381	695	469	552	638	563	0	651	0	385	185	54	3	596
HG02684.mapped.ILLUMINA.bwa.PJL.exome.20121211	596	256	266	0	575	138	526	619	386	0	632	567	357	135	0	62	575

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02685.mapped.ILLUMINA.bwa.PJL.exome.20121211	684	0	0	300	600	388	529	647	0	81	624	0	370	139	0	0	575
HG02687.mapped.ILLUMINA.bwa.PJL.exome.20121211	594	257	264	0	564	133	518	613	0	69	641	568	370	141	0	2	575
HG02688.mapped.ILLUMINA.bwa.PJL.exome.20130415	680	227	249	189	514	278	528	640	469	0	0	0	0	0	0	127	573
HG02690.mapped.ILLUMINA.bwa.PJL.exome.20130415	702	0	0	385	714	477	558	663	575	0	0	0	0	0	72	0	594
HG02691.mapped.ILLUMINA.bwa.PJL.exome.20130415	700	322	365	378	717	467	559	675	469	109	659	546	456	183	52	0	592
HG02694.mapped.ILLUMINA.bwa.PJL.exome.20130415	648	277	299	179	545	414	543	620	425	0	420	511	0	0	0	58	575
HG02696.mapped.ILLUMINA.bwa.PJL.exome.20121211	743	237	250	280	574	318	531	641	448	75	626	558	346	136	0	62	575
HG02697.mapped.ILLUMINA.bwa.PJL.exome.20121211	595	253	262	0	496	133	530	638	466	0	534	566	0	0	0	74	575
HG02699.mapped.ILLUMINA.bwa.PJL.exome.20130415	798	0	0	387	714	466	558	671	584	0	0	0	0	0	0	201	594
HG02700.mapped.ILLUMINA.bwa.PJL.exome.20130415	691	337	371	0	0	0	560	675	578	0	0	0	0	0	0	137	592
HG02702.mapped.ILLUMINA.bwa.GWD.exome.20130415	675	0	0	286	555	383	529	621	392	0	0	0	0	0	35	1	573
HG02703.mapped.ILLUMINA.bwa.GWD.exome.20130415	677	0	0	282	582	381	534	632	474	0	0	0	0	0	39	0	577
HG02715.mapped.ILLUMINA.bwa.GWD.exome.20121211	763	252	258	290	616	382	538	647	487	0	619	563	0	0	43	0	574
HG02716.mapped.ILLUMINA.bwa.GWD.exome.20130415	751	0	247	185	569	278	537	659	473	71	0	0	0	0	24	71	577
HG02721.mapped.ILLUMINA.bwa.GWD.exome.20121211	675	245	253	87	590	375	540	636	435	77	634	567	288	138	28	0	580
HG02722.mapped.ILLUMINA.bwa.GWD.exome.20121211	673	231	220	249	488	327	527	637	464	0	0	0	0	0	17	49	574
HG02724.mapped.ILLUMINA.bwa.PJL.exome.20121211	596	257	272	0	601	136	533	656	0	79	653	568	379	143	0	3	574
HG02725.mapped.ILLUMINA.bwa.PJL.exome.20121211	684	0	0	301	598	381	531	642	466	0	0	0	0	0	37	0	573
HG02727.mapped.ILLUMINA.bwa.PJL.exome.20130415	669	257	263	0	553	131	533	649	455	72	610	528	294	134	0	60	574
HG02728.mapped.ILLUMINA.bwa.PJL.exome.20121211	597	254	268	0	587	141	533	647	461	71	644	572	360	135	28	0	573
HG02731.mapped.ILLUMINA.bwa.PJL.exome.20130415	570	314	332	0	665	181	544	629	411	94	603	522	341	168	0	48	567
HG02733.mapped.ILLUMINA.bwa.PJL.exome.20130415	593	254	267	0	600	140	531	649	371	68	644	574	360	136	0	69	576
HG02734.mapped.ILLUMINA.bwa.PJL.exome.20121211	686	249	268	289	578	371	529	628	0	72	634	0	376	137	0	0	577
HG02736.mapped.ILLUMINA.bwa.PJL.exome.20130415	798	322	370	384	702	460	560	667	580	0	0	0	0	0	55	111	594
HG02737.mapped.ILLUMINA.bwa.PJL.exome.20130415	797	328	377	386	715	473	561	677	568	106	675	588	465	186	0	122	598
HG02756.mapped.ILLUMINA.bwa.GWD.exome.20130415	684	0	0	311	610	384	531	636	473	0	0	0	0	0	40	0	578
HG02757.mapped.ILLUMINA.bwa.GWD.exome.20121211	690	0	0	309	605	395	532	652	487	0	0	0	0	0	0	126	576
HG02759.mapped.ILLUMINA.bwa.GWD.exome.20130415	598	332	378	0	715	190	561	671	579	0	672	589	481	0	61	102	594
HG02760.mapped.ILLUMINA.bwa.GWD.exome.20130415	681	0	373	0	689	185	556	649	473	0	662	0	485	186	50	0	596
HG02763.mapped.ILLUMINA.bwa.GWD.exome.20130415	694	313	331	203	689	450	554	641	539	0	592	533	0	0	39	1	573
HG02768.mapped.ILLUMINA.bwa.GWD.exome.20121211	683	0	0	305	615	389	536	659	390	79	639	0	395	138	38	4	577
HG02769.mapped.ILLUMINA.bwa.GWD.exome.20121211	684	251	265	284	584	136	533	656	480	0	0	0	0	0	32	71	573
HG02771.mapped.ILLUMINA.bwa.GWD.exome.20130415	681	0	0	303	618	381	534	652	473	0	0	0	0	0	41	0	575
HG02772.mapped.ILLUMINA.bwa.GWD.exome.20121211	682	245	252	275	572	135	534	636	478	0	0	0	0	0	43	1	574
HG02774.mapped.ILLUMINA.bwa.PJL.exome.20130415	794	324	365	384	697	460	557	675	558	104	650	0	383	183	50	0	594
HG02775.mapped.ILLUMINA.bwa.PJL.exome.20130415	695	335	376	0	714	189	561	673	0	109	676	595	462	189	0	0	593
HG02778.mapped.ILLUMINA.bwa.PJL.exome.20130415	669	0	0	352	643	438	546	623	529	0	0	0	0	0	24	42	582
HG02780.mapped.ILLUMINA.bwa.PJL.exome.20130415	546	270	0	207	623	415	539	578	286	0	338	0	329	163	0	36	567
HG02783.mapped.ILLUMINA.bwa.PJL.exome.20121211	686	250	251	293	609	373	532	658	458	77	634	565	359	136	0	72	577
HG02784.mapped.ILLUMINA.bwa.PJL.exome.20121211	595	245	262	0	499	129	527	635	456	0	517	545	0	0	0	72	570
HG02786.mapped.ILLUMINA.bwa.PJL.exome.20130415	673	250	259	284	591	369	533	659	483	0	591	569	0	0	30	74	575
HG02787.mapped.ILLUMINA.bwa.PJL.exome.20121211	670	243	258	278	620	377	530	663	458	85	650	579	358	136	27	1	576
HG02789.mapped.ILLUMINA.bwa.PJL.exome.20121211	676	239	248	264	589	136	531	647	395	0	598	563	0	0	39	0	575
HG02790.mapped.ILLUMINA.bwa.PJL.exome.20121211	597	256	274	0	600	132	534	651	0	81	652	522	378	142	0	0	572
HG02792.mapped.ILLUMINA.bwa.PJL.exome.20130415	702	329	374	382	705	473	561	671	470	107	652	8	384	183	0	118	597
HG02793.mapped.ILLUMINA.bwa.PJL.exome.20130415	703	326	370	232	723	382	562	674	585	0	646	588	0	0	55	116	594
HG02798.mapped.ILLUMINA.bwa.GWD.exome.20130415	691	0	0	299	614	282	531	650	483	0	611	573	0	0	45	0	577
HG02799.mapped.ILLUMINA.bwa.GWD.exome.20130415	656	0	0	286	586	381	532	647	470	0	0	0	0	0	26	61	574
HG02804.mapped.ILLUMINA.bwa.GWD.exome.20130415	686	251	262	295	618	387	534	650	480	0	605	0	366	0	0	150	575
HG02805.mapped.ILLUMINA.bwa.GWD.exome.20130415	659	0	235	247	531	262	531	625	465	0	0	0	0	0	27	0	576
HG02807.mapped.ILLUMINA.bwa.GWD.exome.20121211	683	0	0	303	609	381	532	651	475	0	0	0	0	0	25	69	578
HG02808.mapped.ILLUMINA.bwa.GWD.exome.20130415	598	257	275	0	612	281	534	640	481	0	639	570	391	0	45	0	577
HG02810.mapped.ILLUMINA.bwa.GWD.exome.20130415	685	0	0	304	610	388	532	659	485	0	0	0	0	0	34	82	578
HG02811.mapped.ILLUMINA.bwa.GWD.exome.20121211	683	236	256	283	604	380	537	656	469	0	604	0	287	0	28	1	569
HG02813.mapped.ILLUMINA.bwa.GWD.exome.20130415	799	337	370	395	719	475	561	674	586	0	0	0	0	0	93	0	594
HG02814.mapped.ILLUMINA.bwa.GWD.exome.20130415	793	0	375	382	727	465	559	665	584	0	649	0	472	0	51	130	595
HG02816.mapped.ILLUMINA.bwa.GWD.exome.20130415	794	0	0	394	707	469	560	659	571	0	0	0	0	0	69	0	595
HG02817.mapped.ILLUMINA.bwa.GWD.exome.20130415	796	0	0	397	722	479	561	664	581	0	0	0	0	0	0	232	595
HG02819.mapped.ILLUMINA.bwa.GWD.exome.20130415	672	0	251	278	572	367	527	626	462	0	0	0	3	0	34	0	571
HG02820.mapped.ILLUMINA.bwa.GWD.exome.20130415	678	0	0	274	590	372	528	617	396	0	0	0	0	0	0	83	570
HG02836.mapped.ILLUMINA.bwa.GWD.exome.20130415	794	0	0	394	719	470	560	670	576	0	0	0	0	0	0	163	597
HG02837.mapped.ILLUMINA.bwa.GWD.exome.20130415	696	0	359	141	695	472	562	657	573	0	647	0	397	0	61	0	587
HG02839.mapped.ILLUMINA.bwa.GWD.exome.20130415	696	333	371	382	660	459	561	656	0	105	650	0	459	187	0	0	585
HG02840.mapped.ILLUMINA.bwa.GWD.exome.20130415	702	334	372	390	716	466	564	672	588	0	0	0	0	0	0	261	594
HG02851.mapped.ILLUMINA.bwa.GWD.exome.20130415	704	0	374	387	672	477	562	680	585	0	0	0	0	0	60	148	595
HG02852.mapped.ILLUMINA.bwa.GWD.exome.20130415	704	336	374	392	728	480	562	677	584	0	660	589	0	0	0	249	597
HG02854.mapped.ILLUMINA.bwa.GWD.exome.20130415	594	248	268	0	497	131	530	629	462	0	568	504	0	0	26	51	568
HG02855.mapped.ILLUMINA.bwa.GWD.exome.20130415	678	228	258	288	587	364	529	629	476	0	564	492	0	0	0	102	575
HG02860.mapped.ILLUMINA.bwa.GWD.exome.20130415	703	0	0	396	719	476	560	674	573	0	0	0	0	0	52	102	595
HG02861.mapped.ILLUMINA.bwa.GWD.exome.20130415	797	0	0	394	724	394	564	671	581	0	0	0	0	0	73	0	594
HG02870.mapped.ILLUMINA.bwa.GWD.exome.20130415	696	0	331	108	634	166	549	642	551	0	561	530	0	0	61	4	589
HG02878.mapped.ILLUMINA.bwa.GWD.exome.20130415	699	0	0	393	717	479	559	670	576	0	0	0	0	0	78	0	591
HG02879.mapped.ILLUMINA.bwa.GWD.exome.20130415	799	0	0	397	719	470	559	671	582	0	0	0	0	0	76	0	597
HG02881.mapped.ILLUMINA.bwa.GWD.exome.20130415	701	333	370	387	726	476	560	670	582	0	658	587	0	0	75	0	594
HG02882.mapped.ILLUMINA.bwa.GWD.exome.20130415	702	185	377	385	700	460	563	666	561	0	0	0	0	0	0	113	589
HG02884.mapped.ILLUMINA.bwa.GWD.exome.20130415	673	0	0	171	580	302	530	625	371	56	585	497	282	134	21	0	574
HG02885.mapped.ILLUMINA.bwa.GWD.exome.20130415	685	0	0	288	594	277	528	641	459	66	0	0	0	0	33	1	568
HG02887.mapped.ILLUMINA.bwa.GWD.exome.20130415	801	0	0	401	716	481	560	672	589	0	0	0	0	0	71	0	595
HG02888.mapped.ILLUMINA.bwa.GWD.exome.20130415	799	0	0	400	724	474	562	675	582	0	0	0	0	0	86	0	600
HG02890.mapped.ILLUMINA.bwa.GWD.exome.20130415	677	224	241	279	494	359	530	629	376	63	493	0	290	130	24	0	573
HG02891.mapped.ILLUMINA.bwa.GWD.exome.20130415	652	0	247	183	587	296	525	626	468	0	514	0	300	0	31	43	571
HG02895.mapped.ILLUMINA.bwa.GWD.exome.20130415	801	335	377	388	725	472	562	672	578	0	656	590	0	0	57	131	593
HG02896.mapped.ILLUMINA.bwa.GWD.exome.20130415	801	0	0	412	726	480	562	670	587	0	0	0	0	0	86	3	594
HG02922.mapped.ILLUMINA.bwa.ESN.exome.20121211	681	0	0	293	605	378	532	643	477	0	0	0	0	0	36	62	578
HG02923.mapped.ILLUMINA.bwa.ESN.exome.20121211	685	0	0	301	608	387	534	644	477	0	0	0	0	0	42	0	578
HG02938.mapped.ILLUMINA.bwa.ESN.exome.20130415	694	338	376	0	717	192	561	674	584	0	668	592	0	0	61	107	597
HG02941.mapped.ILLUMINA.bwa.ESN.exome.20130415	795	326	372	381	723	478	562	672	479	111	670	559	464	187	0	116	598
HG02943.mapped.ILLUMINA.bwa.ESN.exome.20130415	683	0	0	303	612	389	531	651	482	0	0	0	0	0	0	133	573
HG02944.mapped.ILLUMINA.bwa.ESN.exome.20121211	689	250	257	284	620	378	538	651	485	0	606	565	0	0	32	60	580
HG02946.mapped.ILLUMINA.bwa.ESN.exome.20130415	799	0	0	399	722	477	561	681	589	0	0	0	0	0	60	130	599
HG02947.mapped.ILLUMINA.bwa.ESN.exome.20130415	799	0	0	414	724	473	561	671	581	0	0	0	0	0	85	2	591
HG02952.mapped.ILLUMINA.bwa.ESN.exome.20130415	703	0	0	393	687	477	562	671	581	0	0	0	0	0	0	242	595
HG02953.mapped.ILLUMINA.bwa.ESN.exome.20130415	801	0	0	411	728	460	561	674	584	0	0	0	0	0	81	3	594
HG02968.mapped.ILLUMINA.bwa.ESN.exome.20130415	702	331	369	381	699	193	559	669	585	0	0	0	0	0	54	100	596
HG02970.mapped.ILLUMINA.bwa.ESN.exome.20130415	797	0	0	397	722	477	562	671	583	0	0	0	0	0	68	0	590
HG02971.mapped.ILLUMINA.bwa.ESN.exome.20130415	796	333	372	151	712	472	562	673	584	0	656	588	0	0	59	112	596

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG02973.mapped.ILLUMINA.bwa.ESN.exome.20121211	759	0	0	305	606	389	537	654	478	0	0	0	0	0	38	0	576
HG02974.mapped.ILLUMINA.bwa.ESN.exome.20121211	751	0	0	303	592	384	537	642	475	0	0	0	0	0	36	1	579
HG02976.mapped.ILLUMINA.bwa.ESN.exome.20130415	700	0	373	388	710	468	563	671	580	0	0	0	0	0	79	0	596
HG02977.mapped.ILLUMINA.bwa.ESN.exome.20130415	798	0	373	383	721	477	562	680	585	0	664	0	462	0	62	121	595
HG02979.mapped.ILLUMINA.bwa.ESN.exome.20130415	797	0	0	393	720	477	560	671	580	0	0	0	0	0	72	4	596
HG02981.mapped.ILLUMINA.bwa.ESN.exome.20130415	701	0	0	395	721	479	564	667	583	0	0	0	0	0	0	161	594
HG02982.mapped.ILLUMINA.bwa.GWD.exome.20130415	697	0	374	383	716	473	561	675	582	0	653	0	481	0	61	106	592
HG02983.mapped.ILLUMINA.bwa.GWD.exome.20130415	781	337	379	0	706	184	563	676	588	0	657	589	0	0	60	112	598
HG03006.mapped.ILLUMINA.bwa.BEB.exome.20130415	680	242	251	288	568	372	530	645	399	76	580	0	363	131	0	61	572
HG03007.mapped.ILLUMINA.bwa.BEB.exome.20130415	670	233	253	270	596	362	531	651	469	69	578	564	0	0	0	73	575
HG03009.mapped.ILLUMINA.bwa.BEB.exome.20130422	682	0	0	286	568	369	531	643	385	83	509	496	0	127	0	53	573
HG03012.mapped.ILLUMINA.bwa.BEB.exome.20130422	673	235	239	264	528	359	532	622	366	63	572	0	294	137	0	50	568
HG03015.mapped.ILLUMINA.bwa.PJL.exome.20130415	788	335	376	0	0	0	558	646	470	0	655	0	386	185	0	90	594
HG03016.mapped.ILLUMINA.bwa.PJL.exome.20130415	799	328	372	388	708	468	559	675	583	0	0	0	0	0	60	112	596
HG03018.mapped.ILLUMINA.bwa.PJL.exome.20130415	639	266	289	313	571	414	537	622	530	0	0	0	0	0	0	62	586
HG03019.mapped.ILLUMINA.bwa.PJL.exome.20130415	549	315	344	0	447	168	548	620	530	0	532	492	0	0	30	33	584
HG03021.mapped.ILLUMINA.bwa.PJL.exome.20130415	663	0	0	341	654	453	533	613	285	0	529	0	335	166	31	1	581
HG03022.mapped.ILLUMINA.bwa.PJL.exome.20130415	654	287	310	130	546	413	548	607	383	97	509	0	337	174	0	46	571
HG03024.mapped.ILLUMINA.bwa.GWD.exome.20130415	663	232	242	259	589	371	526	629	367	68	609	504	348	131	23	1	575
HG03025.mapped.ILLUMINA.bwa.GWD.exome.20130415	592	236	262	0	602	269	530	630	138	73	627	505	372	133	0	1	567
HG03027.mapped.ILLUMINA.bwa.GWD.exome.20130415	685	250	264	283	555	378	535	652	488	0	0	0	0	0	31	74	580
HG03028.mapped.ILLUMINA.bwa.GWD.exome.20130415	675	0	256	191	606	317	534	646	485	0	594	0	388	0	39	0	579
HG03039.mapped.ILLUMINA.bwa.GWD.exome.20130415	685	0	256	269	603	276	531	641	471	0	608	0	292	0	36	0	574
HG03040.mapped.ILLUMINA.bwa.GWD.exome.20130415	684	248	267	201	588	318	532	648	487	0	0	0	0	0	0	138	578
HG03045.mapped.ILLUMINA.bwa.GWD.exome.20130415	572	0	259	0	597	141	534	645	476	0	613	0	384	0	24	59	574
HG03046.mapped.ILLUMINA.bwa.GWD.exome.20121211	683	250	264	292	613	377	535	648	480	0	615	569	0	0	30	63	580
HG03048.mapped.ILLUMINA.bwa.GWD.exome.20121211	664	235	244	176	594	293	527	621	394	0	520	569	0	0	36	0	576
HG03049.mapped.ILLUMINA.bwa.GWD.exome.20130415	683	256	259	280	606	378	533	646	478	0	589	0	379	0	38	2	575
HG03052.mapped.ILLUMINA.bwa.MSL.exome.20121211	753	237	257	286	607	376	535	652	373	78	639	563	354	131	25	1	573
HG03054.mapped.ILLUMINA.bwa.MSL.exome.20130415	794	334	373	239	723	453	562	670	578	0	652	586	0	0	89	0	597
HG03055.mapped.ILLUMINA.bwa.MSL.exome.20130415	797	0	0	399	719	479	562	668	566	0	0	0	0	0	0	190	597
HG03057.mapped.ILLUMINA.bwa.MSL.exome.20121211	681	248	272	291	617	380	534	651	481	0	610	515	0	0	36	0	577
HG03058.mapped.ILLUMINA.bwa.MSL.exome.20121211	687	0	0	291	587	355	531	640	468	0	0	0	0	0	22	49	570
HG03060.mapped.ILLUMINA.bwa.MSL.exome.20130415	705	0	0	392	725	472	564	677	584	0	652	587	0	0	65	111	597
HG03061.mapped.ILLUMINA.bwa.MSL.exome.20130415	798	329	373	384	719	467	558	662	574	0	644	0	472	0	0	124	588
HG03063.mapped.ILLUMINA.bwa.MSL.exome.20130415	700	48	0	395	722	468	560	652	576	0	0	0	0	0	0	144	598
HG03064.mapped.ILLUMINA.bwa.MSL.exome.20130415	791	325	369	231	698	469	562	665	577	0	0	0	0	0	72	3	592
HG03066.mapped.ILLUMINA.bwa.MSL.exome.20130415	596	250	264	0	568	131	527	638	460	0	584	508	0	0	32	61	573
HG03069.mapped.ILLUMINA.bwa.MSL.exome.20130415	682	0	0	291	603	381	532	625	462	0	0	0	0	0	37	0	575
HG03072.mapped.ILLUMINA.bwa.MSL.exome.20130415	662	0	247	272	460	349	513	578	380	0	573	0	353	129	28	1	572
HG03073.mapped.ILLUMINA.bwa.MSL.exome.20130415	701	0	0	397	715	481	562	670	581	0	0	0	0	0	76	2	594
HG03074.mapped.ILLUMINA.bwa.MSL.exome.20130415	797	0	0	398	728	477	562	675	574	0	0	0	0	0	0	120	591
HG03077.mapped.ILLUMINA.bwa.MSL.exome.20130415	798	0	0	400	721	475	564	676	581	0	0	0	0	0	61	108	594
HG03078.mapped.ILLUMINA.bwa.MSL.exome.20121211	689	0	0	309	612	388	536	648	485	0	0	0	0	0	38	79	576
HG03079.mapped.ILLUMINA.bwa.MSL.exome.20130415	701	191	369	379	701	459	560	660	201	0	0	0	0	0	0	1	0
HG03081.mapped.ILLUMINA.bwa.MSL.exome.20130415	794	189	375	237	720	388	565	671	569	107	645	0	478	0	0	102	588
HG03082.mapped.ILLUMINA.bwa.MSL.exome.20130415	701	335	373	388	722	474	562	672	581	0	654	0	482	0	62	117	592
HG03084.mapped.ILLUMINA.bwa.MSL.exome.20121211	671	0	274	0	602	139	534	645	476	0	641	0	404	0	42	1	577
HG03085.mapped.ILLUMINA.bwa.MSL.exome.20121211	687	241	254	183	548	366	529	616	383	0	578	0	370	136	0	64	579
HG03086.mapped.ILLUMINA.bwa.MSL.exome.20130415	571	328	369	0	692	187	552	652	472	0	645	585	0	0	37	74	593
HG03088.mapped.ILLUMINA.bwa.MSL.exome.20130415	799	0	0	395	716	475	559	670	577	0	0	0	0	0	53	117	596
HG03091.mapped.ILLUMINA.bwa.MSL.exome.20130415	792	0	0	382	706	462	558	661	573	0	0	0	0	0	52	106	594
HG03095.mapped.ILLUMINA.bwa.MSL.exome.20130415	699	0	0	396	715	479	562	673	585	0	0	0	0	0	57	106	597
HG03096.mapped.ILLUMINA.bwa.MSL.exome.20121211	597	265	279	0	587	140	527	637	0	80	649	563	385	141	0	0	577
HG03097.mapped.ILLUMINA.bwa.MSL.exome.20121211	686	0	0	309	607	389	534	651	470	0	0	0	0	0	32	2	574
HG03099.mapped.ILLUMINA.bwa.ESN.exome.20121211	595	251	272	0	508	282	536	662	486	0	580	0	366	0	0	100	576
HG03100.mapped.ILLUMINA.bwa.ESN.exome.20121211	758	136	251	283	616	366	531	637	464	0	603	567	0	0	38	0	573
HG03103.mapped.ILLUMINA.bwa.ESN.exome.20130415	703	0	372	147	711	474	561	664	0	0	655	0	481	0	68	0	592
HG03105.mapped.ILLUMINA.bwa.ESN.exome.20130415	700	0	73	394	722	470	559	671	585	0	0	0	5	0	83	0	597
HG03108.mapped.ILLUMINA.bwa.ESN.exome.20121211	691	0	0	309	608	380	532	642	476	0	0	0	0	0	37	0	577
HG03109.mapped.ILLUMINA.bwa.ESN.exome.20121211	686	0	0	306	619	393	534	649	474	0	0	0	0	0	33	72	577
HG03111.mapped.ILLUMINA.bwa.ESN.exome.20130415	792	340	381	0	706	191	560	677	584	0	646	559	0	0	0	223	597
HG03112.mapped.ILLUMINA.bwa.ESN.exome.20130415	705	0	0	402	723	473	560	675	582	0	0	0	0	0	94	1	597
HG03114.mapped.ILLUMINA.bwa.ESN.exome.20121211	687	0	0	307	612	381	534	650	480	0	0	0	0	0	44	1	577
HG03115.mapped.ILLUMINA.bwa.ESN.exome.20121211	684	249	265	298	592	381	532	629	460	0	607	0	366	137	34	0	576
HG03117.mapped.ILLUMINA.bwa.ESN.exome.20130415	664	230	258	268	496	350	529	631	467	0	0	0	0	0	0	96	573
HG03118.mapped.ILLUMINA.bwa.ESN.exome.20130415	677	0	0	299	582	377	529	635	468	0	0	0	0	0	28	53	570
HG03120.mapped.ILLUMINA.bwa.ESN.exome.20121211	757	0	0	293	605	389	536	649	475	0	0	0	0	0	37	0	578
HG03121.mapped.ILLUMINA.bwa.ESN.exome.20121211	668	0	259	293	608	389	533	656	471	0	612	0	362	0	35	0	570
HG03123.mapped.ILLUMINA.bwa.ESN.exome.20121211	680	0	0	285	586	377	535	629	460	0	0	0	0	0	20	1	568
HG03124.mapped.ILLUMINA.bwa.ESN.exome.20121211	680	246	259	185	605	281	530	646	477	0	618	566	0	0	27	64	577
HG03126.mapped.ILLUMINA.bwa.ESN.exome.20130415	693	342	385	0	719	192	562	673	586	0	675	590	0	0	86	0	595
HG03127.mapped.ILLUMINA.bwa.ESN.exome.20130415	800	0	0	420	725	480	562	668	576	0	0	63	0	0	0	139	595
HG03129.mapped.ILLUMINA.bwa.ESN.exome.20130415	680	0	0	286	568	367	531	603	398	0	0	0	0	0	35	0	577
HG03130.mapped.ILLUMINA.bwa.ESN.exome.20130415	676	0	250	265	594	375	531	625	462	0	519	0	308	0	32	0	573
HG03132.mapped.ILLUMINA.bwa.ESN.exome.20130415	679	0	0	287	600	383	532	641	473	0	0	0	0	0	31	59	575
HG03133.mapped.ILLUMINA.bwa.ESN.exome.20121211	686	0	0	307	596	388	531	655	471	0	0	0	0	0	32	0	573
HG03135.mapped.ILLUMINA.bwa.ESN.exome.20121211	682	0	0	297	596	370	530	639	454	72	588	0	353	132	27	0	575
HG03136.mapped.ILLUMINA.bwa.ESN.exome.20130415	657	0	250	278	600	370	531	641	464	0	592	0	389	0	37	2	571
HG03139.mapped.ILLUMINA.bwa.ESN.exome.20130415	703	0	0	402	724	478	561	672	582	0	0	0	0	0	88	0	596
HG03157.mapped.ILLUMINA.bwa.ESN.exome.20130415	703	334	370	389	730	468	562	669	575	0	667	0	478	0	0	130	591
HG03159.mapped.ILLUMINA.bwa.ESN.exome.20130415	679	0	0	286	589	378	532	629	394	0	0	0	0	0	35	0	573
HG03160.mapped.ILLUMINA.bwa.ESN.exome.20130422	673	233	249	90	571	370	530	636	403	0	502	0	361	0	27	50	575
HG03162.mapped.ILLUMINA.bwa.ESN.exome.20130415	682	241	262	181	547	368	527	634	472	0	0	0	14	0	0	98	576
HG03163.mapped.ILLUMINA.bwa.ESN.exome.20130415	678	0	0	293	590	373	532	629	468	0	0	0	0	0	37	2	573
HG03166.mapped.ILLUMINA.bwa.ESN.exome.20130415	705	0	0	415	722	478	561	674	580	0	0	0	0	0	60	128	594
HG03168.mapped.ILLUMINA.bwa.ESN.exome.20130415	677	0	0	294	589	331	531	625	459	0	0	5	0	0	0	62	577
HG03169.mapped.ILLUMINA.bwa.ESN.exome.20130415	674	231	120	262	488	352	520	590	368	0	514	0	345	132	22	2	575
HG03172.mapped.ILLUMINA.bwa.ESN.exome.20130415	680	0	0	295	597	381	530	636	396	0	0	0	0	0	22	46	571
HG03175.mapped.ILLUMINA.bwa.ESN.exome.20130415	703	0	368	389	729	476	562	674	572	0	660	0	483	0	84	0	597
HG03189.mapped.ILLUMINA.bwa.ESN.exome.20130415	797	0	378	387	722	477	562	674	584	0	656	0	484	0	89	0	595
HG03190.mapped.ILLUMINA.bwa.ESN.exome.20130415	798	0	0	397	725	476	563	672	585	0	0	0	0	0	88	0	594
HG03193.mapped.ILLUMINA.bwa.ESN.exome.20130415	799	0	0	397	729	478	565	672	586	0	0	0	0	0	91	2	597
HG03195.mapped.ILLUMINA.bwa.ESN.exome.20130415	679	0	0	289	591	383	529	634	463	0	0	0	0	0	30	3	570
HG03196.mapped.ILLUMINA.bwa.ESN.exome.20130415	682	0	0	293	599	380	530	631	473	0	0	0	0	0	0	101	573
HG03198.mapped.ILLUMINA.bwa.ESN.exome.20130415	592	246	263	0	0	0	530	620	468	0	0	0	0	0	0	97	573

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG03199.mapped.ILLUMINA.bwa.ESN.exome.20130415	636	242	242	255	589	89	518	609	0	0	534	474	0	0	27	0	563
HG03202.mapped.ILLUMINA.bwa.ESN.exome.20130415	793	319	368	386	705	464	562	669	583	0	0	0	0	0	58	109	595
HG03209.mapped.ILLUMINA.bwa.MSL.exome.20130415	796	330	373	131	724	191	561	667	578	0	672	592	0	0	72	0	593
HG03212.mapped.ILLUMINA.bwa.MSL.exome.20130415	701	0	0	392	721	474	559	672	580	0	0	0	0	0	0	238	592
HG03224.mapped.ILLUMINA.bwa.MSL.exome.20130415	796	331	370	393	722	478	562	669	587	0	656	591	0	0	68	0	596
HG03225.mapped.ILLUMINA.bwa.MSL.exome.20130415	703	0	0	399	724	482	561	667	586	0	0	0	0	0	77	0	594
HG03228.mapped.ILLUMINA.bwa.PJL.exome.20130415	703	0	0	397	716	471	558	672	0	107	667	0	471	189	0	0	593
HG03229.mapped.ILLUMINA.bwa.PJL.exome.20130415	796	326	365	387	703	466	563	673	581	0	0	0	0	0	48	122	593
HG03234.mapped.ILLUMINA.bwa.PJL.exome.20130415	693	338	379	0	719	190	563	677	478	105	674	592	0	182	0	126	597
HG03235.mapped.ILLUMINA.bwa.PJL.exome.20130415	794	0	0	395	712	479	562	670	567	109	657	0	462	187	0	127	596
HG03237.mapped.ILLUMINA.bwa.PJL.exome.20130415	789	339	380	0	0	0	559	659	572	0	659	0	461	186	0	119	595
HG03238.mapped.ILLUMINA.bwa.PJL.exome.20130415	596	337	380	0	710	189	563	678	582	109	654	586	0	0	0	176	596
HG03240.mapped.ILLUMINA.bwa.GWD.exome.20130415	680	0	0	290	593	366	527	618	466	0	0	0	0	0	31	0	574
HG03241.mapped.ILLUMINA.bwa.GWD.exome.20130415	686	0	0	293	599	375	528	641	472	0	0	0	0	0	22	46	577
HG03246.mapped.ILLUMINA.bwa.GWD.exome.20130415	678	0	0	280	563	367	529	630	438	0	0	0	0	0	25	2	568
HG03247.mapped.ILLUMINA.bwa.GWD.exome.20130415	670	221	257	260	592	366	533	624	440	0	517	0	305	0	0	40	559
HG03258.mapped.ILLUMINA.bwa.GWD.exome.20130415	681	0	264	292	590	380	535	664	485	0	0	0	0	0	25	74	579
HG03259.mapped.ILLUMINA.bwa.GWD.exome.20130415	681	247	251	284	610	364	532	643	475	0	607	538	0	0	37	1	574
HG03265.mapped.ILLUMINA.bwa.ESN.exome.20130415	702	330	377	391	722	476	561	676	590	0	658	587	0	0	54	122	600
HG03267.mapped.ILLUMINA.bwa.ESN.exome.20130415	797	0	0	396	722	475	558	671	584	0	0	0	0	0	74	1	599
HG03268.mapped.ILLUMINA.bwa.ESN.exome.20130415	701	0	0	399	722	479	559	670	575	0	0	0	0	0	62	0	594
HG03270.mapped.ILLUMINA.bwa.ESN.exome.20130415	794	338	373	77	706	299	557	662	116	108	673	587	486	190	0	0	593
HG03271.mapped.ILLUMINA.bwa.ESN.exome.20130415	700	325	369	386	723	475	559	674	469	105	672	594	464	185	55	2	595
HG03279.mapped.ILLUMINA.bwa.ESN.exome.20130415	699	0	0	397	719	471	559	668	583	0	0	0	0	0	73	1	598
HG03280.mapped.ILLUMINA.bwa.ESN.exome.20130415	700	0	0	397	721	475	560	672	583	0	0	0	0	0	59	108	594
HG03291.mapped.ILLUMINA.bwa.ESN.exome.20130415	797	322	368	384	702	467	559	669	575	0	0	0	0	0	0	158	595
HG03294.mapped.ILLUMINA.bwa.ESN.exome.20130415	797	0	368	382	698	470	558	641	468	0	650	0	462	187	0	117	596
HG03295.mapped.ILLUMINA.bwa.ESN.exome.20130415	795	0	367	390	725	194	561	671	584	0	668	0	478	0	80	3	590
HG03297.mapped.ILLUMINA.bwa.ESN.exome.20130415	796	0	0	398	722	482	564	671	583	0	0	0	0	0	84	0	595
HG03298.mapped.ILLUMINA.bwa.ESN.exome.20130415	800	0	0	420	721	479	563	676	589	0	0	0	0	0	70	152	592
HG03300.mapped.ILLUMINA.bwa.ESN.exome.20130415	792	338	378	0	0	0	555	650	477	0	655	0	464	189	0	124	596
HG03301.mapped.ILLUMINA.bwa.ESN.exome.20130415	698	327	362	385	700	418	557	664	575	0	0	0	0	0	0	216	594
HG03303.mapped.ILLUMINA.bwa.ESN.exome.20130415	798	0	379	393	707	467	563	674	586	0	0	0	0	0	62	117	597
HG03304.mapped.ILLUMINA.bwa.ESN.exome.20130415	697	0	0	398	724	480	565	665	584	0	0	0	0	0	83	4	598
HG03311.mapped.ILLUMINA.bwa.ESN.exome.20130415	683	291	322	188	600	385	549	638	436	0	0	0	0	0	0	95	590
HG03313.mapped.ILLUMINA.bwa.ESN.exome.20130415	698	0	0	338	680	471	549	654	548	0	0	0	0	0	0	93	583
HG03342.mapped.ILLUMINA.bwa.ESN.exome.20130415	688	0	0	288	599	376	532	629	471	0	0	0	0	0	33	2	579
HG03343.mapped.ILLUMINA.bwa.ESN.exome.20130415	674	237	258	279	601	365	537	644	462	0	525	9	374	0	25	61	577
HG03351.mapped.ILLUMINA.bwa.ESN.exome.20130415	696	316	340	347	635	445	555	646	555	0	0	0	0	0	54	2	587
HG03352.mapped.ILLUMINA.bwa.ESN.exome.20130415	695	305	345	332	686	187	555	636	552	0	568	0	380	0	28	59	586
HG03354.mapped.ILLUMINA.bwa.ESN.exome.20130415	698	0	0	396	708	470	563	661	580	0	0	0	0	0	0	170	594
HG03363.mapped.ILLUMINA.bwa.ESN.exome.20130415	672	296	337	324	599	430	551	624	446	0	0	0	0	0	30	48	584
HG03366.mapped.ILLUMINA.bwa.ESN.exome.20130415	702	333	365	386	707	472	562	669	583	0	659	583	0	0	0	233	595
HG03367.mapped.ILLUMINA.bwa.ESN.exome.20130415	695	338	375	0	701	188	557	653	573	0	671	0	488	186	0	119	594
HG03369.mapped.ILLUMINA.bwa.ESN.exome.20130415	671	285	305	308	666	183	548	613	446	0	455	523	0	0	44	1	570
HG03370.mapped.ILLUMINA.bwa.ESN.exome.20130415	694	0	0	356	662	454	549	633	555	0	0	0	0	0	48	4	584
HG03372.mapped.ILLUMINA.bwa.ESN.exome.20130415	678	0	0	340	613	439	541	635	427	0	0	0	0	0	44	2	586
HG03376.mapped.ILLUMINA.bwa.MSL.exome.20130415	799	328	185	384	710	473	558	666	572	0	660	0	479	188	62	0	593
HG03378.mapped.ILLUMINA.bwa.MSL.exome.20130415	800	0	0	393	723	472	564	676	583	0	0	0	0	0	96	0	598
HG03380.mapped.ILLUMINA.bwa.MSL.exome.20130415	800	340	379	0	717	190	560	673	588	0	675	593	0	0	83	2	595
HG03382.mapped.ILLUMINA.bwa.MSL.exome.20130415	703	0	0	397	726	472	563	676	584	0	0	0	0	0	90	0	596
HG03385.mapped.ILLUMINA.bwa.MSL.exome.20130415	702	0	0	393	715	474	564	670	582	0	643	559	0	0	57	117	592
HG03388.mapped.ILLUMINA.bwa.MSL.exome.20130415	703	334	375	388	724	472	557	673	583	0	658	591	0	0	76	2	594
HG03391.mapped.ILLUMINA.bwa.MSL.exome.20130415	591	240	264	0	485	129	530	630	457	0	567	0	296	0	33	2	571
HG03394.mapped.ILLUMINA.bwa.MSL.exome.20130415	671	0	0	360	662	456	549	614	435	0	0	0	0	0	48	1	584
HG03397.mapped.ILLUMINA.bwa.MSL.exome.20121211	692	0	0	304	606	389	534	656	481	0	0	0	0	0	30	68	576
HG03401.mapped.ILLUMINA.bwa.MSL.exome.20130415	701	0	0	390	716	470	563	666	580	0	0	0	0	0	76	97	592
HG03410.mapped.ILLUMINA.bwa.MSL.exome.20130415	699	0	0	416	725	478	561	674	586	0	0	0	0	0	92	0	597
HG03419.mapped.ILLUMINA.bwa.MSL.exome.20130415	796	189	373	384	718	478	564	680	578	109	657	0	480	0	59	106	594
HG03428.mapped.ILLUMINA.bwa.MSL.exome.20130415	704	333	367	239	725	477	563	673	479	108	672	591	461	187	0	126	595
HG03432.mapped.ILLUMINA.bwa.MSL.exome.20130415	577	308	347	0	654	182	552	619	202	0	610	488	363	0	0	0	0
HG03433.mapped.ILLUMINA.bwa.MSL.exome.20130415	798	0	0	394	720	474	565	670	581	0	0	0	0	0	74	122	593
HG03436.mapped.ILLUMINA.bwa.MSL.exome.20130415	678	241	255	273	605	362	531	631	466	0	581	497	0	0	27	50	575
HG03437.mapped.ILLUMINA.bwa.MSL.exome.20130415	634	0	250	180	567	303	531	621	389	0	519	0	304	0	35	0	571
HG03439.mapped.ILLUMINA.bwa.MSL.exome.20130415	794	0	0	396	719	479	564	674	578	0	0	0	0	0	56	97	594
HG03442.mapped.ILLUMINA.bwa.MSL.exome.20130415	696	335	375	0	0	0	559	653	570	0	656	0	463	185	62	0	597
HG03445.mapped.ILLUMINA.bwa.MSL.exome.20130415	697	341	379	0	702	386	563	675	582	0	657	0	463	0	67	124	593
HG03446.mapped.ILLUMINA.bwa.MSL.exome.20130415	702	333	369	384	708	466	560	664	583	0	0	0	0	0	0	251	594
HG03449.mapped.ILLUMINA.bwa.MSL.exome.20130415	800	0	0	393	725	475	563	673	585	0	657	589	0	0	74	4	595
HG03451.mapped.ILLUMINA.bwa.MSL.exome.20121211	682	243	248	282	618	378	534	651	477	0	589	563	0	0	32	57	579
HG03452.mapped.ILLUMINA.bwa.MSL.exome.20130415	682	0	244	282	600	138	535	640	465	0	597	0	305	0	36	1	578
HG03455.mapped.ILLUMINA.bwa.MSL.exome.20130415	687	0	0	293	593	361	530	631	458	0	0	0	0	0	27	46	575
HG03457.mapped.ILLUMINA.bwa.MSL.exome.20130415	594	318	361	0	641	175	546	598	430	0	630	547	365	177	0	44	588
HG03458.mapped.ILLUMINA.bwa.MSL.exome.20130415	671	225	241	258	530	359	521	575	371	0	577	0	286	133	21	1	574
HG03460.mapped.ILLUMINA.bwa.MSL.exome.20130415	704	331	375	129	721	191	562	671	585	0	675	588	481	0	77	2	596
HG03461.mapped.ILLUMINA.bwa.MSL.exome.20130415	797	0	375	384	705	477	556	648	467	0	658	0	462	185	0	132	593
HG03464.mapped.ILLUMINA.bwa.MSL.exome.20121211	687	0	0	305	611	381	534	656	480	73	0	0	0	0	33	65	581
HG03469.mapped.ILLUMINA.bwa.MSL.exome.20121211	688	249	255	287	635	383	532	646	487	0	614	518	0	0	37	1	576
HG03470.mapped.ILLUMINA.bwa.MSL.exome.20130415	793	187	371	377	708	464	560	674	577	0	0	0	0	0	60	0	592
HG03472.mapped.ILLUMINA.bwa.MSL.exome.20121211	678	238	248	275	544	373	529	644	475	0	0	0	0	0	28	60	571
HG03473.mapped.ILLUMINA.bwa.MSL.exome.20130415	797	0	0	396	715	470	559	674	582	0	0	0	0	0	75	1	593
HG03476.mapped.ILLUMINA.bwa.MSL.exome.20130415	684	0	0	294	594	282	519	615	463	0	0	0	0	0	33	1	572
HG03478.mapped.ILLUMINA.bwa.MSL.exome.20130415	797	0	0	243	724	466	563	680	579	0	0	0	0	0	63	1	595
HG03479.mapped.ILLUMINA.bwa.MSL.exome.20130415	595	334	373	0	701	188	556	651	474	0	669	585	458	188	58	0	597
HG03484.mapped.ILLUMINA.bwa.MSL.exome.20130415	673	0	0	194	595	374	532	640	451	0	0	0	0	0	31	5	568
HG03485.mapped.ILLUMINA.bwa.MSL.exome.20130415	676	224	249	276	598	366	531	613	443	0	576	0	371	0	30	1	568
HG03488.mapped.ILLUMINA.bwa.PJL.exome.20130422	672	260	277	0	62	0	535	652	443	75	586	0	377	137	0	80	582
HG03490.mapped.ILLUMINA.bwa.PJL.exome.20130415	692	0	0	361	665	451	550	640	543	0	0	0	0	0	0	81	593
HG03491.mapped.ILLUMINA.bwa.PJL.exome.20130415	685	0	0	354	654	452	548	635	529	0	0	0	0	0	0	75	593
HG03499.mapped.ILLUMINA.bwa.ESN.exome.20130415	681	288	322	332	651	450	551	634	454	0	467	515	0	0	30	47	583
HG03511.mapped.ILLUMINA.bwa.ESN.exome.20130415	690	0	0	364	666	451	551	635	543	0	0	0	0	0	31	2	578
HG03514.mapped.ILLUMINA.bwa.ESN.exome.20130415	694	329	378	0	724	386	560	673	577	0	671	588	464	0	60	113	597
HG03515.mapped.ILLUMINA.bwa.ESN.exome.20130415	793	0	0	398	721	474	563	666	585	0	0	0	0	0	0	180	595
HG03517.mapped.ILLUMINA.bwa.ESN.exome.20130415	587	324	363	0	629	185	548	622	437	98	620	559	373	178	0	47	589
HG03518.mapped.ILLUMINA.bwa.ESN.exome.20130415	693	0	0	345	652	438	545	617	547	0	0	0	0	0	0	79	579
HG03520.mapped.ILLUMINA.bwa.ESN.exome.20130415	683	0	0	287	598	373	530	629	473	0	0	0	0	0	32	7	570

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG03521.mapped.ILLUMINA.bwa.ESN.exome.20130415	668	0	254	272	597	373	527	628	468	0	498	0	287	0	35	0	575
HG03538.mapped.ILLUMINA.bwa.GWD.exome.20130415	676	239	255	255	579	370	532	629	466	0	571	558	0	0	37	0	570
HG03539.mapped.ILLUMINA.bwa.GWD.exome.20130415	678	239	257	272	545	346	528	627	442	0	0	0	0	0	0	62	565
HG03547.mapped.ILLUMINA.bwa.MSL.exome.20130415	670	236	242	270	602	365	528	619	394	0	527	505	0	0	32	0	572
HG03548.mapped.ILLUMINA.bwa.MSL.exome.20130415	677	0	0	288	587	382	531	631	464	0	0	0	0	0	34	2	572
HG03556.mapped.ILLUMINA.bwa.MSL.exome.20130415	687	0	0	304	606	383	534	650	469	0	0	0	0	0	31	70	573
HG03557.mapped.ILLUMINA.bwa.MSL.exome.20130415	576	0	264	0	503	268	527	634	465	0	567	0	284	0	26	57	571
HG03558.mapped.ILLUMINA.bwa.MSL.exome.20130415	696	0	0	337	654	356	552	643	454	0	0	0	0	0	28	35	582
HG03559.mapped.ILLUMINA.bwa.MSL.exome.20130415	677	301	314	322	651	390	544	621	541	0	515	516	0	0	28	42	583
HG03563.mapped.ILLUMINA.bwa.MSL.exome.20130422	683	237	242	280	600	367	530	635	459	0	567	0	310	0	33	3	574
HG03565.mapped.ILLUMINA.bwa.MSL.exome.20130415	682	0	0	342	655	453	549	612	445	0	0	0	0	0	30	43	588
HG03567.mapped.ILLUMINA.bwa.MSL.exome.20130415	689	0	0	335	655	445	544	604	304	90	462	0	345	165	28	1	584
HG03571.mapped.ILLUMINA.bwa.MSL.exome.20130415	700	0	0	395	719	479	562	669	582	0	0	0	0	0	72	1	593
HG03572.mapped.ILLUMINA.bwa.MSL.exome.20130415	646	0	255	275	494	363	515	610	142	0	558	0	291	126	0	4	563
HG03575.mapped.ILLUMINA.bwa.MSL.exome.20130415	682	238	253	278	597	361	532	624	465	0	568	0	310	0	26	59	573
HG03577.mapped.ILLUMINA.bwa.MSL.exome.20130415	682	0	0	196	604	321	536	651	476	0	600	562	0	0	30	67	574
HG03578.mapped.ILLUMINA.bwa.MSL.exome.20130415	678	237	255	259	597	371	528	639	466	0	598	508	0	0	26	57	572
HG03583.mapped.ILLUMINA.bwa.MSL.exome.20130415	665	0	251	248	592	362	528	621	452	0	564	0	299	0	37	1	573
HG03585.mapped.ILLUMINA.bwa.BEB.exome.20130422	667	230	237	264	495	261	526	637	393	0	0	0	0	0	28	50	571
HG03589.mapped.ILLUMINA.bwa.BEB.exome.20130422	627	233	246	265	499	366	531	641	361	73	574	0	288	131	0	43	570
HG03593.mapped.ILLUMINA.bwa.BEB.exome.20130422	649	233	261	272	607	278	529	638	371	82	631	567	285	136	0	44	578
HG03594.mapped.ILLUMINA.bwa.BEB.exome.20130415	693	336	375	0	699	183	562	666	574	106	672	591	0	186	0	118	595
HG03595.mapped.ILLUMINA.bwa.BEB.exome.20130415	795	335	375	0	709	189	558	655	569	0	676	592	388	190	63	0	596
HG03598.mapped.ILLUMINA.bwa.BEB.exome.20130415	580	300	319	0	643	177	548	632	304	93	589	502	327	153	0	35	566
HG03600.mapped.ILLUMINA.bwa.BEB.exome.20130415	693	323	368	375	714	467	556	661	576	0	647	588	0	0	0	129	588
HG03603.mapped.ILLUMINA.bwa.BEB.exome.20130415	699	335	376	0	721	190	562	681	587	0	670	594	0	0	66	129	596
HG03604.mapped.ILLUMINA.bwa.BEB.exome.20130415	704	30	107	396	722	477	559	672	568	105	656	160	459	185	56	1	596
HG03607.mapped.ILLUMINA.bwa.BEB.exome.20130415	700	324	373	381	716	473	562	676	579	0	656	586	0	0	58	111	595
HG03611.mapped.ILLUMINA.bwa.BEB.exome.20130415	795	0	0	389	715	482	562	672	585	0	0	0	0	0	64	115	594
HG03615.mapped.ILLUMINA.bwa.BEB.exome.20130415	673	235	257	272	582	277	511	613	383	0	527	0	286	137	33	1	574
HG03616.mapped.ILLUMINA.bwa.BEB.exome.20130415	682	240	256	283	585	366	532	642	473	0	0	0	0	0	0	115	577
HG03619.mapped.ILLUMINA.bwa.PJL.exome.20130415	797	344	388	0	0	0	561	663	574	0	668	0	458	187	0	156	599
HG03624.mapped.ILLUMINA.bwa.PJL.exome.20130415	690	0	0	359	663	467	550	631	432	93	574	0	365	171	0	61	586
HG03625.mapped.ILLUMINA.bwa.PJL.exome.20130415	685	0	0	334	654	446	542	617	538	0	0	0	0	0	0	64	584
HG03629.mapped.ILLUMINA.bwa.PJL.exome.20130415	691	315	173	339	681	175	552	506	338	0	570	535	0	175	0	58	582
HG03631.mapped.ILLUMINA.bwa.PJL.exome.20130415	665	293	329	315	652	363	546	631	404	90	611	545	0	169	0	48	582
HG03634.mapped.ILLUMINA.bwa.PJL.exome.20130415	795	0	0	402	727	478	560	667	565	0	0	0	0	0	0	192	598
HG03636.mapped.ILLUMINA.bwa.PJL.exome.20130415	680	302	330	288	594	348	548	629	447	0	0	0	0	0	53	1	582
HG03640.mapped.ILLUMINA.bwa.PJL.exome.20130415	676	284	0	358	656	443	545	615	381	80	542	0	425	163	0	38	579
HG03642.mapped.ILLUMINA.bwa.STU.exome.20130415	672	231	253	281	599	276	521	639	361	60	620	563	287	134	0	65	575
HG03643.mapped.ILLUMINA.bwa.STU.exome.20130415	681	0	0	295	588	378	532	637	465	0	0	0	0	0	0	81	576
HG03644.mapped.ILLUMINA.bwa.STU.exome.20130415	655	240	270	281	600	282	531	658	472	78	622	520	0	0	0	85	573
HG03645.mapped.ILLUMINA.bwa.STU.exome.20130415	691	332	373	0	714	187	559	666	0	110	678	591	467	189	0	0	594
HG03646.mapped.ILLUMINA.bwa.STU.exome.20130415	703	330	371	388	724	471	560	668	484	109	663	594	0	185	0	130	596
HG03649.mapped.ILLUMINA.bwa.PJL.exome.20130415	560	315	348	0	638	180	549	618	435	0	598	542	0	0	27	35	586
HG03652.mapped.ILLUMINA.bwa.PJL.exome.20130415	568	322	351	0	0	0	524	576	325	0	546	520	0	169	33	1	580
HG03653.mapped.ILLUMINA.bwa.PJL.exome.20130415	661	0	0	343	652	440	540	595	519	0	0	0	0	0	25	40	585
HG03660.mapped.ILLUMINA.bwa.PJL.exome.20130422	752	240	275	302	511	391	523	628	394	0	600	0	382	138	0	73	582
HG03663.mapped.ILLUMINA.bwa.PJL.exome.20130422	671	266	275	0	590	142	529	621	401	0	637	569	305	138	0	73	581
HG03667.mapped.ILLUMINA.bwa.PJL.exome.20130415	701	340	383	0	727	190	562	679	574	109	680	593	468	190	78	0	593
HG03668.mapped.ILLUMINA.bwa.PJL.exome.20130415	700	330	379	390	727	478	561	674	585	0	657	592	0	0	80	2	597
HG03672.mapped.ILLUMINA.bwa.STU.exome.20130415	796	331	375	382	707	478	564	668	580	0	0	0	0	0	0	184	597
HG03673.mapped.ILLUMINA.bwa.STU.exome.20130422	665	243	247	263	602	366	527	648	425	76	631	547	355	133	0	63	574
HG03679.mapped.ILLUMINA.bwa.STU.exome.20130422	688	0	0	297	598	386	532	653	476	0	0	0	16	0	22	60	576
HG03680.mapped.ILLUMINA.bwa.STU.exome.20130415	686	0	0	292	595	383	529	637	467	0	0	0	0	0	28	61	573
HG03681.mapped.ILLUMINA.bwa.STU.exome.20130415	673	245	250	277	608	374	529	642	468	0	586	565	0	0	0	78	574
HG03684.mapped.ILLUMINA.bwa.STU.exome.20130415	643	234	253	275	501	273	500	582	0	75	621	0	371	135	0	1	578
HG03685.mapped.ILLUMINA.bwa.STU.exome.20130415	677	244	263	277	552	356	529	644	392	68	577	0	292	135	0	51	576
HG03686.mapped.ILLUMINA.bwa.STU.exome.20130415	798	0	0	398	720	480	561	674	583	0	0	0	0	0	62	135	597
HG03687.mapped.ILLUMINA.bwa.STU.exome.20130415	598	338	383	0	672	186	562	666	0	110	674	591	472	189	0	0	599
HG03689.mapped.ILLUMINA.bwa.STU.exome.20130415	791	337	381	0	701	187	562	676	573	108	676	589	464	186	65	0	591
HG03690.mapped.ILLUMINA.bwa.STU.exome.20130415	796	332	375	388	727	476	563	675	585	0	662	592	0	0	72	115	597
HG03691.mapped.ILLUMINA.bwa.STU.exome.20130415	798	329	372	388	709	463	563	665	579	0	0	0	0	0	0	253	594
HG03692.mapped.ILLUMINA.bwa.STU.exome.20130422	684	237	255	186	504	274	532	647	469	0	0	0	0	0	22	57	577
HG03693.mapped.ILLUMINA.bwa.STU.exome.20130415	684	0	0	300	591	366	528	633	465	0	0	0	0	0	0	76	573
HG03694.mapped.ILLUMINA.bwa.STU.exome.20130415	801	332	369	390	712	475	564	675	0	110	674	589	462	189	0	0	597
HG03695.mapped.ILLUMINA.bwa.STU.exome.20130415	798	0	0	393	710	477	560	676	580	0	0	0	0	0	0	221	596
HG03696.mapped.ILLUMINA.bwa.STU.exome.20130415	799	0	0	394	714	474	558	666	574	0	0	0	0	0	0	148	595
HG03697.mapped.ILLUMINA.bwa.STU.exome.20130415	694	341	380	0	678	186	558	676	470	109	671	576	387	187	0	101	597
HG03698.mapped.ILLUMINA.bwa.STU.exome.20130415	697	55	58	395	718	481	559	675	583	0	132	35	0	12	55	104	593
HG03702.mapped.ILLUMINA.bwa.PJL.exome.20130415	690	0	0	392	717	478	558	659	454	105	643	0	448	181	0	81	589
HG03703.mapped.ILLUMINA.bwa.PJL.exome.20130415	598	337	363	379	691	379	559	666	576	0	0	0	0	0	54	99	592
HG03705.mapped.ILLUMINA.bwa.PJL.exome.20130415	641	294	311	324	669	428	546	632	321	0	599	493	351	168	24	4	584
HG03706.mapped.ILLUMINA.bwa.PJL.exome.20130415	669	286	0	332	682	433	550	630	420	84	576	0	357	174	0	49	582
HG03708.mapped.ILLUMINA.bwa.PJL.exome.20130415	798	326	375	386	724	472	563	674	476	109	675	590	462	186	56	1	593
HG03709.mapped.ILLUMINA.bwa.PJL.exome.20130415	797	0	0	399	720	481	561	670	561	106	660	0	459	187	53	2	595
HG03711.mapped.ILLUMINA.bwa.STU.exome.20130415	791	344	385	0	728	191	561	672	574	107	677	597	0	187	0	137	594
HG03713.mapped.ILLUMINA.bwa.ITU.exome.20130415	679	0	0	301	604	383	534	645	480	0	0	0	0	0	0	87	578
HG03714.mapped.ILLUMINA.bwa.ITU.exome.20130415	678	0	0	293	594	370	527	643	379	69	608	0	358	129	0	64	576
HG03715.mapped.ILLUMINA.bwa.ITU.exome.20130415	689	0	0	300	609	378	522	646	373	77	535	0	295	136	0	58	574
HG03716.mapped.ILLUMINA.bwa.ITU.exome.20130415	594	255	271	0	585	136	523	623	94	69	632	570	353	135	0	4	574
HG03717.mapped.ILLUMINA.bwa.ITU.exome.20130422	678	245	258	194	503	277	525	645	405	0	0	0	0	0	0	103	576
HG03718.mapped.ILLUMINA.bwa.ITU.exome.20130415	568	315	352	0	0	0	501	477	402	0	451	0	345	177	0	51	584
HG03720.mapped.ILLUMINA.bwa.ITU.exome.20130415	670	247	274	283	613	287	535	654	482	0	590	511	0	0	24	54	581
HG03722.mapped.ILLUMINA.bwa.ITU.exome.20130415	681	0	0	291	595	385	527	635	472	0	0	0	0	0	34	6	574
HG03727.mapped.ILLUMINA.bwa.ITU.exome.20130415	672	230	256	279	508	359	516	618	0	70	613	0	374	138	0	1	574
HG03729.mapped.ILLUMINA.bwa.ITU.exome.20130415	679	0	0	302	601	374	530	637	467	0	0	64	0	0	0	114	577
HG03730.mapped.ILLUMINA.bwa.ITU.exome.20130415	682	0	0	289	589	381	527	624	458	0	0	0	0	0	0	75	575
HG03731.mapped.ILLUMINA.bwa.ITU.exome.20130415	663	238	243	265	500	261	525	643	372	66	528	0	283	129	21	0	572
HG03733.mapped.ILLUMINA.bwa.STU.exome.20130415	803	0	0	403	726	483	561	677	588	0	0	0	0	0	69	143	597
HG03736.mapped.ILLUMINA.bwa.STU.exome.20130415	798	0	0	411	725	399	560	678	583	0	0	0	0	0	0	207	598
HG03738.mapped.ILLUMINA.bwa.STU.exome.20130415	800	336	373	392	700	464	560	674	576	108	668	0	465	183	0	116	597
HG03740.mapped.ILLUMINA.bwa.STU.exome.20130415	676	231	251	279	552	358	532	632	370	75	506	0	286	134	0	58	574
HG03741.mapped.ILLUMINA.bwa.STU.exome.20130422	674	234	271	282	606	268	526	650	467	0	595	554	0	0	29	62	573
HG03742.mapped.ILLUMINA.bwa.ITU.exome.20130415	797	327	364	386	693	462	557	649	563	0	637	0	385	186	50	1	594
HG03743.mapped.ILLUMINA.bwa.STU.exome.20130415	677	0	0	296	603	377	530	634	0	78	620	516	21	135	0	1	571

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG03744.mapped.ILLUMINA.bwa.STU.exome.20130415	683	333	363	0	712	187	559	665	581	0	633	553	0	0	47	102	599
HG03745.mapped.ILLUMINA.bwa.STU.exome.20130415	797	335	373	386	723	473	561	672	471	106	669	594	0	186	0	116	596
HG03746.mapped.ILLUMINA.bwa.STU.exome.20130415	669	231	257	275	556	359	524	607	370	0	559	0	297	133	0	48	578
HG03750.mapped.ILLUMINA.bwa.STU.exome.20130415	671	236	245	282	601	364	531	651	472	0	587	504	0	0	0	95	577
HG03752.mapped.ILLUMINA.bwa.STU.exome.20130415	791	340	384	0	714	187	562	676	577	108	680	592	465	190	0	147	597
HG03753.mapped.ILLUMINA.bwa.STU.exome.20130415	693	342	385	0	730	191	564	681	577	109	682	595	468	188	69	4	595
HG03754.mapped.ILLUMINA.bwa.STU.exome.20130415	680	0	0	288	601	370	524	635	397	0	0	0	0	0	0	94	577
HG03755.mapped.ILLUMINA.bwa.STU.exome.20130415	670	267	285	0	485	135	530	635	80	78	654	573	379	147	0	3	583
HG03756.mapped.ILLUMINA.bwa.STU.exome.20130415	599	260	278	0	606	139	532	647	462	74	637	576	295	136	31	0	577
HG03757.mapped.ILLUMINA.bwa.STU.exome.20130422	683	240	266	289	611	369	532	642	468	0	601	562	0	0	37	9	576
HG03760.mapped.ILLUMINA.bwa.STU.exome.20130415	697	337	377	0	725	193	563	668	570	109	674	595	0	0	0	117	592
HG03762.mapped.ILLUMINA.bwa.PJL.exome.20130415	695	0	0	339	653	447	542	620	444	0	0	0	0	0	0	73	582
HG03765.mapped.ILLUMINA.bwa.PJL.exome.20130415	684	300	330	306	649	429	544	603	0	102	607	520	450	181	0	4	577
HG03767.mapped.ILLUMINA.bwa.PJL.exome.20130415	694	0	0	363	665	459	551	635	0	98	613	0	448	180	0	5	585
HG03770.mapped.ILLUMINA.bwa.ITU.exome.20130415	671	241	261	288	576	272	531	653	477	71	0	0	0	0	0	81	574
HG03771.mapped.ILLUMINA.bwa.ITU.exome.20130415	687	0	0	298	602	372	525	640	473	0	0	0	0	0	24	59	576
HG03772.mapped.ILLUMINA.bwa.ITU.exome.20130415	683	241	258	276	607	277	526	645	383	76	632	516	290	134	0	51	572
HG03773.mapped.ILLUMINA.bwa.ITU.exome.20130415	676	237	251	272	563	355	532	642	472	0	0	0	0	0	28	63	573
HG03774.mapped.ILLUMINA.bwa.ITU.exome.20130415	663	281	302	179	644	420	548	604	418	0	432	520	0	0	0	57	581
HG03775.mapped.ILLUMINA.bwa.ITU.exome.20130415	599	255	268	0	556	134	530	652	463	0	605	512	0	0	25	70	570
HG03777.mapped.ILLUMINA.bwa.ITU.exome.20130415	802	0	0	393	731	479	564	672	574	107	663	19	461	184	0	112	595
HG03778.mapped.ILLUMINA.bwa.ITU.exome.20130415	799	334	372	389	726	475	560	674	480	106	669	597	103	186	0	114	592
HG03779.mapped.ILLUMINA.bwa.ITU.exome.20130415	696	334	375	0	692	185	558	669	478	110	667	587	460	186	0	100	594
HG03780.mapped.ILLUMINA.bwa.ITU.exome.20130415	690	0	0	202	674	363	550	634	326	88	537	0	356	172	0	51	592
HG03781.mapped.ILLUMINA.bwa.ITU.exome.20130415	687	0	0	295	592	377	532	640	358	69	584	508	0	133	26	2	575
HG03782.mapped.ILLUMINA.bwa.ITU.exome.20130415	796	117	124	394	718	478	558	666	568	105	643	250	460	187	0	102	595
HG03784.mapped.ILLUMINA.bwa.ITU.exome.20130415	676	0	0	299	594	376	527	635	366	72	589	0	292	132	29	4	571
HG03785.mapped.ILLUMINA.bwa.ITU.exome.20130415	694	338	376	0	713	190	564	679	479	112	675	594	465	187	0	108	595
HG03786.mapped.ILLUMINA.bwa.ITU.exome.20130415	660	235	253	265	540	273	529	635	473	0	0	0	0	0	0	98	575
HG03787.mapped.ILLUMINA.bwa.ITU.exome.20130415	654	244	261	261	543	262	512	611	382	0	577	0	358	132	31	2	572
HG03788.mapped.ILLUMINA.bwa.ITU.exome.20130415	684	0	0	295	605	378	532	642	443	75	590	0	285	133	0	55	574
HG03789.mapped.ILLUMINA.bwa.ITU.exome.20130415	657	234	255	267	561	276	527	634	359	76	620	570	0	137	0	47	577
HG03790.mapped.ILLUMINA.bwa.ITU.exome.20130415	702	332	368	386	733	475	562	680	582	108	676	593	0	0	66	119	595
HG03792.mapped.ILLUMINA.bwa.ITU.exome.20130415	701	0	0	396	718	474	559	672	579	0	0	0	0	0	57	108	593
HG03793.mapped.ILLUMINA.bwa.BEB.exome.20130415	678	250	267	273	589	374	530	642	382	78	603	0	296	134	0	57	572
HG03796.mapped.ILLUMINA.bwa.BEB.exome.20130415	686	0	0	299	589	382	530	639	468	0	0	0	0	0	25	58	575
HG03800.mapped.ILLUMINA.bwa.BEB.exome.20130415	677	243	259	291	610	286	528	652	478	0	601	562	0	0	31	66	577
HG03802.mapped.ILLUMINA.bwa.BEB.exome.20130415	592	255	272	0	503	133	531	640	453	68	616	572	0	130	0	58	576
HG03803.mapped.ILLUMINA.bwa.BEB.exome.20130415	744	237	0	270	602	373	531	636	382	74	575	0	283	135	0	61	576
HG03805.mapped.ILLUMINA.bwa.BEB.exome.20130415	796	323	370	384	700	462	562	667	0	109	661	0	468	189	0	1	595
HG03808.mapped.ILLUMINA.bwa.BEB.exome.20130415	796	333	376	385	726	472	563	669	582	0	663	587	0	0	0	181	596
HG03809.mapped.ILLUMINA.bwa.BEB.exome.20130415	697	340	378	0	670	188	564	675	568	109	672	592	459	185	62	0	597
HG03812.mapped.ILLUMINA.bwa.BEB.exome.20130422	676	0	0	291	596	367	528	634	389	0	0	0	0	0	0	71	570
HG03814.mapped.ILLUMINA.bwa.BEB.exome.20130415	702	0	0	388	711	465	555	667	575	0	0	0	0	0	47	99	592
HG03815.mapped.ILLUMINA.bwa.BEB.exome.20130415	684	0	0	305	604	377	529	642	0	81	636	0	374	137	0	0	575
HG03817.mapped.ILLUMINA.bwa.BEB.exome.20130422	677	0	0	296	592	373	524	632	470	0	0	0	0	0	21	52	572
HG03821.mapped.ILLUMINA.bwa.BEB.exome.20130415	693	298	332	339	658	359	550	633	547	0	0	0	0	0	0	85	585
HG03823.mapped.ILLUMINA.bwa.BEB.exome.20130415	703	322	365	382	718	460	563	668	557	105	668	558	383	185	0	100	592
HG03824.mapped.ILLUMINA.bwa.BEB.exome.20130415	700	322	368	380	698	466	549	649	0	105	665	0	467	188	0	2	589
HG03826.mapped.ILLUMINA.bwa.BEB.exome.20130415	795	326	371	384	715	468	558	668	0	107	666	593	0	189	0	0	591
HG03829.mapped.ILLUMINA.bwa.BEB.exome.20130415	597	333	373	0	701	183	556	655	569	0	659	591	459	184	57	0	594
HG03830.mapped.ILLUMINA.bwa.BEB.exome.20130415	797	326	367	383	718	470	560	658	577	0	654	581	0	0	0	147	596
HG03832.mapped.ILLUMINA.bwa.BEB.exome.20130415	703	0	0	385	709	474	561	665	573	0	0	0	0	0	69	0	596
HG03833.mapped.ILLUMINA.bwa.BEB.exome.20130415	798	329	369	382	722	472	562	677	0	110	679	590	468	192	0	1	596
HG03836.mapped.ILLUMINA.bwa.STU.exome.20130415	794	0	0	395	711	475	557	669	580	0	0	0	0	0	52	104	594
HG03837.mapped.ILLUMINA.bwa.STU.exome.20130415	793	322	373	385	696	381	559	666	0	111	667	557	459	191	0	0	595
HG03838.mapped.ILLUMINA.bwa.STU.exome.20130415	600	260	277	0	602	140	531	647	487	0	633	580	0	0	0	91	576
HG03844.mapped.ILLUMINA.bwa.STU.exome.20130415	640	233	247	274	604	367	530	641	0	79	638	558	374	138	0	0	573
HG03846.mapped.ILLUMINA.bwa.STU.exome.20130415	759	0	0	360	624	400	533	654	494	0	0	0	0	0	32	64	579
HG03848.mapped.ILLUMINA.bwa.STU.exome.20130415	601	264	278	0	32	0	535	651	486	0	91	52	50	48	0	131	579
HG03849.mapped.ILLUMINA.bwa.STU.exome.20130415	675	237	247	271	552	359	530	643	471	0	0	0	0	0	0	78	576
HG03850.mapped.ILLUMINA.bwa.STU.exome.20130415	565	305	332	0	653	174	549	622	0	98	633	566	364	177	0	3	581
HG03851.mapped.ILLUMINA.bwa.STU.exome.20130415	672	264	281	0	624	144	536	651	479	82	653	582	364	142	0	91	582
HG03854.mapped.ILLUMINA.bwa.STU.exome.20130415	795	323	367	384	695	467	558	669	565	104	647	0	462	181	0	127	591
HG03856.mapped.ILLUMINA.bwa.STU.exome.20130415	758	255	260	290	623	388	531	647	403	71	638	568	360	141	32	0	580
HG03857.mapped.ILLUMINA.bwa.STU.exome.20130415	798	0	0	393	715	477	559	672	568	105	653	0	459	188	0	122	592
HG03858.mapped.ILLUMINA.bwa.STU.exome.20130415	757	0	0	291	590	379	532	647	383	73	588	24	355	138	0	44	577
HG03861.mapped.ILLUMINA.bwa.ITU.exome.20130415	701	0	0	387	711	478	558	660	581	0	0	0	0	0	0	190	592
HG03862.mapped.ILLUMINA.bwa.ITU.exome.20130415	679	237	256	277	583	373	525	640	465	0	514	511	0	0	0	76	574
HG03863.mapped.ILLUMINA.bwa.ITU.exome.20130415	701	323	366	383	703	461	559	669	463	105	656	0	458	188	0	101	594
HG03864.mapped.ILLUMINA.bwa.ITU.exome.20130415	685	0	0	299	599	379	526	638	162	72	561	0	290	134	0	2	571
HG03866.mapped.ILLUMINA.bwa.ITU.exome.20130415	673	0	0	360	639	441	551	594	402	99	478	0	354	159	31	0	584
HG03867.mapped.ILLUMINA.bwa.ITU.exome.20130415	691	0	0	316	624	402	535	650	464	83	587	0	369	139	0	66	580
HG03868.mapped.ILLUMINA.bwa.ITU.exome.20130415	652	0	0	347	655	449	550	616	429	0	0	0	0	0	0	63	585
HG03869.mapped.ILLUMINA.bwa.ITU.exome.20130415	671	242	253	279	576	381	525	640	444	76	632	507	283	135	0	55	576
HG03870.mapped.ILLUMINA.bwa.ITU.exome.20130415	688	0	0	320	619	410	538	649	394	75	600	0	384	138	0	64	580
HG03871.mapped.ILLUMINA.bwa.ITU.exome.20130415	565	313	351	0	0	0	46	0	0	0	606	0	368	182	0	0	580
HG03872.mapped.ILLUMINA.bwa.ITU.exome.20130415	758	0	0	317	612	393	539	656	459	68	593	0	375	134	0	57	582
HG03873.mapped.ILLUMINA.bwa.ITU.exome.20130415	794	324	361	375	714	389	558	669	559	103	662	591	0	179	50	1	595
HG03874.mapped.ILLUMINA.bwa.ITU.exome.20130415	678	241	247	273	571	280	510	614	0	65	626	0	373	138	0	0	572
HG03875.mapped.ILLUMINA.bwa.ITU.exome.20130415	702	0	0	394	715	479	562	672	573	109	652	0	464	186	0	109	594
HG03882.mapped.ILLUMINA.bwa.ITU.exome.20130415	681	0	0	308	606	377	527	650	473	0	7	0	0	0	25	56	575
HG03884.mapped.ILLUMINA.bwa.STU.exome.20130415	598	258	261	283	603	381	529	645	381	67	641	563	364	135	0	66	574
HG03885.mapped.ILLUMINA.bwa.STU.exome.20130415	687	254	267	295	566	375	531	632	5	78	640	568	290	139	0	0	577
HG03886.mapped.ILLUMINA.bwa.STU.exome.20130415	752	0	0	306	601	390	532	636	0	83	626	0	378	137	0	2	573
HG03887.mapped.ILLUMINA.bwa.STU.exome.20130415	673	242	257	294	578	273	528	640	451	75	582	0	295	132	27	0	575
HG03888.mapped.ILLUMINA.bwa.STU.exome.20130415	592	258	275	0	593	137	530	648	375	64	631	566	294	135	0	63	571
HG03890.mapped.ILLUMINA.bwa.STU.exome.20130415	761	0	0	322	626	410	537	650	468	79	594	0	372	139	0	69	579
HG03894.mapped.ILLUMINA.bwa.STU.exome.20130415	684	0	0	366	664	461	549	638	421	89	569	0	365	175	34	5	581
HG03895.mapped.ILLUMINA.bwa.STU.exome.20130415	669	251	262	296	525	370	523	610	451	0	541	103	375	138	0	49	581
HG03896.mapped.ILLUMINA.bwa.STU.exome.20130422	686	0	0	300	601	374	525	639	468	0	0	0	0	0	0	80	575
HG03897.mapped.ILLUMINA.bwa.STU.exome.20130415	673	269	285	0	599	140	540	655	398	80	649	571	377	139	0	71	581
HG03898.mapped.ILLUMINA.bwa.STU.exome.20130415	676	235	247	282	603	283	529	644	385	65	640	507	295	134	27	0	576
HG03899.mapped.ILLUMINA.bwa.STU.exome.20130415	798	0	0	400	721	483	561	678	590	0	0	0	0	0	66	134	597
HG03900.mapped.ILLUMINA.bwa.STU.exome.20130415	760	0	0	294	602	384	534	648	462	72	527	0	358	138	30	4	574
HG03902.mapped.ILLUMINA.bwa.BEB.exome.20130422	672	241	249	270	488	353	527	638	382	0	0	0	0	0	0	72	573

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG03905.mapped.ILLUMINA.bwa.BEB.exome.20130422	596	241	264	0	563	130	530	632	382	61	606	492	282	132	24	3	570
HG03907.mapped.ILLUMINA.bwa.BEB.exome.20130415	688	337	365	382	723	386	558	673	578	0	656	588	0	13	58	112	591
HG03908.mapped.ILLUMINA.bwa.BEB.exome.20130415	701	325	373	381	722	472	560	672	0	110	671	591	470	188	0	0	595
HG03910.mapped.ILLUMINA.bwa.BEB.exome.20130422	593	243	251	262	491	262	527	631	365	70	518	0	286	128	0	46	575
HG03911.mapped.ILLUMINA.bwa.BEB.exome.20130422	682	0	0	301	594	375	526	645	450	74	566	0	292	137	0	74	573
HG03913.mapped.ILLUMINA.bwa.BEB.exome.20130415	702	331	374	387	723	476	563	673	569	104	670	588	464	185	0	121	597
HG03914.mapped.ILLUMINA.bwa.BEB.exome.20130415	796	322	370	384	719	470	562	675	579	0	653	591	0	0	0	153	597
HG03916.mapped.ILLUMINA.bwa.BEB.exome.20130422	668	233	253	267	549	365	528	632	463	0	0	0	0	0	29	59	577
HG03917.mapped.ILLUMINA.bwa.BEB.exome.20130415	704	326	371	385	709	475	563	675	577	108	660	0	463	186	0	116	598
HG03919.mapped.ILLUMINA.bwa.BEB.exome.20130422	594	249	270	0	586	132	530	631	450	0	612	511	0	0	21	56	573
HG03920.mapped.ILLUMINA.bwa.BEB.exome.20130415	696	0	0	416	720	475	561	675	586	0	0	0	0	0	0	255	597
HG03922.mapped.ILLUMINA.bwa.BEB.exome.20130415	703	41	55	396	719	475	562	672	584	0	0	79	0	0	0	160	597
HG03925.mapped.ILLUMINA.bwa.BEB.exome.20130415	798	325	372	377	705	385	560	673	584	0	0	0	0	0	61	122	595
HG03926.mapped.ILLUMINA.bwa.BEB.exome.20130415	699	0	0	388	710	464	561	675	563	104	654	0	456	184	0	102	596
HG03928.mapped.ILLUMINA.bwa.BEB.exome.20130422	678	0	0	288	594	380	526	620	460	0	0	0	0	0	29	43	575
HG03931.mapped.ILLUMINA.bwa.BEB.exome.20130422	638	228	240	247	489	297	530	629	375	72	510	0	351	132	0	50	571
HG03934.mapped.ILLUMINA.bwa.BEB.exome.20130422	673	240	250	274	553	355	515	579	364	0	589	0	297	129	0	49	572
HG03937.mapped.ILLUMINA.bwa.BEB.exome.20130422	679	233	241	266	597	368	524	633	459	0	521	497	0	0	30	1	575
HG03940.mapped.ILLUMINA.bwa.BEB.exome.20130415	701	0	0	394	718	476	562	669	584	0	0	0	0	0	58	119	593
HG03941.mapped.ILLUMINA.bwa.BEB.exome.20130415	695	0	0	386	706	470	561	662	469	103	649	0	378	182	0	93	592
HG03943.mapped.ILLUMINA.bwa.STU.exome.20130415	590	257	273	0	0	0	57	39	0	0	622	0	368	136	0	4	572
HG03944.mapped.ILLUMINA.bwa.STU.exome.20130415	680	306	316	315	582	361	549	614	441	0	0	0	0	0	0	68	583
HG03945.mapped.ILLUMINA.bwa.STU.exome.20130415	701	0	0	399	733	480	563	680	583	105	660	579	0	0	0	161	599
HG03947.mapped.ILLUMINA.bwa.STU.exome.20130415	762	254	272	282	625	376	536	658	459	73	625	568	371	142	0	74	581
HG03948.mapped.ILLUMINA.bwa.STU.exome.20130422	643	239	243	276	612	372	525	639	444	77	618	502	354	137	0	53	573
HG03949.mapped.ILLUMINA.bwa.STU.exome.20130415	681	250	258	296	628	292	539	663	490	0	626	575	0	0	29	67	578
HG03950.mapped.ILLUMINA.bwa.STU.exome.20130415	756	253	264	288	618	373	531	652	456	78	629	566	0	139	0	64	576
HG03951.mapped.ILLUMINA.bwa.STU.exome.20130415	794	329	376	383	721	469	560	675	566	106	673	586	457	186	0	116	593
HG03953.mapped.ILLUMINA.bwa.STU.exome.20130415	668	250	269	298	587	375	537	650	402	82	596	0	369	143	0	72	581
HG03955.mapped.ILLUMINA.bwa.STU.exome.20130415	791	338	375	0	0	0	561	672	475	109	658	0	459	187	0	129	598
HG03960.mapped.ILLUMINA.bwa.ITU.exome.20130415	760	0	0	314	619	389	531	645	0	89	626	59	384	143	0	3	583
HG03963.mapped.ILLUMINA.bwa.ITU.exome.20130415	750	247	260	297	633	394	537	643	463	79	626	565	355	135	0	66	583
HG03965.mapped.ILLUMINA.bwa.ITU.exome.20130415	702	0	0	403	723	396	550	675	591	107	667	0	467	188	0	203	594
HG03967.mapped.ILLUMINA.bwa.ITU.exome.20130415	800	335	374	397	712	480	559	666	0	107	677	0	473	193	0	0	598
HG03968.mapped.ILLUMINA.bwa.ITU.exome.20130415	737	249	256	292	622	392	536	646	491	0	604	563	0	0	0	105	578
HG03969.mapped.ILLUMINA.bwa.ITU.exome.20130415	658	0	0	334	628	439	540	614	334	0	0	0	0	0	0	69	583
HG03971.mapped.ILLUMINA.bwa.ITU.exome.20130415	702	330	370	382	718	470	562	677	577	106	655	586	215	72	0	231	596
HG03973.mapped.ILLUMINA.bwa.ITU.exome.20130415	795	326	375	383	698	460	558	674	580	0	0	0	0	0	63	99	595
HG03974.mapped.ILLUMINA.bwa.ITU.exome.20130415	794	326	373	382	719	461	560	673	566	104	669	590	388	186	0	110	595
HG03976.mapped.ILLUMINA.bwa.ITU.exome.20130415	699	324	369	383	700	459	555	655	474	0	650	0	456	184	52	2	595
HG03977.mapped.ILLUMINA.bwa.ITU.exome.20130415	585	308	341	0	672	180	553	628	285	97	625	582	327	162	25	3	581
HG03978.mapped.ILLUMINA.bwa.ITU.exome.20130415	687	0	0	294	596	387	531	648	449	72	564	0	289	136	0	53	576
HG03985.mapped.ILLUMINA.bwa.STU.exome.20130415	643	283	309	301	590	431	546	615	543	0	0	0	0	0	21	38	581
HG03986.mapped.ILLUMINA.bwa.STU.exome.20130415	663	239	260	275	594	359	529	634	432	67	614	565	0	130	0	50	574
HG03989.mapped.ILLUMINA.bwa.STU.exome.20130415	694	298	321	311	667	439	547	635	398	0	599	516	349	163	0	50	585
HG03990.mapped.ILLUMINA.bwa.STU.exome.20130415	667	293	302	279	647	426	547	629	542	0	467	548	0	0	27	36	586
HG03991.mapped.ILLUMINA.bwa.STU.exome.20130415	679	0	0	350	666	466	551	635	0	100	605	0	441	183	0	3	584
HG03995.mapped.ILLUMINA.bwa.STU.exome.20130415	796	0	0	404	728	478	559	668	585	0	0	0	0	0	0	171	597
HG03998.mapped.ILLUMINA.bwa.STU.exome.20130415	590	281	306	295	666	343	542	612	0	89	624	558	0	174	0	1	582
HG03999.mapped.ILLUMINA.bwa.STU.exome.20130415	688	328	368	371	718	468	559	666	569	106	664	580	384	186	0	107	593
HG04001.mapped.ILLUMINA.bwa.ITU.exome.20130415	559	284	304	265	601	401	544	609	439	0	0	0	0	0	0	74	584
HG04002.mapped.ILLUMINA.bwa.ITU.exome.20130415	700	327	371	385	718	473	563	662	573	0	652	571	0	0	0	137	596
HG04003.mapped.ILLUMINA.bwa.STU.exome.20130415	674	0	0	311	682	440	549	628	0	96	627	528	331	175	0	1	580
HG04006.mapped.ILLUMINA.bwa.STU.exome.20130422	665	135	240	271	571	274	527	642	21	81	645	516	287	137	0	1	574
HG04014.mapped.ILLUMINA.bwa.ITU.exome.20130415	734	251	252	287	618	286	534	663	493	0	523	522	0	0	36	66	579
HG04015.mapped.ILLUMINA.bwa.ITU.exome.20130415	669	269	286	0	621	145	538	655	399	81	648	586	374	142	0	86	583
HG04017.mapped.ILLUMINA.bwa.ITU.exome.20130415	701	0	0	395	721	475	561	670	582	0	0	0	0	0	0	205	596
HG04018.mapped.ILLUMINA.bwa.ITU.exome.20130415	793	0	0	396	718	471	557	673	461	105	650	588	0	185	0	106	596
HG04019.mapped.ILLUMINA.bwa.ITU.exome.20130415	756	0	0	304	619	375	534	639	471	0	0	27	0	0	0	115	582
HG04020.mapped.ILLUMINA.bwa.ITU.exome.20130415	765	0	0	314	619	410	536	656	474	76	609	0	372	140	0	83	581
HG04022.mapped.ILLUMINA.bwa.ITU.exome.20130415	759	0	0	314	616	399	528	651	492	0	0	0	0	0	0	116	581
HG04023.mapped.ILLUMINA.bwa.ITU.exome.20130415	583	265	304	98	648	350	545	625	310	0	592	513	340	166	0	35	585
HG04025.mapped.ILLUMINA.bwa.ITU.exome.20130415	672	269	283	0	7	0	529	638	0	73	639	0	395	142	0	3	581
HG04026.mapped.ILLUMINA.bwa.ITU.exome.20130415	694	324	369	372	714	466	560	649	569	0	641	556	0	0	0	136	591
HG04029.mapped.ILLUMINA.bwa.STU.exome.20130415	670	265	281	0	571	141	538	649	463	81	634	570	372	141	0	75	579
HG04033.mapped.ILLUMINA.bwa.STU.exome.20130415	742	249	260	291	620	398	537	664	380	87	637	571	298	142	34	5	579
HG04035.mapped.ILLUMINA.bwa.STU.exome.20130415	599	269	285	0	590	139	531	616	0	81	646	584	375	145	0	7	579
HG04038.mapped.ILLUMINA.bwa.STU.exome.20130415	663	0	0	331	622	456	535	611	0	91	571	507	345	175	0	4	577
HG04039.mapped.ILLUMINA.bwa.STU.exome.20130415	674	0	0	345	622	440	545	602	362	0	498	0	337	154	0	36	572
HG04042.mapped.ILLUMINA.bwa.STU.exome.20130415	671	259	283	0	568	142	538	657	398	80	642	572	373	144	0	58	581
HG04047.mapped.ILLUMINA.bwa.STU.exome.20130415	680	287	318	310	617	447	536	592	421	0	552	0	352	167	32	1	587
HG04054.mapped.ILLUMINA.bwa.ITU.exome.20130415	675	0	0	363	669	379	545	624	551	0	0	0	0	0	48	3	585
HG04056.mapped.ILLUMINA.bwa.ITU.exome.20130415	658	0	0	355	658	460	549	625	303	89	452	0	406	146	0	39	576
HG04059.mapped.ILLUMINA.bwa.ITU.exome.20130415	581	315	352	0	655	178	550	628	501	84	629	577	0	163	0	47	589
HG04060.mapped.ILLUMINA.bwa.ITU.exome.20130415	699	310	330	351	635	444	526	599	423	0	568	522	0	171	0	47	592
HG04061.mapped.ILLUMINA.bwa.ITU.exome.20130415	580	324	352	0	619	161	551	641	545	0	557	519	0	0	33	58	590
HG04062.mapped.ILLUMINA.bwa.ITU.exome.20130415	680	0	0	361	657	455	552	627	306	91	541	0	354	168	0	52	583
HG04063.mapped.ILLUMINA.bwa.ITU.exome.20130415	756	254	263	288	610	289	522	644	476	0	599	0	294	141	34	0	579
HG04070.mapped.ILLUMINA.bwa.ITU.exome.20130415	790	342	371	384	728	387	558	671	0	111	676	588	472	188	0	2	595
HG04075.mapped.ILLUMINA.bwa.STU.exome.20130415	703	334	375	387	725	473	562	667	578	0	653	587	0	0	0	240	594
HG04076.mapped.ILLUMINA.bwa.ITU.exome.20130415	680	297	312	309	599	430	537	500	297	0	483	0	356	167	0	44	581
HG04080.mapped.ILLUMINA.bwa.ITU.exome.20130415	666	293	320	260	646	426	551	617	536	0	536	504	0	0	30	36	575
HG04090.mapped.ILLUMINA.bwa.ITU.exome.20130415	575	273	321	301	490	339	520	487	403	0	455	0	309	166	0	36	572
HG04093.mapped.ILLUMINA.bwa.ITU.exome.20130415	596	262	281	0	592	139	536	656	466	76	637	575	377	133	0	75	579
HG04094.mapped.ILLUMINA.bwa.ITU.exome.20130415	556	285	311	282	653	418	543	611	441	0	384	489	0	0	0	56	581
HG04096.mapped.ILLUMINA.bwa.ITU.exome.20130415	702	327	378	389	710	472	561	672	0	111	670	0	470	188	0	0	597
HG04098.mapped.ILLUMINA.bwa.ITU.exome.20130415	800	328	372	389	706	463	561	671	578	0	0	0	0	0	0	171	595
HG04099.mapped.ILLUMINA.bwa.STU.exome.20130415	597	264	281	0	622	140	536	656	459	67	640	583	371	137	0	57	580
HG04100.mapped.ILLUMINA.bwa.STU.exome.20130415	698	316	370	376	717	470	558	662	459	102	661	549	375	184	49	1	589
HG04106.mapped.ILLUMINA.bwa.STU.exome.20130415	764	0	0	317	621	388	535	653	442	75	589	571	0	139	0	79	581
HG04107.mapped.ILLUMINA.bwa.STU.exome.20130415	671	267	279	0	592	385	536	652	394	80	643	581	0	139	0	63	582
HG04118.mapped.ILLUMINA.bwa.ITU.exome.20130415	564	319	356	0	611	155	550	612	357	97	595	503	316	157	0	48	577
HG04131.mapped.ILLUMINA.bwa.BEB.exome.20130415	668	284	308	223	634	346	500	599	4	0	593	0	370	177	0	5	583
HG04134.mapped.ILLUMINA.bwa.BEB.exome.20130415	678	0	0	362	662	453	551	623	540	0	0	0	0	0	47	0	584
HG04140.mapped.ILLUMINA.bwa.BEB.exome.20130415	674	0	0	359	676	465	553	644	550	0	0	0	0	0	41	67	587
HG04141.mapped.ILLUMINA.bwa.BEB.exome.20130415	684	0	0	374	658	449	546	646	545	0	0	0	0	0	41	46	582

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
HG04144.mapped.ILLUMINA.bwa.BEB.exome.20130415	697	0	0	397	713	479	558	667	547	108	655	0	459	183	0	117	595
HG04146.mapped.ILLUMINA.bwa.BEB.exome.20130422	676	0	0	294	591	370	529	636	370	72	575	0	291	134	0	52	572
HG04152.mapped.ILLUMINA.bwa.BEB.exome.20130415	799	331	378	0	707	184	562	679	486	108	673	591	387	180	0	146	595
HG04153.mapped.ILLUMINA.bwa.BEB.exome.20130415	794	329	371	389	720	464	563	682	588	0	0	0	0	0	85	168	595
HG04155.mapped.ILLUMINA.bwa.BEB.exome.20130415	700	330	373	393	726	472	563	676	589	0	658	590	0	0	58	124	594
HG04156.mapped.ILLUMINA.bwa.BEB.exome.20130415	692	298	0	342	691	447	547	650	431	99	613	0	359	169	0	60	580
HG04158.mapped.ILLUMINA.bwa.BEB.exome.20130415	581	292	338	337	684	363	554	637	456	0	550	553	0	0	55	2	586
HG04159.mapped.ILLUMINA.bwa.BEB.exome.20130422	677	230	247	266	596	359	526	619	379	68	608	503	287	128	0	53	569
HG04161.mapped.ILLUMINA.bwa.BEB.exome.20130415	793	0	0	402	723	480	564	681	573	110	669	0	459	186	74	0	597
HG04162.mapped.ILLUMINA.bwa.BEB.exome.20130415	703	0	0	396	722	474	561	665	580	0	4	0	0	0	75	4	593
HG04164.mapped.ILLUMINA.bwa.BEB.exome.20130415	788	337	381	0	719	186	563	670	480	107	679	590	467	188	0	132	594
HG04171.mapped.ILLUMINA.bwa.BEB.exome.20130415	798	0	0	403	730	476	561	680	582	109	667	589	0	0	0	239	597
HG04173.mapped.ILLUMINA.bwa.BEB.exome.20130415	686	0	0	347	657	375	545	637	533	0	0	0	0	0	0	79	585
HG04176.mapped.ILLUMINA.bwa.BEB.exome.20130415	795	332	374	380	714	463	561	669	581	0	0	0	0	0	0	241	597
HG04177.mapped.ILLUMINA.bwa.BEB.exome.20130415	794	328	375	0	704	215	554	659	567	0	670	593	458	184	0	134	597
HG04180.mapped.ILLUMINA.bwa.BEB.exome.20130415	782	332	373	0	711	186	558	671	471	104	666	590	460	182	0	99	592
HG04182.mapped.ILLUMINA.bwa.BEB.exome.20130415	674	292	313	322	667	450	549	631	539	0	564	523	0	0	53	1	586
HG04183.mapped.ILLUMINA.bwa.BEB.exome.20130415	675	309	325	317	669	433	545	621	458	0	455	538	0	0	39	27	583
HG04185.mapped.ILLUMINA.bwa.BEB.exome.20130415	695	306	337	236	687	453	555	661	555	0	594	522	0	0	40	54	591
HG04186.mapped.ILLUMINA.bwa.BEB.exome.20130415	655	293	297	328	375	0	534	471	391	0	0	0	0	0	0	35	588
HG04188.mapped.ILLUMINA.bwa.BEB.exome.20130415	797	329	370	386	723	467	562	663	578	0	657	586	0	0	0	149	597
HG04189.mapped.ILLUMINA.bwa.BEB.exome.20130415	700	0	0	393	717	480	562	672	478	104	655	0	464	184	0	108	594
HG04194.mapped.ILLUMINA.bwa.BEB.exome.20130415	696	337	380	0	712	185	560	674	476	105	674	581	462	186	0	127	596
HG04195.mapped.ILLUMINA.bwa.BEB.exome.20130415	700	0	0	394	718	478	559	677	572	0	0	0	0	0	0	170	596
HG04198.mapped.ILLUMINA.bwa.ITU.exome.20130415	702	333	364	387	724	472	561	677	581	0	649	586	0	0	53	121	594
HG04200.mapped.ILLUMINA.bwa.ITU.exome.20130415	791	338	380	0	710	185	561	674	570	109	667	563	461	189	62	2	598
HG04202.mapped.ILLUMINA.bwa.ITU.exome.20130415	703	325	369	385	720	478	561	672	584	0	658	588	0	0	0	223	598
HG04206.mapped.ILLUMINA.bwa.ITU.exome.20130415	801	0	0	395	729	475	560	671	586	0	0	0	0	0	0	114	594
HG04209.mapped.ILLUMINA.bwa.ITU.exome.20130415	705	330	369	387	727	391	559	676	479	106	669	586	462	183	52	3	593
HG04210.mapped.ILLUMINA.bwa.STU.exome.20130415	800	0	0	399	725	394	553	678	588	0	0	0	0	0	89	3	596
HG04211.mapped.ILLUMINA.bwa.ITU.exome.20130415	799	334	379	392	715	471	562	672	587	0	39	8	0	0	0	229	600
HG04212.mapped.ILLUMINA.bwa.ITU.exome.20130415	798	0	0	394	721	477	563	677	570	108	662	0	462	188	61	0	596
HG04214.mapped.ILLUMINA.bwa.ITU.exome.20130415	795	331	367	384	702	471	561	673	565	103	652	0	387	181	0	105	593
HG04216.mapped.ILLUMINA.bwa.ITU.exome.20130415	792	339	384	0	729	194	562	685	571	110	683	598	0	186	70	2	596
HG04219.mapped.ILLUMINA.bwa.ITU.exome.20130415	698	317	364	365	682	458	561	661	0	110	659	0	466	186	0	0	590
HG04222.mapped.ILLUMINA.bwa.ITU.exome.20130415	701	0	0	387	713	469	560	658	469	103	0	0	458	182	0	94	589
HG04225.mapped.ILLUMINA.bwa.ITU.exome.20130415	702	329	371	384	718	475	562	673	476	106	673	583	460	186	0	131	595
HG04227.mapped.ILLUMINA.bwa.STU.exome.20130415	702	0	0	393	716	471	558	668	584	0	0	0	0	0	59	113	596
HG04229.mapped.ILLUMINA.bwa.STU.exome.20130415	595	327	361	0	715	236	558	659	579	0	643	558	0	0	0	143	593
HG04235.mapped.ILLUMINA.bwa.ITU.exome.20130415	701	330	370	378	701	384	560	669	578	0	0	0	0	0	54	122	593
HG04238.mapped.ILLUMINA.bwa.ITU.exome.20130415	700	0	0	396	719	470	557	675	581	0	0	0	0	0	62	111	594
HG04239.mapped.ILLUMINA.bwa.ITU.exome.20130415	695	326	369	375	711	466	562	668	472	104	663	579	381	185	0	103	594
NA06984.mapped.ILLUMINA.bwa.CEU.exome.20120522	646	230	226	242	578	253	525	639	360	62	624	478	281	119	0	54	572
NA06985.mapped.ILLUMINA.bwa.CEU.exome.20130415	660	139	191	177	287	302	524	558	298	0	0	0	0	0	9	25	556
NA06986.mapped.ILLUMINA.bwa.CEU.exome.20121211	674	269	283	0	0	0	538	662	499	0	0	0	0	0	0	218	581
NA06989.mapped.ILLUMINA.bwa.CEU.exome.20120522	682	250	269	294	579	369	537	657	392	65	614	0	361	141	0	80	579
NA06994.mapped.ILLUMINA.bwa.CEU.exome.20120522	787	0	0	373	698	477	556	562	566	0	0	0	0	0	0	165	595
NA07000.mapped.ILLUMINA.bwa.CEU.exome.20130415	667	145	0	97	568	341	481	542	288	0	253	0	254	162	0	30	550
NA07037.mapped.ILLUMINA.bwa.CEU.exome.20121211	698	0	0	358	673	341	531	639	523	0	0	0	0	0	0	123	584
NA07048.mapped.ILLUMINA.bwa.CEU.exome.20120522	685	235	270	295	590	279	533	656	480	0	0	0	0	0	31	69	582
NA07051.mapped.ILLUMINA.bwa.CEU.exome.20120522	757	243	262	277	620	370	530	649	387	66	642	560	0	138	0	67	580
NA07056.mapped.ILLUMINA.bwa.CEU.exome.20130415	606	105	87	86	262	306	480	393	301	0	0	0	0	0	0	42	545
NA07347.mapped.ILLUMINA.bwa.CEU.exome.20121211	761	0	0	315	611	393	531	657	486	0	0	0	0	0	0	133	580
NA07357.mapped.ILLUMINA.bwa.CEU.exome.20130415	611	0	0	237	521	364	499	550	318	0	0	0	0	0	0	57	542
NA10847.mapped.ILLUMINA.bwa.CEU.exome.20121211	704	322	0	271	708	386	557	644	0	100	651	583	448	186	0	0	598
NA10851.mapped.ILLUMINA.bwa.CEU.exome.20130415	643	0	0	255	586	372	488	550	327	0	0	0	0	0	0	64	552
NA11829.mapped.ILLUMINA.bwa.CEU.exome.20130415	647	121	142	220	442	284	502	555	299	0	0	0	0	0	21	0	562
NA11830.mapped.ILLUMINA.bwa.CEU.exome.20130415	543	163	162	0	0	0	463	504	282	0	0	0	0	0	16	0	544
NA11831.mapped.ILLUMINA.bwa.CEU.exome.20130415	660	117	146	207	305	274	485	524	288	0	0	0	0	0	10	20	545
NA11832.mapped.ILLUMINA.bwa.CEU.exome.20130415	630	143	201	219	607	312	501	559	329	0	251	375	0	0	0	43	565
NA11840.mapped.ILLUMINA.bwa.CEU.exome.20120522	688	0	0	379	705	473	555	644	552	0	540	0	367	180	0	92	596
NA11843.mapped.ILLUMINA.bwa.CEU.exome.20120522	676	0	0	267	580	361	526	635	450	0	0	0	0	0	0	78	571
NA11881.mapped.ILLUMINA.bwa.CEU.exome.20130415	624	134	232	225	355	309	530	569	311	0	0	0	0	0	26	0	569
NA11892.mapped.ILLUMINA.bwa.CEU.exome.20121211	593	299	323	0	665	163	545	627	532	0	631	578	0	0	34	63	586
NA11893.mapped.ILLUMINA.bwa.CEU.exome.20121211	697	0	0	351	666	436	545	637	535	0	0	0	0	0	0	139	585
NA11894.mapped.ILLUMINA.bwa.CEU.exome.20121211	699	291	309	340	645	419	546	635	449	0	0	0	0	0	0	104	589
NA11918.mapped.ILLUMINA.bwa.CEU.exome.20121211	766	0	0	315	620	392	534	664	495	0	0	0	0	0	28	97	582
NA11919.mapped.ILLUMINA.bwa.CEU.exome.20121211	679	0	0	291	587	376	523	630	472	0	0	0	0	0	0	98	574
NA11920.mapped.ILLUMINA.bwa.CEU.exome.20121211	756	259	275	297	565	390	536	665	496	0	0	0	0	0	32	88	581
NA11930.mapped.ILLUMINA.bwa.CEU.exome.20121211	596	241	246	0	485	123	528	645	293	61	628	484	276	118	0	52	574
NA11931.mapped.ILLUMINA.bwa.CEU.exome.20121211	698	285	313	343	676	432	541	644	415	99	631	589	0	159	0	63	587
NA11932.mapped.ILLUMINA.bwa.CEU.exome.20121211	784	290	308	344	672	419	543	639	406	97	648	535	334	157	0	70	587
NA11933.mapped.ILLUMINA.bwa.CEU.exome.20121211	691	0	0	352	679	431	543	647	532	0	0	0	0	0	0	149	589
NA11992.mapped.ILLUMINA.bwa.CEU.exome.20130415	634	160	189	207	354	381	494	547	259	0	267	0	257	147	0	29	558
NA11994.mapped.ILLUMINA.bwa.CEU.exome.20130415	643	0	0	334	568	429	499	549	0	93	393	0	344	169	0	0	545
NA11995.mapped.ILLUMINA.bwa.CEU.exome.20130415	624	0	0	209	325	332	449	365	219	0	109	0	0	125	0	15	526
NA12003.mapped.ILLUMINA.bwa.CEU.exome.20130415	481	88	84	42	51	206	409	427	183	0	0	0	0	0	0	19	511
NA12004.mapped.ILLUMINA.bwa.CEU.exome.20130415	617	126	128	171	253	268	474	474	325	0	0	0	0	0	0	36	532
NA12005.mapped.ILLUMINA.bwa.CEU.exome.20130415	631	159	212	209	295	297	471	576	255	0	192	0	282	147	0	29	558
NA12006.mapped.ILLUMINA.bwa.CEU.exome.20130415	553	173	237	0	359	160	522	546	323	0	195	392	0	0	0	56	560
NA12043.mapped.ILLUMINA.bwa.CEU.exome.20130415	654	138	238	212	577	356	516	597	274	0	381	350	263	151	0	27	568
NA12044.mapped.ILLUMINA.bwa.CEU.exome.20130415	649	148	152	219	394	259	476	553	254	94	228	0	224	151	12	0	545
NA12045.mapped.ILLUMINA.bwa.CEU.exome.20121211	687	252	258	284	559	283	532	648	490	0	0	0	0	0	31	60	579
NA12046.mapped.ILLUMINA.bwa.CEU.exome.20130415	535	106	146	158	446	307	501	507	323	0	132	421	0	0	0	46	554
NA12058.mapped.ILLUMINA.bwa.CEU.exome.20120522	757	0	0	303	609	385	534	644	383	65	567	0	358	137	0	63	576
NA12144.mapped.ILLUMINA.bwa.CEU.exome.20130415	631	0	0	339	560	360	496	581	330	0	0	0	0	0	0	50	554
NA12154.mapped.ILLUMINA.bwa.CEU.exome.20130415	642	0	0	241	568	429	490	578	251	0	303	0	261	143	0	26	563
NA12155.mapped.ILLUMINA.bwa.CEU.exome.20130415	618	147	149	214	298	318	488	586	325	0	0	0	0	0	11	25	554
NA12156.mapped.ILLUMINA.bwa.CEU.exome.20130415	624	0	0	229	474	353	484	517	230	0	281	0	194	113	0	23	521
NA12234.mapped.ILLUMINA.bwa.CEU.exome.20130415	648	0	0	265	594	339	501	583	268	0	105	0	253	154	0	24	552
NA12249.mapped.ILLUMINA.bwa.CEU.exome.20120522	799	0	0	380	697	471	555	641	463	0	541	0	449	187	0	85	597
NA12272.mapped.ILLUMINA.bwa.CEU.exome.20120522	698	0	0	388	700	470	554	559	457	88	629	0	377	183	0	94	596
NA12273.mapped.ILLUMINA.bwa.CEU.exome.20120522	600	0	0	374	599	384	544	559	561	0	0	0	0	0	0	104	595
NA12275.mapped.ILLUMINA.bwa.CEU.exome.20120522	593	338	367	0	687	184	556	651	455	89	650	592	370	174	0	78	593
NA12282.mapped.ILLUMINA.bwa.CEU.exome.20121211	699	0	0	373	701	478	552	558	564	0	0	0	0	0	0	138	593
NA12283.mapped.ILLUMINA.bwa.CEU.exome.20121211	695	321	365	274	584	458	555	560	561	0	0	0	0	0	0	132	595

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA12286.mapped.ILLUMINA.bwa.CEU.exome.20121211	792	0	0	372	700	459	554	660	564	0	0	0	0	0	61	100	593
NA12287.mapped.ILLUMINA.bwa.CEU.exome.20121211	699	0	0	356	670	428	540	637	437	99	608	0	330	163	0	60	591
NA12340.mapped.ILLUMINA.bwa.CEU.exome.20120522	671	0	0	276	555	353	525	649	422	60	555	0	334	124	18	0	570
NA12341.mapped.ILLUMINA.bwa.CEU.exome.20120522	742	0	0	280	533	357	528	637	426	0	0	0	0	0	15	47	571
NA12342.mapped.ILLUMINA.bwa.CEU.exome.20120522	666	0	0	252	579	344	526	637	443	0	0	0	0	0	17	65	568
NA12347.mapped.ILLUMINA.bwa.CEU.exome.20121211	699	280	305	346	645	336	541	647	541	0	0	0	0	0	40	65	593
NA12348.mapped.ILLUMINA.bwa.CEU.exome.20121211	702	0	0	350	668	334	544	649	0	106	651	507	327	165	0	0	589
NA12383.mapped.ILLUMINA.bwa.CEU.exome.20121211	697	275	301	336	666	327	545	647	0	104	649	510	349	165	0	0	584
NA12399.mapped.ILLUMINA.bwa.CEU.exome.20120522	676	247	265	294	586	287	531	638	486	0	0	0	0	0	0	127	580
NA12400.mapped.ILLUMINA.bwa.CEU.exome.20121211	690	0	0	303	602	393	533	658	488	0	0	0	0	0	43	3	576
NA12413.mapped.ILLUMINA.bwa.CEU.exome.20121211	698	0	0	357	666	435	545	637	435	101	613	542	0	165	0	76	590
NA12414.mapped.ILLUMINA.bwa.CEU.exome.20130415	645	0	0	342	543	354	487	580	344	0	0	0	0	0	9	33	560
NA12489.mapped.ILLUMINA.bwa.CEU.exome.20130415	648	0	0	252	451	354	498	588	331	0	0	0	0	0	16	37	556
NA12546.mapped.ILLUMINA.bwa.CEU.exome.20121211	698	0	0	358	673	431	543	643	428	101	608	491	0	157	48	0	586
NA12716.mapped.ILLUMINA.bwa.CEU.exome.20121211	694	0	0	380	699	471	555	636	539	0	540	0	379	185	0	106	596
NA12717.mapped.ILLUMINA.bwa.CEU.exome.20121211	696	0	0	367	691	462	554	555	464	0	0	0	0	0	0	106	592
NA12718.mapped.ILLUMINA.bwa.CEU.exome.20120522	680	326	363	363	694	385	556	555	466	0	541	590	0	0	0	132	594
NA12748.mapped.ILLUMINA.bwa.CEU.exome.20121211	720	223	215	247	551	249	526	638	447	0	0	0	0	0	0	87	570
NA12749.mapped.ILLUMINA.bwa.CEU.exome.20121211	698	0	0	356	666	437	544	653	537	0	0	0	0	0	0	132	590
NA12750.mapped.ILLUMINA.bwa.CEU.exome.20130415	700	323	360	359	683	465	556	759	611	0	0	0	0	0	54	88	596
NA12751.mapped.ILLUMINA.bwa.CEU.exome.20121211	694	0	0	379	700	386	548	656	567	0	0	0	0	0	0	141	593
NA12760.mapped.ILLUMINA.bwa.CEU.exome.20120522	693	321	365	363	595	463	556	557	567	0	0	0	0	0	0	129	596
NA12761.mapped.ILLUMINA.bwa.CEU.exome.20121211	593	333	367	0	0	0	556	644	0	92	555	0	460	185	0	0	589
NA12762.mapped.ILLUMINA.bwa.CEU.exome.20130415	615	157	137	157	278	301	497	517	318	0	0	0	0	0	0	41	523
NA12763.mapped.ILLUMINA.bwa.CEU.exome.20121211	692	319	358	271	599	458	556	635	563	0	534	579	0	0	51	71	596
NA12775.mapped.ILLUMINA.bwa.CEU.exome.20121211	594	300	327	0	646	161	548	652	425	103	655	528	335	160	35	1	588
NA12776.mapped.ILLUMINA.bwa.CEU.exome.20121211	699	293	318	346	660	418	545	643	543	0	0	0	0	0	42	87	591
NA12777.mapped.ILLUMINA.bwa.CEU.exome.20121211	700	0	0	360	679	432	550	653	534	0	0	0	0	0	41	74	587
NA12778.mapped.ILLUMINA.bwa.CEU.exome.20121211	782	0	0	358	669	437	546	643	511	98	626	0	423	164	34	1	588
NA12812.mapped.ILLUMINA.bwa.CEU.exome.20130415	642	144	139	215	471	299	493	549	328	0	261	352	0	0	0	43	550
NA12813.mapped.ILLUMINA.bwa.CEU.exome.20130415	561	300	310	0	491	178	538	603	324	0	486	525	0	169	0	57	570
NA12814.mapped.ILLUMINA.bwa.CEU.exome.20130415	649	0	0	242	604	416	483	531	267	89	294	0	231	115	0	34	560
NA12815.mapped.ILLUMINA.bwa.CEU.exome.20130415	600	122	157	201	540	316	509	430	275	0	369	272	214	130	0	23	540
NA12827.mapped.ILLUMINA.bwa.CEU.exome.20121211	701	282	298	220	647	333	524	616	0	102	607	0	336	161	0	0	568
NA12828.mapped.ILLUMINA.bwa.CEU.exome.20121211	700	0	0	366	684	436	545	644	422	102	623	0	427	162	0	83	589
NA12829.mapped.ILLUMINA.bwa.CEU.exome.20121211	676	250	265	295	613	375	532	649	0	80	652	509	381	138	0	0	575
NA12830.mapped.ILLUMINA.bwa.CEU.exome.20121211	673	0	0	276	570	344	523	639	443	0	0	0	0	0	21	54	571
NA12842.mapped.ILLUMINA.bwa.CEU.exome.20121211	758	259	278	309	609	399	537	668	502	0	0	0	0	0	0	228	582
NA12843.mapped.ILLUMINA.bwa.CEU.exome.20121211	672	0	0	268	578	347	527	639	439	0	0	0	0	0	0	106	567
NA12872.mapped.ILLUMINA.bwa.CEU.exome.20130415	596	125	26	165	357	307	460	524	259	0	258	0	176	123	0	17	550
NA12873.mapped.ILLUMINA.bwa.CEU.exome.20130415	624	0	0	246	451	351	485	551	334	0	0	0	0	0	12	24	550
NA12874.mapped.ILLUMINA.bwa.CEU.exome.20130415	600	0	0	240	450	402	479	565	304	0	0	0	0	0	0	35	548
NA12878.mapped.ILLUMINA.bwa.CEU.exome.20121211	683	243	263	291	609	373	532	649	392	82	642	564	364	137	0	66	577
NA12889.mapped.ILLUMINA.bwa.CEU.exome.20121211	761	255	276	300	614	396	540	657	491	0	0	0	0	0	0	154	578
NA12890.mapped.ILLUMINA.bwa.CEU.exome.20121211	766	267	279	207	539	293	540	668	507	0	0	0	0	0	57	116	582
NA18486.mapped.ILLUMINA.bwa.YRI.exome.20120522	751	253	134	202	609	289	533	632	467	0	636	0	367	140	0	84	580
NA18488.mapped.ILLUMINA.bwa.YRI.exome.20120522	683	0	0	271	600	385	531	631	476	0	0	0	0	0	29	73	581
NA18489.mapped.ILLUMINA.bwa.YRI.exome.20121211	679	0	265	294	620	369	535	649	478	0	607	0	316	0	54	0	575
NA18498.mapped.ILLUMINA.bwa.YRI.exome.20120522	659	205	233	159	496	290	526	617	390	0	0	0	0	0	0	91	571
NA18499.mapped.ILLUMINA.bwa.YRI.exome.20121211	692	254	266	286	560	386	531	658	493	0	0	0	0	0	0	140	579
NA18501.mapped.ILLUMINA.bwa.YRI.exome.20121211	760	0	0	351	619	404	536	652	492	0	0	0	0	0	47	0	580
NA18502.mapped.ILLUMINA.bwa.YRI.exome.20130415	655	166	269	226	559	360	528	599	352	0	0	0	0	0	23	53	572
NA18504.mapped.ILLUMINA.bwa.YRI.exome.20120522	685	0	0	311	611	378	533	641	490	0	0	0	0	0	47	1	577
NA18505.mapped.ILLUMINA.bwa.YRI.exome.20130415	676	0	277	248	633	429	545	622	435	0	459	0	351	0	24	50	577
NA18507.mapped.ILLUMINA.bwa.YRI.exome.20130415	639	0	0	233	609	432	524	565	286	0	336	0	322	147	14	0	551
NA18508.mapped.ILLUMINA.bwa.YRI.exome.20130415	697	264	273	236	641	436	548	619	364	0	412	490	0	0	26	55	589
NA18510.mapped.ILLUMINA.bwa.YRI.exome.20121211	759	0	0	310	620	374	536	654	488	0	0	0	0	0	34	78	577
NA18511.mapped.ILLUMINA.bwa.YRI.exome.20121211	701	282	295	338	670	425	544	634	521	0	601	520	0	0	40	0	580
NA18516.mapped.ILLUMINA.bwa.YRI.exome.20120522	758	264	278	302	625	383	536	654	481	0	633	576	0	0	43	0	577
NA18517.mapped.ILLUMINA.bwa.YRI.exome.20121211	699	273	304	328	632	411	543	621	448	0	0	0	0	0	29	67	588
NA18519.mapped.ILLUMINA.bwa.YRI.exome.20121211	730	0	0	292	541	358	528	634	452	0	0	0	0	0	31	0	568
NA18520.mapped.ILLUMINA.bwa.YRI.exome.20120522	762	0	0	320	614	398	536	648	491	0	0	0	0	0	55	0	581
NA18522.mapped.ILLUMINA.bwa.YRI.exome.20120522	755	255	279	206	600	287	534	640	475	0	636	0	377	142	58	0	583
NA18523.mapped.ILLUMINA.bwa.YRI.exome.20121211	596	300	329	0	676	166	544	635	534	0	639	548	0	0	0	123	588
NA18525.mapped.ILLUMINA.bwa.CHB.exome.20130415	655	0	0	245	567	428	495	534	313	0	0	0	0	0	13	15	551
NA18526.mapped.ILLUMINA.bwa.CHB.exome.20121211	696	0	0	363	670	438	536	637	538	0	0	0	0	0	42	51	587
NA18528.mapped.ILLUMINA.bwa.CHB.exome.20130415	648	0	0	340	556	372	513	572	337	0	0	0	0	0	0	63	565
NA18530.mapped.ILLUMINA.bwa.CHB.exome.20120522	697	0	0	357	680	437	542	640	542	0	0	0	0	0	60	0	589
NA18531.mapped.ILLUMINA.bwa.CHB.exome.20130415	626	0	0	236	445	428	511	529	253	93	209	0	221	153	6	2	559
NA18532.mapped.ILLUMINA.bwa.CHB.exome.20121211	703	0	0	366	682	442	545	634	541	0	0	0	0	0	73	0	590
NA18533.mapped.ILLUMINA.bwa.CHB.exome.20121211	756	0	0	306	601	387	531	641	484	0	0	0	0	0	44	0	573
NA18534.mapped.ILLUMINA.bwa.CHB.exome.20120522	692	0	0	351	662	437	538	617	444	0	0	0	0	0	54	0	587
NA18535.mapped.ILLUMINA.bwa.CHB.exome.20120522	767	0	0	320	647	404	537	658	0	89	653	587	0	146	0	0	585
NA18536.mapped.ILLUMINA.bwa.CHB.exome.20121211	692	0	0	358	662	433	547	633	436	102	622	533	0	162	38	0	587
NA18537.mapped.ILLUMINA.bwa.CHB.exome.20120522	694	272	306	344	640	411	520	564	405	0	594	0	322	153	32	0	586
NA18538.mapped.ILLUMINA.bwa.CHB.exome.20120522	756	253	273	298	574	380	534	656	392	76	612	564	0	138	30	1	577
NA18539.mapped.ILLUMINA.bwa.CHB.exome.20121211	686	0	0	306	609	291	525	661	390	81	614	0	368	137	0	79	579
NA18541.mapped.ILLUMINA.bwa.CHB.exome.20121211	682	0	0	308	611	385	529	662	455	75	598	0	293	136	36	0	578
NA18542.mapped.ILLUMINA.bwa.CHB.exome.20121211	702	293	305	345	690	431	549	658	436	105	649	583	423	161	50	1	592
NA18543.mapped.ILLUMINA.bwa.CHB.exome.20121211	699	0	0	385	673	436	543	642	537	0	0	0	0	0	42	62	590
NA18544.mapped.ILLUMINA.bwa.CHB.exome.20121211	694	0	0	356	665	441	545	647	429	103	633	574	0	159	31	0	589
NA18545.mapped.ILLUMINA.bwa.CHB.exome.20121211	700	0	0	388	678	440	545	643	540	0	0	0	0	0	44	64	588
NA18546.mapped.ILLUMINA.bwa.CHB.exome.20121211	693	0	0	351	660	440	543	629	431	99	609	0	410	160	0	72	587
NA18547.mapped.ILLUMINA.bwa.CHB.exome.20121211	688	0	0	353	678	332	535	605	427	101	573	0	325	163	42	0	591
NA18548.mapped.ILLUMINA.bwa.CHB.exome.20121211	697	0	0	354	675	436	546	640	525	0	0	0	0	0	43	67	588
NA18549.mapped.ILLUMINA.bwa.CHB.exome.20121211	690	280	301	340	647	417	539	635	526	0	0	0	0	0	33	66	587
NA18550.mapped.ILLUMINA.bwa.CHB.exome.20121211	695	0	0	358	670	435	536	627	534	0	0	0	0	0	35	40	590
NA18552.mapped.ILLUMINA.bwa.CHB.exome.20121211	786	0	0	365	673	439	534	648	430	98	588	520	0	160	0	42	594
NA18553.mapped.ILLUMINA.bwa.CHB.exome.20120522	689	0	0	310	615	371	533	637	481	0	0	0	0	0	46	0	578
NA18555.mapped.ILLUMINA.bwa.CHB.exome.20121211	782	0	0	358	670	438	546	644	540	0	0	0	0	0	43	76	585
NA18557.mapped.ILLUMINA.bwa.CHB.exome.20121211	698	0	0	360	675	439	548	642	532	0	0	0	0	0	49	74	590
NA18558.mapped.ILLUMINA.bwa.CHB.exome.20121211	699	0	0	360	658	439	545	618	538	0	0	0	0	0	58	0	581
NA18559.mapped.ILLUMINA.bwa.CHB.exome.20121211	702	293	321	353	650	425	544	640	428	99	607	0	418	160	46	0	589
NA18560.mapped.ILLUMINA.bwa.CHB.exome.20120522	758	0	0	312	616	384	534	647	481	0	0	0	0	0	32	0	578
NA18561.mapped.ILLUMINA.bwa.CHB.exome.20121211	695	0	0	357	679	437	543	644	0	105	644	0	437	168	0	0	588
NA18562.mapped.ILLUMINA.bwa.CHB.exome.20121211	696	0	0	360	670	443	543	637	534	0	0	0	0	0	65	0	591

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA18563.mapped.ILLUMINA.bwa.CHB.exome.20121211	695	0	0	358	675	439	543	646	431	99	574	533	0	156	39	0	589
NA18564.mapped.ILLUMINA.bwa.CHB.exome.20121211	783	0	0	357	666	435	545	636	421	104	565	518	0	163	0	47	591
NA18565.mapped.ILLUMINA.bwa.CHB.exome.20120522	676	237	245	270	544	366	534	642	381	62	596	0	299	136	0	51	579
NA18566.mapped.ILLUMINA.bwa.CHB.exome.20121211	693	0	0	359	669	423	538	619	447	0	0	0	0	0	54	0	585
NA18567.mapped.ILLUMINA.bwa.CHB.exome.20120522	753	250	266	292	600	377	534	653	484	0	0	0	0	0	33	83	578
NA18570.mapped.ILLUMINA.bwa.CHB.exome.20121211	695	0	0	351	674	436	536	606	438	0	0	0	0	0	56	0	584
NA18571.mapped.ILLUMINA.bwa.CHB.exome.20121211	697	0	0	356	672	433	545	636	531	0	0	0	0	0	63	0	588
NA18572.mapped.ILLUMINA.bwa.CHB.exome.20120522	700	0	0	357	679	434	544	624	421	96	592	0	331	158	43	0	587
NA18573.mapped.ILLUMINA.bwa.CHB.exome.20121211	699	0	0	359	669	414	527	590	427	0	0	0	0	165	0	68	588
NA18574.mapped.ILLUMINA.bwa.CHB.exome.20120522	756	0	0	307	597	389	535	646	472	0	0	0	0	0	40	0	578
NA18577.mapped.ILLUMINA.bwa.CHB.exome.20121211	785	0	0	365	682	443	545	648	545	0	0	0	0	0	67	0	591
NA18579.mapped.ILLUMINA.bwa.CHB.exome.20121211	782	0	0	365	685	446	547	653	540	0	0	0	0	0	79	0	590
NA18582.mapped.ILLUMINA.bwa.CHB.exome.20121211	791	299	331	354	688	425	550	660	546	0	643	585	0	0	62	0	586
NA18591.mapped.ILLUMINA.bwa.CHB.exome.20130415	659	299	346	338	689	446	555	653	408	100	589	553	0	177	33	0	578
NA18592.mapped.ILLUMINA.bwa.CHB.exome.20121211	676	261	311	340	603	413	517	535	416	0	525	507	0	149	29	0	582
NA18593.mapped.ILLUMINA.bwa.CHB.exome.20121211	698	0	0	356	665	438	542	645	534	0	0	0	0	0	60	1	588
NA18595.mapped.ILLUMINA.bwa.CHB.exome.20121211	698	0	0	354	669	428	540	626	530	0	0	0	0	0	52	0	587
NA18596.mapped.ILLUMINA.bwa.CHB.exome.20121211	699	0	0	359	671	431	547	657	433	104	614	0	322	160	42	0	588
NA18597.mapped.ILLUMINA.bwa.CHB.exome.20121211	696	0	0	354	663	434	544	641	527	0	0	0	0	0	63	0	587
NA18599.mapped.ILLUMINA.bwa.CHB.exome.20121211	775	0	0	350	666	436	540	629	531	0	0	0	0	0	61	0	583
NA18602.mapped.ILLUMINA.bwa.CHB.exome.20120522	700	0	0	355	668	437	548	629	445	0	0	0	0	0	66	0	588
NA18603.mapped.ILLUMINA.bwa.CHB.exome.20121211	700	287	310	344	647	423	543	628	437	99	601	0	324	162	40	0	588
NA18605.mapped.ILLUMINA.bwa.CHB.exome.20121211	782	281	305	338	635	325	543	624	430	99	575	0	332	159	43	0	583
NA18606.mapped.ILLUMINA.bwa.CHB.exome.20121211	784	0	0	353	672	436	544	634	426	99	617	0	332	160	46	0	586
NA18608.mapped.ILLUMINA.bwa.CHB.exome.20121211	699	0	0	354	672	431	536	629	431	100	614	0	335	160	40	0	588
NA18609.mapped.ILLUMINA.bwa.CHB.exome.20120522	698	287	317	339	642	421	525	570	427	0	593	0	334	158	0	80	588
NA18610.mapped.ILLUMINA.bwa.CHB.exome.20121211	701	280	309	342	674	419	545	640	540	0	588	505	0	0	0	127	583
NA18611.mapped.ILLUMINA.bwa.CHB.exome.20120522	697	0	0	359	665	436	535	618	528	0	0	0	0	0	51	73	587
NA18612.mapped.ILLUMINA.bwa.CHB.exome.20121211	687	0	0	360	673	435	544	648	427	101	604	0	418	159	49	0	591
NA18613.mapped.ILLUMINA.bwa.CHB.exome.20120522	697	286	316	335	641	422	519	611	428	0	597	515	0	159	0	76	586
NA18614.mapped.ILLUMINA.bwa.CHB.exome.20130415	658	0	0	260	600	425	514	579	302	0	377	0	260	161	14	0	552
NA18615.mapped.ILLUMINA.bwa.CHB.exome.20130415	657	0	0	255	429	367	496	525	318	0	0	0	0	0	27	0	549
NA18616.mapped.ILLUMINA.bwa.CHB.exome.20120522	758	0	0	317	607	390	533	652	487	0	0	0	0	0	35	76	578
NA18617.mapped.ILLUMINA.bwa.CHB.exome.20130415	667	0	0	360	648	451	530	613	445	0	0	0	0	0	0	87	565
NA18618.mapped.ILLUMINA.bwa.CHB.exome.20130415	651	0	0	249	531	432	510	569	196	87	123	0	308	162	0	34	538
NA18619.mapped.ILLUMINA.bwa.CHB.exome.20130415	653	0	0	241	461	379	484	547	298	0	0	0	0	0	10	34	550
NA18620.mapped.ILLUMINA.bwa.CHB.exome.20121211	696	0	0	355	663	434	538	622	421	101	597	0	332	163	39	1	590
NA18621.mapped.ILLUMINA.bwa.CHB.exome.20121211	697	0	0	359	668	440	539	651	541	0	0	0	0	0	42	66	591
NA18622.mapped.ILLUMINA.bwa.CHB.exome.20121211	785	0	0	359	675	439	546	645	546	0	0	0	0	0	44	74	592
NA18623.mapped.ILLUMINA.bwa.CHB.exome.20121211	701	0	0	360	680	441	547	648	552	0	0	0	0	0	90	0	591
NA18624.mapped.ILLUMINA.bwa.CHB.exome.20121211	695	0	0	351	662	433	539	614	528	0	0	0	0	0	44	62	581
NA18625.mapped.ILLUMINA.bwa.CHB.exome.20130415	632	0	0	238	433	322	478	554	230	0	266	0	131	125	12	0	535
NA18626.mapped.ILLUMINA.bwa.CHB.exome.20130415	673	0	0	360	558	443	509	595	306	0	323	0	338	162	15	0	586
NA18627.mapped.ILLUMINA.bwa.CHB.exome.20130415	650	138	173	239	388	278	504	562	324	0	0	0	0	0	17	32	558
NA18628.mapped.ILLUMINA.bwa.CHB.exome.20130415	641	0	0	357	471	411	481	524	336	0	0	0	0	0	20	0	539
NA18629.mapped.ILLUMINA.bwa.CHB.exome.20130415	679	0	0	357	671	447	544	620	421	89	561	0	338	162	32	1	579
NA18630.mapped.ILLUMINA.bwa.CHB.exome.20130415	657	0	0	246	539	375	473	557	313	0	0	0	0	0	9	21	536
NA18631.mapped.ILLUMINA.bwa.CHB.exome.20120522	751	244	265	296	590	360	532	648	457	84	618	574	0	134	37	1	577
NA18632.mapped.ILLUMINA.bwa.CHB.exome.20121211	692	289	295	338	674	413	542	624	431	98	641	587	0	162	0	60	592
NA18633.mapped.ILLUMINA.bwa.CHB.exome.20121211	701	0	0	362	674	429	542	634	447	0	0	0	0	0	74	0	589
NA18634.mapped.ILLUMINA.bwa.CHB.exome.20120522	754	0	0	314	605	383	535	652	392	82	618	0	360	138	34	0	575
NA18635.mapped.ILLUMINA.bwa.CHB.exome.20121211	700	0	0	352	665	431	535	613	535	0	0	0	0	0	40	46	584
NA18636.mapped.ILLUMINA.bwa.CHB.exome.20121211	699	292	308	345	642	425	546	638	545	0	0	0	0	0	42	85	588
NA18637.mapped.ILLUMINA.bwa.CHB.exome.20121211	694	0	0	359	659	425	538	634	421	105	572	523	0	158	34	0	582
NA18638.mapped.ILLUMINA.bwa.CHB.exome.20121211	755	238	266	300	586	370	529	641	381	66	604	510	0	140	24	1	580
NA18639.mapped.ILLUMINA.bwa.CHB.exome.20130415	656	0	0	250	344	373	485	519	308	0	0	0	0	0	0	4	551
NA18640.mapped.ILLUMINA.bwa.CHB.exome.20130415	616	0	0	323	540	364	483	519	312	0	0	0	0	0	16	0	562
NA18641.mapped.ILLUMINA.bwa.CHB.exome.20130415	658	128	241	206	426	328	522	570	291	0	226	0	317	149	16	0	560
NA18642.mapped.ILLUMINA.bwa.CHB.exome.20130415	655	0	0	244	532	432	497	559	278	0	88	342	0	156	14	1	543
NA18643.mapped.ILLUMINA.bwa.CHB.exome.20130415	631	131	132	175	248	327	389	405	243	0	77	0	215	141	14	0	559
NA18644.mapped.ILLUMINA.bwa.CHB.exome.20130415	673	0	0	360	667	466	547	634	527	0	0	0	0	0	47	2	585
NA18645.mapped.ILLUMINA.bwa.CHB.exome.20130415	630	0	0	225	453	369	504	506	319	0	0	0	0	0	24	0	549
NA18646.mapped.ILLUMINA.bwa.CHB.exome.20130415	697	0	0	360	682	466	557	641	431	98	555	0	361	171	0	55	590
NA18647.mapped.ILLUMINA.bwa.CHB.exome.20130415	582	0	0	232	371	328	456	560	233	0	130	0	101	88	10	2	519
NA18648.mapped.ILLUMINA.bwa.CHB.exome.20130415	667	0	0	355	665	457	549	630	545	0	0	0	0	0	52	4	585
NA18740.mapped.ILLUMINA.bwa.CHB.exome.20130415	595	0	0	252	523	359	491	544	251	0	179	0	210	136	13	0	539
NA18745.mapped.ILLUMINA.bwa.CHB.exome.20130415	625	0	0	240	466	405	466	509	319	0	0	0	0	0	22	0	531
NA18747.mapped.ILLUMINA.bwa.CHB.exome.20130415	673	0	0	258	620	418	535	584	333	0	0	0	0	0	9	31	555
NA18748.mapped.ILLUMINA.bwa.CHB.exome.20130415	622	0	0	241	478	416	493	554	258	0	241	254	0	154	9	1	563
NA18749.mapped.ILLUMINA.bwa.CHB.exome.20130415	645	0	0	356	620	430	530	578	342	0	0	0	0	0	0	62	567
NA18757.mapped.ILLUMINA.bwa.CHB.exome.20130415	629	0	0	259	552	362	472	535	309	0	0	0	0	0	15	0	539
NA18853.mapped.ILLUMINA.bwa.YRI.exome.20120522	748	0	273	295	627	397	534	651	490	0	619	575	0	0	59	0	581
NA18856.mapped.ILLUMINA.bwa.YRI.exome.20120522	664	252	273	0	585	275	511	608	386	0	633	0	385	139	0	64	576
NA18858.mapped.ILLUMINA.bwa.YRI.exome.20121211	700	284	306	222	646	414	547	637	536	0	0	0	0	0	0	149	587
NA18861.mapped.ILLUMINA.bwa.YRI.exome.20121211	697	0	0	355	674	431	548	649	542	0	0	0	0	0	43	79	591
NA18864.mapped.ILLUMINA.bwa.YRI.exome.20130415	794	332	372	384	723	475	562	668	576	0	658	587	0	0	81	3	597
NA18865.mapped.ILLUMINA.bwa.YRI.exome.20130415	798	0	0	391	722	470	560	665	579	0	0	0	0	0	67	0	598
NA18867.mapped.ILLUMINA.bwa.YRI.exome.20120522	775	0	0	316	626	409	539	665	499	0	0	0	0	0	0	252	584
NA18868.mapped.ILLUMINA.bwa.YRI.exome.20120522	753	0	275	289	611	394	533	652	483	0	608	0	390	0	50	0	578
NA18870.mapped.ILLUMINA.bwa.YRI.exome.20121211	688	0	0	315	641	405	536	655	474	0	0	0	0	0	44	0	576
NA18871.mapped.ILLUMINA.bwa.YRI.exome.20120522	751	240	257	289	608	381	535	632	439	0	582	0	365	0	24	0	572
NA18873.mapped.ILLUMINA.bwa.YRI.exome.20120522	757	248	262	297	617	398	534	660	476	0	626	575	0	0	0	67	574
NA18874.mapped.ILLUMINA.bwa.YRI.exome.20120522	741	0	0	287	578	346	529	624	446	0	0	0	0	0	25	0	573
NA18876.mapped.ILLUMINA.bwa.YRI.exome.20130415	799	329	375	393	723	478	560	674	589	0	658	586	0	0	64	113	594
NA18877.mapped.ILLUMINA.bwa.YRI.exome.20130415	800	0	0	404	729	472	562	672	580	0	0	0	0	0	82	0	595
NA18878.mapped.ILLUMINA.bwa.YRI.exome.20130415	796	0	0	398	722	477	561	669	587	0	0	0	0	0	101	0	596
NA18879.mapped.ILLUMINA.bwa.YRI.exome.20130415	798	338	373	240	727	453	563	681	578	109	679	590	467	187	64	1	599
NA18881.mapped.ILLUMINA.bwa.YRI.exome.20130415	787	337	373	0	703	260	560	671	574	0	654	558	0	0	0	119	595
NA18907.mapped.ILLUMINA.bwa.YRI.exome.20121211	697	0	0	226	679	435	546	643	539	0	0	0	0	0	0	159	588
NA18908.mapped.ILLUMINA.bwa.YRI.exome.20120522	753	251	275	194	593	321	534	651	492	0	0	0	0	0	0	179	579
NA18909.mapped.ILLUMINA.bwa.YRI.exome.20121211	783	293	308	344	671	438	538	637	536	0	634	577	0	0	45	60	589
NA18910.mapped.ILLUMINA.bwa.YRI.exome.20120522	669	259	281	0	597	139	527	624	472	0	654	0	399	141	35	1	580
NA18912.mapped.ILLUMINA.bwa.YRI.exome.20120522	687	249	276	209	606	326	531	642	481	0	615	0	379	142	45	0	582
NA18915.mapped.ILLUMINA.bwa.YRI.exome.20130415	799	0	0	398	712	476	559	671	581	0	0	0	0	0	78	3	592
NA18916.mapped.ILLUMINA.bwa.YRI.exome.20121211	700	0	0	128	0	0	512	615	0	0	0	0	0	0	22	0	534
NA18917.mapped.ILLUMINA.bwa.YRI.exome.20120522	593	0	371	0	583	180	555	558	560	0	615	0	475	0	77	0	596

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA18923.mapped.ILLUMINA.bwa.YRI.exome.20120522	691	144	0	378	688	470	549	551	557	0	0	0	0	0	85	0	594
NA18924.mapped.ILLUMINA.bwa.YRI.exome.20120522	696	0	0	387	702	473	556	652	566	0	0	0	0	0	95	0	597
NA18933.mapped.ILLUMINA.bwa.YRI.exome.20120522	692	325	366	272	581	187	558	650	296	0	0	0	0	0	38	0	593
NA18934.mapped.ILLUMINA.bwa.YRI.exome.20120522	696	319	359	263	703	470	558	558	565	0	539	554	0	0	73	0	596
NA18939.mapped.ILLUMINA.bwa.JPT.exome.20130415	648	0	0	247	585	361	475	579	284	0	214	0	260	155	10	3	555
NA18940.mapped.ILLUMINA.bwa.JPT.exome.20121211	696	0	0	356	671	437	542	645	539	0	0	0	0	0	40	60	585
NA18941.mapped.ILLUMINA.bwa.JPT.exome.20130415	651	0	0	351	584	417	499	560	320	0	0	0	0	0	18	0	563
NA18942.mapped.ILLUMINA.bwa.JPT.exome.20121211	698	0	0	357	666	438	545	637	530	0	0	0	0	0	63	0	583
NA18943.mapped.ILLUMINA.bwa.JPT.exome.20121211	698	0	0	360	671	438	542	644	431	101	618	575	0	162	0	71	587
NA18944.mapped.ILLUMINA.bwa.JPT.exome.20121211	699	0	0	355	675	438	542	640	438	102	598	528	0	160	38	0	584
NA18945.mapped.ILLUMINA.bwa.JPT.exome.20121211	699	0	0	362	673	344	538	648	541	0	0	0	0	0	45	67	591
NA18946.mapped.ILLUMINA.bwa.JPT.exome.20130415	647	0	0	332	584	439	510	558	322	0	0	0	0	0	24	0	559
NA18947.mapped.ILLUMINA.bwa.JPT.exome.20121211	702	0	0	357	668	436	544	637	445	0	0	0	0	0	37	71	584
NA18948.mapped.ILLUMINA.bwa.JPT.exome.20121211	694	285	300	340	641	413	542	640	415	103	636	0	439	167	0	63	587
NA18949.mapped.ILLUMINA.bwa.JPT.exome.20121211	701	0	0	348	672	444	545	657	508	101	639	0	433	157	33	0	589
NA18950.mapped.ILLUMINA.bwa.JPT.exome.20120522	680	0	0	291	597	380	521	640	467	0	0	0	0	0	0	85	578
NA18951.mapped.ILLUMINA.bwa.JPT.exome.20121211	700	0	0	362	681	439	531	509	0	0	0	0	0	0	0	1	576
NA18952.mapped.ILLUMINA.bwa.JPT.exome.20121211	701	298	0	340	683	433	540	642	430	101	647	528	334	160	42	0	585
NA18953.mapped.ILLUMINA.bwa.JPT.exome.20120522	771	0	0	314	642	407	540	670	224	85	621	0	386	141	39	0	579
NA18954.mapped.ILLUMINA.bwa.JPT.exome.20130415	622	0	0	311	549	431	505	558	284	0	297	454	0	154	14	1	558
NA18956.mapped.ILLUMINA.bwa.JPT.exome.20130415	669	0	0	356	630	420	509	600	298	83	317	0	260	164	0	45	574
NA18957.mapped.ILLUMINA.bwa.JPT.exome.20130415	591	0	0	225	418	346	485	534	285	0	0	0	0	0	7	22	547
NA18959.mapped.ILLUMINA.bwa.JPT.exome.20121211	763	0	0	355	645	399	535	662	493	0	0	0	0	0	65	0	581
NA18960.mapped.ILLUMINA.bwa.JPT.exome.20120522	772	0	0	361	650	408	536	666	499	0	0	0	0	0	45	109	582
NA18961.mapped.ILLUMINA.bwa.JPT.exome.20120522	763	0	0	313	615	397	535	650	475	83	612	575	0	142	41	0	579
NA18962.mapped.ILLUMINA.bwa.JPT.exome.20130415	618	0	0	241	496	368	504	516	317	0	0	0	0	0	26	0	541
NA18963.mapped.ILLUMINA.bwa.JPT.exome.20130415	661	0	0	343	583	439	530	597	354	0	0	0	0	0	20	47	568
NA18964.mapped.ILLUMINA.bwa.JPT.exome.20120522	766	0	0	313	643	409	538	657	492	0	0	0	0	0	69	0	583
NA18965.mapped.ILLUMINA.bwa.JPT.exome.20130415	664	0	0	247	627	370	531	566	331	0	0	0	0	0	27	0	559
NA18966.mapped.ILLUMINA.bwa.JPT.exome.20121211	700	0	0	388	702	474	557	645	574	0	0	0	0	0	0	155	592
NA18967.mapped.ILLUMINA.bwa.JPT.exome.20121211	699	314	356	272	665	462	557	561	564	0	0	0	0	0	69	1	595
NA18968.mapped.ILLUMINA.bwa.JPT.exome.20120522	784	0	0	379	692	475	554	634	562	0	0	0	0	0	52	82	595
NA18969.mapped.ILLUMINA.bwa.JPT.exome.20120522	696	0	0	373	700	473	551	651	558	0	0	0	0	0	50	78	596
NA18970.mapped.ILLUMINA.bwa.JPT.exome.20120522	698	0	0	366	684	476	556	644	565	0	0	0	0	0	69	0	596
NA18971.mapped.ILLUMINA.bwa.JPT.exome.20120522	694	0	0	406	712	477	557	648	569	0	0	0	0	0	0	133	596
NA18972.mapped.ILLUMINA.bwa.JPT.exome.20121211	793	0	0	384	699	478	553	647	575	0	0	0	0	0	37	74	597
NA18973.mapped.ILLUMINA.bwa.JPT.exome.20121211	788	0	0	378	697	478	559	644	460	0	539	581	0	187	55	0	595
NA18974.mapped.ILLUMINA.bwa.JPT.exome.20120522	797	0	0	373	692	469	557	642	560	0	0	0	0	0	79	0	595
NA18975.mapped.ILLUMINA.bwa.JPT.exome.20120522	690	0	0	378	699	478	557	644	366	0	543	0	376	180	53	0	590
NA18976.mapped.ILLUMINA.bwa.JPT.exome.20120522	786	0	0	375	688	472	555	648	548	0	544	0	452	183	0	84	593
NA18977.mapped.ILLUMINA.bwa.JPT.exome.20130415	673	0	0	366	630	446	537	611	348	0	0	0	0	0	32	0	563
NA18978.mapped.ILLUMINA.bwa.JPT.exome.20130415	675	0	0	344	516	432	512	553	331	0	0	0	0	0	27	0	555
NA18979.mapped.ILLUMINA.bwa.JPT.exome.20130415	607	0	0	227	457	344	452	513	265	0	115	0	195	108	0	13	532
NA18980.mapped.ILLUMINA.bwa.JPT.exome.20130415	685	0	0	363	642	446	547	623	312	85	368	492	0	180	16	1	588
NA18981.mapped.ILLUMINA.bwa.JPT.exome.20120522	789	0	0	389	697	476	556	658	566	0	0	0	0	0	68	70	599
NA18982.mapped.ILLUMINA.bwa.JPT.exome.20120522	765	0	0	310	621	406	535	658	484	0	0	0	0	0	71	0	579
NA18983.mapped.ILLUMINA.bwa.JPT.exome.20120522	761	0	0	314	612	399	537	665	463	77	621	574	0	139	0	78	582
NA18984.mapped.ILLUMINA.bwa.JPT.exome.20121211	687	0	0	304	606	388	535	650	455	75	608	513	0	134	34	0	575
NA18985.mapped.ILLUMINA.bwa.JPT.exome.20120522	688	0	0	303	602	367	529	635	401	0	0	0	0	0	33	1	575
NA18986.mapped.ILLUMINA.bwa.JPT.exome.20120522	689	0	0	349	606	384	534	652	397	73	619	0	305	136	37	1	579
NA18987.mapped.ILLUMINA.bwa.JPT.exome.20120522	702	0	0	376	708	468	557	645	568	0	0	0	0	0	57	80	597
NA18988.mapped.ILLUMINA.bwa.JPT.exome.20120522	680	0	0	294	602	375	530	638	475	0	0	0	0	0	25	78	575
NA18989.mapped.ILLUMINA.bwa.JPT.exome.20120522	763	255	274	302	605	389	537	655	483	0	0	0	0	0	59	0	578
NA18990.mapped.ILLUMINA.bwa.JPT.exome.20120522	690	0	0	382	699	476	560	556	0	94	558	550	454	187	0	1	597
NA18991.mapped.ILLUMINA.bwa.JPT.exome.20120522	787	0	0	374	688	478	559	555	452	0	537	0	456	181	0	74	593
NA18992.mapped.ILLUMINA.bwa.JPT.exome.20130415	644	140	191	211	367	284	471	452	319	0	0	0	0	0	8	40	546
NA18993.mapped.ILLUMINA.bwa.JPT.exome.20130415	585	0	0	245	541	345	454	461	302	0	0	0	0	0	0	39	548
NA18994.mapped.ILLUMINA.bwa.JPT.exome.20130415	631	0	0	246	425	413	478	554	321	0	0	0	0	0	22	1	544
NA18995.mapped.ILLUMINA.bwa.JPT.exome.20130415	613	0	0	219	397	347	424	514	0	0	360	0	289	142	0	1	513
NA18997.mapped.ILLUMINA.bwa.JPT.exome.20130415	596	114	110	192	234	247	438	572	288	0	0	0	0	0	4	16	533
NA18998.mapped.ILLUMINA.bwa.JPT.exome.20130415	645	0	0	251	619	433	518	572	337	0	0	0	0	0	13	32	549
NA18999.mapped.ILLUMINA.bwa.JPT.exome.20120522	768	0	0	321	622	407	535	667	491	0	0	0	0	0	57	0	582
NA19000.mapped.ILLUMINA.bwa.JPT.exome.20120522	762	0	0	316	628	409	536	662	404	78	635	522	0	141	49	1	580
NA19001.mapped.ILLUMINA.bwa.JPT.exome.20130415	599	0	0	231	433	419	481	549	250	0	180	259	0	154	7	0	541
NA19002.mapped.ILLUMINA.bwa.JPT.exome.20130415	682	0	0	259	621	450	534	568	351	0	0	63	0	0	39	0	590
NA19003.mapped.ILLUMINA.bwa.JPT.exome.20120522	763	254	0	196	615	292	533	646	0	84	645	574	0	142	0	0	579
NA19004.mapped.ILLUMINA.bwa.JPT.exome.20120522	762	0	0	311	615	407	533	661	484	0	0	0	0	0	43	95	579
NA19005.mapped.ILLUMINA.bwa.JPT.exome.20130415	670	0	0	243	601	427	522	557	312	0	0	0	0	0	28	0	561
NA19006.mapped.ILLUMINA.bwa.JPT.exome.20130415	795	0	0	404	730	481	563	683	586	0	0	0	0	0	72	152	598
NA19007.mapped.ILLUMINA.bwa.JPT.exome.20120522	767	265	280	308	651	398	540	660	503	0	631	575	0	0	54	58	583
NA19009.mapped.ILLUMINA.bwa.JPT.exome.20130415	654	0	0	329	538	368	476	538	331	0	0	0	0	0	12	18	542
NA19010.mapped.ILLUMINA.bwa.JPT.exome.20130415	681	0	0	359	581	429	540	599	347	0	0	0	0	0	43	2	564
NA19011.mapped.ILLUMINA.bwa.JPT.exome.20130415	803	0	0	399	727	481	565	678	584	0	0	0	0	0	113	0	597
NA19012.mapped.ILLUMINA.bwa.JPT.exome.20120522	760	255	272	304	625	292	535	659	471	78	648	575	370	140	36	0	581
NA19017.mapped.ILLUMINA.bwa.LWK.exome.20121211	689	0	0	296	607	385	531	646	393	67	617	0	366	139	0	59	574
NA19019.mapped.ILLUMINA.bwa.LWK.exome.20121211	748	0	0	285	600	366	529	647	463	71	0	0	0	0	25	61	572
NA19020.mapped.ILLUMINA.bwa.LWK.exome.20130422	636	128	100	203	419	332	452	477	0	0	433	0	348	174	0	1	549
NA19023.mapped.ILLUMINA.bwa.LWK.exome.20121211	685	0	0	299	588	373	535	654	465	0	0	0	0	0	30	0	575
NA19024.mapped.ILLUMINA.bwa.LWK.exome.20121211	677	248	256	285	585	374	533	652	472	0	593	565	0	0	27	60	576
NA19025.mapped.ILLUMINA.bwa.LWK.exome.20130415	703	329	378	387	706	470	560	659	475	0	664	0	484	188	57	0	599
NA19026.mapped.ILLUMINA.bwa.LWK.exome.20121211	684	246	256	277	503	369	530	641	475	0	0	0	0	0	39	1	574
NA19027.mapped.ILLUMINA.bwa.LWK.exome.20130415	588	140	0	145	438	335	491	525	241	0	329	262	203	116	4	0	553
NA19028.mapped.ILLUMINA.bwa.LWK.exome.20130422	657	153	45	130	403	224	423	437	220	0	280	0	270	137	0	34	562
NA19030.mapped.ILLUMINA.bwa.LWK.exome.20121211	684	0	0	298	598	384	530	647	145	73	569	0	286	136	0	0	572
NA19031.mapped.ILLUMINA.bwa.LWK.exome.20130422	634	128	165	50	449	329	478	459	258	0	421	0	341	151	0	20	532
NA19035.mapped.ILLUMINA.bwa.LWK.exome.20130422	614	0	0	249	458	326	507	526	275	0	0	0	0	0	0	18	504
NA19036.mapped.ILLUMINA.bwa.LWK.exome.20130422	660	0	0	226	577	175	495	540	319	0	219	0	311	0	26	0	552
NA19037.mapped.ILLUMINA.bwa.LWK.exome.20130415	699	334	375	235	702	468	562	670	583	0	0	0	0	0	67	125	595
NA19038.mapped.ILLUMINA.bwa.LWK.exome.20130415	634	122	129	188	327	259	506	526	318	0	0	0	0	0	0	44	552
NA19041.mapped.ILLUMINA.bwa.LWK.exome.20130415	515	226	285	0	0	0	438	478	0	0	423	0	361	170	0	0	561
NA19042.mapped.ILLUMINA.bwa.LWK.exome.20130415	799	326	371	378	703	469	560	644	479	0	655	0	464	187	0	115	596
NA19043.mapped.ILLUMINA.bwa.LWK.exome.20121211	682	246	0	292	547	140	533	641	471	0	0	0	0	0	39	1	576
NA19054.mapped.ILLUMINA.bwa.JPT.exome.20120522	687	0	0	299	602	405	529	645	473	0	0	0	0	0	44	0	578
NA19055.mapped.ILLUMINA.bwa.JPT.exome.20120522	688	0	0	301	600	400	533	648	483	0	0	0	0	0	28	77	579
NA19056.mapped.ILLUMINA.bwa.JPT.exome.20120522	761	0	0	311	616	400	535	661	494	0	0	0	0	0	56	88	578
NA19057.mapped.ILLUMINA.bwa.JPT.exome.20120522	688	0	0	310	602	392	534	650	453	51	585	0	367	140	26	0	579

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA19058.mapped.ILLUMINA.bwa.JPT.exome.20120522	765	0	0	308	617	393	535	655	470	84	610	0	377	140	38	0	582
NA19059.mapped.ILLUMINA.bwa.JPT.exome.20120522	761	0	0	305	607	382	519	633	477	0	0	0	0	0	45	0	575
NA19060.mapped.ILLUMINA.bwa.JPT.exome.20120522	776	0	0	317	648	410	539	671	481	82	631	579	0	141	52	0	583
NA19062.mapped.ILLUMINA.bwa.JPT.exome.20120522	676	0	0	301	600	392	534	649	0	76	598	0	293	133	21	0	565
NA19063.mapped.ILLUMINA.bwa.JPT.exome.20120522	763	0	0	360	622	406	538	663	406	85	637	0	379	141	0	106	580
NA19064.mapped.ILLUMINA.bwa.JPT.exome.20120522	767	0	0	313	616	393	531	661	441	80	624	510	0	134	40	0	578
NA19065.mapped.ILLUMINA.bwa.JPT.exome.20120522	764	0	91	317	626	409	540	663	498	0	0	0	0	0	0	80	583
NA19066.mapped.ILLUMINA.bwa.JPT.exome.20120522	759	259	0	294	623	389	536	658	492	0	629	574	0	0	39	1	578
NA19067.mapped.ILLUMINA.bwa.JPT.exome.20120522	761	0	0	308	606	401	535	658	485	0	0	99	0	0	38	77	577
NA19068.mapped.ILLUMINA.bwa.JPT.exome.20120522	690	0	0	313	638	397	534	657	491	0	0	0	0	0	58	1	579
NA19070.mapped.ILLUMINA.bwa.JPT.exome.20120522	759	0	0	314	621	397	534	662	492	0	0	0	0	0	40	84	581
NA19072.mapped.ILLUMINA.bwa.JPT.exome.20120522	797	0	0	384	699	478	559	561	573	0	0	0	0	0	46	88	597
NA19074.mapped.ILLUMINA.bwa.JPT.exome.20120522	593	320	365	358	582	465	545	539	464	0	536	582	0	183	0	77	593
NA19075.mapped.ILLUMINA.bwa.JPT.exome.20120522	777	0	0	375	680	471	558	555	563	0	0	0	0	0	74	0	597
NA19076.mapped.ILLUMINA.bwa.JPT.exome.20120522	697	0	0	380	693	479	555	654	575	0	0	0	0	0	60	82	599
NA19077.mapped.ILLUMINA.bwa.JPT.exome.20120522	697	0	0	373	694	468	559	647	571	0	0	0	0	0	54	79	596
NA19078.mapped.ILLUMINA.bwa.JPT.exome.20130415	695	0	0	375	691	474	556	752	576	0	0	0	0	0	65	0	594
NA19079.mapped.ILLUMINA.bwa.JPT.exome.20120522	786	325	373	365	596	467	557	642	552	89	548	587	0	184	65	0	594
NA19080.mapped.ILLUMINA.bwa.JPT.exome.20120522	693	0	0	374	691	472	556	554	546	0	539	0	455	187	53	0	597
NA19081.mapped.ILLUMINA.bwa.JPT.exome.20120522	692	320	347	355	579	465	550	556	565	0	0	0	0	0	51	69	595
NA19082.mapped.ILLUMINA.bwa.JPT.exome.20120522	699	0	0	375	697	478	555	658	569	0	0	0	0	0	0	173	599
NA19083.mapped.ILLUMINA.bwa.JPT.exome.20120522	697	0	0	384	694	470	555	559	575	0	0	0	0	0	47	66	597
NA19084.mapped.ILLUMINA.bwa.JPT.exome.20120522	694	0	0	379	684	471	557	552	362	0	538	573	0	182	0	78	596
NA19085.mapped.ILLUMINA.bwa.JPT.exome.20120522	703	324	347	270	582	455	553	644	360	0	540	0	452	180	0	64	596
NA19086.mapped.ILLUMINA.bwa.JPT.exome.20130422	629	0	0	335	482	361	497	563	319	0	0	0	0	0	7	36	550
NA19087.mapped.ILLUMINA.bwa.JPT.exome.20120522	701	0	0	366	683	432	545	636	447	104	609	0	333	164	37	0	590
NA19088.mapped.ILLUMINA.bwa.JPT.exome.20120522	700	293	310	355	669	429	546	639	537	0	0	0	0	0	70	0	588
NA19089.mapped.ILLUMINA.bwa.JPT.exome.20130415	800	0	0	399	727	478	563	674	586	0	0	0	0	0	102	0	595
NA19090.mapped.ILLUMINA.bwa.JPT.exome.20130415	797	0	0	418	725	476	564	673	563	0	0	0	0	0	0	209	597
NA19091.mapped.ILLUMINA.bwa.JPT.exome.20130415	781	0	0	413	718	473	559	676	570	106	663	0	459	187	0	139	596
NA19092.mapped.ILLUMINA.bwa.YRI.exome.20120522	759	0	0	309	611	394	535	647	481	0	0	0	0	0	38	0	582
NA19093.mapped.ILLUMINA.bwa.YRI.exome.20121211	687	0	0	299	615	396	534	652	476	0	0	0	0	0	50	0	579
NA19095.mapped.ILLUMINA.bwa.YRI.exome.20130415	665	0	0	354	552	343	507	595	344	0	0	0	0	0	22	1	568
NA19096.mapped.ILLUMINA.bwa.YRI.exome.20130422	583	0	0	120	376	308	434	435	269	0	0	0	0	0	7	0	451
NA19098.mapped.ILLUMINA.bwa.YRI.exome.20121211	786	329	364	376	709	453	558	560	562	0	539	586	0	0	61	83	597
NA19099.mapped.ILLUMINA.bwa.YRI.exome.20130422	675	0	0	255	584	444	527	603	346	0	0	0	0	0	45	1	524
NA19102.mapped.ILLUMINA.bwa.YRI.exome.20121211	762	0	0	313	622	397	536	661	492	0	0	0	0	0	52	87	581
NA19107.mapped.ILLUMINA.bwa.YRI.exome.20121211	699	294	307	341	650	421	547	641	433	104	625	0	414	152	51	0	586
NA19108.mapped.ILLUMINA.bwa.YRI.exome.20121211	702	286	315	346	677	432	547	639	538	0	627	0	344	0	0	111	582
NA19113.mapped.ILLUMINA.bwa.YRI.exome.20130415	640	0	0	245	411	411	438	527	333	0	0	0	0	0	20	0	549
NA19114.mapped.ILLUMINA.bwa.YRI.exome.20121211	688	0	0	355	665	430	543	638	427	99	600	0	406	157	39	0	587
NA19116.mapped.ILLUMINA.bwa.YRI.exome.20120522	748	250	273	102	590	137	535	654	493	0	592	524	0	0	45	91	582
NA19117.mapped.ILLUMINA.bwa.YRI.exome.20130415	648	156	143	210	306	340	514	555	343	0	0	0	0	0	15	38	546
NA19118.mapped.ILLUMINA.bwa.YRI.exome.20130415	543	0	314	0	336	320	527	592	338	0	319	0	310	0	20	32	558
NA19119.mapped.ILLUMINA.bwa.YRI.exome.20120522	694	327	361	352	674	460	549	554	552	0	549	0	457	184	0	84	597
NA19121.mapped.ILLUMINA.bwa.YRI.exome.20130415	635	0	0	349	483	392	512	532	314	0	0	0	0	0	0	12	509
NA19129.mapped.ILLUMINA.bwa.YRI.exome.20121211	697	0	314	346	677	434	545	643	532	0	592	0	415	0	34	67	586
NA19130.mapped.ILLUMINA.bwa.YRI.exome.20120522	762	263	276	316	639	410	538	670	496	0	0	0	0	0	69	107	581
NA19131.mapped.ILLUMINA.bwa.YRI.exome.20120522	693	322	352	354	587	190	559	637	560	0	0	0	0	0	91	0	593
NA19137.mapped.ILLUMINA.bwa.YRI.exome.20130415	634	335	400	0	86	22	303	0	0	0	715	0	495	183	0	4	595
NA19138.mapped.ILLUMINA.bwa.YRI.exome.20121211	698	0	0	375	688	476	558	644	562	0	0	0	0	0	74	0	592
NA19141.mapped.ILLUMINA.bwa.YRI.exome.20120522	599	334	369	0	584	183	547	546	458	0	650	557	397	178	0	89	597
NA19143.mapped.ILLUMINA.bwa.YRI.exome.20120522	691	321	363	363	582	454	548	629	456	0	545	0	373	183	49	0	596
NA19144.mapped.ILLUMINA.bwa.YRI.exome.20121211	596	334	376	0	701	189	560	633	461	93	659	439	481	185	0	89	596
NA19146.mapped.ILLUMINA.bwa.YRI.exome.20130422	658	135	254	193	446	319	459	401	281	0	329	0	275	145	17	0	576
NA19147.mapped.ILLUMINA.bwa.YRI.exome.20121211	699	284	158	348	647	429	523	623	438	0	617	0	334	159	45	0	590
NA19149.mapped.ILLUMINA.bwa.YRI.exome.20130415	641	0	154	227	525	342	497	567	316	0	274	0	281	0	18	24	558
NA19152.mapped.ILLUMINA.bwa.YRI.exome.20120522	798	0	0	358	699	474	558	654	555	0	530	577	0	0	0	176	595
NA19153.mapped.ILLUMINA.bwa.YRI.exome.20121211	788	0	0	382	699	472	555	660	572	0	0	0	0	0	53	90	594
NA19159.mapped.ILLUMINA.bwa.YRI.exome.20121211	695	0	0	379	689	474	553	656	565	0	0	0	0	0	64	66	594
NA19160.mapped.ILLUMINA.bwa.YRI.exome.20120522	791	0	0	385	694	474	554	634	472	0	0	0	0	0	87	0	591
NA19171.mapped.ILLUMINA.bwa.YRI.exome.20120522	701	323	363	374	682	468	556	562	580	0	0	0	0	0	57	85	596
NA19172.mapped.ILLUMINA.bwa.YRI.exome.20120522	764	259	279	305	624	383	538	657	491	0	623	573	0	0	58	0	577
NA19175.mapped.ILLUMINA.bwa.YRI.exome.20130422	608	0	0	327	554	419	488	514	308	0	0	0	0	0	15	0	548
NA19184.mapped.ILLUMINA.bwa.YRI.exome.20130415	623	0	197	174	263	283	410	286	277	0	127	0	279	118	12	0	560
NA19185.mapped.ILLUMINA.bwa.YRI.exome.20130415	622	0	0	261	510	345	510	547	315	0	0	0	0	0	10	26	544
NA19189.mapped.ILLUMINA.bwa.YRI.exome.20120522	700	0	0	353	671	441	548	650	536	0	0	0	0	0	76	0	587
NA19190.mapped.ILLUMINA.bwa.YRI.exome.20121211	698	0	0	358	676	431	543	639	538	0	0	0	0	0	59	0	565
NA19197.mapped.ILLUMINA.bwa.YRI.exome.20120522	697	330	370	0	580	181	556	552	573	0	530	591	0	0	0	162	597
NA19198.mapped.ILLUMINA.bwa.YRI.exome.20120522	793	0	0	390	716	477	560	661	573	0	0	0	0	0	0	196	597
NA19200.mapped.ILLUMINA.bwa.YRI.exome.20120522	688	331	365	364	706	474	554	566	577	0	636	562	0	0	61	100	599
NA19201.mapped.ILLUMINA.bwa.YRI.exome.20121211	696	0	0	377	687	464	558	647	553	0	0	0	0	0	65	105	595
NA19204.mapped.ILLUMINA.bwa.YRI.exome.20120522	695	323	180	372	666	412	553	613	454	0	542	0	398	185	0	95	592
NA19206.mapped.ILLUMINA.bwa.YRI.exome.20121211	796	0	0	388	708	480	558	563	576	0	0	0	0	0	76	95	601
NA19207.mapped.ILLUMINA.bwa.YRI.exome.20121211	696	325	366	362	699	470	555	561	577	0	630	552	0	0	61	86	598
NA19209.mapped.ILLUMINA.bwa.YRI.exome.20121211	695	0	0	382	709	478	557	661	570	0	0	0	0	0	64	105	596
NA19210.mapped.ILLUMINA.bwa.YRI.exome.20121211	694	0	0	224	694	432	557	640	565	0	541	583	0	0	54	93	595
NA19213.mapped.ILLUMINA.bwa.YRI.exome.20120522	690	0	0	314	643	396	536	657	487	0	0	0	0	0	51	0	577
NA19214.mapped.ILLUMINA.bwa.YRI.exome.20130422	647	0	0	256	573	431	494	563	311	0	0	0	0	0	12	0	510
NA19222.mapped.ILLUMINA.bwa.YRI.exome.20130422	616	84	119	166	503	243	497	483	308	0	98	310	0	0	15	1	544
NA19223.mapped.ILLUMINA.bwa.YRI.exome.20120522	696	0	0	382	705	474	556	561	567	0	0	0	0	0	60	88	594
NA19225.mapped.ILLUMINA.bwa.YRI.exome.20121211	693	0	0	356	680	434	546	641	452	0	0	0	0	0	63	0	588
NA19235.mapped.ILLUMINA.bwa.YRI.exome.20120522	760	0	0	321	631	404	540	660	497	0	0	0	0	0	48	111	583
NA19236.mapped.ILLUMINA.bwa.YRI.exome.20120522	686	253	272	294	523	377	532	627	393	0	609	0	365	137	39	1	579
NA19238.mapped.ILLUMINA.bwa.YRI.exome.20130415	700	331	183	224	688	475	555	650	568	0	648	0	478	183	90	2	600
NA19239.mapped.ILLUMINA.bwa.YRI.exome.20130415	689	0	16	357	651	464	550	615	447	0	0	0	0	0	44	46	587
NA19240.mapped.ILLUMINA.bwa.YRI.exome.20130415	671	285	153	310	484	428	533	548	504	0	434	0	346	170	48	1	579
NA19247.mapped.ILLUMINA.bwa.YRI.exome.20120522	691	0	0	315	639	407	539	670	492	0	0	0	0	0	37	108	580
NA19248.mapped.ILLUMINA.bwa.YRI.exome.20120522	625	0	230	246	490	269	520	600	359	0	594	0	336	121	0	52	572
NA19256.mapped.ILLUMINA.bwa.YRI.exome.20121211	695	0	315	340	674	434	547	638	549	0	603	0	340	0	39	78	585
NA19257.mapped.ILLUMINA.bwa.YRI.exome.20121211	591	305	329	0	665	166	546	638	535	0	645	546	0	0	0	107	588
NA19307.mapped.ILLUMINA.bwa.LWK.exome.20130415	665	140	147	232	361	313	420	472	271	0	347	0	289	158	11	0	554
NA19308.mapped.ILLUMINA.bwa.LWK.exome.20130422	539	260	270	0	376	165	0	0	0	0	437	0	464	175	0	0	561
NA19309.mapped.ILLUMINA.bwa.LWK.exome.20130415	579	116	135	158	244	318	411	423	208	0	122	0	177	118	9	0	538
NA19310.mapped.ILLUMINA.bwa.LWK.exome.20130422	626	119	6	191	267	224	378	355	228	0	208	0	252	140	7	0	537
NA19311.mapped.ILLUMINA.bwa.LWK.exome.20120522	694	336	367	376	673	460	557	552	458	0	528	0	400	187	55	0	599

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA19312.mapped.ILLUMINA.bwa.LWK.exome.20130422	668	158	170	238	387	325	470	490	303	0	253	0	289	145	0	39	556
NA19313.mapped.ILLUMINA.bwa.LWK.exome.20120522	703	324	360	366	676	470	559	650	566	0	0	0	0	0	79	0	594
NA19314.mapped.ILLUMINA.bwa.LWK.exome.20130422	607	136	117	179	340	307	465	533	178	0	167	0	228	0	0	0	0
NA19315.mapped.ILLUMINA.bwa.LWK.exome.20120522	696	0	0	378	696	475	555	655	565	0	0	0	0	0	61	81	595
NA19316.mapped.ILLUMINA.bwa.LWK.exome.20120522	695	342	372	0	711	186	559	658	571	0	642	590	0	0	103	0	600
NA19317.mapped.ILLUMINA.bwa.LWK.exome.20120522	795	0	0	384	707	473	560	651	569	0	0	0	0	0	0	105	598
NA19318.mapped.ILLUMINA.bwa.LWK.exome.20120522	687	0	0	268	684	445	553	548	551	0	522	535	0	0	37	65	590
NA19319.mapped.ILLUMINA.bwa.LWK.exome.20120522	597	0	375	0	675	372	548	546	540	0	554	0	472	184	0	68	594
NA19320.mapped.ILLUMINA.bwa.LWK.exome.20130415	801	0	0	415	726	481	564	678	586	0	0	0	0	0	115	2	596
NA19321.mapped.ILLUMINA.bwa.LWK.exome.20120522	794	0	0	384	711	475	556	653	571	0	0	0	0	0	0	163	597
NA19323.mapped.ILLUMINA.bwa.LWK.exome.20130415	685	0	0	295	608	379	528	643	386	69	508	0	288	135	32	0	577
NA19324.mapped.ILLUMINA.bwa.LWK.exome.20120522	699	0	0	375	702	469	560	648	568	0	0	0	0	0	0	196	596
NA19327.mapped.ILLUMINA.bwa.LWK.exome.20120522	794	0	0	376	704	474	557	559	461	0	0	0	0	0	43	0	591
NA19328.mapped.ILLUMINA.bwa.LWK.exome.20120522	692	0	371	376	706	191	564	650	560	0	619	0	478	0	0	108	592
NA19331.mapped.ILLUMINA.bwa.LWK.exome.20120522	799	345	382	0	0	0	562	668	586	0	0	0	0	0	134	0	601
NA19332.mapped.ILLUMINA.bwa.LWK.exome.20120522	681	252	269	293	610	385	528	625	454	0	636	0	401	134	34	1	577
NA19334.mapped.ILLUMINA.bwa.LWK.exome.20120522	599	254	285	0	587	143	534	656	485	0	628	570	0	0	55	0	578
NA19338.mapped.ILLUMINA.bwa.LWK.exome.20120522	680	244	273	290	605	373	532	640	471	0	608	520	0	0	48	0	581
NA19346.mapped.ILLUMINA.bwa.LWK.exome.20120522	764	0	0	318	617	393	535	654	490	0	0	0	0	0	54	0	577
NA19347.mapped.ILLUMINA.bwa.LWK.exome.20120522	676	274	284	0	613	135	538	667	491	0	613	0	406	0	54	0	580
NA19350.mapped.ILLUMINA.bwa.LWK.exome.20120522	760	0	0	310	617	383	534	652	478	0	0	0	0	0	0	89	572
NA19351.mapped.ILLUMINA.bwa.LWK.exome.20130415	639	0	0	241	448	314	488	553	324	0	0	0	0	0	12	28	570
NA19355.mapped.ILLUMINA.bwa.LWK.exome.20130415	537	169	270	0	283	147	489	506	303	0	267	368	0	0	0	18	520
NA19360.mapped.ILLUMINA.bwa.LWK.exome.20130415	528	143	256	0	534	178	506	569	320	0	409	323	314	0	11	23	568
NA19372.mapped.ILLUMINA.bwa.LWK.exome.20130422	631	123	12	208	369	406	445	499	288	0	278	0	247	145	0	40	557
NA19374.mapped.ILLUMINA.bwa.LWK.exome.20130415	623	0	0	244	604	425	487	600	283	87	82	0	247	0	0	32	556
NA19375.mapped.ILLUMINA.bwa.LWK.exome.20130422	636	0	0	224	605	373	507	569	309	0	0	0	0	0	13	0	520
NA19376.mapped.ILLUMINA.bwa.LWK.exome.20130415	632	154	92	102	519	316	489	554	284	0	2	153	196	0	0	27	476
NA19377.mapped.ILLUMINA.bwa.LWK.exome.20130422	642	152	217	224	405	407	511	572	327	0	0	0	0	0	28	0	561
NA19378.mapped.ILLUMINA.bwa.LWK.exome.20130415	680	248	253	193	603	283	534	642	480	0	589	510	0	0	28	65	573
NA19379.mapped.ILLUMINA.bwa.LWK.exome.20130415	626	155	138	102	448	336	480	587	310	0	271	390	0	0	13	33	550
NA19380.mapped.ILLUMINA.bwa.LWK.exome.20120522	792	0	0	383	697	478	552	644	562	0	0	0	0	0	86	0	593
NA19383.mapped.ILLUMINA.bwa.LWK.exome.20130422	592	0	0	302	510	368	512	593	300	0	0	0	0	0	18	1	548
NA19384.mapped.ILLUMINA.bwa.LWK.exome.20130422	657	144	154	101	316	323	514	594	328	0	0	0	0	0	0	51	551
NA19385.mapped.ILLUMINA.bwa.LWK.exome.20120522	692	323	355	274	588	463	552	542	553	0	524	0	379	179	51	0	596
NA19390.mapped.ILLUMINA.bwa.LWK.exome.20130415	630	154	127	195	278	319	398	331	252	0	34	0	258	139	0	24	543
NA19391.mapped.ILLUMINA.bwa.LWK.exome.20130415	500	0	90	178	336	239	424	369	287	0	174	0	162	0	0	30	519
NA19393.mapped.ILLUMINA.bwa.LWK.exome.20130422	636	0	0	228	524	171	499	578	330	0	190	0	256	0	14	14	549
NA19394.mapped.ILLUMINA.bwa.LWK.exome.20130422	666	0	0	257	587	433	528	578	352	0	0	0	0	0	20	22	573
NA19395.mapped.ILLUMINA.bwa.LWK.exome.20130422	633	0	0	238	389	369	461	544	316	0	0	0	0	0	20	0	553
NA19397.mapped.ILLUMINA.bwa.LWK.exome.20130422	622	143	193	98	582	335	487	531	155	0	360	371	224	146	0	0	506
NA19399.mapped.ILLUMINA.bwa.LWK.exome.20130422	673	0	192	221	626	412	486	597	327	0	334	0	317	0	31	1	568
NA19401.mapped.ILLUMINA.bwa.LWK.exome.20130415	499	0	187	0	439	322	510	536	292	0	356	0	339	0	0	12	503
NA19403.mapped.ILLUMINA.bwa.LWK.exome.20130415	629	0	0	207	432	317	480	432	316	0	0	0	0	0	0	35	537
NA19404.mapped.ILLUMINA.bwa.LWK.exome.20130422	638	0	0	178	304	232	401	455	223	0	101	0	179	147	0	28	548
NA19428.mapped.ILLUMINA.bwa.LWK.exome.20130422	609	0	116	177	591	359	497	572	312	0	278	0	275	0	16	29	546
NA19429.mapped.ILLUMINA.bwa.LWK.exome.20130422	629	161	146	92	552	363	494	537	279	0	79	0	209	0	11	0	518
NA19430.mapped.ILLUMINA.bwa.LWK.exome.20130415	617	0	0	231	481	417	476	570	294	0	0	0	0	0	24	0	539
NA19431.mapped.ILLUMINA.bwa.LWK.exome.20130422	655	0	0	230	458	374	499	572	316	0	0	0	0	0	7	21	543
NA19434.mapped.ILLUMINA.bwa.LWK.exome.20130422	647	0	0	325	468	430	513	533	327	0	0	0	0	0	0	50	556
NA19435.mapped.ILLUMINA.bwa.LWK.exome.20130415	616	0	0	256	425	338	487	512	311	0	0	0	0	0	15	0	547
NA19436.mapped.ILLUMINA.bwa.LWK.exome.20130415	592	0	0	224	392	325	456	504	293	0	0	0	0	0	4	10	502
NA19437.mapped.ILLUMINA.bwa.LWK.exome.20130415	669	0	0	241	471	371	512	585	154	95	286	0	297	164	0	0	516
NA19438.mapped.ILLUMINA.bwa.LWK.exome.20130415	591	0	0	223	336	334	457	497	310	0	0	0	0	0	20	1	547
NA19439.mapped.ILLUMINA.bwa.LWK.exome.20130422	625	155	230	202	443	400	488	564	340	0	116	116	260	0	0	39	551
NA19440.mapped.ILLUMINA.bwa.LWK.exome.20130422	582	0	0	233	357	327	409	542	318	0	0	0	0	0	9	18	542
NA19443.mapped.ILLUMINA.bwa.LWK.exome.20130422	671	165	240	305	320	306	490	589	294	87	248	0	264	142	0	32	555
NA19445.mapped.ILLUMINA.bwa.LWK.exome.20130415	653	0	0	250	336	330	491	563	298	0	0	0	0	0	9	21	553
NA19446.mapped.ILLUMINA.bwa.LWK.exome.20130415	629	0	0	236	414	409	471	533	320	0	0	0	0	0	14	0	546
NA19448.mapped.ILLUMINA.bwa.LWK.exome.20130415	630	0	0	315	483	358	496	531	330	0	0	0	0	0	10	21	523
NA19449.mapped.ILLUMINA.bwa.LWK.exome.20130422	679	158	242	233	334	392	462	533	297	0	283	0	314	128	17	0	571
NA19451.mapped.ILLUMINA.bwa.LWK.exome.20130422	609	0	0	240	332	350	465	531	308	0	0	0	0	0	16	0	540
NA19452.mapped.ILLUMINA.bwa.LWK.exome.20130422	627	0	0	113	551	418	499	523	261	0	256	0	196	145	13	0	545
NA19454.mapped.ILLUMINA.bwa.LWK.exome.20130415	682	0	0	300	595	388	531	641	0	84	623	0	372	136	0	1	577
NA19455.mapped.ILLUMINA.bwa.LWK.exome.20130422	656	0	0	234	606	375	487	611	309	0	230	0	293	0	12	1	522
NA19456.mapped.ILLUMINA.bwa.LWK.exome.20130422	513	165	290	0	296	245	466	568	293	0	108	0	256	0	14	0	486
NA19457.mapped.ILLUMINA.bwa.LWK.exome.20120522	701	0	0	385	711	475	559	653	573	0	0	0	0	0	79	0	596
NA19461.mapped.ILLUMINA.bwa.LWK.exome.20130422	659	0	0	258	472	374	494	597	318	0	0	0	0	0	22	0	562
NA19462.mapped.ILLUMINA.bwa.LWK.exome.20130422	602	122	89	217	255	207	249	347	273	0	0	0	99	111	8	0	544
NA19463.mapped.ILLUMINA.bwa.LWK.exome.20130422	665	157	235	233	384	396	509	591	321	0	0	0	0	0	10	28	572
NA19466.mapped.ILLUMINA.bwa.LWK.exome.20130422	655	137	124	218	309	292	492	551	329	0	0	0	0	0	0	64	557
NA19467.mapped.ILLUMINA.bwa.LWK.exome.20130415	622	0	161	177	516	346	504	563	309	0	135	317	0	0	9	25	555
NA19468.mapped.ILLUMINA.bwa.LWK.exome.20130422	554	247	235	0	584	361	502	591	316	0	430	0	394	0	0	24	524
NA19471.mapped.ILLUMINA.bwa.LWK.exome.20120522	690	0	273	302	619	388	537	661	490	0	630	0	392	0	67	0	582
NA19472.mapped.ILLUMINA.bwa.LWK.exome.20120522	665	0	264	196	603	302	532	648	480	0	603	0	370	0	28	75	579
NA19473.mapped.ILLUMINA.bwa.LWK.exome.20120522	581	253	269	0	0	0	479	571	366	0	545	0	270	128	19	0	570
NA19474.mapped.ILLUMINA.bwa.LWK.exome.20120522	688	255	272	304	592	391	535	662	491	0	0	0	0	0	38	84	580
NA19475.mapped.ILLUMINA.bwa.LWK.exome.20130415	803	336	376	397	684	478	561	666	539	0	670	0	484	191	0	172	598
NA19625.mapped.ILLUMINA.bwa.ASW.exome.20120522	763	248	264	281	614	384	536	649	487	0	603	561	0	0	25	57	581
NA19648.mapped.ILLUMINA.bwa.MXL.exome.20120522	673	266	276	0	619	143	537	659	0	85	670	0	391	144	0	0	581
NA19649.mapped.ILLUMINA.bwa.MXL.exome.20120522	745	0	0	286	580	365	527	637	448	0	0	0	0	0	23	47	572
NA19651.mapped.ILLUMINA.bwa.MXL.exome.20120522	737	232	243	258	591	345	528	652	445	0	605	489	0	0	21	62	571
NA19652.mapped.ILLUMINA.bwa.MXL.exome.20120522	739	231	231	260	511	342	526	633	444	0	0	0	0	0	0	112	574
NA19654.mapped.ILLUMINA.bwa.MXL.exome.20120522	677	221	227	245	581	336	529	639	439	0	575	567	0	0	28	0	569
NA19655.mapped.ILLUMINA.bwa.MXL.exome.20120522	676	0	0	284	585	356	531	652	448	0	0	0	0	0	18	59	573
NA19657.mapped.ILLUMINA.bwa.MXL.exome.20120522	683	0	0	275	540	363	528	644	442	0	0	0	0	0	0	78	571
NA19658.mapped.ILLUMINA.bwa.MXL.exome.20120522	663	216	210	245	513	337	521	639	435	0	0	0	0	0	18	55	565
NA19660.mapped.ILLUMINA.bwa.MXL.exome.20120522	738	214	225	215	502	338	530	648	356	63	570	490	0	117	14	0	572
NA19661.mapped.ILLUMINA.bwa.MXL.exome.20120522	746	0	0	276	570	333	526	631	410	59	579	0	271	119	0	52	571
NA19663.mapped.ILLUMINA.bwa.MXL.exome.20120522	705	221	223	235	594	272	523	642	453	0	627	0	376	0	0	89	572
NA19664.mapped.ILLUMINA.bwa.MXL.exome.20120522	641	224	215	212	588	315	527	632	0	72	637	567	263	129	0	0	572
NA19669.mapped.ILLUMINA.bwa.MXL.exome.20120522	655	219	0	252	558	242	521	642	294	66	562	0	264	121	0	49	568
NA19670.mapped.ILLUMINA.bwa.MXL.exome.20120522	681	0	0	280	541	349	526	632	297	45	554	0	270	123	0	45	569
NA19675.mapped.ILLUMINA.bwa.MXL.exome.20120522	674	0	0	272	545	351	526	632	449	0	0	0	0	0	19	56	572
NA19676.mapped.ILLUMINA.bwa.MXL.exome.20120522	670	220	214	246	579	332	528	627	349	55	595	491	267	118	0	49	568
NA19678.mapped.ILLUMINA.bwa.MXL.exome.20120522	675	0	0	268	575	360	523	639	445	0	0	0	0	0	17	46	574

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA19679.mapped.ILLUMINA.bwa.MXL.exome.20120522	663	225	227	244	575	256	528	642	443	0	579	536	0	0	0	88	570
NA19681.mapped.ILLUMINA.bwa.MXL.exome.20120522	744	0	0	275	578	361	527	631	448	0	0	0	0	0	13	61	570
NA19682.mapped.ILLUMINA.bwa.MXL.exome.20120522	747	0	0	288	582	362	528	646	433	0	0	0	0	0	29	63	572
NA19684.mapped.ILLUMINA.bwa.MXL.exome.20120522	595	208	227	247	516	245	524	648	346	66	578	0	261	122	0	41	569
NA19685.mapped.ILLUMINA.bwa.MXL.exome.20120522	679	0	0	270	571	340	525	635	461	0	0	0	0	0	23	47	574
NA19700.mapped.ILLUMINA.bwa.ASW.exome.20120522	657	228	223	247	461	333	531	631	448	0	0	0	0	0	0	77	572
NA19701.mapped.ILLUMINA.bwa.ASW.exome.20120522	668	226	234	246	448	321	527	634	448	0	0	0	0	0	0	93	573
NA19703.mapped.ILLUMINA.bwa.ASW.exome.20120522	716	220	228	236	533	327	525	636	447	0	0	0	0	0	0	99	570
NA19704.mapped.ILLUMINA.bwa.ASW.exome.20120522	679	0	0	288	575	345	526	645	440	0	0	0	0	0	0	105	571
NA19707.mapped.ILLUMINA.bwa.ASW.exome.20120522	679	0	0	264	578	350	528	640	446	0	0	0	0	0	14	53	574
NA19711.mapped.ILLUMINA.bwa.ASW.exome.20120522	631	224	231	224	576	123	525	635	429	0	577	536	0	0	19	39	576
NA19712.mapped.ILLUMINA.bwa.ASW.exome.20120522	595	239	242	0	0	0	509	570	351	0	575	0	249	122	0	51	571
NA19713.mapped.ILLUMINA.bwa.ASW.exome.20120522	738	0	0	196	573	342	523	637	454	0	0	0	0	0	36	1	573
NA19716.mapped.ILLUMINA.bwa.MXL.exome.20120522	670	222	224	147	485	250	527	653	442	0	0	0	0	0	21	48	570
NA19717.mapped.ILLUMINA.bwa.MXL.exome.20120522	672	0	0	276	568	357	526	642	0	76	627	0	360	127	0	3	568
NA19719.mapped.ILLUMINA.bwa.MXL.exome.20120522	678	0	0	283	586	343	524	641	449	0	0	0	0	0	0	97	572
NA19720.mapped.ILLUMINA.bwa.MXL.exome.20120522	676	0	0	255	574	354	527	635	409	54	586	0	330	119	25	0	574
NA19722.mapped.ILLUMINA.bwa.MXL.exome.20120522	667	215	229	266	489	327	527	641	451	0	0	0	0	0	20	50	571
NA19723.mapped.ILLUMINA.bwa.MXL.exome.20120522	702	230	0	237	548	251	522	641	416	44	590	0	274	122	0	46	572
NA19725.mapped.ILLUMINA.bwa.MXL.exome.20120522	736	0	0	279	577	357	526	646	372	0	0	0	0	0	18	41	570
NA19726.mapped.ILLUMINA.bwa.MXL.exome.20120522	676	0	0	282	572	355	528	639	444	0	0	0	0	0	0	87	569
NA19728.mapped.ILLUMINA.bwa.MXL.exome.20120522	690	324	367	376	699	475	563	660	461	97	664	587	453	184	59	0	598
NA19729.mapped.ILLUMINA.bwa.MXL.exome.20120522	697	0	0	375	693	473	555	649	563	0	0	0	0	0	83	0	596
NA19731.mapped.ILLUMINA.bwa.MXL.exome.20120522	695	0	358	363	699	473	558	556	570	0	532	0	467	0	75	0	595
NA19732.mapped.ILLUMINA.bwa.MXL.exome.20120522	699	0	0	381	701	471	549	646	553	96	629	0	450	183	64	0	591
NA19734.mapped.ILLUMINA.bwa.MXL.exome.20130422	670	0	0	355	602	429	506	578	349	0	0	0	0	0	22	38	582
NA19735.mapped.ILLUMINA.bwa.MXL.exome.20130422	636	152	242	223	472	368	503	597	300	0	406	449	325	160	0	22	554
NA19740.mapped.ILLUMINA.bwa.MXL.exome.20130415	649	0	0	269	616	370	520	574	339	0	0	0	0	0	0	62	575
NA19741.mapped.ILLUMINA.bwa.MXL.exome.20130422	615	123	165	210	307	292	434	402	245	0	194	0	203	156	0	24	547
NA19746.mapped.ILLUMINA.bwa.MXL.exome.20120522	794	0	0	385	709	481	559	643	557	94	638	588	0	186	69	0	599
NA19747.mapped.ILLUMINA.bwa.MXL.exome.20120522	700	0	0	387	695	476	559	658	548	95	548	0	456	182	0	102	596
NA19749.mapped.ILLUMINA.bwa.MXL.exome.20130415	700	0	0	386	704	476	558	756	555	93	634	0	459	184	0	99	596
NA19750.mapped.ILLUMINA.bwa.MXL.exome.20120522	683	329	366	361	597	470	556	552	560	0	0	0	0	0	78	0	596
NA19752.mapped.ILLUMINA.bwa.MXL.exome.20130422	670	0	0	241	551	434	532	540	264	0	140	0	254	150	0	47	550
NA19755.mapped.ILLUMINA.bwa.MXL.exome.20120522	600	329	353	370	700	469	557	643	552	0	655	560	453	186	62	0	598
NA19756.mapped.ILLUMINA.bwa.MXL.exome.20120522	601	322	359	367	701	467	556	557	553	0	557	551	455	183	53	0	596
NA19758.mapped.ILLUMINA.bwa.MXL.exome.20120522	791	0	0	379	694	468	555	644	546	0	533	0	458	184	58	0	595
NA19759.mapped.ILLUMINA.bwa.MXL.exome.20120522	693	0	0	381	702	477	558	664	569	0	0	0	0	0	67	106	596
NA19761.mapped.ILLUMINA.bwa.MXL.exome.20120522	788	0	0	366	686	475	555	560	567	0	0	0	0	0	85	0	592
NA19762.mapped.ILLUMINA.bwa.MXL.exome.20120522	597	325	378	375	694	473	563	653	456	0	546	0	464	191	0	94	599
NA19764.mapped.ILLUMINA.bwa.MXL.exome.20130415	644	0	0	244	468	413	511	585	252	0	314	0	231	154	10	0	543
NA19770.mapped.ILLUMINA.bwa.MXL.exome.20120522	792	322	369	373	711	455	564	563	366	0	656	557	455	184	0	85	599
NA19771.mapped.ILLUMINA.bwa.MXL.exome.20120522	695	0	0	383	695	479	559	563	0	99	554	558	372	187	0	0	597
NA19773.mapped.ILLUMINA.bwa.MXL.exome.20120522	688	0	0	386	704	469	559	558	568	0	0	0	0	0	57	103	597
NA19774.mapped.ILLUMINA.bwa.MXL.exome.20120522	690	0	0	388	701	475	555	657	567	0	0	0	0	0	57	83	594
NA19776.mapped.ILLUMINA.bwa.MXL.exome.20120522	691	309	356	271	583	458	553	546	456	0	542	0	372	181	0	67	593
NA19777.mapped.ILLUMINA.bwa.MXL.exome.20120522	693	0	0	378	687	474	555	654	550	0	0	0	0	0	0	115	596
NA19779.mapped.ILLUMINA.bwa.MXL.exome.20120522	693	0	0	375	690	474	553	638	562	0	0	0	0	0	68	0	594
NA19780.mapped.ILLUMINA.bwa.MXL.exome.20120522	694	0	0	377	712	478	558	559	563	0	0	0	0	0	0	171	600
NA19782.mapped.ILLUMINA.bwa.MXL.exome.20120522	700	0	0	373	684	474	561	640	572	0	0	0	0	0	95	0	596
NA19783.mapped.ILLUMINA.bwa.MXL.exome.20120522	605	326	366	361	592	371	559	559	460	0	624	0	377	185	0	95	597
NA19785.mapped.ILLUMINA.bwa.MXL.exome.20120522	700	0	0	386	711	481	559	655	555	0	646	0	461	183	75	0	597
NA19786.mapped.ILLUMINA.bwa.MXL.exome.20120522	699	0	0	378	608	476	557	657	570	0	0	0	0	0	68	91	596
NA19788.mapped.ILLUMINA.bwa.MXL.exome.20120522	691	313	364	269	575	451	554	559	558	0	0	0	0	0	50	70	593
NA19789.mapped.ILLUMINA.bwa.MXL.exome.20120522	692	0	0	378	686	377	530	541	537	0	0	0	0	185	0	79	594
NA19792.mapped.ILLUMINA.bwa.MXL.exome.20121211	686	0	0	294	595	384	530	645	364	79	579	0	344	135	0	71	579
NA19794.mapped.ILLUMINA.bwa.MXL.exome.20130422	527	153	226	0	0	0	448	557	325	0	0	0	0	0	7	18	531
NA19795.mapped.ILLUMINA.bwa.MXL.exome.20130415	607	0	0	237	518	352	494	560	335	0	0	0	0	0	14	10	552
NA19818.mapped.ILLUMINA.bwa.ASW.exome.20120522	654	213	230	251	495	332	530	644	445	0	0	0	0	0	36	0	574
NA19819.mapped.ILLUMINA.bwa.ASW.exome.20120522	729	0	0	282	578	352	525	635	455	0	0	0	0	0	25	0	571
NA19834.mapped.ILLUMINA.bwa.ASW.exome.20120522	742	0	0	256	488	328	509	593	365	0	571	0	260	122	0	52	571
NA19835.mapped.ILLUMINA.bwa.ASW.exome.20120522	670	227	234	254	584	331	525	649	353	59	626	558	270	120	20	0	576
NA19900.mapped.ILLUMINA.bwa.ASW.exome.20121211	688	0	0	288	627	381	537	641	477	0	602	0	388	0	42	0	576
NA19901.mapped.ILLUMINA.bwa.ASW.exome.20120522	716	0	0	283	578	354	525	643	448	0	0	0	0	0	0	92	571
NA19904.mapped.ILLUMINA.bwa.ASW.exome.20120522	676	0	0	273	544	358	522	638	423	0	0	0	0	0	37	1	571
NA19908.mapped.ILLUMINA.bwa.ASW.exome.20120522	726	223	233	253	481	127	528	640	432	0	0	0	0	0	17	48	565
NA19909.mapped.ILLUMINA.bwa.ASW.exome.20120522	646	226	219	246	505	254	500	600	349	0	584	0	333	113	0	60	572
NA19913.mapped.ILLUMINA.bwa.ASW.exome.20130415	798	319	361	384	706	459	562	678	582	0	0	0	0	0	87	0	595
NA19914.mapped.ILLUMINA.bwa.ASW.exome.20120522	735	224	220	256	571	341	525	642	405	0	542	0	341	0	19	1	558
NA19916.mapped.ILLUMINA.bwa.ASW.exome.20120522	685	0	0	285	576	242	523	645	449	0	0	0	0	0	29	56	571
NA19917.mapped.ILLUMINA.bwa.ASW.exome.20120522	720	119	238	251	578	335	526	634	451	0	570	483	0	0	18	51	571
NA19920.mapped.ILLUMINA.bwa.ASW.exome.20120522	724	227	241	227	441	333	520	614	399	0	571	0	268	118	0	61	574
NA19921.mapped.ILLUMINA.bwa.ASW.exome.20120522	658	233	247	0	511	113	529	639	301	54	620	462	265	124	0	53	572
NA19922.mapped.ILLUMINA.bwa.ASW.exome.20130415	598	66	117	186	448	287	458	529	321	0	140	372	0	0	14	1	551
NA19923.mapped.ILLUMINA.bwa.ASW.exome.20130415	573	0	0	231	413	288	452	557	250	0	65	0	184	105	0	15	527
NA19982.mapped.ILLUMINA.bwa.ASW.exome.20120522	581	248	232	0	551	131	527	646	0	79	651	574	357	123	0	1	570
NA19984.mapped.ILLUMINA.bwa.ASW.exome.20130422	660	0	0	244	493	369	497	535	251	0	160	0	244	151	13	1	550
NA19985.mapped.ILLUMINA.bwa.ASW.exome.20120522	690	0	0	221	687	464	553	634	549	0	0	0	0	0	64	0	589
NA20126.mapped.ILLUMINA.bwa.ASW.exome.20120522	592	330	371	0	685	186	553	644	452	0	653	588	448	176	0	74	593
NA20127.mapped.ILLUMINA.bwa.ASW.exome.20120522	695	0	0	365	601	451	552	553	540	0	528	0	291	183	0	79	596
NA20274.mapped.ILLUMINA.bwa.ASW.exome.20130415	802	333	373	395	725	464	566	673	578	0	656	559	0	0	65	118	593
NA20276.mapped.ILLUMINA.bwa.ASW.exome.20120522	790	186	370	273	708	474	558	565	572	0	546	589	0	0	86	0	594
NA20278.mapped.ILLUMINA.bwa.ASW.exome.20120522	695	0	0	371	691	476	554	563	459	90	617	0	450	183	56	0	595
NA20281.mapped.ILLUMINA.bwa.ASW.exome.20120522	687	0	0	379	690	476	555	558	575	0	0	0	0	0	47	77	596
NA20282.mapped.ILLUMINA.bwa.ASW.exome.20120522	696	325	353	366	579	466	548	549	548	0	543	0	451	188	52	0	594
NA20287.mapped.ILLUMINA.bwa.ASW.exome.20120522	685	321	357	275	702	382	557	562	571	0	628	582	0	0	51	73	593
NA20289.mapped.ILLUMINA.bwa.ASW.exome.20120522	693	0	0	379	699	474	556	559	557	0	0	0	0	0	0	77	587
NA20291.mapped.ILLUMINA.bwa.ASW.exome.20120522	696	317	363	270	701	471	560	559	557	0	633	0	472	0	66	79	598
NA20294.mapped.ILLUMINA.bwa.ASW.exome.20120522	698	0	0	271	666	465	550	536	462	0	535	0	447	182	48	0	594
NA20296.mapped.ILLUMINA.bwa.ASW.exome.20120522	785	326	357	267	692	468	554	550	566	0	534	558	0	0	0	162	595
NA20298.mapped.ILLUMINA.bwa.ASW.exome.20130415	658	0	0	252	541	423	492	566	313	0	0	0	0	0	20	0	537
NA20299.mapped.ILLUMINA.bwa.ASW.exome.20120522	695	0	0	382	692	476	559	648	546	0	537	0	456	188	0	89	595
NA20314.mapped.ILLUMINA.bwa.ASW.exome.20120522	697	0	0	383	696	476	556	644	456	86	546	0	449	188	60	0	597
NA20317.mapped.ILLUMINA.bwa.ASW.exome.20120522	692	326	366	122	579	460	555	637	563	0	525	549	0	0	70	1	593
NA20318.mapped.ILLUMINA.bwa.ASW.exome.20130415	801	0	0	397	726	477	564	676	487	0	650	580	0	0	57	126	598
NA20320.mapped.ILLUMINA.bwa.ASW.exome.20130415	799	0	0	419	727	480	564	674	590	0	0	0	0	0	67	145	595

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA20321.mapped.ILLUMINA.bwa.ASW.exome.20130415	801	332	373	399	713	461	566	678	586	0	0	0	0	0	61	128	595
NA20322.mapped.ILLUMINA.bwa.ASW.exome.20120522	689	321	349	270	585	463	554	556	550	0	0	0	0	0	60	84	587
NA20332.mapped.ILLUMINA.bwa.ASW.exome.20120522	784	328	361	278	707	473	555	648	461	0	642	591	0	181	64	0	593
NA20334.mapped.ILLUMINA.bwa.ASW.exome.20120522	696	0	0	382	694	473	559	553	562	0	0	0	0	0	50	74	593
NA20336.mapped.ILLUMINA.bwa.ASW.exome.20120522	690	183	361	350	694	381	550	558	560	0	525	586	0	0	71	0	599
NA20339.mapped.ILLUMINA.bwa.ASW.exome.20130415	606	133	0	212	344	286	417	450	241	0	238	0	244	144	10	0	552
NA20340.mapped.ILLUMINA.bwa.ASW.exome.20120522	694	322	358	269	679	471	554	657	564	0	523	0	397	0	49	80	593
NA20341.mapped.ILLUMINA.bwa.ASW.exome.20120522	698	0	0	364	708	468	555	564	553	85	561	583	449	184	0	102	599
NA20342.mapped.ILLUMINA.bwa.ASW.exome.20120522	683	323	361	268	575	468	546	545	552	0	534	0	453	177	65	0	594
NA20344.mapped.ILLUMINA.bwa.ASW.exome.20120522	699	0	0	389	699	481	556	659	557	0	0	0	0	0	57	100	596
NA20346.mapped.ILLUMINA.bwa.ASW.exome.20120522	696	323	361	358	701	421	555	558	563	0	538	582	0	0	55	80	591
NA20348.mapped.ILLUMINA.bwa.ASW.exome.20120522	786	0	0	376	696	473	557	656	567	0	0	0	0	0	65	84	596
NA20351.mapped.ILLUMINA.bwa.ASW.exome.20130415	635	0	0	240	602	371	501	571	331	0	333	0	313	0	28	2	560
NA20355.mapped.ILLUMINA.bwa.ASW.exome.20130415	802	330	373	394	729	479	565	673	588	0	647	592	0	0	76	3	597
NA20356.mapped.ILLUMINA.bwa.ASW.exome.20120522	692	332	369	0	699	187	558	633	569	0	643	591	0	0	101	0	595
NA20357.mapped.ILLUMINA.bwa.ASW.exome.20130422	630	0	0	245	552	374	475	528	323	0	0	0	0	0	14	22	555
NA20359.mapped.ILLUMINA.bwa.ASW.exome.20130422	618	0	0	231	423	413	495	547	338	0	0	0	0	0	9	19	531
NA20362.mapped.ILLUMINA.bwa.ASW.exome.20130415	692	295	326	334	591	437	552	618	548	0	0	0	0	0	52	3	590
NA20412.mapped.ILLUMINA.bwa.ASW.exome.20130415	519	142	154	209	308	312	492	509	235	0	97	0	258	113	0	28	546
NA20502.mapped.ILLUMINA.bwa.TSI.exome.20130415	666	0	0	356	584	369	505	586	279	89	282	317	0	159	0	56	562
NA20503.mapped.ILLUMINA.bwa.TSI.exome.20130415	607	197	133	216	439	332	491	559	0	96	435	428	304	166	0	0	572
NA20504.mapped.ILLUMINA.bwa.TSI.exome.20130422	639	0	0	332	542	365	494	551	339	0	0	0	0	0	10	23	550
NA20505.mapped.ILLUMINA.bwa.TSI.exome.20130415	634	137	174	171	539	322	442	542	225	0	315	451	0	127	0	25	556
NA20506.mapped.ILLUMINA.bwa.TSI.exome.20130422	616	132	194	179	263	276	396	357	235	0	255	0	191	144	0	24	550
NA20507.mapped.ILLUMINA.bwa.TSI.exome.20130422	675	0	0	261	602	379	524	604	349	0	0	0	0	0	21	43	567
NA20508.mapped.ILLUMINA.bwa.TSI.exome.20130415	630	139	243	206	556	338	503	576	302	0	350	502	0	140	0	41	551
NA20509.mapped.ILLUMINA.bwa.TSI.exome.20130422	641	147	170	237	600	331	541	606	301	94	448	491	248	154	16	0	550
NA20510.mapped.ILLUMINA.bwa.TSI.exome.20130422	673	258	230	231	613	353	514	597	309	85	438	490	326	155	0	43	567
NA20511.mapped.ILLUMINA.bwa.TSI.exome.20130415	804	0	0	404	726	475	563	673	589	0	0	0	0	0	0	246	597
NA20512.mapped.ILLUMINA.bwa.TSI.exome.20130415	537	214	228	0	560	174	502	563	313	0	387	482	0	0	0	70	555
NA20513.mapped.ILLUMINA.bwa.TSI.exome.20130422	616	139	114	201	448	290	489	474	0	92	385	287	310	169	0	0	530
NA20514.mapped.ILLUMINA.bwa.TSI.exome.20130422	651	158	231	231	605	331	509	589	292	0	426	405	296	166	0	31	565
NA20515.mapped.ILLUMINA.bwa.TSI.exome.20130422	644	0	0	327	538	347	491	575	254	0	211	0	250	166	16	0	543
NA20516.mapped.ILLUMINA.bwa.TSI.exome.20130415	646	145	194	221	329	319	532	571	341	0	0	0	0	0	0	52	564
NA20517.mapped.ILLUMINA.bwa.TSI.exome.20130415	633	0	0	257	576	364	492	544	296	80	323	0	276	153	0	34	561
NA20518.mapped.ILLUMINA.bwa.TSI.exome.20130422	629	111	123	227	352	282	488	545	258	0	166	0	225	141	0	22	571
NA20519.mapped.ILLUMINA.bwa.TSI.exome.20130422	628	133	150	190	317	297	502	563	314	0	0	0	0	0	0	69	559
NA20520.mapped.ILLUMINA.bwa.TSI.exome.20130422	676	0	0	266	526	437	530	573	345	0	0	0	0	0	26	1	571
NA20521.mapped.ILLUMINA.bwa.TSI.exome.20130422	618	0	0	227	551	332	476	555	321	0	0	0	0	0	0	41	548
NA20522.mapped.ILLUMINA.bwa.TSI.exome.20130422	654	0	0	255	555	417	498	515	265	0	130	0	242	148	14	0	552
NA20524.mapped.ILLUMINA.bwa.TSI.exome.20130415	633	178	169	188	439	282	476	517	224	0	382	461	0	116	0	16	539
NA20525.mapped.ILLUMINA.bwa.TSI.exome.20130422	616	0	0	244	517	433	501	593	250	92	427	411	244	129	0	31	543
NA20526.mapped.ILLUMINA.bwa.TSI.exome.20130415	671	0	0	266	494	365	521	560	326	0	0	0	0	0	21	44	546
NA20527.mapped.ILLUMINA.bwa.TSI.exome.20130422	667	161	274	231	396	360	502	428	0	0	456	483	336	183	0	0	571
NA20528.mapped.ILLUMINA.bwa.TSI.exome.20130415	674	0	0	263	600	361	532	582	330	0	0	0	0	0	0	81	566
NA20529.mapped.ILLUMINA.bwa.TSI.exome.20130415	663	0	0	352	660	457	548	641	351	0	292	506	0	0	22	47	573
NA20530.mapped.ILLUMINA.bwa.TSI.exome.20130415	595	147	134	172	343	241	477	533	291	0	0	0	0	0	12	27	533
NA20531.mapped.ILLUMINA.bwa.TSI.exome.20130415	671	158	243	240	300	324	501	590	277	0	308	0	324	157	17	2	558
NA20532.mapped.ILLUMINA.bwa.TSI.exome.20130415	656	124	137	200	244	258	476	473	304	0	0	0	0	0	0	55	547
NA20533.mapped.ILLUMINA.bwa.TSI.exome.20130415	659	0	0	336	447	424	494	543	311	0	0	0	0	0	18	32	565
NA20534.mapped.ILLUMINA.bwa.TSI.exome.20130415	668	173	266	233	641	347	522	583	312	0	446	406	341	159	20	1	573
NA20535.mapped.ILLUMINA.bwa.TSI.exome.20130415	682	0	0	362	502	372	518	603	309	95	371	0	321	153	0	29	567
NA20536.mapped.ILLUMINA.bwa.TSI.exome.20130415	660	0	0	351	619	369	521	564	330	0	0	0	0	0	8	23	566
NA20538.mapped.ILLUMINA.bwa.TSI.exome.20130415	667	232	262	231	622	376	531	595	301	96	416	533	0	164	18	0	564
NA20539.mapped.ILLUMINA.bwa.TSI.exome.20130415	588	0	0	240	441	366	480	535	190	0	150	0	256	138	0	21	559
NA20540.mapped.ILLUMINA.bwa.TSI.exome.20130415	665	141	236	229	426	312	510	583	332	0	0	0	0	0	0	67	565
NA20541.mapped.ILLUMINA.bwa.TSI.exome.20130415	654	161	196	214	348	326	523	590	333	0	0	0	0	0	16	27	559
NA20542.mapped.ILLUMINA.bwa.TSI.exome.20121211	592	293	329	0	648	158	542	633	0	101	644	581	322	162	0	1	585
NA20543.mapped.ILLUMINA.bwa.TSI.exome.20121211	702	294	318	351	679	337	541	645	544	0	624	537	0	0	0	127	588
NA20544.mapped.ILLUMINA.bwa.TSI.exome.20121211	700	0	309	339	652	323	541	658	540	0	0	0	0	0	47	80	587
NA20581.mapped.ILLUMINA.bwa.TSI.exome.20121211	699	290	313	339	673	330	545	647	0	101	655	580	327	166	0	2	586
NA20582.mapped.ILLUMINA.bwa.TSI.exome.20120522	700	0	0	356	678	439	543	648	530	0	0	0	0	0	40	77	591
NA20585.mapped.ILLUMINA.bwa.TSI.exome.20121211	692	0	0	360	677	428	546	640	535	0	0	0	0	0	0	128	586
NA20586.mapped.ILLUMINA.bwa.TSI.exome.20120522	701	283	306	335	646	425	545	634	525	0	0	0	0	0	0	157	584
NA20587.mapped.ILLUMINA.bwa.TSI.exome.20121211	682	0	0	304	592	379	533	642	381	68	600	0	350	131	0	66	576
NA20588.mapped.ILLUMINA.bwa.TSI.exome.20121211	597	300	334	0	630	160	545	638	419	100	641	586	0	164	0	79	582
NA20589.mapped.ILLUMINA.bwa.TSI.exome.20121211	700	0	0	357	674	440	548	635	544	0	0	0	0	0	45	80	591
NA20752.mapped.ILLUMINA.bwa.TSI.exome.20121211	782	0	0	357	676	437	543	641	535	0	0	0	0	0	0	137	588
NA20753.mapped.ILLUMINA.bwa.TSI.exome.20121211	701	0	0	357	678	433	548	652	544	0	0	0	0	0	45	86	588
NA20754.mapped.ILLUMINA.bwa.TSI.exome.20121211	788	279	0	343	673	431	545	636	535	0	0	0	0	0	0	145	586
NA20755.mapped.ILLUMINA.bwa.TSI.exome.20121211	577	298	322	0	0	0	540	645	0	102	643	0	431	165	0	0	588
NA20756.mapped.ILLUMINA.bwa.TSI.exome.20121211	702	289	312	347	686	436	547	645	525	104	647	589	0	159	0	76	589
NA20757.mapped.ILLUMINA.bwa.TSI.exome.20121211	697	0	0	351	663	341	536	643	537	0	0	0	0	0	0	122	590
NA20758.mapped.ILLUMINA.bwa.TSI.exome.20121211	697	280	303	341	647	416	510	616	424	0	585	0	327	159	0	62	589
NA20759.mapped.ILLUMINA.bwa.TSI.exome.20121211	773	0	0	354	672	430	528	608	407	99	587	0	325	157	0	58	591
NA20760.mapped.ILLUMINA.bwa.TSI.exome.20120522	697	280	300	342	664	428	540	640	531	0	610	535	0	0	36	49	587
NA20761.mapped.ILLUMINA.bwa.TSI.exome.20121211	694	0	0	347	670	432	538	623	438	0	0	0	0	0	0	110	585
NA20762.mapped.ILLUMINA.bwa.TSI.exome.20130415	799	334	372	395	729	397	563	680	590	0	665	589	0	0	74	106	599
NA20763.mapped.ILLUMINA.bwa.TSI.exome.20130415	798	348	383	0	728	189	565	681	576	112	680	599	0	188	0	142	599
NA20764.mapped.ILLUMINA.bwa.TSI.exome.20130415	798	157	167	419	729	479	564	684	485	111	669	424	463	185	63	4	598
NA20765.mapped.ILLUMINA.bwa.TSI.exome.20121211	784	282	0	346	681	431	542	638	426	100	596	0	338	158	0	66	584
NA20766.mapped.ILLUMINA.bwa.TSI.exome.20121211	596	244	247	0	578	127	524	644	350	45	641	567	340	122	0	45	570
NA20767.mapped.ILLUMINA.bwa.TSI.exome.20130415	697	342	384	0	711	191	566	675	587	0	670	595	0	0	0	309	597
NA20768.mapped.ILLUMINA.bwa.TSI.exome.20121211	662	0	0	276	563	350	524	644	448	0	0	0	0	0	0	85	571
NA20769.mapped.ILLUMINA.bwa.TSI.exome.20120522	678	0	0	287	579	355	522	643	460	0	0	0	0	0	19	46	573
NA20770.mapped.ILLUMINA.bwa.TSI.exome.20121211	671	219	232	247	580	332	526	628	448	0	558	485	0	0	0	98	573
NA20771.mapped.ILLUMINA.bwa.TSI.exome.20121211	745	0	0	284	580	267	519	651	452	0	0	0	0	0	21	47	572
NA20772.mapped.ILLUMINA.bwa.TSI.exome.20121211	677	224	237	251	522	328	524	641	444	0	0	0	0	0	0	110	573
NA20773.mapped.ILLUMINA.bwa.TSI.exome.20121211	598	247	252	0	536	128	528	648	449	0	629	575	0	0	0	123	573
NA20774.mapped.ILLUMINA.bwa.TSI.exome.20121211	658	118	220	251	580	328	526	627	339	56	615	483	265	119	0	48	568
NA20775.mapped.ILLUMINA.bwa.TSI.exome.20121211	735	222	236	237	504	328	524	627	0	70	633	0	353	130	0	0	572
NA20778.mapped.ILLUMINA.bwa.TSI.exome.20121211	652	216	233	249	592	338	529	632	451	0	588	545	0	0	24	54	573
NA20783.mapped.ILLUMINA.bwa.TSI.exome.20121211	668	232	237	180	578	253	530	650	444	0	604	520	0	0	15	66	571
NA20785.mapped.ILLUMINA.bwa.TSI.exome.20121211	745	0	0	287	573	346	523	640	301	58	573	0	279	121	0	52	568
NA20786.mapped.ILLUMINA.bwa.TSI.exome.20121211	598	242	244	0	550	129	528	635	394	54	638	573	0	122	0	39	573
NA20787.mapped.ILLUMINA.bwa.TSI.exome.20121211	680	0	0	283	586	347	523	627	441	0	0	0	0	0	0	104	573

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA20790.mapped.ILLUMINA.bwa.TSI.exome.20121211	678	0	0	280	577	338	525	636	441	0	0	0	0	0	0	78	570
NA20792.mapped.ILLUMINA.bwa.TSI.exome.20120522	673	0	0	280	574	266	517	649	445	0	0	0	0	0	26	51	567
NA20795.mapped.ILLUMINA.bwa.TSI.exome.20121211	673	204	220	241	510	320	528	642	444	0	0	0	0	0	0	108	570
NA20796.mapped.ILLUMINA.bwa.TSI.exome.20120522	691	0	0	357	639	380	529	665	395	74	619	0	365	133	0	82	578
NA20797.mapped.ILLUMINA.bwa.TSI.exome.20121211	597	252	274	0	0	0	532	631	475	0	0	0	0	0	0	85	577
NA20798.mapped.ILLUMINA.bwa.TSI.exome.20121211	757	0	0	306	600	397	534	648	480	0	0	0	0	0	0	121	580
NA20799.mapped.ILLUMINA.bwa.TSI.exome.20121211	752	247	257	287	560	280	533	639	473	0	0	0	0	0	28	63	579
NA20800.mapped.ILLUMINA.bwa.TSI.exome.20120522	748	0	0	302	594	286	525	647	482	0	0	0	0	0	0	123	578
NA20801.mapped.ILLUMINA.bwa.TSI.exome.20121211	759	0	0	302	613	387	533	646	459	77	618	0	302	136	0	58	576
NA20802.mapped.ILLUMINA.bwa.TSI.exome.20120522	690	0	0	306	614	387	528	643	489	0	0	0	0	0	27	64	579
NA20803.mapped.ILLUMINA.bwa.TSI.exome.20121211	752	0	0	305	608	381	533	646	442	81	592	0	362	132	0	83	579
NA20804.mapped.ILLUMINA.bwa.TSI.exome.20121211	757	251	269	286	637	368	536	646	400	71	645	577	0	137	0	71	579
NA20805.mapped.ILLUMINA.bwa.TSI.exome.20121211	674	0	0	311	601	387	536	642	484	0	0	0	0	0	0	117	580
NA20806.mapped.ILLUMINA.bwa.TSI.exome.20121211	758	0	0	304	584	391	531	647	373	74	594	0	305	138	0	66	580
NA20807.mapped.ILLUMINA.bwa.TSI.exome.20121211	598	324	353	267	581	374	552	642	555	0	0	0	0	0	63	1	593
NA20808.mapped.ILLUMINA.bwa.TSI.exome.20121211	691	0	0	278	695	470	555	643	555	0	0	0	0	0	0	128	597
NA20809.mapped.ILLUMINA.bwa.TSI.exome.20121211	693	0	0	374	694	385	549	639	556	0	0	0	0	0	0	169	592
NA20810.mapped.ILLUMINA.bwa.TSI.exome.20121211	595	319	346	274	696	466	556	643	454	0	552	550	446	181	48	0	592
NA20811.mapped.ILLUMINA.bwa.TSI.exome.20121211	597	321	364	365	691	373	552	645	457	84	640	590	0	183	0	84	595
NA20812.mapped.ILLUMINA.bwa.TSI.exome.20121211	696	323	366	373	709	468	561	560	471	0	543	585	0	0	0	158	597
NA20813.mapped.ILLUMINA.bwa.TSI.exome.20121211	597	328	361	365	704	474	561	565	454	0	649	587	456	188	0	95	595
NA20814.mapped.ILLUMINA.bwa.TSI.exome.20121211	600	332	355	271	697	380	555	559	359	0	558	558	0	182	0	106	596
NA20815.mapped.ILLUMINA.bwa.TSI.exome.20121211	780	332	367	368	685	382	557	564	561	0	0	0	0	0	0	242	598
NA20818.mapped.ILLUMINA.bwa.TSI.exome.20121211	799	0	0	405	721	478	561	674	574	95	643	593	0	0	78	125	598
NA20819.mapped.ILLUMINA.bwa.TSI.exome.20121211	603	322	361	278	707	388	555	649	0	83	661	593	461	191	0	0	597
NA20821.mapped.ILLUMINA.bwa.TSI.exome.20130415	701	0	0	390	714	386	557	666	580	0	0	0	0	0	0	137	594
NA20822.mapped.ILLUMINA.bwa.TSI.exome.20130415	792	0	0	395	716	479	562	668	464	105	644	0	476	184	0	114	597
NA20826.mapped.ILLUMINA.bwa.TSI.exome.20121211	784	329	368	373	682	466	558	650	574	0	0	0	0	0	0	186	594
NA20827.mapped.ILLUMINA.bwa.TSI.exome.20130415	571	293	344	0	0	0	500	449	381	0	396	0	286	152	0	30	574
NA20828.mapped.ILLUMINA.bwa.TSI.exome.20121211	698	326	370	376	591	380	556	643	576	0	0	0	0	0	67	102	596
NA20832.mapped.ILLUMINA.bwa.TSI.exome.20130415	685	0	0	222	670	366	551	639	325	83	468	0	344	168	40	0	593
NA20845.mapped.ILLUMINA.bwa.GIH.exome.20120522	685	249	266	284	570	399	532	648	486	0	0	0	0	0	0	119	578
NA20846.mapped.ILLUMINA.bwa.GIH.exome.20120522	685	0	0	355	625	399	533	660	472	76	604	0	373	140	0	80	581
NA20847.mapped.ILLUMINA.bwa.GIH.exome.20120522	755	253	265	294	617	381	536	653	487	0	594	518	0	0	0	112	578
NA20849.mapped.ILLUMINA.bwa.GIH.exome.20120522	680	254	275	285	602	281	534	656	463	79	609	0	307	140	0	74	582
NA20850.mapped.ILLUMINA.bwa.GIH.exome.20120522	596	263	276	0	585	139	535	643	492	0	585	515	0	0	0	121	578
NA20851.mapped.ILLUMINA.bwa.GIH.exome.20120522	751	256	271	285	623	284	534	657	475	78	645	575	378	138	32	1	576
NA20852.mapped.ILLUMINA.bwa.GIH.exome.20120522	762	0	0	313	610	393	535	656	489	0	0	0	0	0	35	86	578
NA20853.mapped.ILLUMINA.bwa.GIH.exome.20120522	597	259	281	0	572	138	534	640	459	75	637	568	293	135	0	78	579
NA20854.mapped.ILLUMINA.bwa.GIH.exome.20121211	685	257	279	302	613	386	533	654	468	76	642	575	376	140	0	78	581
NA20856.mapped.ILLUMINA.bwa.GIH.exome.20120522	754	252	275	288	614	392	538	656	469	77	644	521	300	136	41	0	579
NA20858.mapped.ILLUMINA.bwa.GIH.exome.20120522	672	266	279	0	0	405	540	656	490	0	0	0	0	0	0	134	578
NA20859.mapped.ILLUMINA.bwa.GIH.exome.20120522	755	250	273	287	621	284	535	660	483	0	617	569	0	0	35	75	576
NA20861.mapped.ILLUMINA.bwa.GIH.exome.20121211	673	266	282	0	589	138	535	649	479	81	649	579	0	140	0	70	579
NA20862.mapped.ILLUMINA.bwa.GIH.exome.20120522	687	0	0	312	614	400	532	656	0	85	652	573	380	142	0	0	577
NA20863.mapped.ILLUMINA.bwa.GIH.exome.20121211	697	292	318	341	645	329	541	640	538	0	0	0	0	0	0	114	589
NA20864.mapped.ILLUMINA.bwa.GIH.exome.20121211	699	0	0	359	665	436	545	638	535	0	0	0	0	0	0	109	591
NA20866.mapped.ILLUMINA.bwa.GIH.exome.20120522	667	263	284	0	0	380	536	651	490	0	0	0	0	0	0	114	574
NA20867.mapped.ILLUMINA.bwa.GIH.exome.20120522	595	301	327	0	671	165	540	649	0	105	657	583	427	165	0	0	587
NA20868.mapped.ILLUMINA.bwa.GIH.exome.20120522	699	288	305	344	630	422	525	594	0	97	648	0	432	166	0	0	588
NA20869.mapped.ILLUMINA.bwa.GIH.exome.20120522	746	256	273	301	579	380	531	634	0	64	634	70	385	142	0	0	580
NA20870.mapped.ILLUMINA.bwa.GIH.exome.20120522	670	261	278	0	605	138	535	649	487	0	632	578	0	0	0	115	581
NA20871.mapped.ILLUMINA.bwa.GIH.exome.20120522	758	0	0	346	621	390	535	656	0	86	642	0	389	145	0	1	580
NA20872.mapped.ILLUMINA.bwa.GIH.exome.20120522	760	0	0	307	619	288	533	646	453	80	622	0	372	137	0	77	577
NA20874.mapped.ILLUMINA.bwa.GIH.exome.20120522	601	262	278	0	570	139	535	656	471	76	643	581	0	138	0	82	581
NA20875.mapped.ILLUMINA.bwa.GIH.exome.20120522	757	251	274	286	601	383	537	659	488	0	0	0	0	0	0	112	577
NA20876.mapped.ILLUMINA.bwa.GIH.exome.20120522	752	251	277	293	595	282	533	658	472	81	613	0	374	142	0	80	576
NA20877.mapped.ILLUMINA.bwa.GIH.exome.20120522	763	0	0	306	611	388	535	649	486	0	0	0	14	0	29	61	579
NA20878.mapped.ILLUMINA.bwa.GIH.exome.20120522	685	246	274	287	588	286	519	629	455	0	609	0	366	139	0	77	580
NA20881.mapped.ILLUMINA.bwa.GIH.exome.20120522	765	0	0	313	612	396	535	660	485	0	0	0	0	0	0	149	580
NA20882.mapped.ILLUMINA.bwa.GIH.exome.20130415	499	259	245	0	369	130	496	541	247	0	371	449	0	142	0	18	546
NA20884.mapped.ILLUMINA.bwa.GIH.exome.20130415	610	142	192	175	560	336	457	527	279	0	348	315	286	136	0	32	564
NA20885.mapped.ILLUMINA.bwa.GIH.exome.20120522	755	0	0	308	617	398	533	652	482	0	0	0	0	0	0	105	574
NA20886.mapped.ILLUMINA.bwa.GIH.exome.20120522	754	254	273	196	593	287	533	658	493	0	0	0	0	0	0	166	579
NA20887.mapped.ILLUMINA.bwa.GIH.exome.20120522	760	257	270	298	636	388	535	651	0	87	658	569	392	144	0	2	578
NA20888.mapped.ILLUMINA.bwa.GIH.exome.20120522	753	257	270	301	596	282	519	641	465	0	619	0	372	140	0	98	577
NA20889.mapped.ILLUMINA.bwa.GIH.exome.20120522	755	259	274	301	622	391	534	653	473	86	635	572	370	139	0	80	579
NA20890.mapped.ILLUMINA.bwa.GIH.exome.20120522	762	0	0	308	631	391	537	670	489	74	640	575	0	0	39	80	579
NA20891.mapped.ILLUMINA.bwa.GIH.exome.20120522	691	0	0	304	613	387	535	654	478	0	0	0	0	0	0	114	579
NA20892.mapped.ILLUMINA.bwa.GIH.exome.20120522	677	253	265	294	595	380	536	652	481	0	0	0	0	0	0	120	576
NA20893.mapped.ILLUMINA.bwa.GIH.exome.20120522	687	0	0	302	606	394	532	646	483	0	0	0	0	0	0	134	577
NA20894.mapped.ILLUMINA.bwa.GIH.exome.20120522	762	254	274	287	601	386	530	628	0	83	635	0	389	143	0	1	581
NA20895.mapped.ILLUMINA.bwa.GIH.exome.20120522	683	256	268	298	568	386	534	635	454	0	606	0	371	141	0	89	577
NA20896.mapped.ILLUMINA.bwa.GIH.exome.20120522	669	266	275	0	603	138	536	663	488	0	0	0	0	0	0	126	578
NA20897.mapped.ILLUMINA.bwa.GIH.exome.20120522	759	0	0	309	616	386	532	658	457	79	615	0	378	141	0	83	580
NA20898.mapped.ILLUMINA.bwa.GIH.exome.20120522	759	248	272	202	620	295	535	660	493	0	610	573	0	0	0	123	576
NA20899.mapped.ILLUMINA.bwa.GIH.exome.20120522	669	262	280	0	0	0	13	0	0	0	630	71	389	144	0	1	579
NA20900.mapped.ILLUMINA.bwa.GIH.exome.20130415	703	336	367	235	722	390	560	670	573	111	665	591	0	181	0	112	595
NA20901.mapped.ILLUMINA.bwa.GIH.exome.20120522	687	256	272	302	623	386	533	649	0	85	652	571	388	144	0	0	577
NA20902.mapped.ILLUMINA.bwa.GIH.exome.20120522	760	0	0	310	612	392	531	652	0	81	653	0	380	143	0	1	581
NA20903.mapped.ILLUMINA.bwa.GIH.exome.20120522	688	0	0	311	610	396	535	655	0	88	629	0	381	142	0	0	574
NA20904.mapped.ILLUMINA.bwa.GIH.exome.20120522	690	0	0	300	613	393	533	658	497	0	0	0	0	0	33	87	578
NA20905.mapped.ILLUMINA.bwa.GIH.exome.20120522	671	263	279	0	606	136	535	643	480	0	630	572	0	0	0	103	575
NA20906.mapped.ILLUMINA.bwa.GIH.exome.20120522	686	256	270	299	620	393	533	658	480	76	638	575	375	139	0	90	579
NA20908.mapped.ILLUMINA.bwa.GIH.exome.20120522	743	252	272	298	621	287	533	655	487	0	617	564	0	0	34	77	578
NA20910.mapped.ILLUMINA.bwa.GIH.exome.20120522	760	0	0	312	614	394	533	656	485	0	0	0	0	0	0	100	577
NA20911.mapped.ILLUMINA.bwa.GIH.exome.20120522	751	253	0	294	617	387	534	656	467	80	585	0	374	138	0	78	579
NA21086.mapped.ILLUMINA.bwa.GIH.exome.20120522	690	0	0	309	614	396	535	652	487	0	0	0	0	0	0	116	578
NA21087.mapped.ILLUMINA.bwa.GIH.exome.20120522	685	251	266	294	605	379	528	624	0	74	639	0	384	142	0	0	578
NA21088.mapped.ILLUMINA.bwa.GIH.exome.20120522	764	0	0	307	615	393	534	654	401	82	541	0	375	140	0	78	576
NA21089.mapped.ILLUMINA.bwa.GIH.exome.20120522	795	324	0	369	708	472	560	566	552	89	636	0	378	185	0	93	597
NA21090.mapped.ILLUMINA.bwa.GIH.exome.20120522	794	0	0	387	712	476	559	661	572	0	0	0	0	0	0	156	597
NA21091.mapped.ILLUMINA.bwa.GIH.exome.20120522	688	329	357	355	674	376	549	531	0	81	651	0	468	188	0	0	599
NA21092.mapped.ILLUMINA.bwa.GIH.exome.20120522	697	337	379	0	0	0	555	633	569	0	553	0	461	185	0	98	601
NA21093.mapped.ILLUMINA.bwa.GIH.exome.20120522	757	0	0	302	606	396	534	651	482	0	0	0	0	0	0	101	578
NA21094.mapped.ILLUMINA.bwa.GIH.exome.20121211	698	328	364	273	697	468	556	651	567	0	534	558	0	0	0	145	599

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
NA21095.mapped.ILLUMINA.bwa.GIH.exome.20121211	676	245	270	299	612	387	531	650	492	0	591	563	0	0	0	145	579
NA21097.mapped.ILLUMINA.bwa.GIH.exome.20120522	599	338	381	0	0	0	0	0	0	0	666	0	468	193	0	0	599
NA21098.mapped.ILLUMINA.bwa.GIH.exome.20120522	695	336	375	0	689	180	559	566	568	0	630	587	0	0	63	99	600
NA21099.mapped.ILLUMINA.bwa.GIH.exome.20120522	695	331	367	360	715	473	562	659	551	88	644	590	385	184	0	96	597
NA21100.mapped.ILLUMINA.bwa.GIH.exome.20120522	601	335	373	0	687	187	552	640	0	98	671	587	472	189	0	0	600
NA21101.mapped.ILLUMINA.bwa.GIH.exome.20120522	695	338	378	0	682	184	556	647	551	91	654	556	378	185	0	91	598
NA21102.mapped.ILLUMINA.bwa.GIH.exome.20120522	698	0	0	391	718	470	558	658	576	0	0	0	0	0	59	117	597
NA21103.mapped.ILLUMINA.bwa.GIH.exome.20120522	694	0	0	374	707	474	561	563	563	0	0	0	0	0	0	185	597
NA21104.mapped.ILLUMINA.bwa.GIH.exome.20130415	620	129	138	161	311	307	469	527	305	0	0	0	0	0	3	29	541
NA21105.mapped.ILLUMINA.bwa.GIH.exome.20130415	643	161	0	255	606	431	533	626	327	0	0	0	0	0	0	49	554
NA21106.mapped.ILLUMINA.bwa.GIH.exome.20130415	642	130	0	263	551	365	492	532	267	0	237	0	269	153	0	30	564
NA21107.mapped.ILLUMINA.bwa.GIH.exome.20130415	650	141	229	227	495	341	506	572	260	0	368	383	242	161	13	0	550
NA21108.mapped.ILLUMINA.bwa.GIH.exome.20130415	648	0	0	354	505	437	519	580	332	0	0	0	0	0	0	69	560
NA21109.mapped.ILLUMINA.bwa.GIH.exome.20130415	648	146	203	48	359	294	467	370	277	0	299	0	311	163	0	44	548
NA21110.mapped.ILLUMINA.bwa.GIH.exome.20130415	653	0	0	350	610	419	510	587	279	0	292	0	261	165	12	0	569
NA21111.mapped.ILLUMINA.bwa.GIH.exome.20130415	639	0	0	356	538	431	508	524	350	0	0	0	0	0	0	64	559
NA21112.mapped.ILLUMINA.bwa.GIH.exome.20130415	663	135	204	210	330	343	512	561	0	95	423	0	351	178	0	0	555
NA21113.mapped.ILLUMINA.bwa.GIH.exome.20130415	616	0	0	317	514	346	472	496	275	0	0	0	0	0	0	49	547
NA21114.mapped.ILLUMINA.bwa.GIH.exome.20120522	669	267	279	0	587	141	534	658	481	0	618	567	0	0	31	73	577
NA21115.mapped.ILLUMINA.bwa.GIH.exome.20130415	633	146	116	206	297	349	491	562	340	0	0	0	0	0	12	31	539
NA21116.mapped.ILLUMINA.bwa.GIH.exome.20130415	615	0	0	326	541	418	496	552	292	0	230	0	234	142	8	0	558
NA21117.mapped.ILLUMINA.bwa.GIH.exome.20130415	626	141	106	188	312	320	485	559	261	0	239	0	153	136	0	24	538
NA21118.mapped.ILLUMINA.bwa.GIH.exome.20130415	657	0	0	229	403	363	475	570	236	0	207	0	265	140	6	0	548
NA21119.mapped.ILLUMINA.bwa.GIH.exome.20130415	653	0	0	220	366	356	488	536	283	0	0	0	0	0	10	32	540
NA21120.mapped.ILLUMINA.bwa.GIH.exome.20130415	648	0	0	216	518	362	450	510	177	0	58	0	260	132	8	1	540
NA21122.mapped.ILLUMINA.bwa.GIH.exome.20130415	652	145	249	214	328	339	494	517	310	0	0	0	0	0	0	50	539
NA21123.mapped.ILLUMINA.bwa.GIH.exome.20130415	651	165	143	193	410	305	487	507	218	0	350	434	231	136	0	29	548
NA21124.mapped.ILLUMINA.bwa.GIH.exome.20130415	599	256	271	0	551	134	528	631	0	74	645	513	373	141	0	0	575
NA21125.mapped.ILLUMINA.bwa.GIH.exome.20130415	639	120	125	181	292	240	476	487	0	0	389	0	304	161	0	0	557
NA21126.mapped.ILLUMINA.bwa.GIH.exome.20121211	666	257	266	0	549	132	533	645	476	0	528	560	0	0	31	65	576
NA21127.mapped.ILLUMINA.bwa.GIH.exome.20130415	597	335	375	0	0	0	559	674	560	104	648	0	458	185	0	103	597
NA21128.mapped.ILLUMINA.bwa.GIH.exome.20130415	798	331	374	395	732	474	561	676	481	112	676	589	462	190	0	131	598
NA21129.mapped.ILLUMINA.bwa.GIH.exome.20130415	647	236	242	261	508	336	531	628	466	0	0	0	0	0	36	0	572
NA21130.mapped.ILLUMINA.bwa.GIH.exome.20130415	802	331	372	396	738	476	568	678	582	112	672	594	0	0	0	228	597
NA21133.mapped.ILLUMINA.bwa.GIH.exome.20130415	701	328	369	384	725	387	560	675	582	0	650	590	0	0	56	103	595
NA21135.mapped.ILLUMINA.bwa.GIH.exome.20130415	794	340	380	0	708	185	556	657	0	108	677	597	462	190	0	1	597
NA21137.mapped.ILLUMINA.bwa.GIH.exome.20120522	760	0	0	313	617	402	535	652	491	0	0	0	0	0	0	118	576
NA21141.mapped.ILLUMINA.bwa.GIH.exome.20121211	779	278	302	345	658	432	539	628	529	0	0	0	0	0	0	122	587
NA21142.mapped.ILLUMINA.bwa.GIH.exome.20121211	701	0	0	356	676	435	541	638	533	0	0	0	0	0	0	129	590
NA21143.mapped.ILLUMINA.bwa.GIH.exome.20121211	697	0	0	358	674	441	544	649	438	101	615	0	333	163	0	81	589
NA21144.mapped.ILLUMINA.bwa.GIH.exome.20121211	672	302	331	0	671	166	544	643	430	100	655	587	331	162	0	76	588
TCGA-02-0003-10A-01D-1490-08_GBM	758	0	0	303	615	292	523	662	479	0	0	0	0	0	0	168	581
TCGA-02-0033-10A-01D-1490-08_GBM	684	257	269	295	601	385	533	640	465	0	628	0	376	140	39	2	580
TCGA-02-0047-10A-01D-1490-08_GBM	681	254	268	289	515	384	534	653	484	0	0	0	0	0	41	89	575
TCGA-02-0055-10A-01D-1490-08_GBM	676	252	275	292	595	283	529	666	474	0	0	0	0	0	36	76	579
TCGA-02-2470-10A-01D-1494-08_GBM	685	0	0	312	586	291	524	662	463	80	605	0	373	138	0	84	578
TCGA-02-2483-10A-01D-1494-08_GBM	688	0	0	305	610	401	534	652	0	85	635	0	381	141	0	0	581
TCGA-02-2485-10A-01D-1494-08_GBM	760	0	0	310	615	386	532	666	484	0	0	0	0	0	0	128	581
TCGA-02-2486-10A-01D-1494-08_GBM	596	259	281	0	0	0	536	659	482	0	0	0	0	0	49	1	580
TCGA-05-4244-10A-01D-1105-08_LUAD	680	247	258	297	581	374	534	661	468	75	606	0	367	139	0	69	574
TCGA-05-4249-10A-01D-1105-08_LUAD	684	0	0	307	612	401	530	656	482	0	0	0	0	0	0	88	580
TCGA-05-4250-10A-01D-1105-08_LUAD	685	0	0	344	609	387	532	651	483	0	0	0	0	0	0	124	579
TCGA-05-4382-10A-01D-1265-08_LUAD	669	252	257	287	586	278	531	648	381	73	606	0	296	135	26	1	576
TCGA-05-4384-10A-01D-1753-08_LUAD	686	0	0	303	599	376	528	629	397	0	0	0	0	0	0	71	573
TCGA-05-4389-10A-01D-1265-08_LUAD	677	247	259	300	610	288	530	643	0	86	658	577	376	138	0	0	577
TCGA-05-4390-10A-01D-1753-08_LUAD	683	0	0	307	594	381	524	630	377	73	573	0	278	133	0	44	576
TCGA-05-4395-10A-01D-1265-08_LUAD	693	0	0	308	614	383	531	664	488	0	0	0	0	0	0	100	578
TCGA-05-4396-10A-01D-1855-08_LUAD	686	0	0	305	619	397	535	656	460	82	640	509	365	137	0	65	578
TCGA-05-4397-10A-01D-1265-08_LUAD	687	0	0	303	611	290	524	654	474	0	0	0	0	0	0	89	577
TCGA-05-4398-10A-01D-1265-08_LUAD	683	0	0	307	611	384	535	651	481	0	0	0	0	0	49	0	578
TCGA-05-4402-10A-01D-1265-08_LUAD	682	0	0	302	608	381	528	633	392	0	0	0	0	142	30	0	574
TCGA-05-4403-10A-01D-1265-08_LUAD	595	258	279	0	598	137	535	659	443	78	637	512	364	135	0	70	578
TCGA-05-4405-10A-01D-1855-08_LUAD	682	0	0	305	611	285	530	651	476	0	0	0	0	0	25	68	577
TCGA-05-4410-10A-01D-1855-08_LUAD	676	252	256	288	599	369	532	652	485	0	0	0	0	0	35	66	579
TCGA-05-4415-10A-01D-1855-08_LUAD	688	0	0	306	614	373	533	651	488	0	0	0	0	0	0	132	578
TCGA-05-4417-10A-01D-1855-08_LUAD	688	253	260	295	609	136	532	629	0	78	643	573	0	141	0	0	574
TCGA-05-4418-10A-01D-1265-08_LUAD	759	242	266	291	611	383	535	650	464	81	644	564	375	135	0	58	576
TCGA-05-4420-10A-01D-1265-08_LUAD	689	0	0	308	610	385	528	648	453	75	613	0	366	137	0	75	577
TCGA-05-4422-10A-01D-1265-08_LUAD	674	252	269	191	520	290	533	652	477	0	0	0	0	0	0	98	578
TCGA-05-4424-10A-01D-1855-08_LUAD	686	0	0	305	617	381	532	637	483	0	0	0	0	0	0	91	574
TCGA-05-4425-10A-01D-1753-08_LUAD	660	230	245	287	535	279	530	635	481	0	0	0	0	0	0	95	578
TCGA-05-4426-10A-01D-1265-08_LUAD	667	256	276	0	598	143	535	648	0	82	661	577	370	139	0	1	579
TCGA-05-4427-10A-01D-1855-08_LUAD	686	253	256	291	593	367	535	641	485	0	0	0	0	0	0	120	578
TCGA-05-4430-10A-01D-1265-08_LUAD	687	0	0	299	608	380	532	651	456	75	617	0	366	140	0	74	576
TCGA-05-4432-10A-01D-1265-08_LUAD	684	0	0	298	612	396	534	646	404	0	0	0	0	0	0	120	578
TCGA-05-4433-10A-01D-1855-08_LUAD	676	250	265	269	607	279	531	637	468	0	604	513	0	0	0	90	579
TCGA-05-4434-10A-01D-1265-08_LUAD	757	0	0	305	610	379	531	660	454	78	616	0	366	139	0	68	578
TCGA-05-5423-10A-01D-1625-08_LUAD	679	0	0	293	605	367	525	644	468	0	0	0	0	0	0	95	579
TCGA-05-5425-10A-01D-1625-08_LUAD	678	0	0	297	607	371	527	641	475	0	0	0	0	0	0	105	576
TCGA-05-5428-10A-01D-1625-08_LUAD	743	0	0	299	560	372	532	642	377	68	570	0	294	135	0	61	573
TCGA-05-5429-10A-01D-1625-08_LUAD	675	237	256	274	556	356	528	646	473	0	0	0	0	0	0	100	575
TCGA-05-5715-10A-01D-1625-08_LUAD	667	242	261	253	545	363	528	636	362	75	583	0	296	139	0	49	577
TCGA-06-0119-10A-01D-1490-08_GBM	682	0	0	310	603	292	524	653	453	72	600	0	369	137	0	75	578
TCGA-06-0122-10A-01D-1490-08_GBM	681	250	270	188	579	281	532	657	479	0	0	0	0	0	34	73	575
TCGA-06-0124-10A-01D-1490-08_GBM	683	251	274	288	583	282	532	656	388	82	642	0	374	135	0	69	578
TCGA-06-0125-10A-01D-1490-08_GBM	680	258	266	291	611	285	529	652	487	0	616	510	0	0	0	128	574
TCGA-06-0126-10A-01D-1490-08_GBM	756	250	266	289	569	368	534	651	381	75	616	509	0	139	0	61	577
TCGA-06-0128-10A-01D-1490-08_GBM	686	0	0	301	603	395	536	650	481	0	0	0	0	0	0	99	576
TCGA-06-0129-10A-01D-1490-08_GBM	677	245	265	292	608	377	531	647	385	76	638	569	374	136	32	0	575
TCGA-06-0130-10A-01D-1490-08_GBM	672	253	273	288	578	284	529	653	478	0	0	0	0	0	33	68	574
TCGA-06-0132-10A-01D-1491-08_GBM	682	251	267	283	580	283	531	657	477	0	0	0	0	0	0	93	577
TCGA-06-0137-10A-01D-1490-08_GBM	738	252	263	285	589	376	534	646	471	0	0	0	0	0	54	3	580
TCGA-06-0139-10A-01D-1490-08_GBM	685	249	265	284	612	383	530	653	457	73	643	578	0	136	0	71	579
TCGA-06-0140-10A-01D-1490-08_GBM	685	0	0	302	609	398	535	633	481	0	0	0	0	0	0	90	579
TCGA-06-0141-10A-01D-1490-08_GBM	661	237	239	242	547	262	527	641	296	75	515	505	0	134	0	38	573
TCGA-06-0142-10A-01D-1490-08_GBM	655	241	260	284	606	282	531	652	378	73	618	508	359	136	0	69	577

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-06-0145-10A-01D-1490-08_GBM	688	0	0	304	599	394	532	648	470	0	0	0	0	0	0	95	577
TCGA-06-0151-10A-01D-1491-08_GBM	690	0	0	300	603	392	530	649	438	81	607	0	300	139	0	74	575
TCGA-06-0152-10A-01D-1492-08_GBM	690	0	0	303	604	387	534	653	390	78	614	0	294	134	0	86	577
TCGA-06-0154-10A-01D-1491-08_GBM	686	250	274	303	607	379	531	666	461	82	639	0	381	137	0	76	575
TCGA-06-0155-10A-01D-1492-08_GBM	685	248	265	297	602	381	532	659	476	0	0	0	0	0	33	75	578
TCGA-06-0157-10A-01D-1491-08_GBM	690	0	0	299	606	392	533	657	489	0	0	0	0	0	0	152	577
TCGA-06-0158-10A-01D-1491-08_GBM	687	0	0	307	611	385	525	635	0	81	609	0	303	140	0	1	575
TCGA-06-0165-10A-01D-1491-08_GBM	689	0	0	307	602	392	534	661	457	78	605	0	367	136	0	79	576
TCGA-06-0166-10A-01D-1491-08_GBM	687	249	269	292	585	287	529	649	471	0	0	0	0	0	48	0	579
TCGA-06-0167-10A-01D-1491-08_GBM	758	0	0	304	604	384	530	654	468	0	0	0	0	0	42	82	575
TCGA-06-0168-10A-01D-1491-08_GBM	686	0	0	299	609	390	529	657	454	81	616	0	367	136	0	81	577
TCGA-06-0169-10A-01D-1490-08_GBM	687	0	0	306	604	387	532	655	478	0	0	0	0	0	35	75	576
TCGA-06-0171-10A-01D-1491-08_GBM	682	252	0	191	611	286	531	659	457	77	610	0	367	141	33	0	578
TCGA-06-0173-10B-01D-1491-08_GBM	664	246	267	277	610	278	532	651	486	0	604	516	0	0	33	74	575
TCGA-06-0174-10B-01D-1491-08_GBM	593	255	274	0	598	138	532	640	387	78	644	575	0	136	0	69	572
TCGA-06-0178-10B-01D-1491-08_GBM	687	0	0	300	607	288	521	645	477	0	0	0	0	0	0	147	575
TCGA-06-0184-10B-01D-1491-08_GBM	687	248	271	292	594	382	532	645	0	81	645	0	379	140	0	2	577
TCGA-06-0185-10B-01D-1491-08_GBM	682	0	0	303	607	383	527	657	482	0	0	0	0	0	35	74	577
TCGA-06-0187-10B-01D-1491-08_GBM	674	249	263	296	594	384	533	658	481	0	0	0	0	0	37	80	576
TCGA-06-0188-10B-01D-1491-08_GBM	687	0	0	306	607	389	533	656	486	0	0	0	0	0	34	80	577
TCGA-06-0189-10A-01D-1491-08_GBM	684	248	268	297	596	285	532	653	473	0	0	0	0	0	49	11	578
TCGA-06-0190-10B-01D-1491-08_GBM	687	254	272	208	623	295	533	663	473	79	652	575	376	138	34	4	575
TCGA-06-0192-10A-01D-1492-08_GBM	679	248	271	198	614	288	534	653	484	0	614	513	0	0	0	167	581
TCGA-06-0195-10A-01D-1491-08_GBM	681	0	0	300	599	378	511	618	437	0	0	0	0	136	0	70	572
TCGA-06-0209-10A-01D-1491-08_GBM	761	0	0	307	611	390	530	651	481	0	0	0	0	0	35	74	576
TCGA-06-0210-10A-01D-1491-08_GBM	688	0	0	306	608	385	529	650	450	73	590	567	0	137	0	77	578
TCGA-06-0211-10A-01D-1491-08_GBM	687	0	0	305	611	287	526	654	478	0	0	0	0	0	0	102	580
TCGA-06-0213-10A-01D-1491-08_GBM	677	0	0	291	608	389	532	640	471	0	0	0	0	0	54	1	574
TCGA-06-0214-10A-01D-1491-08_GBM	687	249	276	298	591	382	533	657	461	80	631	0	370	137	0	79	577
TCGA-06-0216-10A-01D-1492-08_GBM	684	0	0	304	591	396	532	650	480	0	0	0	0	0	0	147	578
TCGA-06-0219-10A-01D-1491-08_GBM	687	0	0	305	610	390	530	656	481	0	0	0	0	0	0	140	578
TCGA-06-0221-10A-01D-1491-08_GBM	687	249	268	301	633	385	532	657	391	78	638	571	370	135	0	85	576
TCGA-06-0237-10A-01D-1491-08_GBM	684	251	268	288	612	381	532	656	392	74	630	572	0	137	31	3	578
TCGA-06-0238-10A-01D-1492-08_GBM	674	247	266	289	566	379	532	651	475	0	0	0	0	0	0	110	575
TCGA-06-0240-10A-01D-1491-08_GBM	687	0	0	304	613	393	532	655	455	76	613	0	363	136	0	83	575
TCGA-06-0241-10A-01D-1491-08_GBM	598	261	274	0	564	136	531	648	474	0	609	566	0	0	0	116	577
TCGA-06-0644-10A-01D-1492-08_GBM	592	257	268	0	499	131	532	657	459	81	626	570	0	131	33	0	573
TCGA-06-0645-10A-01D-1492-08_GBM	678	252	264	284	587	380	532	660	469	0	0	0	0	0	31	83	574
TCGA-06-0646-10A-01D-1492-08_GBM	683	255	264	285	590	379	532	658	479	0	0	0	0	0	0	131	575
TCGA-06-0648-10A-01D-1492-08_GBM	688	0	0	304	609	385	532	640	474	0	0	0	0	0	0	142	575
TCGA-06-0649-10A-01D-1492-08_GBM	753	246	269	190	614	288	535	663	481	0	608	565	0	0	0	105	577
TCGA-06-0650-10A-01D-1696-08_GBM	647	250	270	275	572	279	527	646	476	0	0	0	0	0	28	57	577
TCGA-06-0686-10A-01D-1492-08_GBM	681	0	0	314	615	392	533	668	480	0	0	0	0	0	0	165	578
TCGA-06-0743-10A-01D-1492-08_GBM	677	258	270	286	606	284	530	646	475	0	596	519	0	0	0	117	581
TCGA-06-0744-10A-01D-1492-08_GBM	599	264	277	0	0	0	532	655	447	66	614	0	295	138	32	1	578
TCGA-06-0745-10A-01D-1492-08_GBM	685	0	0	303	608	389	533	654	442	76	591	0	306	137	0	90	578
TCGA-06-0747-10A-01D-1492-08_GBM	668	255	263	288	569	384	531	650	472	0	0	0	0	0	35	76	575
TCGA-06-0749-10A-01D-1492-08_GBM	758	0	0	295	602	394	533	654	470	79	613	0	306	139	32	1	578
TCGA-06-0750-10A-01D-1492-08_GBM	681	244	270	280	613	382	532	655	451	79	642	579	0	137	0	72	577
TCGA-06-0875-10A-01D-1492-08_GBM	684	254	269	198	611	290	533	654	479	0	623	569	0	0	54	1	581
TCGA-06-0876-10A-01D-1492-08_GBM	686	246	265	292	540	386	534	665	389	80	608	0	368	137	36	1	573
TCGA-06-0877-10A-01D-1492-08_GBM	597	259	280	0	586	134	533	659	444	78	651	573	301	137	0	89	580
TCGA-06-0878-10A-01D-1492-08_GBM	688	0	0	302	606	386	530	655	472	76	625	0	305	139	36	2	581
TCGA-06-0879-10A-01D-1492-08_GBM	687	254	267	293	613	387	533	649	479	0	617	518	0	0	0	170	578
TCGA-06-0881-10A-01D-1492-08_GBM	688	260	268	293	609	390	534	649	473	0	623	572	0	0	51	1	577
TCGA-06-0882-10A-01D-1492-08_GBM	756	0	0	306	620	398	534	648	483	0	32	0	0	0	0	121	579
TCGA-06-0939-10A-01D-1353-08_GBM	688	254	273	299	624	392	532	658	391	82	647	569	369	138	0	81	582
TCGA-06-1804-10A-01D-1696-08_GBM	669	241	264	282	553	370	532	650	478	0	0	0	0	0	32	60	577
TCGA-06-1806-10B-01D-1845-08_GBM	688	0	0	298	618	401	533	650	483	0	0	0	0	0	34	70	576
TCGA-06-2557-10A-01D-1494-08_GBM	757	0	0	299	611	389	533	658	469	0	0	0	0	0	31	0	571
TCGA-06-2558-10A-01D-1494-08_GBM	666	248	272	293	611	284	529	646	475	0	599	519	0	0	53	3	578
TCGA-06-2559-10A-01D-1494-08_GBM	686	0	0	308	614	394	533	662	482	0	0	0	0	0	32	81	577
TCGA-06-2561-10A-01D-1494-08_GBM	686	0	0	306	610	398	532	656	469	80	625	570	0	139	0	73	578
TCGA-06-2562-10A-01D-1494-08_GBM	690	0	0	312	609	400	532	657	479	0	0	0	0	0	44	2	577
TCGA-06-2563-10A-01D-1494-08_GBM	686	0	0	310	611	393	535	657	395	81	623	0	365	135	37	3	578
TCGA-06-2564-10A-01D-1494-08_GBM	688	253	271	297	622	383	535	659	471	77	656	570	376	134	36	1	577
TCGA-06-2565-10A-01D-1494-08_GBM	598	265	264	0	590	139	522	624	0	81	656	517	383	140	0	0	578
TCGA-06-2567-10A-01D-1494-08_GBM	593	258	281	0	0	0	533	661	488	0	0	0	0	0	37	73	578
TCGA-06-2569-10A-01D-1494-08_GBM	681	250	268	291	598	282	532	655	468	79	605	0	304	139	0	70	577
TCGA-06-2570-10A-01D-1495-08_GBM	686	0	0	309	614	392	531	653	486	0	0	0	0	0	0	112	575
TCGA-06-5408-10A-01D-1696-08_GBM	662	246	261	285	615	285	531	645	480	0	600	514	0	0	0	121	578
TCGA-06-5410-10A-01D-1696-08_GBM	678	245	255	293	595	382	535	649	452	83	628	562	292	136	0	67	576
TCGA-06-5411-10A-01D-1696-08_GBM	684	0	0	299	601	392	530	639	474	0	0	0	0	0	26	63	579
TCGA-06-5412-10A-01D-1696-08_GBM	664	238	261	285	585	369	522	608	374	0	564	0	293	136	27	1	575
TCGA-06-5413-10A-01D-1696-08_GBM	684	0	0	299	605	380	529	646	486	0	0	0	0	0	26	57	578
TCGA-06-5414-10A-01D-1486-08_GBM	682	251	270	292	611	291	530	657	462	79	639	573	368	136	0	74	578
TCGA-06-5415-10A-01D-1486-08_GBM	687	257	265	300	620	390	535	665	489	0	610	570	0	0	0	160	578
TCGA-06-5416-10A-01D-1486-08_GBM	680	0	0	345	611	390	533	652	482	0	0	0	0	0	0	100	577
TCGA-06-5417-10A-01D-1486-08_GBM	685	0	0	306	615	387	531	659	487	0	0	0	0	0	37	88	578
TCGA-06-5418-10A-01D-1486-08_GBM	674	255	264	295	617	289	531	656	391	79	650	570	368	135	0	81	579
TCGA-06-5856-10A-01D-1696-08_GBM	687	0	0	294	598	391	532	642	461	0	0	0	0	0	34	59	577
TCGA-06-5858-10A-01D-1696-08_GBM	675	0	0	303	598	381	528	655	470	0	0	0	0	0	29	56	578
TCGA-06-5859-10A-01D-1696-08_GBM	685	0	0	308	607	384	529	640	467	0	0	0	0	0	0	80	577
TCGA-06-6388-10A-01D-1845-08_GBM	675	248	265	291	615	380	534	647	388	69	647	573	302	137	33	0	578
TCGA-06-6389-10A-01D-1696-08_GBM	682	245	258	280	584	369	527	652	461	73	586	0	292	134	0	70	575
TCGA-06-6390-10A-01D-1696-08_GBM	684	247	253	297	509	373	527	648	483	0	0	0	0	0	23	54	577
TCGA-06-6391-10A-01D-1696-08_GBM	683	0	0	302	606	385	528	647	450	73	607	0	359	135	0	74	576
TCGA-06-6693-10A-01D-1845-08_GBM	736	250	263	289	608	379	535	654	392	72	642	569	361	138	0	62	576
TCGA-06-6694-10A-01D-1845-08_GBM	678	252	277	287	591	0	534	645	0	82	633	0	384	139	0	0	570
TCGA-06-6695-10A-01D-1845-08_GBM	692	0	0	314	618	394	531	652	487	0	0	0	0	0	0	128	578
TCGA-06-6697-10A-01D-1845-08_GBM	684	0	0	307	612	387	531	652	489	0	0	0	0	0	0	129	580
TCGA-06-6698-10A-01D-1845-08_GBM	656	245	262	281	507	375	533	651	483	0	0	0	0	0	33	64	578
TCGA-06-6699-10A-01D-1845-08_GBM	747	249	268	186	575	381	534	646	491	0	0	0	0	0	32	79	579
TCGA-06-6700-10A-01D-1845-08_GBM	757	248	266	291	565	385	530	618	373	0	621	0	357	138	0	73	576
TCGA-06-6701-10A-01D-1845-08_GBM	684	252	266	291	589	378	534	647	481	0	0	0	0	0	0	100	576
TCGA-06-A5U0-10A-01D-A33W-08_GBM	674	240	242	262	553	137	526	637	460	0	0	0	0	0	34	0	572

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-06-A5U1-10A-01D-A33W-08_GBM	682	0	0	288	576	319	529	644	392	0	0	0	0	0	20	52	570
TCGA-06-A6S0-10A-01D-A33W-08_GBM	594	246	237	0	587	136	527	620	434	76	613	467	290	127	0	47	574
TCGA-06-A6S1-10A-01D-A33W-08_GBM	686	0	0	203	593	367	530	632	399	0	556	508	0	0	34	0	577
TCGA-09-2044-10A-01D-0704-01_OV	681	246	265	282	581	383	537	637	454	85	604	0	369	134	0	68	577
TCGA-12-0615-10A-01D-1492-08_GBM	690	0	0	307	626	288	523	650	484	0	0	0	0	0	0	135	575
TCGA-12-0616-10A-01D-1492-08_GBM	676	251	262	282	591	383	534	662	477	0	0	0	0	0	41	80	577
TCGA-12-0618-10A-01D-1492-08_GBM	686	0	0	298	597	385	528	648	471	0	0	0	0	0	35	66	578
TCGA-12-0619-10A-01D-1492-08_GBM	674	247	258	275	556	277	530	654	482	0	0	0	0	0	0	140	576
TCGA-12-0688-10A-01D-1492-08_GBM	685	253	268	288	561	377	530	657	481	0	0	0	0	0	41	85	578
TCGA-12-0692-10A-01D-1492-08_GBM	648	0	0	275	505	351	522	613	370	0	0	0	0	0	0	62	574
TCGA-12-0821-10A-01D-1492-08_GBM	751	252	273	295	592	0	531	638	458	0	0	0	0	137	35	4	571
TCGA-12-1597-10A-01D-1495-08_GBM	683	246	269	182	517	283	525	613	452	0	606	0	367	132	0	68	577
TCGA-12-3649-10A-01D-1495-08_GBM	689	0	0	304	629	388	533	648	489	0	0	0	0	0	0	114	578
TCGA-12-3650-10A-01D-1495-08_GBM	676	247	267	284	612	373	530	655	458	74	639	510	297	135	0	61	578
TCGA-12-3652-10A-01D-1495-08_GBM	667	257	278	0	602	138	534	660	386	74	655	577	368	137	0	76	578
TCGA-12-3653-10A-01D-1495-08_GBM	667	251	269	287	605	289	531	651	376	77	640	561	294	139	0	64	575
TCGA-12-5295-10A-01D-1486-08_GBM	690	0	0	314	615	392	534	655	483	0	0	0	0	0	43	2	578
TCGA-12-5299-10A-01D-1486-08_GBM	601	259	277	0	0	0	531	654	460	82	623	0	375	138	32	0	578
TCGA-12-5301-10A-01D-1486-08_GBM	759	0	0	306	609	400	533	651	393	72	593	0	301	138	33	6	580
TCGA-13-0751-10A-01D-0446-08_OV	693	0	0	313	628	410	538	663	0	87	653	0	402	145	0	0	583
TCGA-13-0757-10A-01D-0356-01_OV	761	264	275	303	623	389	534	663	472	83	649	580	382	138	39	0	580
TCGA-13-0758-10A-01D-0356-01_OV	765	267	274	309	628	298	538	661	489	0	623	580	0	0	58	2	583
TCGA-13-0883-10A-01D-0399-01_OV	780	275	284	310	659	413	541	664	484	83	658	595	71	147	0	203	583
TCGA-13-0886-10A-01D-0399-01_OV	766	0	0	319	651	412	539	664	501	0	0	0	0	0	0	290	583
TCGA-13-0888-10A-01D-0399-01_OV	696	267	280	310	611	300	537	657	495	0	0	0	0	0	0	229	584
TCGA-13-0891-10A-01D-0399-01_OV	762	261	278	305	614	403	537	659	500	0	0	0	0	0	0	245	584
TCGA-13-0899-10A-01D-0399-01_OV	693	267	279	303	635	298	537	655	477	85	630	0	388	141	53	0	583
TCGA-13-0904-10A-01D-0399-01_OV	770	272	284	307	621	302	539	666	493	0	0	0	0	0	0	222	583
TCGA-13-0911-10A-01D-0399-01_OV	763	0	0	316	630	409	534	665	491	0	0	0	0	0	68	0	581
TCGA-13-0913-10A-01D-0399-01_OV	693	263	279	297	609	405	538	656	497	0	0	0	0	0	0	279	583
TCGA-13-0916-10A-01D-0399-01_OV	691	0	25	308	625	300	534	654	491	0	0	74	0	0	0	221	582
TCGA-13-0921-10A-01D-0399-01_OV	776	272	282	301	622	409	539	665	495	0	0	0	0	0	0	152	586
TCGA-13-0923-10A-01D-0399-01_OV	766	0	0	315	628	413	538	661	485	86	642	0	388	139	0	129	581
TCGA-13-1477-10A-01D-0472-01_OV	603	272	285	0	620	142	538	662	478	84	657	592	0	139	0	98	582
TCGA-13-1485-10A-01D-0472-01_OV	690	265	279	299	628	297	536	656	489	0	624	582	0	0	0	137	582
TCGA-13-1495-10A-01D-0472-01_OV	693	0	0	318	649	407	536	665	502	0	0	0	0	0	0	261	584
TCGA-13-1500-10A-01D-0472-01_OV	694	0	0	317	623	410	538	666	480	86	633	0	378	144	0	99	583
TCGA-13-1505-10A-01D-0472-01_OV	767	0	0	313	628	412	536	661	502	0	0	0	0	0	0	260	581
TCGA-13-2057-10A-01D-1526-09_OV	800	340	383	0	0	0	555	543	476	0	628	0	457	187	0	124	597
TCGA-13-2059-10A-01D-1526-09_OV	704	0	0	393	712	471	554	647	451	103	609	0	454	185	0	92	592
TCGA-13-2061-10A-01D-1526-09_OV	802	0	0	399	725	478	558	645	562	0	0	0	0	0	0	190	594
TCGA-13-2065-10A-01D-1526-09_OV	799	0	0	416	727	478	565	663	590	0	0	0	0	0	93	156	594
TCGA-13-2066-10A-01D-1526-09_OV	702	0	0	399	722	477	556	646	564	0	0	0	0	0	0	198	597
TCGA-13-2071-10A-01D-1526-09_OV	801	329	368	388	722	477	563	667	0	109	677	590	469	189	0	0	600
TCGA-14-0736-10C-01D-2280-08_GBM	596	252	266	0	559	135	531	633	470	0	579	0	374	0	35	0	579
TCGA-14-0740-10B-01D-1845-08_GBM	759	0	0	316	614	291	527	657	479	0	0	0	0	0	43	3	577
TCGA-14-0781-10A-01D-1696-08_GBM	675	247	265	185	608	320	533	637	480	0	514	513	0	0	36	2	574
TCGA-14-0786-10A-01D-1492-08_GBM	595	262	275	0	0	0	532	659	494	0	0	0	0	0	0	159	578
TCGA-14-0787-10A-01D-1492-08_GBM	686	258	277	297	600	393	537	656	469	77	612	0	372	138	43	0	580
TCGA-14-0789-10A-01D-1492-08_GBM	689	0	0	298	604	379	532	655	481	0	0	0	0	0	31	71	580
TCGA-14-0790-10A-01D-1494-08_GBM	686	0	0	305	633	388	529	660	382	79	601	0	364	141	0	76	577
TCGA-14-0813-10A-01D-1492-08_GBM	754	0	0	306	608	387	531	659	485	0	0	0	0	0	34	63	576
TCGA-14-0817-10A-01D-1492-08_GBM	688	0	0	304	603	395	530	650	470	0	0	0	0	0	0	100	578
TCGA-14-0862-10C-01D-1845-08_GBM	755	0	0	301	602	380	533	647	483	0	0	0	0	0	35	64	579
TCGA-14-0871-10A-01D-1492-08_GBM	599	262	278	0	592	137	535	653	0	87	654	576	371	142	0	1	574
TCGA-14-1034-10A-01D-1492-08_GBM	686	0	0	312	616	390	531	654	483	0	0	0	0	0	35	74	577
TCGA-14-1043-10A-01D-1845-08_GBM	758	244	268	291	600	379	535	660	487	0	0	0	0	0	36	67	573
TCGA-14-1395-10A-01D-1845-08_GBM	686	0	0	306	613	386	535	645	479	0	0	0	0	0	0	95	578
TCGA-14-1450-10B-01D-1845-08_GBM	671	262	276	0	603	143	534	639	450	62	653	580	297	138	30	0	577
TCGA-14-1456-10A-01D-1494-08_GBM	759	0	0	348	611	386	534	660	477	0	0	0	0	0	31	70	578
TCGA-14-1823-10A-01D-1494-08_GBM	678	0	0	298	606	394	530	642	471	0	0	0	0	0	31	71	581
TCGA-14-1825-10A-01D-1494-08_GBM	758	0	0	308	615	393	532	640	459	80	632	0	371	139	0	79	579
TCGA-14-1829-10A-01D-1494-08_GBM	687	251	274	288	618	386	535	656	481	0	617	571	0	0	68	0	580
TCGA-14-2554-10A-01D-1494-08_GBM	686	249	267	302	597	381	527	646	462	0	593	521	0	140	0	86	581
TCGA-14-3476-10A-01D-1353-08_GBM	682	248	256	300	619	387	532	656	464	81	638	577	0	137	0	71	578
TCGA-14-4157-10A-01D-1353-08_GBM	673	265	279	0	598	140	537	648	483	0	598	573	0	0	0	123	578
TCGA-15-0742-10A-01D-1492-08_GBM	679	248	271	186	519	286	533	653	463	0	0	0	0	0	0	118	577
TCGA-15-1444-10A-01D-1696-08_GBM	592	260	274	0	562	139	534	647	471	0	591	513	0	0	0	89	580
TCGA-16-0846-10A-01D-1492-08_GBM	667	263	275	0	552	136	530	661	480	61	604	565	0	0	0	105	576
TCGA-16-0848-10A-01D-1492-08_GBM	686	0	0	300	612	391	530	655	477	0	0	0	0	0	36	82	577
TCGA-16-0861-10A-01D-1492-08_GBM	689	0	0	306	610	393	534	655	465	80	631	0	379	139	0	90	580
TCGA-16-1045-10B-01D-1492-08_GBM	760	0	0	308	610	400	535	658	0	87	649	569	371	140	0	0	578
TCGA-16-1048-10A-01D-1353-08_GBM	762	0	0	314	644	387	530	659	489	0	0	0	0	0	0	148	578
TCGA-19-1390-10C-01D-1495-08_GBM	686	252	0	298	622	381	533	655	394	74	611	0	372	137	0	80	576
TCGA-19-1787-10A-01D-1495-08_GBM	689	0	0	303	609	383	530	654	482	0	0	0	0	0	39	74	577
TCGA-19-1790-10B-01D-1353-08_GBM	690	0	0	359	644	394	535	662	503	0	0	0	0	0	41	92	580
TCGA-19-2619-10A-01D-1495-08_GBM	679	245	267	289	613	284	532	660	461	82	649	519	363	134	31	13	577
TCGA-19-2620-10A-01D-1495-08_GBM	680	0	0	312	613	386	530	661	477	0	0	0	0	0	30	72	574
TCGA-19-2623-10A-01D-1495-08_GBM	681	253	267	292	590	377	532	651	479	0	0	0	0	0	0	139	576
TCGA-19-2624-10A-01D-1495-08_GBM	679	0	0	307	608	283	518	625	458	0	0	0	0	137	29	1	573
TCGA-19-2625-10A-01D-1495-08_GBM	689	0	0	297	623	391	534	661	454	86	644	568	364	135	0	72	577
TCGA-19-2629-10A-01D-1495-08_GBM	756	246	259	189	616	285	534	656	478	0	612	562	0	0	49	0	575
TCGA-19-2631-10B-01D-1353-08_GBM	761	0	0	312	615	387	535	662	486	0	0	0	0	0	35	73	581
TCGA-19-4065-10A-01D-2280-08_GBM	758	239	248	279	552	367	531	652	469	0	0	0	0	0	25	59	576
TCGA-19-4068-10A-01D-1353-08_GBM	756	251	274	301	619	286	533	663	487	0	615	568	0	0	37	74	578
TCGA-19-5947-10A-01D-1696-08_GBM	689	0	0	299	608	391	532	644	485	0	0	0	0	0	42	64	576
TCGA-19-5950-10A-01D-1696-08_GBM	682	0	0	307	607	283	522	650	482	0	0	0	0	0	0	111	578
TCGA-19-5951-10A-01D-1696-08_GBM	682	0	0	301	599	387	532	655	369	85	586	0	365	136	0	62	575
TCGA-19-5952-10A-01D-1696-08_GBM	667	243	261	273	605	283	530	653	477	0	592	512	0	0	25	69	574
TCGA-19-5953-10A-01D-1845-08_GBM	670	258	281	0	589	134	536	644	486	0	591	534	0	0	0	110	577
TCGA-19-5954-10A-01D-1696-08_GBM	674	242	258	273	605	278	530	637	369	79	625	573	0	137	0	61	574
TCGA-19-5955-10A-01D-1696-08_GBM	753	0	0	306	604	373	532	639	456	62	584	0	295	136	0	60	578
TCGA-19-5956-10A-01D-1696-08_GBM	680	231	273	281	582	370	530	636	473	0	0	0	0	0	37	72	577
TCGA-19-5958-10A-01D-1696-08_GBM	660	237	258	286	571	369	531	643	364	73	592	0	361	136	0	66	575
TCGA-19-5959-10A-01D-1696-08_GBM	681	0	0	297	589	381	525	628	361	64	569	472	0	136	0	39	572
TCGA-19-5960-10A-01D-1696-08_GBM	671	238	253	280	535	265	523	641	366	69	592	0	284	139	0	51	572

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-19-A60I-10A-01D-A33W-08_GBM	665	241	263	283	602	372	530	630	466	0	580	505	0	0	29	62	571
TCGA-19-A6J4-10A-01D-A33W-08_GBM	676	0	0	298	590	375	527	626	463	0	0	0	0	0	0	76	574
TCGA-19-A6J5-10A-01D-A33W-08_GBM	645	227	239	264	590	368	527	626	372	0	499	0	284	0	30	0	556
TCGA-20-0991-10A-01D-0428-01_OV	762	0	0	306	636	298	527	660	500	0	0	0	0	0	0	221	582
TCGA-21-1081-10B-01D-1521-08_LUSC	758	254	272	299	617	380	535	658	490	0	611	574	0	0	0	175	581
TCGA-21-1082-10B-01D-1521-08_LUSC	688	0	0	305	609	397	534	655	478	0	0	0	0	0	0	109	579
TCGA-21-5782-10A-01D-1632-08_LUSC	593	258	272	0	504	129	531	644	318	73	617	556	0	134	0	50	579
TCGA-21-5783-10A-01D-2184-08_LUSC	680	0	0	291	592	380	531	629	364	68	584	0	284	137	0	56	574
TCGA-21-5784-10A-01D-1632-08_LUSC	672	242	260	259	537	363	531	633	0	76	609	0	371	139	0	2	572
TCGA-21-5786-10A-01D-1632-08_LUSC	729	0	0	301	579	372	524	647	467	0	0	0	0	0	23	62	578
TCGA-21-5787-10A-01D-1632-08_LUSC	740	240	256	175	487	364	532	635	470	0	0	0	0	0	21	59	574
TCGA-21-A5DI-10A-01D-A26K-08_LUSC	684	0	0	299	594	381	528	637	432	0	567	0	288	132	30	2	575
TCGA-22-A5C4-10A-01D-A27N-08_LUSC	678	0	0	290	559	370	529	625	464	0	0	0	0	0	0	98	575
TCGA-23-1110-10A-01D-0428-01_OV	766	0	0	314	644	410	538	658	496	0	0	0	0	0	52	124	582
TCGA-23-2641-10A-01D-1526-09_OV	794	330	360	383	700	383	553	648	570	0	0	0	0	0	0	167	595
TCGA-23-2643-10A-01D-1526-09_OV	602	334	373	0	693	182	560	666	580	0	637	586	0	0	87	137	594
TCGA-23-2647-10A-01D-1526-09_OV	796	323	370	387	723	473	560	634	581	0	602	589	0	0	98	111	596
TCGA-23-2649-10A-01D-1526-09_OV	696	342	376	0	700	184	556	656	577	0	639	582	0	0	74	118	596
TCGA-24-1430-10A-01D-0472-01_OV	676	275	293	0	0	0	538	648	481	0	632	0	395	142	0	138	585
TCGA-24-1431-10A-01D-0472-01_OV	767	0	0	318	633	411	537	662	484	84	641	0	396	142	0	138	586
TCGA-25-1319-10A-01D-0452-01_OV	761	0	0	307	609	388	532	660	488	0	0	0	0	0	45	84	580
TCGA-25-2397-10A-01D-0704-01_OV	685	251	267	289	586	382	531	653	451	76	609	0	369	135	0	75	576
TCGA-25-2398-10A-01D-0704-01_OV	761	0	0	313	639	394	534	658	495	0	0	0	0	0	0	178	582
TCGA-26-1439-10A-01D-1353-08_GBM	680	244	258	300	565	276	531	656	478	0	0	0	0	0	25	67	578
TCGA-26-1442-10A-01D-1696-08_GBM	595	252	273	0	563	138	534	657	466	68	586	558	0	0	30	63	577
TCGA-26-5132-10A-01D-1486-08_GBM	679	254	268	199	614	288	534	653	481	0	602	568	0	0	45	10	577
TCGA-26-5133-10A-01D-1486-08_GBM	679	254	274	297	592	286	533	652	479	0	0	0	0	0	0	101	577
TCGA-26-5134-10A-01D-1486-08_GBM	760	0	0	302	610	400	533	649	484	0	0	0	0	0	0	158	579
TCGA-26-5135-10A-01D-1486-08_GBM	688	0	0	308	606	392	535	649	473	0	0	0	0	0	0	105	577
TCGA-26-5136-10A-01D-1486-08_GBM	678	248	262	293	585	284	531	647	476	0	0	0	0	0	0	107	579
TCGA-26-5139-10A-01D-1486-08_GBM	759	0	0	311	620	393	532	658	468	75	640	0	306	139	42	0	576
TCGA-26-6173-10A-01D-1845-08_GBM	759	0	0	310	614	384	530	650	397	68	615	0	294	138	0	73	577
TCGA-26-6174-10A-01D-1845-08_GBM	598	264	278	0	575	137	534	657	465	65	628	578	0	139	0	82	579
TCGA-27-1830-10A-01D-1494-08_GBM	687	0	0	308	617	399	531	651	480	0	0	0	0	0	0	134	574
TCGA-27-1831-10A-01D-1494-08_GBM	756	251	268	297	595	290	522	646	0	77	634	0	378	141	0	0	582
TCGA-27-1832-10A-01D-1494-08_GBM	682	0	0	302	612	387	528	628	390	0	0	0	0	0	0	74	576
TCGA-27-1833-10A-01D-1494-08_GBM	761	253	272	298	600	391	535	664	485	0	0	0	0	0	41	89	580
TCGA-27-1834-10A-01D-1494-08_GBM	686	0	0	304	609	297	526	655	482	0	0	0	0	0	0	138	579
TCGA-27-1835-10A-01D-1494-08_GBM	680	254	264	294	617	289	534	658	490	0	606	576	0	0	0	161	577
TCGA-27-1836-10A-01D-1494-08_GBM	690	0	0	349	615	384	533	654	477	0	0	0	0	0	47	0	575
TCGA-27-1837-10A-01D-1494-08_GBM	685	252	273	293	596	378	534	660	485	0	0	0	0	0	0	110	580
TCGA-27-1838-10A-01D-1494-08_GBM	684	249	277	290	597	386	535	664	483	0	0	0	0	0	0	119	578
TCGA-27-2518-10A-01D-1494-08_GBM	688	251	271	197	587	286	533	659	482	0	0	0	0	0	39	77	579
TCGA-27-2519-10A-01D-1494-08_GBM	682	243	266	296	567	389	525	634	0	77	651	0	387	141	0	2	578
TCGA-27-2521-10A-01D-1494-08_GBM	759	0	0	349	610	396	534	657	485	0	0	0	0	0	0	120	577
TCGA-27-2523-10A-01D-1494-08_GBM	689	0	0	308	609	295	521	655	482	0	0	0	0	0	0	158	579
TCGA-27-2524-10A-01D-1494-08_GBM	691	0	0	307	605	397	535	659	483	0	0	0	0	0	36	80	576
TCGA-27-2526-10A-01D-1494-08_GBM	754	0	0	316	611	387	533	652	478	0	0	0	0	0	0	93	577
TCGA-27-2527-10A-01D-1494-08_GBM	758	253	273	303	614	382	533	634	0	79	650	571	370	139	0	1	578
TCGA-27-2528-10A-01D-1494-08_GBM	685	0	0	300	613	388	530	656	396	83	620	0	374	136	35	0	578
TCGA-28-1747-10B-01D-1494-08_GBM	692	0	0	309	613	392	531	663	483	0	0	0	0	0	29	77	578
TCGA-28-1753-10B-01D-1494-08_GBM	684	0	0	310	618	393	534	664	485	0	0	0	0	0	37	78	576
TCGA-28-2499-10A-01D-1494-08_GBM	688	0	0	302	614	394	535	661	482	0	0	0	0	0	0	139	579
TCGA-28-2501-10A-01D-1696-08_GBM	674	0	0	293	599	381	524	639	0	79	622	0	376	142	0	0	575
TCGA-28-2502-10A-01D-1494-08_GBM	681	252	272	303	622	287	534	660	496	0	632	571	0	0	0	161	576
TCGA-28-2509-10A-01D-1494-08_GBM	667	262	277	0	565	138	533	655	390	83	653	577	0	138	36	0	576
TCGA-28-2510-10A-01D-1696-08_GBM	662	240	257	280	598	371	533	634	479	0	610	563	0	0	39	1	575
TCGA-28-2513-10A-01D-1494-08_GBM	690	0	0	307	615	394	533	661	484	0	0	0	0	0	41	79	578
TCGA-28-2514-10A-01D-1494-08_GBM	688	0	0	308	608	401	533	655	480	0	0	0	0	0	0	101	579
TCGA-28-5204-10A-01D-1486-08_GBM	594	260	278	0	596	137	534	652	386	74	645	519	370	137	0	78	578
TCGA-28-5207-10A-01D-1486-08_GBM	756	0	0	306	619	292	528	648	483	0	0	2	0	0	0	107	579
TCGA-28-5208-10A-01D-1486-08_GBM	683	253	265	293	595	381	534	661	486	0	0	0	0	0	0	155	579
TCGA-28-5209-10A-01D-1486-08_GBM	690	0	0	313	625	396	535	672	462	84	653	569	373	137	0	88	580
TCGA-28-5211-10B-01D-1845-08_GBM	687	0	0	303	610	390	535	646	480	0	0	0	0	0	47	0	576
TCGA-28-5213-10A-01D-1486-08_GBM	759	254	271	298	616	292	536	655	488	0	624	572	0	0	0	163	581
TCGA-28-5214-10A-01D-1486-08_GBM	757	258	272	292	601	286	530	656	481	0	0	0	0	0	49	1	575
TCGA-28-5215-10A-01D-1486-08_GBM	685	251	274	299	592	285	536	654	476	0	0	0	0	0	51	0	576
TCGA-28-5216-10A-01D-1486-08_GBM	761	253	270	299	596	393	533	657	480	0	0	0	0	0	0	116	575
TCGA-28-5218-10A-01D-1486-08_GBM	672	254	273	299	600	288	531	659	0	85	652	0	385	140	0	1	576
TCGA-28-5219-10A-01D-1486-08_GBM	688	0	0	307	612	390	533	660	485	0	0	0	0	0	37	74	577
TCGA-28-5220-10A-01D-1486-08_GBM	691	0	0	309	610	383	525	659	490	0	0	0	0	0	39	71	576
TCGA-28-6450-10A-01D-1696-08_GBM	593	245	272	0	578	137	530	640	450	76	650	574	0	131	0	61	577
TCGA-29-2429-10A-01D-1526-09_OV	697	327	363	378	701	382	559	658	582	0	0	0	0	0	70	107	594
TCGA-29-2431-10A-01D-1526-09_OV	704	329	369	386	692	371	559	641	568	0	0	0	0	0	0	191	596
TCGA-29-2432-10A-01D-1526-09_OV	800	0	0	396	720	469	555	646	580	0	0	0	0	0	0	199	590
TCGA-29-2434-10A-01D-1526-09_OV	798	0	0	394	715	476	560	651	467	0	0	0	0	0	0	202	597
TCGA-29-2436-10A-01D-1526-09_OV	703	0	0	398	720	391	553	654	584	0	0	0	0	0	0	296	596
TCGA-32-1970-10A-01D-1494-08_GBM	682	255	273	298	620	285	530	655	487	0	635	575	0	0	0	144	577
TCGA-32-1977-10C-01D-1353-08_GBM	751	254	261	296	615	373	533	655	395	82	654	567	374	139	0	66	580
TCGA-32-1979-10A-01D-1696-08_GBM	682	0	0	298	601	379	530	634	470	0	0	0	0	0	0	116	573
TCGA-32-1980-10A-01D-1696-08_GBM	669	247	249	190	500	283	531	635	468	0	0	0	0	0	35	0	573
TCGA-32-1982-10A-01D-1494-08_GBM	601	264	279	0	597	141	534	659	487	0	621	0	0	0	0	153	580
TCGA-32-1986-10A-01D-1494-08_GBM	688	0	0	303	616	383	531	650	487	0	0	0	0	0	0	136	577
TCGA-32-1991-10C-01D-1353-08_GBM	694	0	0	313	624	390	534	656	492	0	0	0	0	0	0	153	579
TCGA-32-2491-10A-01D-1353-08_GBM	756	254	264	297	613	361	533	653	400	77	631	573	0	131	0	67	578
TCGA-32-2494-10A-01D-1353-08_GBM	772	249	264	297	566	378	534	659	403	82	584	0	370	135	30	1	576
TCGA-32-2495-10B-01D-1353-08_GBM	763	250	265	295	599	376	533	654	487	0	0	0	0	0	0	104	578
TCGA-32-2498-10B-01D-1353-08_GBM	692	246	265	291	620	381	535	659	468	80	625	581	0	137	33	0	577
TCGA-32-2615-10A-01D-1495-08_GBM	690	0	0	302	599	290	522	660	475	0	0	0	0	0	0	91	577
TCGA-32-2616-10A-01D-1495-08_GBM	684	0	0	301	605	388	532	645	389	73	591	568	89	135	34	5	574
TCGA-32-2632-10A-01D-1495-08_GBM	682	253	265	289	585	382	532	649	0	86	645	0	379	143	0	1	576
TCGA-32-2634-10A-01D-1495-08_GBM	594	253	272	0	509	134	530	645	387	72	639	568	366	135	0	68	574
TCGA-32-2638-10A-01D-1495-08_GBM	676	246	264	280	606	379	533	653	382	76	633	566	0	137	34	0	573
TCGA-32-4208-10A-01D-1353-08_GBM	692	0	0	313	616	294	528	652	486	0	0	0	0	0	0	113	578
TCGA-32-4209-10A-01D-1353-08_GBM	691	241	258	298	596	376	533	655	488	0	0	0	0	0	49	0	582
TCGA-32-4210-10A-01D-1353-08_GBM	683	247	269	202	622	282	539	660	491	81	590	573	0	0	38	73	578

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-32-4211-10A-01D-1353-08_GBM	690	0	0	347	615	390	530	654	400	78	627	0	302	140	0	74	579
TCGA-32-4213-10A-01D-1353-08_GBM	667	263	279	0	580	134	531	654	458	79	640	516	370	141	28	1	579
TCGA-32-4719-10A-01D-1353-08_GBM	762	0	0	312	617	392	538	655	479	0	0	0	0	0	47	0	579
TCGA-32-5222-10A-01D-1486-08_GBM	692	258	275	298	618	387	532	657	467	81	648	582	0	136	37	4	579
TCGA-33-A4WN-10A-01D-A25L-08_LUSC	662	245	257	256	593	370	527	623	364	75	636	551	290	129	0	58	573
TCGA-33-A5GW-10A-01D-A27N-08_LUSC	683	0	0	292	598	389	530	631	465	0	0	0	0	0	0	81	571
TCGA-34-5231-10A-01D-1817-08_LUSC	685	0	0	308	607	289	520	652	480	0	0	0	0	0	29	66	575
TCGA-34-5232-10A-01D-1817-08_LUSC	688	0	0	305	608	387	535	660	478	79	0	0	0	0	36	0	578
TCGA-34-5234-10A-01D-1632-08_LUSC	595	257	274	0	604	144	532	643	478	0	625	568	0	0	0	85	577
TCGA-34-5236-10A-01D-1817-08_LUSC	689	0	0	301	602	391	532	649	480	0	0	0	0	0	33	64	578
TCGA-34-5239-10A-01D-1817-08_LUSC	596	256	276	0	0	0	533	656	460	77	597	0	293	138	0	68	575
TCGA-34-5240-10A-01D-1441-08_LUSC	686	0	0	299	602	386	533	651	377	81	581	0	302	136	36	2	576
TCGA-34-5241-10A-01D-1441-08_LUSC	686	0	0	296	607	397	533	655	473	0	0	0	0	0	32	84	574
TCGA-34-5927-10A-01D-1817-08_LUSC	688	0	0	301	609	385	532	651	484	0	0	0	0	0	0	84	577
TCGA-34-5928-10A-01D-1817-08_LUSC	676	243	258	292	553	376	527	623	440	0	615	564	0	135	0	54	577
TCGA-34-7107-10A-01D-1945-08_LUSC	680	249	269	287	587	371	532	641	379	76	575	560	0	139	0	68	573
TCGA-34-8454-10A-01D-2323-08_LUSC	689	246	269	289	605	385	533	650	461	76	624	569	368	138	34	0	575
TCGA-34-8455-10A-01D-2323-08_LUSC	599	260	276	0	561	139	535	647	454	77	621	577	0	141	0	75	577
TCGA-34-8456-10A-01D-2323-08_LUSC	668	0	0	290	589	369	531	640	462	0	0	0	0	0	24	49	574
TCGA-34-A5IX-10A-01D-A27N-08_LUSC	686	0	0	296	604	385	528	642	465	0	0	0	0	0	31	0	572
TCGA-35-3615-10A-01D-1489-08_LUAD	689	75	0	310	590	397	534	664	489	0	43	9	0	0	44	83	578
TCGA-35-4122-10A-01D-1105-08_LUAD	690	0	0	344	607	385	531	646	0	83	650	564	373	140	0	1	580
TCGA-35-4123-10A-01D-1105-08_LUAD	684	246	269	292	584	380	531	646	476	0	0	0	0	0	0	104	576
TCGA-35-5375-10A-01D-1625-08_LUAD	642	252	259	276	602	273	527	637	374	65	629	570	0	136	0	63	580
TCGA-36-2530-10A-01D-1526-09_OV	704	0	0	393	712	474	555	636	458	98	604	0	456	184	0	106	595
TCGA-36-2532-10A-01D-1526-09_OV	703	0	0	413	711	475	559	656	562	100	646	0	458	184	90	0	597
TCGA-36-2533-10A-01D-1526-09_OV	701	0	0	380	705	474	510	440	278	90	410	0	359	177	0	69	583
TCGA-36-2534-10A-01D-1526-09_OV	801	0	0	398	721	479	563	666	586	0	0	0	0	0	141	0	596
TCGA-36-2537-10A-01D-1526-09_OV	704	0	0	409	716	474	560	658	577	0	0	0	0	0	117	0	597
TCGA-36-2538-10A-01D-1526-09_OV	804	0	0	402	726	479	563	674	480	111	639	0	465	185	0	146	597
TCGA-36-2539-10A-01D-1526-09_OV	704	0	0	413	722	473	557	667	581	0	0	0	0	0	74	120	595
TCGA-36-2540-10A-01D-1526-09_OV	801	331	364	385	705	475	562	664	575	0	0	0	0	0	86	125	597
TCGA-36-2542-10A-01D-1526-09_OV	601	336	377	0	685	184	557	630	545	100	648	591	0	185	0	128	593
TCGA-36-2543-10A-01D-1526-09_OV	700	327	364	378	695	469	554	611	570	0	0	0	0	0	85	100	593
TCGA-36-2544-10A-01D-1526-09_OV	600	333	369	0	692	180	558	545	574	0	596	553	0	0	0	135	587
TCGA-36-2545-10A-01D-1526-09_OV	798	0	0	395	721	386	559	665	583	0	0	0	0	0	71	127	596
TCGA-36-2547-10A-01D-1526-09_OV	703	331	365	387	692	457	563	665	473	108	636	0	460	182	108	0	596
TCGA-36-2548-10A-01D-1526-09_OV	798	0	0	416	720	477	554	662	581	0	0	0	0	0	75	103	597
TCGA-36-2551-10A-01D-1526-09_OV	703	330	371	239	696	379	562	669	560	102	645	0	462	182	0	146	595
TCGA-36-2552-10A-01D-1526-09_OV	704	317	361	371	712	371	554	644	567	0	590	568	0	0	62	84	590
TCGA-37-3783-10A-01D-1267-08_LUSC	691	0	0	321	626	293	526	649	484	0	0	0	0	144	0	119	579
TCGA-37-3789-10A-01D-0983-08_LUSC	717	244	252	270	616	260	529	653	473	0	596	553	0	0	0	122	577
TCGA-37-3792-10A-01D-0983-08_LUSC	761	250	240	274	506	354	528	621	373	0	580	0	289	130	27	0	575
TCGA-37-4129-10A-01D-1352-08_LUSC	762	0	0	349	621	295	534	657	492	0	0	0	0	0	0	113	579
TCGA-37-4130-10A-01D-1352-08_LUSC	692	264	282	310	636	294	538	669	503	0	0	0	0	0	0	202	583
TCGA-37-4132-10A-01D-1352-08_LUSC	765	0	0	359	636	404	538	675	501	0	0	0	0	0	37	106	583
TCGA-37-4133-10A-01D-1352-08_LUSC	768	260	282	314	616	399	540	670	502	0	0	0	0	0	0	171	581
TCGA-37-4135-10A-01D-1352-08_LUSC	759	0	0	316	628	391	534	664	492	0	0	0	0	0	0	151	581
TCGA-37-4141-10A-01D-1352-08_LUSC	764	0	0	358	644	402	536	670	498	0	0	0	0	0	0	165	581
TCGA-37-5819-10A-01D-1632-08_LUSC	676	244	257	280	574	369	529	637	475	0	0	0	0	0	0	101	573
TCGA-37-A5EL-10A-01D-A26K-08_LUSC	669	243	265	274	577	379	525	627	376	67	616	568	0	133	0	59	575
TCGA-37-A5EM-10A-01D-A27N-08_LUSC	680	240	257	277	603	368	528	641	366	75	623	507	353	136	23	1	574
TCGA-37-A5EN-10A-01D-A26K-08_LUSC	671	248	259	291	607	382	533	652	474	0	573	571	0	0	0	85	579
TCGA-38-6178-10A-01D-1753-08_LUAD	755	0	0	306	601	376	520	645	475	0	0	0	0	0	28	43	574
TCGA-38-A44F-10A-01D-A24F-08_LUAD	676	240	258	285	563	372	514	611	3	72	611	0	375	138	0	1	574
TCGA-41-2571-10A-01D-1495-08_GBM	683	252	271	285	609	379	531	643	444	76	639	568	304	133	0	60	576
TCGA-41-2572-10A-01D-1353-08_GBM	681	252	272	300	603	282	534	659	486	0	0	0	0	0	36	70	579
TCGA-41-2573-10A-01D-1495-08_GBM	680	248	266	192	610	289	529	652	459	80	648	517	293	135	0	55	578
TCGA-41-2575-10A-01D-1495-08_GBM	682	251	266	285	592	385	535	646	474	0	0	0	0	0	39	3	575
TCGA-41-3392-10A-01D-1495-08_GBM	679	246	269	285	584	281	531	659	481	0	0	0	0	0	32	59	575
TCGA-41-3393-10A-01D-1353-08_GBM	684	0	0	353	616	388	534	647	479	0	0	0	0	0	0	114	576
TCGA-41-3915-10A-01D-1353-08_GBM	764	0	0	314	621	397	534	660	478	82	626	0	300	138	0	74	578
TCGA-41-4097-10A-01D-1353-08_GBM	771	0	0	318	617	385	533	666	462	81	603	0	374	138	0	87	577
TCGA-41-5651-10A-01D-1696-08_GBM	678	246	256	277	559	369	525	636	481	0	0	0	0	0	31	60	574
TCGA-41-6646-10A-01D-1845-08_GBM	687	0	0	305	610	392	533	657	451	76	596	0	372	138	0	79	577
TCGA-42-2582-10A-01D-1526-09_OV	803	0	0	417	721	479	561	652	582	0	0	0	0	0	0	270	596
TCGA-42-2587-10A-01D-1526-09_OV	799	336	369	380	704	378	555	657	576	0	0	0	0	0	82	132	596
TCGA-42-2588-10A-01D-1526-09_OV	689	334	378	0	0	0	554	635	578	0	0	0	0	0	63	110	595
TCGA-42-2589-10A-01D-1526-09_OV	703	331	367	381	701	384	556	665	582	0	0	0	0	0	92	130	598
TCGA-42-2590-10A-01D-1526-09_OV	802	0	0	398	726	389	554	663	585	0	0	0	0	0	87	146	595
TCGA-42-2591-10A-01D-1526-09_OV	695	339	377	0	0	0	556	664	565	106	653	587	0	184	0	138	601
TCGA-42-2593-10A-01D-1764-09_OV	799	0	0	414	719	477	560	670	558	102	650	0	461	185	92	0	597
TCGA-43-3394-10A-01D-0983-08_LUSC	735	236	123	104	498	131	517	620	371	0	645	566	343	131	31	1	575
TCGA-43-3920-10A-01D-0983-08_LUSC	739	233	248	280	598	263	528	643	468	0	592	559	0	0	0	114	577
TCGA-43-5668-10A-01D-1632-08_LUSC	671	237	263	274	499	368	532	639	452	63	509	0	303	136	25	0	576
TCGA-43-5670-10A-01D-2122-08_LUSC	681	243	264	289	610	380	531	647	384	80	638	572	0	131	0	63	577
TCGA-43-6143-10A-01D-1817-08_LUSC	687	0	0	306	601	374	530	659	476	0	0	0	0	0	29	67	572
TCGA-43-6647-10A-01D-1817-08_LUSC	686	0	0	303	612	394	531	649	463	77	592	0	369	135	0	66	574
TCGA-43-6770-10A-01D-1817-08_LUSC	680	248	272	280	603	142	531	645	477	0	599	561	0	0	26	49	575
TCGA-43-6771-10A-01D-1817-08_LUSC	693	0	0	305	613	382	531	657	483	0	0	0	0	0	32	77	575
TCGA-43-6773-10A-01D-1945-08_LUSC	691	0	0	305	601	286	523	644	474	0	0	0	0	0	0	129	577
TCGA-43-7656-10A-01D-2122-08_LUSC	685	0	0	303	602	387	530	642	475	0	0	0	0	0	0	80	573
TCGA-43-7657-10A-01D-2122-08_LUSC	687	0	0	300	601	287	521	643	462	0	0	0	0	0	0	78	573
TCGA-43-7658-10A-01D-2122-08_LUSC	678	241	266	277	575	366	530	644	443	74	593	0	365	136	22	1	574
TCGA-43-8115-10A-01D-2244-08_LUSC	680	0	0	287	593	375	529	632	462	0	0	0	0	0	0	86	573
TCGA-43-8116-10A-01D-2244-08_LUSC	673	235	254	276	585	275	528	634	463	0	0	0	0	0	0	72	573
TCGA-43-8118-10A-01D-2395-08_LUSC	668	249	258	283	606	375	529	639	387	75	625	567	0	132	31	0	576
TCGA-43-A474-10A-01D-A24F-08_LUSC	685	0	9	299	590	361	523	630	465	0	0	0	0	0	0	73	571
TCGA-43-A475-10A-01D-A24F-08_LUSC	681	0	0	288	586	373	528	628	456	0	0	0	0	0	0	65	569
TCGA-43-A56U-10A-01D-A26K-08_LUSC	597	261	274	0	549	136	532	636	476	0	580	564	0	0	0	132	573
TCGA-43-A56V-10A-01D-A26K-08_LUSC	664	238	125	255	367	356	483	517	368	0	500	0	273	128	0	50	574
TCGA-44-2656-10A-01D-0969-08_LUAD	686	0	0	309	609	394	530	657	469	0	0	0	0	0	0	104	577
TCGA-44-2657-10A-01D-1105-08_LUAD	679	248	275	292	595	378	531	650	482	0	0	0	0	0	28	77	578
TCGA-44-2659-10A-01D-0969-08_LUAD	678	259	275	297	592	381	532	658	467	78	615	518	0	136	0	78	574
TCGA-44-2661-10A-01D-1105-08_LUAD	600	256	282	0	0	0	535	647	474	0	0	0	0	0	0	106	578
TCGA-44-2662-10A-01D-0969-08_LUAD	674	138	277	300	589	283	529	659	487	0	0	0	0	0	37	90	579

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-44-2665-10A-01D-1040-01_LUAD	596	259	281	0	567	141	532	657	453	75	636	577	0	138	0	74	577
TCGA-44-2666-10A-01D-A271-08_LUAD	683	0	0	351	608	384	528	629	474	0	0	0	0	0	0	85	575
TCGA-44-2668-10A-01D-1489-08_LUAD	691	0	0	306	630	400	535	664	462	85	612	0	372	140	0	86	577
TCGA-44-3396-10A-01D-1265-08_LUAD	689	0	0	305	608	393	533	652	485	0	0	0	0	0	50	1	578
TCGA-44-3398-10A-01D-1105-08_LUAD	763	0	0	308	608	399	532	644	477	0	0	0	0	0	0	129	579
TCGA-44-3917-10A-01D-A271-08_LUAD	676	0	0	291	598	389	528	626	466	0	0	0	0	0	0	112	573
TCGA-44-3918-10A-01D-A271-08_LUAD	758	0	0	299	609	385	532	646	401	0	0	0	0	0	0	95	581
TCGA-44-3919-10A-01D-1458-08_LUAD	686	254	265	300	620	288	532	666	480	0	0	0	0	0	42	80	577
TCGA-44-4112-10A-01D-1458-08_LUAD	667	258	266	301	620	290	532	663	464	79	638	521	375	141	38	0	577
TCGA-44-5643-10A-01D-1625-08_LUAD	683	0	0	293	594	384	527	640	372	66	528	0	297	138	28	0	577
TCGA-44-5644-10A-01D-2036-08_LUAD	690	0	0	303	609	381	531	645	470	0	0	0	0	0	0	133	577
TCGA-44-5645-10A-01D-1625-08_LUAD	680	0	0	294	595	391	530	636	478	0	0	0	0	0	19	47	573
TCGA-44-6144-10A-01D-1753-08_LUAD	681	0	0	305	614	375	529	638	473	0	0	0	0	0	0	68	581
TCGA-44-6145-10A-01D-1753-08_LUAD	640	236	251	280	603	283	528	643	373	76	613	572	0	132	0	52	574
TCGA-44-6146-10A-01D-1753-08_LUAD	660	233	260	279	606	368	529	635	0	83	636	520	362	139	0	0	574
TCGA-44-6147-10A-01D-1753-08_LUAD	755	0	0	300	598	290	523	638	471	0	0	0	0	0	0	99	578
TCGA-44-6148-10A-01D-1753-08_LUAD	684	0	0	305	611	372	529	642	477	0	0	0	0	0	0	73	577
TCGA-44-6774-10A-01D-1855-08_LUAD	599	261	275	0	0	0	535	645	460	72	619	0	301	137	32	7	578
TCGA-44-6775-10A-01D-1855-08_LUAD	674	251	268	292	612	284	534	647	485	0	599	567	0	0	0	131	579
TCGA-44-6776-10A-01D-1855-08_LUAD	597	260	280	0	586	139	534	656	485	0	585	565	0	0	30	75	579
TCGA-44-6777-10A-01D-1855-08_LUAD	690	0	0	304	605	383	533	647	479	0	0	0	0	0	0	117	576
TCGA-44-6778-10A-01D-1855-08_LUAD	680	0	0	289	607	380	535	648	482	0	614	0	319	0	25	77	575
TCGA-44-7659-10A-01D-2063-08_LUAD	680	240	258	281	581	361	530	643	464	0	0	0	0	0	0	85	573
TCGA-44-7660-10A-01D-2063-08_LUAD	597	256	271	0	0	0	533	648	483	0	0	0	0	0	30	69	575
TCGA-44-7661-10A-01D-2063-08_LUAD	674	244	246	281	580	271	530	653	4	83	636	0	376	139	0	1	575
TCGA-44-7662-10A-01D-2063-08_LUAD	595	257	269	0	592	135	528	648	483	0	596	563	0	0	33	76	571
TCGA-44-7667-10A-01D-2063-08_LUAD	685	0	0	307	604	384	531	651	476	0	0	0	0	0	30	67	576
TCGA-44-7669-10A-01D-2063-08_LUAD	597	251	274	0	565	137	530	648	482	0	586	509	0	0	0	90	574
TCGA-44-7670-10A-01D-2063-08_LUAD	691	0	0	305	607	394	531	642	475	0	0	0	0	0	0	85	576
TCGA-44-7671-10A-01D-2063-08_LUAD	684	0	0	301	605	395	534	647	476	0	0	0	0	0	32	81	580
TCGA-44-7672-10A-01D-2063-08_LUAD	683	0	0	306	596	382	533	652	407	0	0	0	0	0	35	60	577
TCGA-44-8117-10A-01D-2238-08_LUAD	683	0	0	301	605	386	534	638	475	0	0	0	0	0	0	128	576
TCGA-44-8119-10A-01D-2238-08_LUAD	754	243	231	275	539	274	513	615	371	0	594	0	290	130	20	2	576
TCGA-44-8120-10A-01D-2238-08_LUAD	590	250	261	0	571	132	530	640	377	0	632	565	354	132	0	54	575
TCGA-44-A479-10A-01D-A24F-08_LUAD	665	243	260	287	599	377	528	630	466	0	587	0	363	0	33	1	574
TCGA-44-A47A-10A-01D-A24F-08_LUAD	677	0	0	295	590	376	529	647	469	0	0	0	0	0	27	54	573
TCGA-44-A47B-10A-01D-A24F-08_LUAD	661	237	252	264	500	268	525	620	429	67	585	500	0	134	27	0	578
TCGA-44-A47F-10A-01D-A24F-08_LUAD	677	240	258	280	601	366	532	634	371	70	629	560	296	134	0	57	573
TCGA-44-A47G-10A-01D-A24F-08_LUAD	679	0	0	295	593	379	529	628	303	72	568	560	0	129	0	64	570
TCGA-44-A4SS-10A-01D-A24P-08_LUAD	678	0	0	295	595	284	519	635	465	0	0	0	0	0	0	115	572
TCGA-44-A4SU-10A-01D-A24P-08_LUAD	685	0	0	299	596	386	529	646	466	0	0	0	0	0	34	72	573
TCGA-46-3765-10A-01D-0983-08_LUSC	670	250	267	0	548	124	531	650	464	0	620	564	0	0	29	60	575
TCGA-46-3766-10A-01D-0983-08_LUSC	742	239	246	269	543	341	532	659	475	0	0	0	0	0	25	68	575
TCGA-46-3767-10A-01D-0983-08_LUSC	745	0	0	308	602	361	530	649	440	68	599	0	365	132	0	72	575
TCGA-46-3768-10A-01D-0983-08_LUSC	726	235	243	283	561	268	530	636	463	0	0	0	0	0	24	54	571
TCGA-46-3769-10A-01D-0983-08_LUSC	745	235	228	267	527	344	530	658	463	0	0	0	0	0	0	131	576
TCGA-46-6025-10A-01D-1817-08_LUSC	756	254	268	295	600	380	534	661	464	86	646	568	370	137	0	64	576
TCGA-46-6026-10A-01D-1817-08_LUSC	686	248	264	291	582	379	531	653	476	0	0	0	0	0	33	60	575
TCGA-50-5044-10A-01D-1855-08_LUAD	749	247	265	288	611	377	534	644	445	72	643	561	361	136	0	64	574
TCGA-50-5045-10A-01D-1625-08_LUAD	755	0	0	284	597	375	531	629	472	0	0	0	0	0	0	96	575
TCGA-50-5049-10A-01D-1625-08_LUAD	593	236	256	260	576	275	531	640	469	0	0	0	0	0	0	98	574
TCGA-50-5051-10A-01D-1855-08_LUAD	683	253	270	290	615	380	531	642	489	0	610	511	0	0	0	93	579
TCGA-50-5055-10A-01D-1625-08_LUAD	669	247	261	285	613	282	532	641	388	73	628	561	357	133	0	69	573
TCGA-50-5066-10A-01D-1625-08_LUAD	673	235	265	261	472	372	534	642	482	0	0	0	0	0	27	62	577
TCGA-50-5068-10A-01D-1625-08_LUAD	679	0	0	294	603	384	531	636	470	0	0	0	0	0	0	98	576
TCGA-50-5072-10A-01D-1855-08_LUAD	754	0	0	302	605	392	532	646	483	0	0	0	0	0	40	0	580
TCGA-50-5941-10A-01D-1753-08_LUAD	755	0	0	298	603	369	527	632	483	0	0	0	0	0	18	58	574
TCGA-50-5942-10A-01D-1753-08_LUAD	687	0	0	303	604	383	529	652	474	0	0	0	0	0	27	56	578
TCGA-50-5944-10A-01D-1753-08_LUAD	677	237	240	283	548	359	530	649	463	78	586	554	0	138	0	53	575
TCGA-50-5946-10A-01D-1753-08_LUAD	739	243	250	286	612	368	529	635	390	76	620	566	0	136	28	0	578
TCGA-50-6597-10A-01D-1855-08_LUAD	678	251	271	291	586	282	521	618	460	0	618	556	0	136	29	0	577
TCGA-50-8457-10A-01D-2323-08_LUAD	760	0	0	305	612	293	525	655	484	0	0	0	0	0	31	71	575
TCGA-50-8459-10A-01D-2323-08_LUAD	670	260	279	0	0	0	535	641	481	0	0	0	0	0	31	70	579
TCGA-50-8460-10A-01D-2323-08_LUAD	670	264	280	0	607	144	535	651	396	78	633	583	0	138	0	65	579
TCGA-52-7622-10A-01D-2122-08_LUSC	687	0	0	298	602	378	530	648	476	0	0	0	0	0	29	57	572
TCGA-52-7809-10A-01D-2122-08_LUSC	668	243	256	283	560	371	530	635	477	0	0	0	0	0	0	109	575
TCGA-52-7810-10A-01D-2122-08_LUSC	685	0	0	302	601	289	520	646	0	79	639	0	371	137	0	3	573
TCGA-52-7811-10A-01D-2122-08_LUSC	761	0	0	305	606	382	531	647	482	0	0	0	0	0	0	130	577
TCGA-52-7812-10A-01D-2122-08_LUSC	690	0	0	300	614	391	537	653	377	83	633	569	300	133	0	75	575
TCGA-53-7624-10A-01D-2063-08_LUAD	678	237	251	287	571	261	531	650	481	0	0	0	0	0	0	83	577
TCGA-53-7626-10A-01D-2063-08_LUAD	686	0	0	306	601	370	529	642	474	0	0	0	0	0	25	55	579
TCGA-53-7813-10A-01D-2167-08_LUAD	727	214	218	248	537	348	495	592	367	0	602	0	270	130	0	60	576
TCGA-53-A4EZ-10A-01D-A24P-08_LUAD	675	236	264	288	578	366	530	649	462	0	0	0	0	0	30	68	571
TCGA-55-5899-10A-01D-1625-08_LUAD	680	0	0	289	594	375	530	639	307	66	509	465	0	131	0	52	577
TCGA-55-6543-10A-01D-1753-08_LUAD	675	225	248	258	555	361	530	640	455	0	0	0	0	0	0	77	578
TCGA-55-6712-10A-01D-1855-08_LUAD	653	251	267	292	617	287	531	645	455	75	639	566	0	136	0	68	573
TCGA-55-7227-10A-01D-2036-08_LUAD	671	248	261	275	552	270	532	614	466	0	0	0	0	0	34	1	575
TCGA-55-7281-10A-01D-2036-08_LUAD	680	0	0	305	592	379	525	641	392	0	0	0	0	0	0	108	579
TCGA-55-7283-10A-01D-2036-08_LUAD	674	245	266	284	617	374	531	640	474	0	539	557	0	0	27	53	576
TCGA-55-7284-10A-01D-2238-08_LUAD	684	0	0	302	603	383	532	650	457	75	589	0	357	135	32	0	580
TCGA-55-7570-10A-01D-2036-08_LUAD	683	0	0	296	604	387	532	650	473	0	0	0	0	0	31	56	576
TCGA-55-7574-10A-01D-2036-08_LUAD	677	0	0	301	611	288	530	643	402	0	0	0	0	0	0	126	578
TCGA-55-7576-10A-01D-2063-08_LUAD	683	0	0	289	610	372	533	635	483	0	0	0	0	0	20	42	578
TCGA-55-7724-10A-01D-2167-08_LUAD	742	0	0	300	608	378	533	661	444	0	0	0	0	0	0	96	576
TCGA-55-7725-10A-01D-2167-08_LUAD	684	0	0	334	605	354	532	651	454	0	0	0	0	0	32	70	574
TCGA-55-7726-10A-01D-2167-08_LUAD	678	0	0	298	580	370	531	640	464	0	0	0	0	0	25	49	576
TCGA-55-7727-10A-01D-2167-08_LUAD	731	0	0	303	596	371	526	639	0	79	628	464	333	139	0	0	575
TCGA-55-7728-10A-01D-2184-08_LUAD	686	0	0	297	598	294	525	642	478	0	0	0	0	0	0	82	577
TCGA-55-7815-10A-01D-2167-08_LUAD	738	0	0	305	600	380	532	653	468	0	0	0	0	0	0	89	576
TCGA-55-7816-10A-01D-2167-08_LUAD	728	243	240	270	607	264	529	657	452	0	557	562	0	0	28	65	576
TCGA-55-7903-10A-01D-2167-08_LUAD	732	232	222	266	614	356	533	665	346	81	641	571	343	129	0	57	575
TCGA-55-7907-10A-01D-2167-08_LUAD	733	0	0	292	590	356	530	652	394	0	0	0	0	0	0	89	577
TCGA-55-7911-10A-01D-2167-08_LUAD	724	230	231	262	502	268	528	656	456	0	0	0	0	0	23	50	579
TCGA-55-7913-10A-01D-2238-08_LUAD	598	253	265	0	562	129	533	638	477	0	583	0	386	0	0	92	573
TCGA-55-7914-10A-01D-2167-08_LUAD	650	211	234	262	480	252	528	655	390	0	0	0	0	0	17	47	576
TCGA-55-7994-10A-01D-2184-08_LUAD	593	253	269	0	580	129	531	647	473	0	604	566	0	0	0	105	572

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-55-7995-10A-01D-2184-08_LUAD	684	0	0	305	599	377	529	650	467	0	0	0	0	0	0	82	578
TCGA-55-8085-10A-01D-2238-08_LUAD	679	0	0	296	611	384	535	647	382	69	594	0	366	132	0	68	576
TCGA-55-8087-10A-01D-2238-08_LUAD	687	243	256	284	551	368	531	652	444	74	613	0	352	137	29	0	576
TCGA-55-8089-10A-01D-2238-08_LUAD	676	252	265	278	575	372	533	638	475	0	0	0	0	0	41	1	575
TCGA-55-8090-10A-01D-2238-08_LUAD	681	0	0	296	599	284	520	644	455	72	583	0	355	133	28	1	580
TCGA-55-8091-10A-01D-2238-08_LUAD	685	0	0	301	605	385	533	642	470	0	0	0	0	0	0	81	570
TCGA-55-8092-10A-01D-2238-08_LUAD	748	0	0	300	600	287	525	644	475	0	0	0	0	0	0	134	573
TCGA-55-8094-10A-01D-2238-08_LUAD	683	0	0	303	612	376	534	642	490	0	0	0	0	0	0	139	579
TCGA-55-8096-10A-01D-2238-08_LUAD	681	244	263	297	589	288	531	651	480	0	0	0	0	0	35	60	579
TCGA-55-8097-10A-01D-2238-08_LUAD	687	0	0	303	608	385	532	645	0	81	633	0	378	138	0	1	576
TCGA-55-8203-10A-01D-2238-08_LUAD	676	0	0	303	598	283	529	646	479	0	0	0	0	0	0	128	579
TCGA-55-8204-10A-01D-2238-08_LUAD	757	0	0	303	602	388	532	646	486	0	0	0	0	0	0	143	578
TCGA-55-8205-10A-01D-2238-08_LUAD	679	237	255	294	561	278	527	645	451	80	526	0	356	138	0	70	576
TCGA-55-8206-10A-01D-2238-08_LUAD	687	0	0	303	599	385	532	647	479	0	0	0	0	0	0	126	574
TCGA-55-8207-10A-01D-2238-08_LUAD	675	248	253	288	590	280	531	651	477	0	0	0	0	0	0	97	577
TCGA-55-8208-10A-01D-2238-08_LUAD	651	247	256	279	579	281	531	654	476	0	0	0	0	0	33	68	576
TCGA-55-8299-10B-01D-2323-08_LUAD	594	264	275	0	0	0	533	657	487	0	0	0	0	0	37	72	577
TCGA-55-8301-10A-01D-2284-08_LUAD	760	0	0	306	615	387	537	656	389	81	622	571	367	139	0	66	576
TCGA-55-8302-10A-01D-2323-08_LUAD	672	252	257	295	589	279	532	657	484	0	0	0	0	0	32	63	574
TCGA-55-8505-10A-01D-2393-08_LUAD	672	251	260	291	609	280	532	651	460	79	643	561	290	134	0	69	576
TCGA-55-8506-10A-01D-2393-08_LUAD	682	251	269	294	591	384	531	654	481	0	0	0	0	0	37	81	574
TCGA-55-8507-10A-01D-2393-08_LUAD	669	258	276	0	0	0	534	653	490	0	0	0	0	0	0	148	577
TCGA-55-8508-10A-01D-2393-08_LUAD	682	255	268	280	614	334	527	653	485	0	624	567	0	0	36	78	573
TCGA-55-8510-10A-01D-2393-08_LUAD	669	259	275	0	518	140	529	649	480	0	545	567	0	0	47	1	576
TCGA-55-8511-10A-01D-2393-08_LUAD	690	0	0	306	609	396	531	640	390	72	576	0	358	136	0	60	578
TCGA-55-8512-10A-01D-2393-08_LUAD	684	251	266	299	605	382	529	651	473	73	638	572	0	136	28	5	574
TCGA-55-8513-10A-01D-2393-08_LUAD	687	0	0	291	595	373	528	635	462	0	0	0	0	0	0	72	573
TCGA-55-8514-10A-01D-2393-08_LUAD	753	250	251	182	578	378	532	645	477	0	0	0	0	0	0	129	578
TCGA-55-8614-10A-01D-2393-08_LUAD	685	0	0	308	609	395	529	649	390	76	590	0	368	137	0	67	576
TCGA-55-8615-10A-01D-2393-08_LUAD	689	0	0	304	606	387	531	651	462	81	611	0	365	135	0	65	579
TCGA-55-8616-10A-01D-2393-08_LUAD	680	250	268	288	613	375	534	656	394	78	640	567	372	139	0	65	578
TCGA-55-8619-10A-01D-2393-08_LUAD	596	256	274	0	575	135	530	645	382	74	631	566	0	134	0	72	579
TCGA-55-8620-10A-01D-2393-08_LUAD	686	0	0	308	617	291	523	648	459	72	572	0	371	139	0	59	578
TCGA-55-8621-10A-01D-2393-08_LUAD	758	0	0	310	610	399	533	651	388	76	603	0	371	137	0	65	576
TCGA-55-A48X-10A-01D-A24F-08_LUAD	686	0	0	299	571	280	520	636	448	75	609	0	290	134	0	60	577
TCGA-55-A48Y-10A-01D-A24F-08_LUAD	687	0	0	298	593	377	527	630	479	0	77	87	0	0	0	110	570
TCGA-55-A48Z-10A-01D-A24P-08_LUAD	689	249	262	285	586	375	529	635	460	0	0	0	0	0	0	84	574
TCGA-55-A490-10A-01D-A24F-08_LUAD	684	0	0	289	599	386	533	654	374	80	640	562	296	135	0	62	571
TCGA-55-A491-10A-01D-A24F-08_LUAD	674	241	259	272	511	370	527	636	464	0	0	0	0	0	0	83	572
TCGA-55-A492-10A-01D-A24F-08_LUAD	679	0	0	292	587	383	529	623	460	0	0	55	0	0	0	72	572
TCGA-55-A493-10A-01D-A24F-08_LUAD	595	255	267	0	508	133	529	637	460	0	531	511	0	0	39	0	572
TCGA-55-A494-10A-01D-A24P-08_LUAD	679	0	0	300	594	379	528	641	365	63	589	0	294	135	0	58	570
TCGA-55-A4DF-10A-01D-A24F-08_LUAD	596	259	276	0	601	139	531	644	452	72	636	579	0	134	30	1	577
TCGA-55-A4DG-10A-01D-A24F-08_LUAD	678	233	263	284	604	383	531	642	0	80	633	575	372	138	0	0	578
TCGA-56-5897-10A-01D-1632-08_LUSC	682	0	0	285	604	290	531	650	478	0	0	0	0	0	26	59	579
TCGA-56-5898-10A-01D-1632-08_LUSC	687	0	0	296	606	376	526	646	370	51	558	0	291	133	0	54	575
TCGA-56-6545-10A-01D-1817-08_LUSC	672	248	266	287	563	278	529	643	474	0	0	0	0	0	36	56	580
TCGA-56-6546-10A-01D-1817-08_LUSC	685	0	0	298	594	289	524	646	457	75	590	0	286	136	0	65	576
TCGA-56-7221-10A-01D-2042-08_LUSC	673	247	258	281	605	386	531	635	460	0	581	567	0	0	0	84	577
TCGA-56-7222-10A-01D-2042-08_LUSC	685	0	0	298	590	388	534	635	474	0	0	0	0	0	0	131	571
TCGA-56-7223-10A-01D-2042-08_LUSC	674	245	259	270	586	376	529	642	480	0	582	562	0	0	31	61	573
TCGA-56-7579-10A-01D-2042-08_LUSC	682	245	253	274	592	376	535	652	469	66	556	512	0	0	29	59	574
TCGA-56-7580-10A-01D-2042-08_LUSC	684	247	267	264	514	378	534	646	383	75	534	0	363	136	0	70	578
TCGA-56-7582-10A-01D-2042-08_LUSC	748	0	0	301	600	394	532	653	485	0	0	0	0	0	26	58	576
TCGA-56-7731-10A-01D-2122-08_LUSC	684	0	0	302	593	363	526	632	471	0	0	0	0	0	0	92	572
TCGA-56-7822-10A-01D-2122-08_LUSC	690	236	262	284	602	375	532	640	475	0	603	512	0	0	0	115	575
TCGA-56-7823-10A-01D-2244-08_LUSC	685	257	265	249	623	288	533	653	471	84	649	569	373	137	0	91	579
TCGA-56-8082-10A-01D-2244-08_LUSC	685	0	0	287	593	371	529	646	462	0	0	0	0	0	0	71	578
TCGA-56-8083-10A-01D-2244-08_LUSC	679	0	0	299	600	374	529	636	382	77	610	0	356	134	23	0	577
TCGA-56-8201-10A-01D-2244-08_LUSC	671	239	256	277	594	363	531	647	307	61	622	560	350	135	0	55	575
TCGA-56-8304-10A-01D-2323-08_LUSC	593	260	271	0	576	131	532	648	479	0	601	515	0	0	0	120	577
TCGA-56-8307-10A-01D-2293-08_LUSC	688	0	0	303	607	390	532	645	470	0	0	0	0	0	0	89	575
TCGA-56-8308-10A-01D-2293-08_LUSC	676	0	0	306	600	287	521	655	456	76	612	0	365	130	0	63	574
TCGA-56-8309-10A-01D-2293-08_LUSC	685	0	0	303	606	386	530	645	473	0	0	0	0	0	0	82	571
TCGA-56-8503-10A-01D-2395-08_LUSC	594	252	269	0	30	0	530	642	51	83	628	0	377	137	0	3	575
TCGA-56-8504-10A-01D-2395-08_LUSC	676	244	264	286	611	284	528	649	473	0	619	561	0	0	28	75	575
TCGA-56-8622-10A-01D-2395-08_LUSC	671	248	260	289	566	284	528	640	404	0	0	0	0	0	0	118	574
TCGA-56-8623-10A-01D-2395-08_LUSC	683	0	0	301	606	383	531	650	485	0	0	0	0	0	30	63	577
TCGA-56-8624-10A-01D-2395-08_LUSC	594	256	270	0	515	135	530	656	476	78	593	560	0	0	30	67	579
TCGA-56-8625-10A-01D-2395-08_LUSC	683	0	0	301	595	385	530	636	472	0	0	0	0	0	0	114	574
TCGA-56-8626-10A-01D-2395-08_LUSC	755	255	270	285	514	375	534	644	472	0	0	0	0	0	0	93	576
TCGA-56-8628-10A-01D-2395-08_LUSC	684	238	265	289	604	286	527	642	1	80	647	510	379	137	0	4	574
TCGA-56-8629-10A-01D-2395-08_LUSC	687	0	0	300	602	380	533	646	476	0	0	0	0	0	0	118	574
TCGA-56-A49D-10A-01D-A24F-08_LUSC	670	0	0	293	592	373	527	618	391	0	0	0	0	0	0	66	575
TCGA-56-A4BW-10A-01D-A24F-08_LUSC	660	241	255	269	540	276	525	626	381	60	561	0	290	132	24	1	572
TCGA-56-A4BX-10A-01D-A24F-08_LUSC	744	244	260	295	611	373	529	646	378	77	629	511	364	135	0	71	574
TCGA-56-A4BY-10A-01D-A24F-08_LUSC	594	255	268	0	0	0	526	645	466	0	0	0	0	0	29	53	573
TCGA-56-A4ZJ-10A-01D-A25L-08_LUSC	591	256	280	0	86	0	530	657	471	71	603	29	298	0	32	71	573
TCGA-56-A4ZK-10A-01D-A25L-08_LUSC	685	0	0	300	601	381	531	646	459	67	580	0	360	136	30	8	571
TCGA-56-A5DR-10A-01D-A27N-08_LUSC	669	237	265	284	559	277	528	632	0	77	624	0	382	138	0	1	574
TCGA-56-A5DS-10A-01D-A27N-08_LUSC	688	0	0	297	603	386	533	631	467	0	0	0	0	0	0	124	574
TCGA-58-8386-10A-01D-2293-08_LUSC	676	248	267	192	516	279	532	656	456	79	608	0	294	139	0	71	578
TCGA-58-8387-10A-01D-2293-08_LUSC	682	229	234	277	628	366	530	640	478	0	591	557	0	0	0	108	575
TCGA-58-8388-10A-01D-2323-08_LUSC	677	248	0	284	614	284	533	646	449	75	592	0	299	135	0	69	577
TCGA-58-8390-10A-01D-2323-08_LUSC	755	0	0	306	614	388	532	635	482	0	0	0	0	0	0	120	576
TCGA-58-8391-10A-01D-2323-08_LUSC	693	0	0	306	612	393	534	643	482	0	0	0	0	0	0	97	577
TCGA-58-8392-10A-01D-2323-08_LUSC	762	0	0	315	619	403	535	656	458	78	591	562	0	140	0	59	576
TCGA-58-8393-10A-01D-2323-08_LUSC	746	251	256	298	618	375	535	659	483	0	532	570	0	0	0	87	580
TCGA-58-A46J-10A-01D-A24F-08_LUSC	598	256	275	0	551	134	530	647	448	73	631	562	294	135	0	67	576
TCGA-58-A46K-10A-01D-A24F-08_LUSC	666	245	254	277	608	376	531	643	465	0	604	504	0	0	30	59	576
TCGA-58-A46L-10A-01D-A24F-08_LUSC	665	247	267	283	568	282	528	635	378	54	579	0	298	136	0	69	575
TCGA-58-A46M-10A-01D-A24F-08_LUSC	676	0	0	293	598	284	528	636	477	0	0	0	26	0	0	99	574
TCGA-58-A46N-10A-01D-A24F-08_LUSC	668	238	256	266	608	373	530	633	371	71	622	562	0	134	0	52	573
TCGA-59-2372-10A-01D-1526-09_OV	697	335	375	0	716	190	561	663	583	0	668	594	0	0	0	232	596
TCGA-62-8394-10A-01D-2323-08_LUAD	762	0	0	355	616	393	535	645	487	0	0	0	0	0	35	96	579
TCGA-62-8395-10A-01D-2323-08_LUAD	758	0	0	352	631	401	536	649	460	71	585	0	380	140	0	92	580

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-62-8397-10A-01D-2323-08_LUAD	689	0	0	308	615	388	534	651	466	71	612	0	376	138	29	0	577
TCGA-62-8398-10A-01D-2323-08_LUAD	680	236	257	285	512	361	513	611	375	0	522	0	365	141	0	64	573
TCGA-62-8399-10A-01D-2323-08_LUAD	733	246	267	288	584	276	528	644	475	0	0	0	0	0	0	96	578
TCGA-62-8402-10A-01D-2323-08_LUAD	741	249	267	287	615	377	537	646	389	77	640	578	0	139	0	69	579
TCGA-62-A46O-10A-01D-A24F-08_LUAD	676	235	255	271	574	366	528	635	367	72	520	0	292	135	0	51	571
TCGA-62-A46P-10A-01D-A24F-08_LUAD	677	254	270	291	560	376	534	645	483	0	0	0	0	0	0	126	577
TCGA-62-A46R-10A-01D-A24F-08_LUAD	664	245	264	273	574	367	530	635	0	81	634	556	292	139	0	1	573
TCGA-62-A46S-10A-01D-A24F-08_LUAD	682	0	0	295	598	377	528	633	373	72	576	0	292	135	0	51	571
TCGA-62-A46U-10A-01D-A24F-08_LUAD	591	249	270	0	485	131	523	623	306	74	613	561	0	135	0	58	570
TCGA-62-A46V-10A-01D-A24F-08_LUAD	687	0	0	286	598	284	527	626	365	73	614	0	288	135	0	57	572
TCGA-62-A46Y-10A-01D-A24F-08_LUAD	665	241	255	95	166	0	514	607	379	0	0	0	0	132	0	56	576
TCGA-62-A470-10A-01D-A24F-08_LUAD	670	247	254	285	579	371	524	637	385	72	628	512	361	133	32	1	572
TCGA-62-A471-10A-01D-A24F-08_LUAD	666	242	266	267	593	374	530	627	382	66	633	510	294	133	35	3	573
TCGA-62-A472-10A-01D-A24F-08_LUAD	675	0	0	280	585	280	524	626	365	61	497	505	0	123	0	50	577
TCGA-63-5128-10A-01D-1441-08_LUSC	690	0	0	299	599	391	532	644	470	0	0	0	0	0	0	99	575
TCGA-63-5131-10A-01D-1441-08_LUSC	686	247	0	295	612	382	530	650	461	79	597	0	301	135	0	73	579
TCGA-63-6202-10A-01D-1817-08_LUSC	688	0	0	299	593	380	529	647	469	0	0	0	0	0	0	81	577
TCGA-63-7020-10A-01D-1945-08_LUSC	596	259	274	0	579	138	531	642	481	0	627	574	0	0	0	128	577
TCGA-63-7021-10A-01D-1945-08_LUSC	684	0	0	304	610	393	532	648	489	0	0	0	0	0	0	139	577
TCGA-63-7022-10A-01D-1945-08_LUSC	760	0	0	309	617	391	535	652	482	0	0	0	0	0	44	3	578
TCGA-63-7023-10A-01D-1945-08_LUSC	684	0	0	304	605	378	529	632	478	0	0	0	0	0	0	119	577
TCGA-63-A5M9-10A-01D-A26K-08_LUSC	760	0	0	305	605	385	526	640	456	0	0	0	0	0	0	90	579
TCGA-63-A5MB-10A-01D-A26K-08_LUSC	747	240	252	283	555	367	527	622	465	0	0	0	0	0	0	95	576
TCGA-63-A5MG-10A-01D-A27N-08_LUSC	676	239	257	281	560	364	530	640	465	0	0	0	0	0	30	61	574
TCGA-63-A5MH-10A-01D-A27N-08_LUSC	685	0	0	289	595	378	530	639	479	0	0	0	0	0	24	54	575
TCGA-63-A5MI-10A-01D-A27N-08_LUSC	661	238	256	276	567	270	529	650	478	0	0	0	0	0	32	57	575
TCGA-63-A5MJ-10A-01D-A27N-08_LUSC	683	0	0	296	596	280	520	632	0	82	632	0	376	137	0	0	571
TCGA-63-A5ML-10A-01D-A27N-08_LUSC	677	244	256	283	608	377	529	649	463	0	601	565	0	0	25	61	572
TCGA-63-A5MM-10A-01D-A26K-08_LUSC	680	0	0	298	607	391	530	634	476	0	0	0	0	0	0	89	580
TCGA-63-A5MN-10A-01D-A27N-08_LUSC	686	0	0	292	598	386	530	643	469	0	0	0	0	0	0	78	576
TCGA-63-A5MP-10A-01D-A26K-08_LUSC	755	0	0	287	594	388	531	630	469	0	0	0	0	0	39	1	574
TCGA-63-A5MR-10A-01D-A27N-08_LUSC	665	233	244	270	553	375	527	641	462	0	0	0	0	0	34	1	573
TCGA-63-A5MS-10A-01D-A26K-08_LUSC	681	0	0	293	602	382	528	625	311	69	528	0	286	137	29	6	576
TCGA-63-A5MT-10A-01D-A26K-08_LUSC	660	234	254	279	570	377	532	631	383	64	523	0	369	135	31	6	575
TCGA-63-A5MU-10A-01D-A26K-08_LUSC	670	0	0	297	600	380	527	627	461	0	0	0	0	0	0	91	575
TCGA-63-A5MV-10A-01D-A26K-08_LUSC	592	259	272	0	582	129	531	637	0	77	641	574	361	142	0	5	577
TCGA-63-A5MW-10A-01D-A26K-08_LUSC	676	236	259	274	504	372	530	644	458	0	0	0	0	0	31	58	578
TCGA-63-A5MY-10A-01D-A26K-08_LUSC	686	0	0	301	571	371	520	639	469	0	0	0	0	0	0	91	574
TCGA-64-1676-10A-01D-0969-08_LUAD	756	0	0	308	608	385	531	654	461	76	615	0	301	131	0	88	580
TCGA-64-1678-10A-01D-1489-08_LUAD	684	0	0	305	611	400	532	658	471	76	613	0	301	138	0	78	578
TCGA-64-1679-10A-01D-2063-08_LUAD	686	243	252	276	577	365	534	649	403	0	0	0	0	0	0	76	576
TCGA-64-1680-10A-01D-1040-01_LUAD	594	245	267	0	460	124	528	631	384	0	568	490	0	0	24	49	573
TCGA-64-1681-10A-01D-2063-08_LUAD	687	0	0	297	606	383	533	644	482	0	0	0	0	0	26	58	577
TCGA-64-5774-10A-01D-1625-08_LUAD	748	0	0	306	605	377	533	650	480	0	0	0	0	0	23	63	575
TCGA-64-5775-10A-01D-1625-08_LUAD	683	0	0	293	564	389	535	643	373	76	566	0	296	135	25	0	575
TCGA-64-5778-10A-01D-1625-08_LUAD	679	249	264	283	580	367	529	643	0	75	647	520	297	142	0	0	576
TCGA-64-5779-10A-01D-1625-08_LUAD	594	265	281	0	539	136	536	647	482	0	523	506	0	0	23	60	574
TCGA-64-5781-10A-01D-1625-08_LUAD	671	0	0	291	585	378	519	624	359	64	506	0	278	127	0	58	579
TCGA-64-5815-10A-01D-1625-08_LUAD	599	234	255	272	592	137	518	601	0	70	628	518	295	142	0	1	572
TCGA-67-3770-10A-01D-0969-08_LUAD	763	0	0	302	612	396	536	650	479	0	0	0	0	0	47	3	578
TCGA-67-3771-10A-01D-1040-01_LUAD	671	257	279	0	0	0	534	665	494	0	0	0	0	0	45	81	576
TCGA-67-3773-10A-01D-1489-08_LUAD	688	0	0	307	612	395	530	656	479	0	0	0	0	0	0	108	579
TCGA-67-3774-10A-01D-1489-08_LUAD	689	0	0	310	619	397	535	656	484	0	0	0	0	0	37	95	578
TCGA-67-4679-10A-01D-1753-08_LUAD	672	229	258	266	610	284	526	638	470	0	544	500	0	0	0	104	577
TCGA-67-6215-10A-01D-1753-08_LUAD	655	234	260	275	604	276	526	643	393	60	628	499	296	136	0	49	576
TCGA-67-6216-10A-01D-1753-08_LUAD	671	228	261	169	494	367	533	643	370	54	566	0	276	136	0	42	578
TCGA-67-6217-10A-01D-1753-08_LUAD	689	0	0	298	607	288	529	643	400	0	0	0	0	0	24	44	575
TCGA-68-7755-10A-01D-2122-08_LUSC	685	0	0	294	596	379	532	643	386	66	608	0	296	132	24	2	573
TCGA-68-7756-10A-01D-2122-08_LUSC	687	0	0	302	610	370	533	635	0	80	630	0	379	140	0	0	574
TCGA-68-7757-10A-01D-2293-08_LUSC	650	240	255	274	551	272	529	644	384	75	599	564	0	134	0	57	575
TCGA-68-8250-10A-01D-2293-08_LUSC	687	0	0	303	605	380	534	655	477	0	0	0	0	0	36	77	578
TCGA-68-8251-10A-01D-2293-08_LUSC	601	256	266	0	0	0	531	650	479	0	0	0	0	0	30	63	576
TCGA-68-A59J-10A-01D-A26K-08_LUSC	680	0	0	302	608	374	526	635	381	67	526	0	292	136	0	64	575
TCGA-69-7760-10A-01D-2167-08_LUAD	638	229	239	274	606	262	525	655	364	66	636	573	0	129	0	75	577
TCGA-69-7761-10A-01D-2167-08_LUAD	729	0	0	297	559	275	519	655	445	0	0	0	0	0	30	57	578
TCGA-69-7763-10A-01D-2167-08_LUAD	699	232	233	278	585	278	527	657	380	71	633	530	355	126	0	50	576
TCGA-69-7764-10A-01D-2167-08_LUAD	651	250	258	0	564	130	532	661	467	0	596	554	0	0	32	71	576
TCGA-69-7765-10A-01D-2167-08_LUAD	592	224	220	254	595	356	538	646	432	0	573	0	344	0	27	1	576
TCGA-69-7973-10A-01D-2184-08_LUAD	674	243	253	279	601	364	529	648	0	85	648	570	369	139	0	2	574
TCGA-69-7974-10A-01D-2184-08_LUAD	687	0	0	295	600	377	532	642	384	70	580	0	364	133	30	1	576
TCGA-69-7978-10A-01D-2184-08_LUAD	594	254	268	0	603	139	531	655	483	0	628	570	0	0	0	127	575
TCGA-69-7979-10A-01D-2184-08_LUAD	598	251	269	0	547	132	534	653	467	72	595	562	0	0	37	1	575
TCGA-69-7980-10A-01D-2184-08_LUAD	687	250	242	282	601	375	530	649	369	73	627	571	0	133	0	55	573
TCGA-69-8253-10A-01D-2284-08_LUAD	673	232	265	270	555	366	531	641	470	0	0	0	0	0	28	52	577
TCGA-69-8254-10A-01D-2284-08_LUAD	682	246	268	275	603	385	535	644	472	68	519	562	0	0	44	0	575
TCGA-69-8255-10A-01D-2284-08_LUAD	759	0	0	301	602	390	535	646	485	0	0	0	0	0	44	0	575
TCGA-69-A59K-10A-01D-A25L-08_LUAD	682	0	0	304	599	382	532	634	468	0	0	0	0	0	37	4	574
TCGA-70-6722-10A-01D-1817-08_LUSC	688	0	0	306	607	383	532	645	446	79	601	0	366	137	0	59	576
TCGA-70-6723-10A-01D-1817-08_LUSC	672	254	255	288	584	271	532	651	481	0	0	0	0	0	43	2	577
TCGA-71-6725-10A-01D-1855-08_LUAD	759	0	0	309	610	401	534	649	486	0	0	0	0	0	36	70	577
TCGA-71-8520-10A-01D-2393-08_LUAD	738	242	248	271	609	380	529	644	447	68	624	511	363	136	0	57	581
TCGA-73-7498-10A-01D-2184-08_LUAD	683	0	0	304	603	289	524	644	476	0	0	0	0	0	0	125	579
TCGA-73-7499-10A-01D-2184-08_LUAD	689	0	0	298	600	376	531	639	464	0	0	0	0	0	0	88	575
TCGA-74-6575-10A-01D-1845-08_GBM	597	265	277	0	583	136	535	652	483	0	605	559	0	0	49	1	577
TCGA-74-6577-10A-01D-1845-08_GBM	677	254	262	287	587	290	535	660	482	0	0	0	0	0	34	67	580
TCGA-74-6578-10A-01D-1845-08_GBM	690	253	267	293	612	288	535	658	490	0	617	566	0	0	37	69	579
TCGA-74-6581-10A-01D-1845-08_GBM	688	0	0	312	615	387	534	659	491	0	0	0	0	0	40	81	578
TCGA-74-6584-10A-01D-1845-08_GBM	763	0	0	354	641	297	535	664	494	0	0	0	0	0	0	104	578
TCGA-75-5122-10A-01D-1753-08_LUAD	675	0	0	278	593	282	529	651	461	0	0	0	0	0	20	40	569
TCGA-75-5125-10A-01D-1753-08_LUAD	688	0	0	303	604	368	521	635	460	0	0	0	0	0	0	70	575
TCGA-75-5126-10A-01D-1753-08_LUAD	670	242	256	276	614	357	535	660	479	73	588	562	0	0	0	106	577
TCGA-75-5146-10A-01D-1625-08_LUAD	688	0	0	301	604	379	522	642	447	62	589	0	282	135	0	58	578
TCGA-75-5147-10A-01D-1625-08_LUAD	597	255	275	0	507	140	533	641	436	68	625	504	291	0	16	0	574
TCGA-75-6203-10A-01D-1753-08_LUAD	644	234	251	275	557	267	532	632	474	0	0	0	0	0	0	72	576
TCGA-75-6205-10A-01D-1753-08_LUAD	684	0	0	303	600	388	537	648	474	0	0	0	0	0	28	51	576
TCGA-75-6206-10A-01D-1753-08_LUAD	675	234	0	280	607	285	524	632	380	78	577	0	293	135	0	51	577

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-75-6207-10A-01D-1753-08_LUAD	683	0	0	301	601	378	534	635	401	0	0	0	0	0	29	54	573
TCGA-75-6211-10A-01D-1753-08_LUAD	728	239	256	277	610	272	531	640	372	67	617	573	0	134	0	50	577
TCGA-75-6212-10A-01D-1753-08_LUAD	684	0	0	304	605	373	527	636	473	0	0	0	0	0	0	116	576
TCGA-75-6214-10A-01D-1946-08_LUAD	675	0	0	304	603	383	531	634	384	74	585	0	370	135	27	0	575
TCGA-75-7025-10A-01D-1946-08_LUAD	687	0	0	302	610	383	532	644	478	0	0	0	0	0	0	91	578
TCGA-75-7027-10A-01D-1946-08_LUAD	692	0	0	315	619	396	537	653	485	0	0	0	0	0	0	105	580
TCGA-75-7030-10A-01D-1946-08_LUAD	678	0	0	298	596	366	516	588	449	0	0	0	0	135	23	0	568
TCGA-75-7031-10A-01D-1946-08_LUAD	683	248	267	292	592	287	533	660	401	70	616	0	371	140	0	84	575
TCGA-76-4925-10A-01D-1486-08_GBM	756	0	0	309	612	289	522	658	484	0	0	0	0	0	0	107	576
TCGA-76-4926-10A-01D-1486-08_GBM	685	0	0	307	613	392	532	662	459	83	606	574	0	136	0	86	578
TCGA-76-4927-10A-01D-1486-08_GBM	759	0	0	312	610	391	532	656	482	0	0	0	0	0	0	157	579
TCGA-76-4928-10A-01D-1486-08_GBM	683	0	0	309	606	398	532	663	488	0	0	0	0	0	0	165	580
TCGA-76-4929-10A-01D-1486-08_GBM	684	0	0	308	616	400	537	662	468	82	617	533	0	137	0	84	578
TCGA-76-4931-10A-01D-1486-08_GBM	670	265	278	0	0	0	533	658	471	76	624	0	373	140	0	78	578
TCGA-76-4932-10A-01D-1486-08_GBM	600	264	281	0	0	0	531	667	487	0	0	0	0	0	38	81	577
TCGA-76-4934-10A-01D-1486-08_GBM	691	252	269	299	615	385	530	651	0	86	649	578	371	143	0	1	576
TCGA-76-4935-10A-01D-1486-08_GBM	762	0	0	307	621	389	531	660	460	77	613	0	305	136	0	77	577
TCGA-76-6191-10A-01D-1696-08_GBM	682	0	0	301	569	388	529	629	475	0	0	0	0	0	0	107	574
TCGA-76-6192-10A-01D-1696-08_GBM	680	0	0	303	618	386	534	657	468	76	597	502	0	0	27	61	575
TCGA-76-6193-10A-01D-1696-08_GBM	676	0	0	301	601	288	520	639	481	0	0	0	0	0	0	113	574
TCGA-76-6280-10A-01D-1845-08_GBM	751	254	266	291	597	0	534	640	455	0	0	0	0	141	0	79	578
TCGA-76-6282-10A-01D-1696-08_GBM	756	0	0	306	602	375	527	638	384	72	578	496	0	133	0	63	578
TCGA-76-6283-10A-01D-1845-08_GBM	761	0	0	306	611	395	533	648	484	0	0	0	0	0	34	75	579
TCGA-76-6285-10A-01D-1696-08_GBM	658	237	264	278	551	277	528	630	375	72	577	0	299	140	25	0	575
TCGA-76-6286-10A-01D-1845-08_GBM	741	253	269	294	567	284	534	646	489	0	0	0	0	0	0	154	579
TCGA-76-6656-10A-01D-1845-08_GBM	755	0	0	307	611	387	534	642	451	76	612	0	367	137	0	68	577
TCGA-76-6657-10A-01D-1845-08_GBM	670	261	279	0	621	141	534	659	489	0	643	576	0	0	33	68	579
TCGA-76-6660-10A-01D-1845-08_GBM	756	251	259	288	594	280	534	648	485	0	0	0	0	0	0	98	578
TCGA-76-6661-10A-01D-1845-08_GBM	757	253	269	299	618	284	530	645	490	0	600	567	0	0	0	140	576
TCGA-76-6662-10A-01D-1845-08_GBM	760	250	261	283	562	380	533	651	491	0	0	0	0	0	39	77	578
TCGA-76-6663-10A-01D-1845-08_GBM	674	242	277	297	574	283	533	652	477	0	0	0	0	0	0	95	577
TCGA-76-6664-10A-01D-1845-08_GBM	690	250	259	292	582	373	535	637	486	0	0	0	0	0	40	2	576
TCGA-77-6842-10A-01D-1945-08_LUSC	652	248	263	269	606	364	533	647	481	0	599	512	0	0	30	54	570
TCGA-77-6843-10A-01D-1945-08_LUSC	647	246	235	263	606	273	526	646	469	0	540	557	0	0	32	55	574
TCGA-77-6844-10A-01D-1945-08_LUSC	660	245	260	280	612	282	529	640	476	0	604	562	0	0	0	85	574
TCGA-77-6845-10A-01D-1945-08_LUSC	664	0	0	299	513	360	528	635	458	0	0	0	0	0	26	52	576
TCGA-77-7138-10A-01D-2042-08_LUSC	681	0	0	297	599	387	523	635	377	58	585	0	295	135	35	0	571
TCGA-77-7139-10A-01D-2042-08_LUSC	683	0	0	302	600	383	528	651	474	0	0	0	0	0	28	69	573
TCGA-77-7140-10A-01D-2042-08_LUSC	660	233	256	279	544	275	530	651	473	0	0	0	0	0	29	65	574
TCGA-77-7463-10A-01D-2042-08_LUSC	658	245	262	286	504	275	527	640	472	0	0	0	0	0	0	130	575
TCGA-77-7465-10A-01D-2042-08_LUSC	687	0	0	297	599	384	532	635	440	72	587	0	358	133	0	63	573
TCGA-77-8128-10A-01D-2244-08_LUSC	676	240	0	287	610	377	531	640	459	0	0	0	0	0	0	82	571
TCGA-77-8130-10A-01D-2244-08_LUSC	682	0	0	299	589	374	530	627	458	0	0	0	0	0	0	74	571
TCGA-77-8131-10A-01D-2244-08_LUSC	684	235	246	259	599	353	529	641	468	0	523	487	0	0	25	54	575
TCGA-77-8133-10A-01D-2244-08_LUSC	653	229	236	263	536	343	520	623	461	0	0	0	0	0	33	0	575
TCGA-77-8136-10A-01D-2244-08_LUSC	691	0	0	321	626	393	536	667	488	0	0	0	0	67	41	83	580
TCGA-77-8138-10A-01D-2244-08_LUSC	593	253	266	0	586	135	529	651	367	84	630	574	0	128	0	68	573
TCGA-77-8139-10A-01D-2244-08_LUSC	680	0	0	277	595	288	524	639	470	0	0	0	0	0	23	64	575
TCGA-77-8140-10A-01D-2244-08_LUSC	679	237	256	268	545	357	530	636	458	0	0	0	0	0	0	69	572
TCGA-77-8143-10A-01D-2244-08_LUSC	674	0	0	299	584	283	520	631	440	0	0	0	0	0	0	75	571
TCGA-77-8144-10A-01D-2244-08_LUSC	656	247	259	269	544	275	529	642	442	70	586	0	353	131	31	0	576
TCGA-77-8145-10A-01D-2244-08_LUSC	686	0	0	292	598	367	528	630	471	0	0	0	0	0	0	102	574
TCGA-77-8146-10A-01D-2244-08_LUSC	635	237	242	268	596	277	524	631	0	76	627	527	362	138	0	0	574
TCGA-77-8148-10A-01D-2244-08_LUSC	662	241	249	283	605	131	524	606	449	0	513	515	0	138	27	0	577
TCGA-77-8150-10A-01D-2244-08_LUSC	670	0	0	285	567	279	529	639	465	66	0	0	0	0	25	42	575
TCGA-77-8154-10A-01D-2244-08_LUSC	668	237	242	277	559	274	522	646	371	76	586	0	361	130	25	0	575
TCGA-77-8156-10A-01D-2244-08_LUSC	676	233	235	278	602	365	532	636	452	0	583	508	0	0	0	74	574
TCGA-77-A5FZ-10A-01D-A27N-08_LUSC	664	237	258	256	512	275	530	623	380	0	0	0	0	0	0	72	574
TCGA-77-A5G1-10A-01D-A27N-08_LUSC	677	0	0	292	596	381	529	631	466	0	0	0	0	0	0	82	573
TCGA-77-A5G3-10A-01D-A27N-08_LUSC	666	244	259	283	559	274	527	642	455	0	0	0	0	0	0	79	570
TCGA-77-A5G6-10A-01D-A27N-08_LUSC	677	0	0	294	563	280	521	633	471	0	0	0	0	0	33	57	572
TCGA-77-A5G7-10A-01D-A27N-08_LUSC	634	233	254	279	493	358	527	634	462	0	0	0	0	0	27	55	572
TCGA-77-A5G8-10A-01D-A27N-08_LUSC	667	232	263	285	605	380	529	635	470	0	602	511	0	0	0	129	573
TCGA-77-A5GA-10A-01D-A27N-08_LUSC	685	0	0	294	606	381	529	651	470	0	0	0	0	0	0	82	575
TCGA-77-A5GB-10A-01D-A27N-08_LUSC	670	240	247	264	553	265	530	627	467	0	0	0	0	0	0	105	573
TCGA-77-A5GF-10A-01D-A27N-08_LUSC	595	252	268	0	582	134	530	641	444	74	642	567	366	135	0	58	574
TCGA-77-A5GH-10A-01D-A27N-08_LUSC	685	0	0	293	602	380	535	640	440	73	590	0	363	134	0	55	577
TCGA-78-7143-10A-01D-2036-08_LUAD	754	0	0	307	608	385	530	654	474	0	0	0	0	0	0	82	577
TCGA-78-7145-10A-01D-2036-08_LUAD	680	0	0	299	602	398	531	640	386	74	529	0	300	136	0	61	577
TCGA-78-7146-10A-01D-2036-08_LUAD	680	251	265	285	586	284	529	635	461	0	0	0	0	0	0	82	573
TCGA-78-7147-10A-01D-2036-08_LUAD	681	251	259	287	580	381	531	635	463	0	539	569	0	0	0	86	575
TCGA-78-7148-10A-01D-2036-08_LUAD	682	249	258	282	566	281	529	657	479	0	0	0	0	0	32	63	574
TCGA-78-7149-10A-01D-2036-08_LUAD	681	0	0	296	593	386	534	631	462	0	0	0	0	0	0	81	572
TCGA-78-7150-10A-01D-2036-08_LUAD	670	244	262	182	601	276	531	637	466	0	594	559	0	0	0	76	570
TCGA-78-7152-10A-01D-2036-08_LUAD	673	247	266	186	608	284	531	650	468	0	584	570	0	0	33	69	574
TCGA-78-7153-10A-01D-2036-08_LUAD	676	249	268	291	599	382	531	639	386	78	623	450	370	136	0	65	572
TCGA-78-7154-10A-01D-2036-08_LUAD	687	0	0	304	604	386	530	640	468	0	0	0	0	0	0	83	573
TCGA-78-7155-10A-01D-2036-08_LUAD	671	0	0	296	590	376	525	637	378	62	568	0	293	130	0	53	575
TCGA-78-7156-10A-01D-2036-08_LUAD	688	0	0	306	609	392	536	657	469	82	625	566	0	139	0	72	576
TCGA-78-7158-10A-01D-2036-08_LUAD	597	254	271	0	0	0	532	636	458	0	0	0	0	0	0	116	575
TCGA-78-7159-10A-01D-2036-08_LUAD	684	0	0	299	599	376	530	638	448	72	537	0	299	136	0	51	574
TCGA-78-7160-10A-01D-2036-08_LUAD	679	244	262	271	609	373	529	644	436	71	610	567	0	134	0	70	574
TCGA-78-7161-10A-01D-2036-08_LUAD	675	0	0	289	598	374	529	632	390	0	0	0	0	0	0	95	573
TCGA-78-7220-10A-01D-2036-08_LUAD	687	0	0	295	599	393	531	636	399	0	0	0	0	0	0	120	580
TCGA-78-7535-10A-01D-2063-08_LUAD	661	244	262	278	554	281	529	639	393	75	615	0	366	132	0	66	574
TCGA-78-7536-10A-01D-2063-08_LUAD	595	256	272	0	555	136	531	648	388	78	637	573	0	137	26	2	575
TCGA-78-7537-10A-01D-2063-08_LUAD	687	0	0	304	591	388	533	639	452	77	602	0	297	138	0	66	575
TCGA-78-7539-10A-01D-2063-08_LUAD	682	238	255	280	556	363	534	640	464	0	0	0	0	0	0	85	572
TCGA-78-7633-10A-01D-2063-08_LUAD	681	0	0	306	598	373	526	635	364	66	599	0	285	135	0	55	572
TCGA-78-8648-10A-01D-2393-08_LUAD	682	0	0	203	594	290	532	648	398	76	588	0	295	137	34	0	579
TCGA-78-8655-10A-01D-2393-08_LUAD	669	261	272	0	562	136	532	656	466	75	640	568	372	138	0	72	579
TCGA-78-8660-10A-01D-2393-08_LUAD	765	0	0	303	611	390	532	634	481	0	0	0	0	0	0	136	575
TCGA-78-8662-10A-01D-2393-08_LUAD	687	252	271	287	613	382	532	659	385	71	639	577	0	136	29	1	576
TCGA-79-5596-10A-01D-1945-08_LUSC	665	247	262	270	602	280	525	643	369	54	610	568	0	134	0	60	571
TCGA-80-5607-10A-01D-1946-08_LUAD	687	0	0	302	611	385	532	650	487	0	0	0	0	0	0	108	577
TCGA-80-5608-10A-01D-1946-08_LUAD	690	0	0	305	607	387	532	647	468	77	546	0	374	139	0	81	577

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-80-5611-10A-01D-1625-08_LUAD	666	235	253	273	511	359	534	636	470	0	0	0	0	0	12	42	576
TCGA-81-5910-10A-01D-1696-08_GBM	658	243	265	279	600	286	523	647	470	0	594	507	0	0	24	55	574
TCGA-81-5911-10A-01D-1845-08_GBM	757	0	0	308	609	388	533	643	387	74	617	0	299	140	0	67	578
TCGA-83-5908-10A-01D-2284-08_LUAD	685	246	257	291	561	373	532	637	448	79	609	0	295	133	0	65	577
TCGA-85-6175-10A-01D-1817-08_LUSC	674	251	0	288	616	289	532	646	393	84	605	0	370	137	24	0	578
TCGA-85-6560-10A-01D-1817-08_LUSC	597	255	273	0	585	134	534	651	469	78	640	566	369	137	0	71	576
TCGA-85-6561-10A-01D-1817-08_LUSC	757	248	267	291	582	376	535	654	475	0	0	0	0	0	27	63	573
TCGA-85-6798-10A-01D-1945-08_LUSC	596	261	279	0	0	0	533	647	488	0	0	0	0	0	0	109	580
TCGA-85-7696-10A-01D-2122-08_LUSC	681	244	273	284	588	373	533	651	391	79	631	0	373	135	21	3	574
TCGA-85-7697-10A-01D-2122-08_LUSC	678	249	257	295	609	376	530	644	452	76	634	572	0	136	0	68	578
TCGA-85-7698-10A-01D-2122-08_LUSC	686	0	0	303	598	382	529	644	477	0	0	0	0	0	0	129	576
TCGA-85-7699-10A-01D-2122-08_LUSC	759	259	276	304	626	291	531	667	474	84	652	580	0	143	0	101	578
TCGA-85-7710-10A-01D-2122-08_LUSC	598	262	273	0	577	128	533	641	3	83	643	576	350	141	0	0	579
TCGA-85-7843-10A-01D-2122-08_LUSC	680	239	255	290	605	369	528	640	470	0	612	511	0	0	0	112	577
TCGA-85-7844-10A-01D-2122-08_LUSC	661	246	255	288	581	367	528	637	473	0	0	0	0	0	0	76	572
TCGA-85-7950-10A-01D-2184-08_LUSC	678	233	263	291	600	362	530	649	383	71	630	557	290	134	0	50	579
TCGA-85-8048-10A-01D-2244-08_LUSC	679	238	232	274	555	362	522	612	365	0	598	0	358	134	0	56	575
TCGA-85-8049-10A-01D-2244-08_LUSC	648	238	237	240	589	273	525	642	463	0	518	561	0	0	28	59	574
TCGA-85-8052-10A-01D-2244-08_LUSC	665	239	227	279	602	134	525	606	362	0	574	513	0	131	29	0	570
TCGA-85-8070-10A-01D-2244-08_LUSC	683	0	0	293	593	371	529	636	469	0	0	0	0	0	0	75	573
TCGA-85-8071-10A-01D-2244-08_LUSC	680	0	0	294	586	379	531	648	303	71	572	0	349	131	0	61	574
TCGA-85-8072-10A-01D-2244-08_LUSC	678	0	0	288	595	372	529	619	470	0	0	0	0	0	0	109	576
TCGA-85-8276-10A-01D-2293-08_LUSC	688	0	0	348	608	380	533	651	449	68	605	0	365	136	0	68	577
TCGA-85-8277-10A-01D-2293-08_LUSC	682	245	257	289	582	283	529	646	471	0	0	0	0	0	0	129	580
TCGA-85-8287-10A-01D-2293-08_LUSC	684	246	249	286	610	374	531	639	0	86	642	571	292	136	0	0	573
TCGA-85-8288-10A-01D-2293-08_LUSC	684	251	250	290	558	282	530	640	477	0	0	0	0	0	0	125	578
TCGA-85-8350-10A-01D-2293-08_LUSC	681	0	0	303	606	283	520	655	477	0	0	0	0	0	0	83	577
TCGA-85-8351-10A-01D-2293-08_LUSC	689	0	0	349	616	385	533	660	478	76	0	0	0	0	32	66	574
TCGA-85-8352-10A-01D-2323-08_LUSC	741	246	262	284	587	282	531	659	382	58	583	0	304	139	0	70	579
TCGA-85-8353-10A-01D-2293-08_LUSC	691	0	0	308	609	380	535	641	485	0	0	0	0	0	0	122	574
TCGA-85-8354-10A-01D-2323-08_LUSC	691	0	0	317	618	386	532	660	475	68	603	567	0	0	0	118	579
TCGA-85-8355-10A-01D-2293-08_LUSC	760	0	0	303	604	387	529	654	479	0	0	0	0	0	0	127	578
TCGA-85-8479-10A-01D-2323-08_LUSC	594	257	276	0	604	139	533	642	477	0	628	573	0	0	48	0	577
TCGA-85-8481-10A-01D-2323-08_LUSC	672	260	270	0	565	140	516	623	0	80	653	506	385	142	0	0	575
TCGA-85-8580-10A-01D-2395-08_LUSC	679	243	261	293	613	368	533	645	474	0	603	508	0	0	35	68	575
TCGA-85-8582-10A-01D-2395-08_LUSC	679	250	266	284	616	284	529	638	396	75	633	512	363	129	0	71	574
TCGA-85-8584-10A-01D-2395-08_LUSC	671	247	253	279	596	278	527	631	463	0	575	508	0	0	0	81	578
TCGA-85-8664-10A-01D-2395-08_LUSC	756	0	0	301	606	380	528	637	478	0	0	0	0	0	0	81	571
TCGA-85-8666-10A-01D-2395-08_LUSC	677	245	260	273	611	371	530	638	476	0	554	509	0	0	26	61	572
TCGA-85-A4CL-10A-01D-A26K-08_LUSC	639	237	247	280	602	278	526	634	443	0	507	494	0	0	0	73	576
TCGA-85-A4CN-10A-01D-A24F-08_LUSC	665	239	242	289	544	357	529	629	459	0	0	0	0	0	0	71	575
TCGA-85-A4JB-10A-01D-A25L-08_LUSC	637	247	263	275	606	276	531	629	470	0	595	493	0	0	28	55	574
TCGA-85-A4JC-10A-01D-A25A-08_LUSC	591	251	269	0	586	134	533	650	384	81	646	568	356	134	32	0	575
TCGA-85-A4PA-10A-01D-A25A-08_LUSC	681	245	254	289	606	377	535	648	378	73	625	507	291	135	0	62	577
TCGA-85-A4QQ-10A-01D-A25L-08_LUSC	679	0	0	289	600	373	525	631	399	0	0	0	0	0	0	76	574
TCGA-85-A4QR-10A-01D-A25A-08_LUSC	673	235	261	296	550	0	522	622	370	0	0	0	0	134	0	63	570
TCGA-85-A50M-10A-01D-A25L-08_LUSC	688	0	0	305	605	388	534	648	478	0	0	0	0	0	32	65	579
TCGA-85-A50Z-10A-01D-A25L-08_LUSC	686	0	0	303	589	368	502	594	382	0	0	0	0	131	0	68	569
TCGA-85-A510-10A-01D-A26K-08_LUSC	679	0	0	302	608	389	535	637	469	0	0	0	0	0	0	90	576
TCGA-85-A511-10A-01D-A25L-08_LUSC	676	0	0	291	562	380	527	612	460	0	0	0	0	0	0	102	576
TCGA-85-A512-10A-01D-A26K-08_LUSC	746	249	268	295	574	286	530	645	481	0	0	0	0	0	29	63	577
TCGA-85-A513-10A-01D-A26K-08_LUSC	687	0	0	299	599	379	527	636	0	82	614	566	0	140	0	1	577
TCGA-85-A53L-10A-01D-A26K-08_LUSC	679	0	0	295	594	379	530	623	377	67	579	0	363	136	25	5	574
TCGA-85-A5B5-10A-01D-A26K-08_LUSC	660	240	250	270	605	283	528	642	368	69	613	568	0	133	0	65	578
TCGA-86-6562-10A-01D-1753-08_LUAD	686	0	0	297	601	282	520	638	477	0	0	0	0	0	27	46	576
TCGA-86-6851-10A-01D-1946-08_LUAD	688	0	0	305	609	382	531	644	470	0	0	0	0	0	0	101	580
TCGA-86-7701-10A-01D-2167-08_LUAD	728	222	238	261	534	343	532	642	467	0	0	0	0	0	0	84	577
TCGA-86-7711-10A-01D-2063-08_LUAD	646	237	230	279	603	266	527	634	480	0	569	503	0	0	20	46	576
TCGA-86-7713-10A-01D-2063-08_LUAD	676	249	261	286	559	284	531	653	487	0	0	0	0	0	30	71	578
TCGA-86-7714-10A-01D-2167-08_LUAD	667	224	219	0	582	286	528	629	462	0	589	0	298	0	26	55	575
TCGA-86-7953-10A-01D-2184-08_LUAD	680	0	0	342	607	377	528	648	379	68	592	0	351	134	0	51	574
TCGA-86-7954-10A-01D-2184-08_LUAD	599	251	264	0	0	0	534	639	468	0	0	0	0	0	36	3	578
TCGA-86-7955-10A-01D-2184-08_LUAD	691	0	0	296	603	381	529	634	382	76	592	0	360	136	0	58	574
TCGA-86-8054-10A-01D-2238-08_LUAD	684	0	0	304	606	363	530	626	442	0	0	0	0	129	0	64	576
TCGA-86-8055-10A-01D-2238-08_LUAD	688	0	0	307	607	383	534	656	481	0	0	0	0	0	0	86	578
TCGA-86-8056-10A-01D-2238-08_LUAD	677	244	239	295	616	282	531	644	453	82	639	572	365	131	33	0	576
TCGA-86-8073-10A-01D-2238-08_LUAD	675	243	235	281	570	363	531	648	449	71	598	0	357	134	32	0	576
TCGA-86-8074-10A-01D-2238-08_LUAD	667	257	273	0	586	134	534	654	450	76	638	575	0	136	36	1	575
TCGA-86-8075-10A-01D-2238-08_LUAD	682	244	269	287	611	377	531	647	448	68	647	581	0	138	0	68	575
TCGA-86-8076-10A-01D-2238-08_LUAD	682	0	0	300	602	373	520	629	389	0	0	0	0	137	0	57	569
TCGA-86-8278-10A-01D-2284-08_LUAD	678	245	257	287	568	362	529	650	477	0	0	0	0	0	28	66	578
TCGA-86-8279-10A-01D-2284-08_LUAD	759	0	0	303	602	292	522	631	399	0	0	0	0	0	25	64	574
TCGA-86-8280-10A-01D-2284-08_LUAD	689	0	0	306	603	278	516	616	395	0	0	0	0	137	0	66	568
TCGA-86-8281-10A-01D-2284-08_LUAD	732	230	261	280	509	268	516	637	393	0	0	0	0	0	0	103	574
TCGA-86-8358-10A-01D-2323-08_LUAD	756	247	262	289	616	284	530	651	478	0	598	570	0	0	0	141	575
TCGA-86-8359-10A-01D-2323-08_LUAD	762	0	0	310	621	299	526	663	453	82	621	0	388	138	0	85	581
TCGA-86-8585-10A-01D-2393-08_LUAD	683	244	265	298	595	375	532	650	480	0	0	0	0	0	32	67	574
TCGA-86-8668-10A-01D-2393-08_LUAD	596	257	273	0	117	0	532	658	478	0	0	0	0	0	0	69	579
TCGA-86-8669-10A-01D-2393-08_LUAD	684	0	0	305	604	288	530	651	475	0	0	11	0	0	0	91	576
TCGA-86-8671-10A-01D-2393-08_LUAD	749	253	266	282	611	281	530	646	479	0	609	512	59	17	0	127	578
TCGA-86-8672-10A-01D-2393-08_LUAD	682	258	269	293	610	379	533	652	461	82	640	572	7	137	0	82	580
TCGA-86-8673-10A-01D-2393-08_LUAD	671	244	262	292	581	280	531	645	485	0	0	0	38	0	0	137	578
TCGA-86-8674-10A-01D-2393-08_LUAD	756	0	0	311	611	382	533	636	478	0	0	0	0	0	0	104	577
TCGA-86-A456-10A-01D-A24F-08_LUAD	684	0	0	297	593	380	525	623	459	0	0	0	0	0	21	43	572
TCGA-86-A4D0-10A-01D-A24F-08_LUAD	686	0	0	294	593	379	525	622	458	0	0	0	0	0	0	71	572
TCGA-86-A4JF-10A-01D-A24P-08_LUAD	688	0	0	303	597	379	528	648	480	0	0	0	0	0	29	63	574
TCGA-86-A4P7-10A-01D-A24P-08_LUAD	589	254	272	0	41	0	528	646	471	0	0	0	0	0	29	64	575
TCGA-86-A4P8-10A-01D-A24P-08_LUAD	679	0	0	304	605	375	528	639	378	67	605	0	295	134	0	54	575
TCGA-87-5896-10A-01D-1696-08_GBM	652	225	258	266	568	277	526	621	475	0	0	0	0	0	27	51	579
TCGA-90-6837-10A-01D-1945-08_LUSC	761	261	276	309	626	391	535	670	478	89	657	577	383	140	39	3	581
TCGA-90-7766-10A-01D-2122-08_LUSC	675	246	261	284	549	373	532	641	457	73	587	0	297	130	24	6	576
TCGA-90-7767-10A-01D-2122-08_LUSC	684	244	259	280	581	365	530	638	390	72	592	0	286	131	20	3	573
TCGA-90-7769-10A-01D-2122-08_LUSC	683	0	0	300	608	383	529	654	482	0	0	0	0	0	25	60	572
TCGA-90-7964-10A-01D-2184-08_LUSC	687	0	0	299	604	382	529	637	477	0	0	0	0	0	0	110	577
TCGA-90-A4ED-10A-01D-A25A-08_LUSC	679	253	265	287	563	374	530	643	445	72	596	0	298	131	0	66	576
TCGA-90-A4EE-10B-01D-A25A-08_LUSC	675	247	259	271	537	362	530	640	469	0	0	0	0	0	34	63	573

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-90-A59Q-10A-01D-A26K-08_LUSC	684	0	0	295	557	395	533	631	460	0	0	0	0	0	0	94	574
TCGA-91-6828-10A-01D-1855-08_LUAD	685	0	0	302	604	384	532	650	480	0	0	0	0	0	29	55	573
TCGA-91-6840-10A-01D-1946-08_LUAD	593	261	276	0	577	137	531	654	475	74	596	565	0	0	23	58	577
TCGA-91-7771-10A-01D-2167-08_LUAD	688	0	0	295	597	379	533	652	479	0	0	0	0	0	33	62	576
TCGA-91-8496-10A-01D-2393-08_LUAD	756	0	0	303	605	399	535	649	484	0	0	0	0	0	0	79	579
TCGA-91-8497-10A-01D-2393-08_LUAD	730	222	247	280	557	274	527	643	439	78	578	0	290	134	27	9	574
TCGA-91-8499-10A-01D-2393-08_LUAD	688	0	0	304	608	291	532	652	483	0	0	0	0	0	0	149	576
TCGA-91-A4BC-10A-01D-A24F-08_LUAD	673	223	241	274	603	361	529	643	386	69	620	563	0	133	0	58	570
TCGA-91-A4BD-10A-01D-A24F-08_LUAD	679	238	258	278	578	371	529	630	383	75	636	501	296	136	0	55	570
TCGA-92-7340-10A-01D-2042-08_LUSC	682	0	0	297	594	381	531	639	365	74	529	0	361	133	0	59	576
TCGA-92-7341-10A-01D-2042-08_LUSC	597	254	266	0	0	0	531	632	472	0	0	0	0	0	0	92	575
TCGA-92-8063-10A-01D-2244-08_LUSC	656	239	238	268	600	277	524	628	309	66	616	500	281	131	23	2	572
TCGA-92-8064-10A-01D-2244-08_LUSC	675	0	0	291	594	286	517	637	459	0	0	0	0	0	29	56	571
TCGA-92-8065-10A-01D-2244-08_LUSC	682	0	0	297	582	366	531	632	451	0	0	0	0	0	0	74	572
TCGA-93-7347-10A-01D-2184-08_LUAD	688	0	0	308	605	382	532	646	478	0	0	0	0	0	33	1	574
TCGA-93-7348-10A-01D-2036-08_LUAD	644	243	249	287	509	278	533	635	463	0	0	0	0	0	0	81	574
TCGA-93-8067-10A-01D-2284-08_LUAD	681	0	0	308	604	392	533	643	384	82	612	0	363	138	0	64	572
TCGA-93-A4JN-10A-01D-A24P-08_LUAD	685	0	0	305	606	382	528	644	450	82	605	0	302	133	0	66	575
TCGA-93-A4JO-10A-01D-A24P-08_LUAD	682	0	0	299	587	280	519	644	468	0	0	0	0	0	0	119	575
TCGA-93-A4JP-10A-01D-A24P-08_LUAD	686	0	0	303	606	383	532	653	476	0	0	0	55	0	33	71	574
TCGA-93-A4JQ-10A-01D-A24P-08_LUAD	671	251	262	284	555	274	508	615	439	0	600	0	366	132	0	67	574
TCGA-94-7033-10A-01D-1946-08_LUSC	734	245	266	282	612	282	533	657	481	72	582	513	0	0	27	66	578
TCGA-94-7557-10A-01D-2122-08_LUSC	677	247	245	289	610	288	530	645	474	0	600	566	0	0	38	4	574
TCGA-94-7943-10A-01D-2184-08_LUSC	684	0	0	298	591	379	529	643	472	0	0	0	0	0	0	102	576
TCGA-94-8035-10A-01D-2244-08_LUSC	654	218	0	240	572	266	524	638	442	0	0	0	0	0	21	57	574
TCGA-94-8490-10A-01D-2323-08_LUSC	688	0	0	310	615	386	530	652	483	0	0	0	0	0	34	63	579
TCGA-94-8491-10A-01D-2323-08_LUSC	596	258	268	0	0	0	533	643	473	0	0	0	0	0	36	0	576
TCGA-94-A4VJ-10A-01D-A25A-08_LUSC	680	0	0	304	596	372	527	638	464	0	0	0	0	0	0	85	578
TCGA-94-A5I4-10A-01D-A26K-08_LUSC	685	0	0	306	598	390	532	642	472	0	0	0	0	0	0	128	574
TCGA-94-A5I6-10A-01D-A27N-08_LUSC	673	241	259	278	509	366	529	646	446	76	600	0	368	133	29	0	572
TCGA-95-7039-10A-01D-1946-08_LUAD	683	0	0	297	599	384	532	628	472	0	0	0	0	0	23	64	574
TCGA-95-7043-10A-01D-1946-08_LUAD	685	0	0	301	599	385	531	648	474	0	0	0	0	0	24	59	580
TCGA-95-7562-10B-01D-2238-08_LUAD	689	0	0	305	601	380	532	642	478	0	0	0	0	0	30	69	577
TCGA-95-7567-10A-01D-2063-08_LUAD	672	244	252	288	583	278	528	641	485	0	0	0	0	0	33	65	573
TCGA-95-7944-10A-01D-2184-08_LUAD	677	232	252	180	610	282	533	648	375	68	632	563	287	135	0	51	576
TCGA-95-7947-10A-01D-2184-08_LUAD	671	241	232	281	584	273	533	651	470	0	0	0	0	0	26	64	577
TCGA-95-7948-10A-01D-2184-08_LUAD	664	246	255	288	612	283	531	656	482	0	612	515	0	0	0	120	581
TCGA-95-8039-10A-01D-2238-08_LUAD	682	0	0	295	596	283	518	648	476	0	0	0	0	0	28	67	574
TCGA-95-8494-10A-01D-2323-08_LUAD	751	245	253	182	609	378	537	649	384	63	631	566	290	134	0	57	575
TCGA-95-A4VK-10A-01D-A25L-08_LUAD	684	0	0	304	598	377	527	636	468	0	13	0	0	0	0	114	577
TCGA-95-A4VN-10A-01D-A25L-08_LUAD	683	0	0	301	602	381	529	640	450	81	595	0	293	141	0	62	575
TCGA-95-A4VP-10A-01D-A25L-08_LUAD	683	0	0	292	589	283	523	643	471	0	0	0	0	0	29	56	576
TCGA-96-7544-10A-01D-2042-08_LUSC	670	0	0	293	597	287	522	636	370	73	592	0	361	136	0	67	571
TCGA-96-7545-10A-01D-2042-08_LUSC	682	0	0	300	597	383	531	626	468	0	0	0	0	0	0	83	573
TCGA-96-8169-10A-01D-2293-08_LUSC	685	0	0	302	617	382	531	655	476	0	0	0	0	0	35	61	575
TCGA-96-8170-10A-01D-2293-08_LUSC	679	251	248	273	543	360	530	638	469	0	0	0	0	0	25	51	571
TCGA-96-A4JK-10A-01D-A25A-08_LUSC	677	248	248	284	576	371	524	641	450	0	52	0	0	0	0	82	576
TCGA-96-A4JL-10A-01D-A25A-08_LUSC	755	0	0	305	612	386	528	646	384	79	603	0	357	136	32	2	575
TCGA-97-7546-10A-01D-2036-08_LUAD	681	235	266	184	507	275	530	653	466	0	0	0	0	0	31	62	574
TCGA-97-7547-10A-01D-2036-08_LUAD	684	0	0	302	602	389	531	635	310	61	580	0	364	137	0	64	575
TCGA-97-7552-10A-01D-2036-08_LUAD	683	0	0	303	601	389	530	649	478	0	0	0	0	0	0	134	580
TCGA-97-7553-10A-01D-2036-08_LUAD	674	252	262	275	613	366	534	628	372	74	616	560	300	137	28	1	575
TCGA-97-7554-10A-01D-2036-08_LUAD	680	0	0	298	571	387	533	637	440	0	566	0	292	132	27	0	579
TCGA-97-7937-10A-01D-2167-08_LUAD	684	0	0	295	583	365	531	654	0	84	637	0	364	136	0	2	575
TCGA-97-7938-10A-01D-2167-08_LUAD	733	0	0	297	588	377	535	647	304	68	583	0	357	130	0	58	575
TCGA-97-7941-10A-01D-2184-08_LUAD	686	0	0	294	557	372	530	648	468	0	0	0	0	0	28	65	575
TCGA-97-8171-10A-01D-2284-08_LUAD	683	244	256	281	555	360	534	644	477	0	0	0	0	0	30	57	574
TCGA-97-8172-10A-01D-2284-08_LUAD	753	245	259	284	462	372	531	642	386	77	579	0	294	135	26	0	577
TCGA-97-8174-10A-01D-2284-08_LUAD	675	239	254	281	513	361	531	621	378	72	574	0	291	135	0	44	579
TCGA-97-8175-10A-01D-2284-08_LUAD	669	237	236	272	504	349	527	635	370	63	531	0	347	134	0	50	577
TCGA-97-8176-10B-01D-2393-08_LUAD	679	0	0	304	609	397	528	643	480	0	0	0	0	0	0	116	578
TCGA-97-8177-10A-01D-2284-08_LUAD	687	0	0	297	604	287	530	634	476	0	0	0	0	0	0	107	574
TCGA-97-8179-10A-01D-2284-08_LUAD	687	0	0	311	610	386	532	634	468	0	0	0	0	0	0	89	576
TCGA-97-8547-10A-01D-2393-08_LUAD	689	0	0	296	601	284	521	637	474	0	0	0	54	16	0	119	576
TCGA-97-8552-10A-01D-2393-08_LUAD	734	241	253	285	579	280	531	652	478	0	0	0	0	0	0	101	580
TCGA-97-A4LX-10A-01D-A24P-08_LUAD	683	245	266	296	607	379	529	644	469	0	601	562	14	0	28	66	573
TCGA-97-A4M0-10A-01D-A24P-08_LUAD	678	0	0	294	578	286	517	620	374	64	561	0	289	134	0	54	572
TCGA-97-A4M1-10A-01D-A24P-08_LUAD	680	239	253	280	584	367	528	632	301	63	635	561	293	133	0	50	574
TCGA-97-A4M2-10A-01D-A24P-08_LUAD	672	136	266	279	552	377	527	630	370	70	574	0	293	133	25	3	570
TCGA-97-A4M3-10A-01D-A24P-08_LUAD	684	0	0	300	597	382	527	652	476	0	0	0	0	0	27	72	572
TCGA-97-A4M5-10A-01D-A24P-08_LUAD	671	244	264	276	575	275	514	609	451	0	611	0	292	134	0	60	569
TCGA-97-A4M6-10A-01D-A24P-08_LUAD	591	248	266	0	592	135	529	635	0	79	645	508	374	135	0	1	571
TCGA-97-A4M7-10A-01D-A24P-08_LUAD	684	0	0	294	609	284	528	651	474	0	0	0	0	0	31	69	577
TCGA-98-7454-10A-01D-2042-08_LUSC	679	0	0	305	602	384	529	643	471	0	0	0	0	0	0	91	576
TCGA-98-8020-10A-01D-2244-08_LUSC	680	243	245	268	605	141	530	639	398	0	584	565	0	0	0	68	569
TCGA-98-8021-10A-01D-2244-08_LUSC	680	0	0	285	601	370	527	589	370	0	0	0	0	0	26	0	570
TCGA-98-8022-10A-01D-2244-08_LUSC	684	0	0	285	598	366	530	630	400	0	0	0	0	0	0	89	572
TCGA-98-8023-10A-01D-2244-08_LUSC	679	0	0	293	591	282	520	643	359	74	589	0	363	131	0	63	576
TCGA-98-A538-10A-01D-A25L-08_LUSC	680	0	0	301	602	288	523	642	470	0	0	0	0	0	29	62	572
TCGA-98-A539-10A-01D-A25L-08_LUSC	683	0	0	300	598	372	525	635	464	0	0	0	0	0	31	61	570
TCGA-98-A53A-10A-01D-A25L-08_LUSC	676	243	259	187	575	281	530	648	388	0	0	0	0	0	25	6	565
TCGA-98-A53B-10A-01D-A25L-08_LUSC	668	248	256	283	513	277	527	636	468	0	0	0	0	0	0	116	573
TCGA-98-A53C-10A-01D-A25L-08_LUSC	645	238	254	265	551	268	515	626	292	70	550	0	286	131	0	61	572
TCGA-98-A53D-10A-01D-A25L-08_LUSC	683	0	0	301	600	376	529	635	466	0	0	0	0	0	0	127	574
TCGA-98-A53H-10A-01D-A25L-08_LUSC	638	238	245	268	544	275	526	632	378	70	505	0	280	128	0	43	574
TCGA-98-A53I-10A-01D-A25L-08_LUSC	678	248	260	289	560	278	519	644	435	72	609	0	298	135	0	65	575
TCGA-98-A53J-10A-01D-A26K-08_LUSC	676	0	0	304	597	377	532	634	467	0	0	0	38	0	0	86	575
TCGA-99-7458-10A-01D-2036-08_LUAD	679	0	0	303	611	387	533	654	462	76	585	0	304	139	35	3	574
TCGA-99-8025-10A-01D-2238-08_LUAD	681	0	0	302	589	382	534	644	476	0	0	0	0	0	29	53	575
TCGA-99-8028-10A-01D-2238-08_LUAD	688	0	0	304	606	380	533	652	487	0	0	0	0	0	39	66	579
TCGA-99-8032-10A-01D-2238-08_LUAD	685	0	0	305	606	387	532	657	479	0	0	0	0	0	33	69	577
TCGA-99-8033-10A-01D-2238-08_LUAD	684	0	0	302	602	387	529	657	469	0	0	0	0	0	0	134	579
TCGA-A1-A0SB-10B-01D-A142-09_BRCA	681	280	327	349	638	402	538	639	0	99	632	512	354	179	0	0	570
TCGA-A1-A0SD-10A-01D-A110-09_BRCA	690	328	370	0	0	0	562	658	571	0	0	0	0	0	0	194	598
TCGA-A1-A0SE-10A-03D-A099-09_BRCA	788	322	368	373	707	471	558	669	0	106	668	590	386	193	0	0	595
TCGA-A1-A0SF-10B-01D-A142-09_BRCA	665	236	311	333	673	430	534	621	455	0	567	512	0	0	24	35	546

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-A1-A0SG-10B-01D-A17G-09_BRCA	689	332	372	0	698	186	561	661	461	106	669	557	385	186	0	97	595
TCGA-A1-A0SH-10A-03D-A099-09_BRCA	800	328	369	386	724	450	559	666	0	111	677	589	387	194	0	0	591
TCGA-A1-A0SI-10B-01D-A142-09_BRCA	633	0	0	350	656	361	547	619	416	93	570	476	0	156	20	0	569
TCGA-A1-A0SJ-10A-02D-A099-09_BRCA	794	0	0	375	717	456	564	665	578	0	629	589	0	0	72	0	594
TCGA-A1-A0SK-10A-03D-A099-09_BRCA	700	0	0	389	713	466	557	657	477	0	0	0	0	0	62	0	598
TCGA-A1-A0SM-10A-02D-A10G-09_BRCA	698	318	364	231	719	380	556	666	576	0	644	558	0	0	47	93	592
TCGA-A1-A0SN-10B-01D-A142-09_BRCA	666	0	0	223	679	376	551	641	446	0	0	0	0	0	19	46	581
TCGA-A1-A0SO-10A-03D-A099-09_BRCA	682	312	360	360	704	378	555	652	446	101	652	547	437	181	0	67	587
TCGA-A1-A0SP-10A-02D-A099-09_BRCA	694	319	355	371	707	381	555	646	568	0	602	548	0	0	0	148	591
TCGA-A2-A04N-10A-01D-A110-09_BRCA	700	0	0	391	722	474	558	666	469	0	0	0	0	0	0	164	595
TCGA-A2-A04R-10B-01D-A10G-09_BRCA	683	313	349	365	702	458	556	654	440	100	644	0	402	172	31	3	579
TCGA-A2-A04U-10A-01D-A110-09_BRCA	697	0	0	393	711	475	558	673	569	0	0	0	0	0	58	95	594
TCGA-A2-A04W-10A-01D-A110-09_BRCA	703	0	0	391	717	475	557	664	584	0	0	0	0	0	57	92	598
TCGA-A2-A0CK-10A-01D-A22A-09_BRCA	555	294	329	0	599	173	519	574	295	0	619	537	0	153	0	28	568
TCGA-A2-A0CL-10A-01D-A110-09_BRCA	597	318	381	0	723	191	562	672	491	0	674	580	478	0	52	91	599
TCGA-A2-A0CO-10A-01D-A22A-09_BRCA	642	276	294	288	634	328	532	616	282	92	602	493	297	167	0	29	585
TCGA-A2-A0CR-10A-01D-A22A-09_BRCA	664	0	0	341	642	429	549	618	544	0	0	0	0	0	35	0	582
TCGA-A2-A0CS-10A-01D-A110-09_BRCA	694	0	0	390	711	474	557	658	458	108	640	0	386	178	0	113	595
TCGA-A2-A0CV-10A-01D-A110-09_BRCA	789	0	0	393	712	466	554	663	481	0	0	0	0	0	44	82	597
TCGA-A2-A0CW-10A-01D-A110-09_BRCA	800	330	371	390	715	388	562	677	583	0	0	0	0	0	100	0	600
TCGA-A2-A0D3-10A-01D-A110-09_BRCA	691	315	363	380	679	455	553	650	0	101	657	591	0	185	0	0	593
TCGA-A2-A0EN-10A-01D-A099-09_BRCA	783	313	367	376	692	382	556	664	351	107	634	0	458	182	0	88	595
TCGA-A2-A0EP-10A-01D-A22X-09_BRCA	683	0	0	346	664	457	549	632	452	0	0	0	0	0	0	86	591
TCGA-A2-A0ES-10A-01D-A110-09_BRCA	792	332	381	0	698	178	560	667	0	110	670	595	0	189	0	1	598
TCGA-A2-A0EW-10A-01D-A110-09_BRCA	794	316	362	386	699	455	559	674	575	0	0	0	0	0	59	112	600
TCGA-A2-A0ST-10A-01D-A099-09_BRCA	698	0	0	393	712	473	558	663	470	103	647	577	0	183	0	103	591
TCGA-A2-A0SU-10A-01D-A099-09_BRCA	795	0	0	395	716	476	553	668	461	107	645	0	380	187	32	0	594
TCGA-A2-A0SX-10A-01D-A099-09_BRCA	798	0	0	399	720	483	562	671	579	0	0	0	0	0	47	102	597
TCGA-A2-A0SY-10A-01D-A099-09_BRCA	697	324	367	380	702	378	559	661	578	0	0	0	0	0	0	159	594
TCGA-A2-A0T0-10A-01D-A099-09_BRCA	741	282	324	361	692	447	552	641	453	0	559	517	0	0	0	53	585
TCGA-A2-A0T1-10A-01D-A099-09_BRCA	790	335	373	0	698	184	561	660	469	105	663	593	0	183	0	98	596
TCGA-A2-A0T2-10A-01D-A099-09_BRCA	676	0	0	376	684	463	555	652	448	106	586	0	361	175	0	58	580
TCGA-A2-A0T3-10A-01D-A110-09_BRCA	684	308	347	368	702	457	558	656	574	0	625	567	0	0	0	137	594
TCGA-A2-A0T4-10A-01D-A099-09_BRCA	690	317	359	371	677	455	556	666	578	0	0	0	0	0	45	86	594
TCGA-A2-A0T5-10A-01D-A099-09_BRCA	696	313	360	232	710	383	560	648	455	108	644	588	0	173	0	60	595
TCGA-A2-A0T6-10A-01D-A099-09_BRCA	700	0	0	390	707	477	560	652	565	0	0	0	0	0	0	123	595
TCGA-A2-A0T7-10A-01D-A099-09_BRCA	792	0	0	389	706	467	556	663	559	105	643	0	384	181	50	0	593
TCGA-A2-A0YC-10A-01D-A10G-09_BRCA	692	308	353	373	673	367	553	661	572	0	0	0	0	0	42	70	592
TCGA-A2-A0YD-10A-01D-A10G-09_BRCA	686	0	0	381	698	384	549	648	465	0	0	0	0	0	0	118	591
TCGA-A2-A0YE-10A-01D-A10G-09_BRCA	702	0	0	392	707	461	557	668	574	0	0	0	0	0	48	92	600
TCGA-A2-A0YF-10A-01D-A10G-09_BRCA	659	278	317	325	690	381	540	645	466	0	601	0	359	0	13	27	586
TCGA-A2-A0YG-10A-01D-A10G-09_BRCA	652	0	0	379	680	442	537	626	457	0	0	0	0	0	0	72	592
TCGA-A2-A0YH-10A-01D-A10G-09_BRCA	683	0	0	391	707	459	557	653	480	0	0	0	0	0	0	161	592
TCGA-A2-A0YI-10A-01D-A10M-09_BRCA	695	0	0	397	711	471	562	673	582	0	0	0	0	0	62	95	596
TCGA-A2-A0YJ-10A-01D-A10G-09_BRCA	592	244	296	305	569	331	534	620	455	0	0	0	0	0	11	21	549
TCGA-A2-A0YK-10A-01D-A117-09_BRCA	798	0	0	402	733	398	556	673	583	0	0	0	0	0	0	202	594
TCGA-A2-A0YL-10A-01D-A10G-09_BRCA	696	0	0	389	710	475	558	664	466	102	652	0	449	185	0	78	594
TCGA-A2-A0YM-10A-01D-A10G-09_BRCA	684	307	342	363	694	376	554	640	438	101	637	552	0	169	0	56	595
TCGA-A2-A0YT-10A-01D-A10G-09_BRCA	796	319	362	231	686	377	556	661	568	0	0	0	0	0	49	89	592
TCGA-A2-A1FV-10A-01D-A13O-09_BRCA	671	0	0	368	685	457	549	655	467	0	0	0	0	0	37	54	586
TCGA-A2-A1FW-10A-01D-A13O-09_BRCA	788	293	337	330	620	425	526	648	469	0	0	0	0	0	33	46	572
TCGA-A2-A1FX-10A-01D-A13O-09_BRCA	680	286	341	341	637	422	544	616	466	0	0	0	0	0	0	75	587
TCGA-A2-A1FZ-10A-01D-A14G-09_BRCA	567	302	359	0	590	167	530	636	315	100	623	539	0	174	0	36	575
TCGA-A2-A1G0-10A-01D-A13O-09_BRCA	659	0	0	366	670	448	543	642	456	0	0	0	0	0	18	39	581
TCGA-A2-A1G1-10A-01D-A13O-09_BRCA	573	315	321	0	683	180	551	652	544	0	598	514	0	0	31	39	587
TCGA-A2-A1G6-10A-01D-A13O-09_BRCA	671	0	0	365	662	455	545	634	423	91	597	0	362	161	0	37	569
TCGA-A2-A259-10A-01D-A16D-09_BRCA	681	0	0	383	698	452	555	643	564	0	0	0	0	0	0	98	588
TCGA-A2-A25A-10A-01D-A16D-09_BRCA	676	0	0	378	675	363	551	630	454	0	0	0	0	0	0	63	559
TCGA-A2-A25B-10A-01D-A167-09_BRCA	675	0	0	359	691	450	558	649	473	0	0	0	0	0	51	0	577
TCGA-A2-A25C-10A-01D-A167-09_BRCA	660	0	0	348	639	409	517	593	353	0	0	0	0	0	0	58	565
TCGA-A2-A25D-10A-01D-A16D-09_BRCA	693	0	0	391	713	469	560	652	478	0	0	0	0	0	0	128	593
TCGA-A2-A25E-10A-01D-A167-09_BRCA	657	0	0	357	660	439	542	618	439	0	0	0	0	0	0	55	567
TCGA-A2-A25F-10A-01D-A167-09_BRCA	663	281	311	323	593	403	541	616	438	0	0	0	0	0	19	26	561
TCGA-A2-A3KC-10A-01D-A20S-09_BRCA	551	256	263	87	502	360	509	405	372	0	369	0	310	140	23	3	576
TCGA-A2-A3KD-10A-01D-A20S-09_BRCA	659	277	327	318	586	316	540	625	304	0	430	0	345	169	0	41	584
TCGA-A2-A3XS-10A-01D-A22X-09_BRCA	698	314	332	341	679	455	555	635	456	0	573	0	381	0	0	103	589
TCGA-A2-A3XT-10A-01D-A22X-09_BRCA	696	175	361	330	595	447	548	628	328	0	0	0	0	0	0	58	563
TCGA-A2-A3XU-10A-01D-A22X-09_BRCA	699	298	334	336	676	437	548	630	555	0	589	559	0	0	33	60	590
TCGA-A2-A3XV-10A-01D-A23C-09_BRCA	690	0	0	368	657	457	554	638	460	0	0	0	0	0	0	88	581
TCGA-A2-A3XW-10A-01D-A23C-09_BRCA	675	0	0	364	669	450	547	642	433	0	479	0	347	175	0	55	578
TCGA-A2-A3XX-10A-01D-A23C-09_BRCA	696	0	338	188	679	463	554	630	548	0	510	0	385	0	48	1	584
TCGA-A2-A3XY-10A-01D-A23C-09_BRCA	695	302	335	328	677	416	557	635	553	0	573	0	369	0	34	50	583
TCGA-A2-A3XZ-10A-01D-A23C-09_BRCA	700	0	0	379	690	466	554	633	562	0	0	0	0	0	41	75	586
TCGA-A2-A3Y0-10A-01D-A23C-09_BRCA	694	0	0	356	641	445	542	629	435	0	0	0	0	0	0	35	560
TCGA-A2-A4RW-10A-01D-A25Q-09_BRCA	696	0	0	332	654	359	553	623	328	87	465	489	0	171	0	39	582
TCGA-A2-A4RX-10A-01D-A25Q-09_BRCA	692	0	0	367	663	459	557	630	535	0	0	0	0	0	37	47	587
TCGA-A2-A4RY-10A-01D-A25Q-09_BRCA	687	305	338	297	645	436	550	652	425	94	578	0	440	173	0	60	588
TCGA-A2-A4S0-10A-01D-A25Q-09_BRCA	697	65	14	375	675	468	555	667	563	0	0	0	0	0	35	66	588
TCGA-A2-A4S1-10A-01D-A25Q-09_BRCA	687	306	343	344	637	353	548	646	545	0	0	0	0	0	0	97	587
TCGA-A2-A4S2-10A-01D-A25Q-09_BRCA	700	0	0	356	687	460	552	638	559	0	0	0	0	0	38	64	582
TCGA-A2-A4S3-10A-01D-A25Q-09_BRCA	694	0	0	356	666	452	551	624	547	0	0	0	0	0	40	4	585
TCGA-A4-7286-10A-01D-2136-08_KIRP	682	243	263	297	582	374	531	646	389	83	610	173	359	136	31	1	573
TCGA-A4-7287-10A-01D-2136-08_KIRP	683	0	0	306	605	383	530	636	473	0	0	0	0	0	0	117	576
TCGA-A4-7583-10A-01D-2136-08_KIRP	672	245	253	281	547	275	527	635	467	0	0	0	0	0	0	118	574
TCGA-A4-7584-10A-01D-2136-08_KIRP	689	0	0	305	607	390	528	641	466	0	0	0	0	0	0	96	575
TCGA-A4-7732-10A-01D-2136-08_KIRP	687	0	0	300	603	396	529	648	472	0	0	0	0	0	33	67	574
TCGA-A4-7734-10A-01D-2136-08_KIRP	754	0	0	303	612	288	524	653	455	77	629	0	353	139	0	71	574
TCGA-A4-7828-10A-01D-2136-08_KIRP	597	255	271	0	589	138	532	652	483	0	602	512	0	0	30	68	574
TCGA-A4-7915-10A-01D-2201-08_KIRP	690	0	0	304	620	398	531	655	478	0	0	0	0	0	31	69	573
TCGA-A4-7996-10A-01D-2201-08_KIRP	683	0	0	304	608	290	523	653	482	0	0	0	0	0	0	143	578
TCGA-A4-7997-10A-01D-2201-08_KIRP	684	0	0	299	602	386	529	657	481	0	0	0	0	0	32	60	575
TCGA-A4-8098-10A-01D-2396-08_KIRP	686	0	0	290	608	382	532	639	471	0	0	0	0	0	30	63	580
TCGA-A4-8310-10A-01D-2396-08_KIRP	654	252	261	272	550	279	527	646	467	0	0	0	0	0	0	129	577
TCGA-A4-8311-10A-01D-2396-08_KIRP	672	240	262	187	510	270	529	636	464	0	0	0	0	0	38	0	574
TCGA-A4-8312-10A-01D-2396-08_KIRP	686	0	0	303	611	378	530	649	478	0	0	0	0	0	38	4	572
TCGA-A4-8515-10A-01D-2396-08_KIRP	684	0	0	300	613	389	533	648	387	86	630	569	0	136	0	69	572

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-A4-8517-10A-01D-2396-08_KIRP	685	0	0	302	616	397	532	661	453	60	596	0	369	141	0	77	581
TCGA-A4-8518-10A-01D-2396-08_KIRP	747	252	261	291	602	282	532	652	452	81	604	0	370	140	0	82	579
TCGA-A4-8630-10A-01D-2396-08_KIRP	675	244	261	281	614	284	528	644	441	79	633	512	294	132	0	57	574
TCGA-A4-A48D-10A-01D-A25F-10_KIRP	665	235	268	332	646	421	536	623	361	0	402	476	0	0	20	35	590
TCGA-A4-A4ZT-10A-01D-A26P-10_KIRP	672	242	283	261	559	441	548	612	322	0	465	496	345	176	0	55	584
TCGA-A4-A57E-10A-01D-A26P-10_KIRP	660	262	243	257	558	433	528	600	353	0	397	475	0	0	0	80	575
TCGA-A4-A5DU-10A-01D-A28G-10_KIRP	572	239	298	247	556	371	534	621	320	0	487	552	0	161	0	55	580
TCGA-A4-A5XZ-10A-01D-A31X-10_KIRP	541	0	0	255	518	425	505	566	295	0	313	424	0	153	0	30	555
TCGA-A4-A6HP-10A-01D-A31X-10_KIRP	496	0	0	239	452	418	493	471	252	0	282	0	200	88	0	22	515
TCGA-A5-A0G1-10A-01D-A122-09_UCEC	798	0	0	395	724	472	560	672	568	108	653	587	0	187	0	126	596
TCGA-A5-A0GG-10A-01D-A122-09_UCEC	800	328	372	385	709	475	561	673	580	87	422	461	0	131	0	164	597
TCGA-A5-A0GQ-10A-01D-A122-09_UCEC	796	0	0	399	722	472	561	681	581	0	0	0	0	0	73	122	600
TCGA-A5-A0GR-10A-01D-A122-09_UCEC	799	330	373	386	725	392	561	677	585	0	662	589	0	0	69	102	597
TCGA-A5-A0R6-10A-01D-A10B-09_UCEC	684	301	362	377	681	454	557	665	478	0	0	0	0	0	32	67	585
TCGA-A5-A0R7-10A-01D-A10B-09_UCEC	704	319	367	378	687	463	557	664	560	103	643	0	384	184	0	101	594
TCGA-A5-A0R8-10A-01D-A10B-09_UCEC	638	0	0	365	679	438	538	642	463	0	0	0	0	0	0	68	588
TCGA-A5-A0R9-10A-01D-A10B-09_UCEC	698	311	364	373	707	467	557	658	564	105	656	581	0	184	0	91	594
TCGA-A5-A0RA-10A-01D-A10B-09_UCEC	569	322	361	0	0	0	555	649	441	100	617	0	373	180	26	0	588
TCGA-A5-A0VO-10A-01D-A10G-09_UCEC	700	320	359	374	718	460	558	664	359	103	664	543	384	183	0	78	595
TCGA-A5-A0VP-10A-01D-A10B-09_UCEC	697	311	366	375	718	468	557	666	482	0	639	557	0	0	46	90	590
TCGA-A5-A0VQ-10A-01D-A10B-09_UCEC	695	306	353	363	682	454	557	654	474	0	0	0	0	0	0	105	596
TCGA-A5-A1OF-10A-01D-A14G-09_UCEC	683	297	310	189	608	336	542	642	549	0	0	0	0	0	31	45	585
TCGA-A5-A1OG-10A-01D-A14G-09_UCEC	763	0	0	385	704	459	553	670	536	102	627	0	362	176	37	0	591
TCGA-A5-A1OH-10A-01D-A22A-09_UCEC	697	0	0	358	674	453	547	637	551	0	0	0	0	0	0	114	590
TCGA-A5-A1OJ-10A-01D-A14G-09_UCEC	673	0	0	355	645	442	549	613	435	0	0	0	0	0	32	40	579
TCGA-A5-A1OK-10A-01D-A14K-09_UCEC	686	0	0	355	670	434	546	612	0	95	614	524	353	179	0	2	584
TCGA-A5-A2K2-10A-01D-A18P-09_UCEC	682	293	314	313	611	353	547	609	448	0	0	0	0	0	0	66	583
TCGA-A5-A2K3-10A-01D-A17W-09_UCEC	691	0	0	363	654	461	552	637	401	94	467	0	361	171	0	46	589
TCGA-A5-A2K4-10B-01D-A18P-09_UCEC	698	0	0	355	666	453	543	626	338	91	543	0	359	170	0	47	588
TCGA-A5-A2K5-10A-01D-A17W-09_UCEC	688	299	331	229	580	436	546	628	0	95	620	0	374	180	0	0	572
TCGA-A5-A2K7-10A-01D-A17W-09_UCEC	687	280	300	134	607	439	534	464	297	0	548	0	362	170	33	1	586
TCGA-A5-A3LO-10A-01D-A22A-09_UCEC	556	302	346	0	474	165	544	617	268	92	585	497	311	168	0	39	582
TCGA-A5-A3LP-10A-01D-A22A-09_UCEC	700	305	323	323	631	405	552	647	538	0	0	0	0	0	0	120	587
TCGA-A6-2671-10A-01D-1408-10_COAD	630	0	0	344	484	328	454	560	322	0	0	0	0	0	0	40	545
TCGA-A6-2674-10A-01D-A270-10_COAD	538	0	0	273	540	369	534	613	341	0	0	0	0	0	0	75	578
TCGA-A6-2675-10A-01D-1719-10_COAD	703	0	0	396	705	465	553	653	573	0	0	0	0	0	31	53	592
TCGA-A6-2677-10A-01D-A270-10_COAD	524	300	305	0	488	172	524	583	0	0	503	525	256	170	0	0	564
TCGA-A6-2684-10A-01D-A270-10_COAD	517	134	194	201	316	302	498	567	0	0	418	0	308	177	0	0	524
TCGA-A6-3809-10A-01D-A270-10_COAD	494	262	278	0	354	133	513	518	278	0	391	412	238	151	12	0	554
TCGA-A6-3810-10A-01D-A270-10_COAD	542	156	199	241	432	314	508	587	341	0	0	0	0	0	0	72	557
TCGA-A6-4105-10A-01D-1771-10_COAD	682	0	0	363	643	452	544	626	334	99	534	0	338	155	0	58	584
TCGA-A6-5656-10A-01D-A270-10_COAD	647	0	0	266	515	390	523	594	300	0	322	0	309	172	0	36	563
TCGA-A6-5657-10A-01D-1650-10_COAD	703	0	351	382	707	458	557	656	558	0	593	0	380	0	29	0	580
TCGA-A6-5659-10A-01D-1650-10_COAD	701	0	0	372	653	347	535	621	455	0	0	0	0	0	0	66	590
TCGA-A6-5662-10A-01D-1650-10_COAD	800	0	0	413	708	457	556	656	472	0	0	0	0	0	0	117	594
TCGA-A6-5664-10A-01D-1835-10_COAD	597	0	0	212	526	393	413	454	295	0	0	0	0	0	0	4	527
TCGA-A6-5665-10A-01D-1650-10_COAD	702	0	0	401	701	453	555	647	465	0	0	0	0	0	0	99	596
TCGA-A6-5666-10A-01D-1650-10_COAD	683	0	0	403	688	447	547	632	473	0	0	0	0	0	31	41	595
TCGA-A6-6137-10A-01D-1806-10_COAD	672	0	0	347	667	367	516	630	447	0	0	0	0	0	0	64	582
TCGA-A6-6138-10A-01D-1771-10_COAD	668	295	346	0	496	156	555	651	449	94	367	464	0	0	19	53	590
TCGA-A6-6141-10A-01D-1771-10_COAD	640	217	272	323	485	405	481	552	324	0	416	0	286	140	0	30	589
TCGA-A6-6142-10A-01D-1771-10_COAD	659	0	0	358	613	409	534	597	418	0	0	0	0	0	0	53	573
TCGA-A6-6648-10A-01D-1771-10_COAD	641	211	283	181	420	310	518	595	321	97	387	0	271	155	0	23	570
TCGA-A6-6649-10A-01D-1771-10_COAD	639	0	0	308	551	347	506	593	274	0	391	0	178	136	0	33	555
TCGA-A6-6650-10A-01D-1771-10_COAD	609	0	0	325	436	401	440	422	299	0	0	0	0	0	9	0	528
TCGA-A6-6651-10A-01D-1835-10_COAD	578	7	0	95	385	241	433	514	231	0	115	0	59	125	0	14	536
TCGA-A6-6652-10A-01D-1771-10_COAD	645	119	128	303	417	300	462	492	318	0	335	0	306	146	0	41	587
TCGA-A6-6653-10A-01D-1771-10_COAD	560	286	331	0	0	0	437	379	321	0	317	0	277	154	0	36	570
TCGA-A6-6654-10A-01D-1835-10_COAD	674	0	0	368	637	453	526	625	454	0	0	0	0	0	16	51	571
TCGA-A6-6780-10A-01D-A270-10_COAD	626	0	0	261	451	330	542	595	0	91	411	0	328	172	0	0	536
TCGA-A6-6781-10A-01D-1924-10_COAD	660	0	0	353	635	368	506	604	306	95	368	0	221	132	0	32	559
TCGA-A6-6782-10A-01D-1835-10_COAD	580	115	72	0	264	228	454	426	252	0	165	202	0	58	9	0	515
TCGA-A6-A565-10A-01D-A28G-10_COAD	684	0	0	263	677	436	536	620	348	0	507	0	469	0	46	0	572
TCGA-A6-A566-10A-01D-A28G-10_COAD	658	0	0	279	551	444	550	631	359	0	0	0	0	0	0	108	571
TCGA-A6-A567-10A-01D-A28G-10_COAD	663	231	280	103	507	180	536	611	361	0	479	535	364	0	17	38	575
TCGA-A6-A56B-10A-01D-A28G-10_COAD	662	0	0	256	552	373	544	622	352	0	451	0	365	0	41	1	584
TCGA-A6-A5ZU-10A-01D-A28G-10_COAD	675	0	333	254	584	437	547	639	359	0	462	0	365	0	46	2	590
TCGA-A7-A0DA-10A-01D-A110-09_BRCA	798	0	0	416	731	481	565	674	587	0	0	0	0	0	67	154	600
TCGA-A7-A0DB-10A-02D-A272-09_BRCA	687	291	323	313	676	443	548	631	428	91	625	538	346	172	27	1	585
TCGA-A7-A13D-10A-02D-A12Q-09_BRCA	702	0	0	236	721	390	561	681	586	0	663	559	0	0	74	106	598
TCGA-A7-A13E-10A-01D-A12Q-09_BRCA	692	318	364	376	692	452	558	666	571	0	0	0	0	0	63	1	595
TCGA-A7-A13F-10A-01D-A12Q-09_BRCA	800	333	374	383	725	388	562	685	485	105	677	597	0	184	72	0	600
TCGA-A7-A13H-10A-01D-A22A-09_BRCA	681	0	0	358	672	468	551	647	557	0	0	0	0	0	0	88	584
TCGA-A7-A26E-10A-01D-A167-09_BRCA	774	0	0	365	690	457	552	651	0	103	648	524	379	183	0	0	584
TCGA-A7-A26F-10A-01D-A167-09_BRCA	626	0	0	338	642	425	528	611	409	0	0	0	0	0	21	21	553
TCGA-A7-A26G-10A-01D-A167-09_BRCA	664	295	166	207	652	430	522	572	338	0	600	0	368	161	0	54	582
TCGA-A7-A26H-10A-01D-A167-09_BRCA	669	284	327	343	659	356	536	642	563	0	0	0	0	0	24	40	578
TCGA-A7-A26I-10A-01D-A167-09_BRCA	677	289	338	354	645	432	554	636	468	0	0	0	0	0	0	84	579
TCGA-A7-A26J-10A-01D-A167-09_BRCA	669	0	0	372	688	442	530	629	463	0	0	0	0	0	0	98	574
TCGA-A7-A2KD-10A-01D-A21Q-09_BRCA	674	273	0	346	634	433	548	609	429	0	0	0	0	0	0	56	572
TCGA-A7-A3IY-10A-01D-A21Q-09_BRCA	690	0	0	341	645	367	538	619	431	0	0	0	0	0	0	64	584
TCGA-A7-A3IZ-10A-01D-A20S-09_BRCA	655	0	0	320	611	420	541	609	0	86	595	0	355	182	0	3	568
TCGA-A7-A3J0-10A-01D-A20S-09_BRCA	678	258	273	273	479	402	547	608	445	0	0	0	0	0	29	0	577
TCGA-A7-A3J1-10A-01D-A20S-09_BRCA	641	0	0	317	604	419	525	569	336	0	0	0	0	0	0	45	570
TCGA-A7-A3RF-10A-01D-A22A-09_BRCA	701	0	0	369	682	474	555	656	361	96	599	0	367	177	0	65	589
TCGA-A7-A425-10A-01D-A243-09_BRCA	648	73	75	315	628	419	542	516	422	0	0	0	0	0	0	31	569
TCGA-A7-A426-10A-01D-A243-09_BRCA	691	295	336	338	609	418	552	642	406	92	583	559	0	175	0	55	582
TCGA-A7-A4SA-10A-01D-A25Q-09_BRCA	689	306	335	334	678	448	552	636	547	0	555	520	0	0	41	51	582
TCGA-A7-A4SB-10A-01D-A25Q-09_BRCA	589	317	353	0	642	213	554	625	406	96	608	506	365	170	0	44	589
TCGA-A7-A4SC-10A-01D-A25Q-09_BRCA	696	0	0	345	675	447	546	627	548	0	0	0	0	0	27	45	581
TCGA-A7-A4SD-10A-01D-A25Q-09_BRCA	687	0	0	366	682	458	555	627	553	0	0	0	0	0	51	1	590
TCGA-A7-A4SE-10A-01D-A25Q-09_BRCA	702	0	0	370	695	464	559	654	558	0	0	0	0	0	55	0	593
TCGA-A7-A4SF-10A-01D-A25Q-09_BRCA	686	309	341	197	612	404	550	643	552	0	0	0	0	0	37	61	586
TCGA-A7-A56D-10A-01D-A27P-09_BRCA	593	171	341	96	661	182	551	610	533	0	608	544	0	0	43	1	582
TCGA-A7-A5ZV-10A-01D-A28E-09_BRCA	698	0	0	337	675	453	546	622	549	0	0	0	0	0	32	56	592
TCGA-A7-A5ZW-10A-01D-A29N-09_BRCA	680	0	0	349	683	456	552	642	537	87	560	0	361	0	42	2	586

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-A7-A5ZX-10A-01D-A29N-09_BRCA	687	291	340	320	665	450	551	613	454	0	574	526	0	0	0	106	581
TCGA-A8-A075-10B-01D-A099-09_BRCA	793	0	0	392	714	466	558	663	479	0	0	0	0	0	46	78	591
TCGA-A8-A07R-10B-01D-A047-09_BRCA	795	0	0	408	718	388	554	674	473	109	661	0	468	186	0	99	595
TCGA-A8-A097-10A-01D-A047-09_BRCA	702	0	0	393	721	482	558	669	584	0	0	0	0	0	0	160	597
TCGA-AC-A23C-10A-01D-A167-09_BRCA	670	287	331	336	631	421	553	628	463	0	0	0	0	0	23	38	580
TCGA-AC-A23E-10A-01D-A159-09_BRCA	697	306	349	357	693	451	554	651	438	103	644	525	436	177	0	55	582
TCGA-AC-A2B8-10A-01D-A17D-09_BRCA	640	0	0	352	660	366	532	629	387	89	577	0	351	160	0	34	582
TCGA-AC-A2QH-10A-01D-A18P-09_BRCA	581	312	355	0	614	165	553	632	453	0	603	520	0	0	0	78	575
TCGA-AC-A2QI-10A-01D-A19Y-09_BRCA	685	0	0	357	660	443	548	623	445	0	0	0	26	35	10	72	586
TCGA-AC-A3BB-10A-01D-A19Y-09_BRCA	632	0	0	345	631	430	538	606	450	0	0	0	0	0	0	12	578
TCGA-AC-A3HN-10A-01D-A20S-09_BRCA	641	0	0	334	633	426	542	596	327	0	0	0	0	0	20	19	576
TCGA-AC-A3QP-10B-01D-A22X-09_BRCA	672	270	312	317	659	431	542	608	326	89	587	509	335	163	0	39	571
TCGA-AC-A3TM-10A-01D-A22A-09_BRCA	546	307	326	0	0	22	543	580	253	0	452	0	326	150	19	2	574
TCGA-AC-A3TN-10A-01D-A22A-09_BRCA	669	0	0	352	658	442	547	645	412	101	549	0	344	172	29	0	587
TCGA-AC-A3W5-10A-01D-A22A-09_BRCA	685	0	0	351	678	448	551	616	441	0	0	0	0	0	54	7	586
TCGA-AC-A3W6-10A-01D-A22A-09_BRCA	669	288	0	308	657	440	547	624	296	82	453	0	346	162	0	43	581
TCGA-AC-A3W7-10A-01D-A22A-09_BRCA	680	324	323	350	670	357	550	651	0	98	650	533	451	186	0	1	587
TCGA-AC-A3YI-10A-01D-A23C-09_BRCA	582	311	312	0	648	179	552	634	316	0	622	515	354	176	0	53	585
TCGA-AC-A3YJ-10A-01D-A22X-09_BRCA	684	0	0	383	684	466	556	646	443	98	612	0	367	174	0	71	588
TCGA-AC-A5EH-10A-01D-A28E-09_BRCA	582	283	306	247	646	428	548	604	439	0	517	515	0	0	0	84	581
TCGA-AC-A5EI-10A-01D-A27P-09_BRCA	684	277	331	269	536	425	552	616	543	0	0	0	0	0	0	106	590
TCGA-AC-A5XS-10A-01D-A29N-09_BRCA	691	0	0	356	664	467	553	629	455	0	0	0	0	0	0	85	585
TCGA-AC-A5XU-10A-01D-A28E-09_BRCA	692	0	332	326	616	169	551	634	566	0	0	0	0	0	41	52	589
TCGA-AC-A62V-10A-01D-A31U-09_BRCA	693	0	331	195	612	340	541	497	416	0	463	0	356	169	37	0	588
TCGA-AC-A62X-10A-01D-A29N-09_BRCA	697	0	0	327	658	446	548	623	410	91	545	0	360	174	33	0	577
TCGA-AC-A62Y-10A-01D-A29N-09_BRCA	698	288	328	317	521	337	547	632	550	0	0	0	0	0	52	0	587
TCGA-AD-5900-10A-01D-1650-10_COAD	794	0	0	393	690	454	552	646	477	0	0	0	0	0	18	53	594
TCGA-AD-6548-10A-01D-1835-10_COAD	578	0	0	157	436	238	432	401	294	0	0	0	0	0	0	21	513
TCGA-AD-6888-10A-01D-1924-10_COAD	669	0	0	347	647	434	521	623	301	102	411	431	273	132	18	0	559
TCGA-AD-6889-10A-01D-1924-10_COAD	564	272	286	0	0	0	488	613	426	0	0	0	0	0	24	0	583
TCGA-AD-6890-10A-01D-1924-10_COAD	667	154	255	229	441	369	473	529	429	0	0	0	0	0	11	38	569
TCGA-AD-6895-10A-01D-1924-10_COAD	653	0	0	318	622	422	510	587	431	0	0	0	0	0	0	45	565
TCGA-AD-6899-10A-01D-1924-10_COAD	623	148	119	182	347	309	481	546	337	0	0	0	0	0	15	20	569
TCGA-AD-6901-10A-01D-1924-10_COAD	664	0	0	326	586	420	489	554	332	0	0	0	0	0	0	50	557
TCGA-AD-6963-10A-01D-1924-10_COAD	584	0	0	245	472	293	430	534	261	0	252	0	229	124	0	18	542
TCGA-AD-6964-10A-01D-1924-10_COAD	573	276	311	0	454	155	546	609	0	97	585	469	424	173	0	0	569
TCGA-AD-6965-10A-01D-1924-10_COAD	665	0	0	273	642	341	512	594	343	0	0	0	0	0	0	33	561
TCGA-AD-A5EK-10A-01D-A28G-10_COAD	647	0	308	112	468	179	550	615	355	0	454	508	0	0	39	0	583
TCGA-AF-2687-10A-01D-1733-10_READ	683	0	0	377	657	442	519	611	446	0	0	0	0	0	0	47	583
TCGA-AF-2690-10A-01D-1733-10_READ	678	0	0	359	668	361	521	630	446	0	0	0	0	0	16	40	578
TCGA-AF-2693-10A-01D-1733-10_READ	679	265	264	220	453	413	537	581	301	88	334	0	296	153	10	0	581
TCGA-AF-3911-10A-01D-1733-10_READ	671	0	0	343	652	369	517	610	346	0	0	0	0	0	0	62	574
TCGA-AF-4110-10A-01D-1733-10_READ	660	0	0	338	595	365	518	599	347	0	0	0	0	0	7	25	560
TCGA-AF-5654-10A-01D-1657-10_READ	696	253	264	336	676	362	533	617	352	0	455	486	0	0	0	66	582
TCGA-AG-3591-10A-01D-1733-10_READ	622	164	281	238	421	310	531	614	312	93	339	0	276	167	0	16	581
TCGA-AG-3592-10A-01D-1733-10_READ	649	0	0	368	624	440	524	599	322	96	363	0	278	162	0	25	580
TCGA-AG-4021-10A-01D-1733-10_READ	655	266	295	307	452	371	547	613	338	93	365	0	286	165	0	25	585
TCGA-AH-6544-10A-01D-1826-10_READ	641	130	225	197	398	307	500	586	289	93	344	0	229	135	0	36	554
TCGA-AH-6897-10A-01D-1924-10_READ	614	0	0	323	546	329	485	533	326	0	0	0	0	0	0	44	557
TCGA-AH-6903-10A-01D-1924-10_READ	626	103	124	169	468	384	449	558	263	0	384	453	0	128	0	18	566
TCGA-AJ-A23M-10A-01D-A159-09_UCEC	667	299	340	357	651	363	553	656	470	0	0	0	0	0	30	52	588
TCGA-AJ-A23N-10A-01D-A22A-09_UCEC	679	267	317	292	494	399	534	527	430	0	0	0	0	0	0	59	578
TCGA-AJ-A23O-10A-01D-A159-09_UCEC	676	0	0	354	661	443	548	613	446	0	0	0	0	0	49	1	585
TCGA-AJ-A2QK-10A-01D-A18P-09_UCEC	586	312	356	0	672	186	551	635	410	99	639	586	0	173	41	4	588
TCGA-AJ-A2QL-10A-01D-A18P-09_UCEC	688	310	347	321	643	0	537	599	420	0	0	0	0	167	37	0	590
TCGA-AJ-A2QM-10A-01D-A18P-09_UCEC	694	0	0	356	647	455	550	631	454	0	0	0	0	0	32	61	584
TCGA-AJ-A2QN-10A-01D-A18P-09_UCEC	688	299	334	181	681	360	550	649	542	0	563	525	0	0	32	47	585
TCGA-AJ-A2QO-10A-01D-A18P-09_UCEC	691	0	0	351	661	369	541	625	540	0	0	0	0	0	0	75	586
TCGA-AJ-A3BD-10A-01D-A19Y-09_UCEC	696	0	0	368	674	464	551	621	442	0	0	0	0	0	0	113	588
TCGA-AJ-A3BF-10A-01D-A20S-09_UCEC	579	320	358	0	616	177	554	637	549	0	571	544	0	0	31	62	586
TCGA-AJ-A3BG-10A-01D-A19Y-09_UCEC	683	0	0	360	664	368	543	646	412	90	574	0	350	168	0	50	582
TCGA-AJ-A3BH-10A-01D-A19Y-09_UCEC	691	306	322	338	679	460	545	626	317	84	612	581	0	174	0	52	585
TCGA-AJ-A3BI-10A-01D-A20S-09_UCEC	687	0	0	353	668	443	548	617	455	0	0	0	0	0	47	4	588
TCGA-AJ-A3BK-10A-01D-A19Y-09_UCEC	684	293	335	324	632	429	551	631	543	0	0	0	0	0	57	2	584
TCGA-AJ-A3EJ-10A-01D-A19Y-09_UCEC	700	0	0	363	692	377	556	642	554	0	0	0	0	0	0	129	589
TCGA-AJ-A3EL-10A-01D-A20S-09_UCEC	700	0	0	380	699	473	555	657	452	102	637	556	0	177	0	100	591
TCGA-AJ-A3I9-10A-01D-A22A-09_UCEC	701	0	0	373	685	450	551	655	558	0	0	0	0	0	42	51	583
TCGA-AJ-A3IA-10A-01D-A20S-09_UCEC	697	308	346	341	647	359	551	647	547	0	0	0	0	0	34	76	587
TCGA-AJ-A3NC-10A-01D-A22A-09_UCEC	694	0	0	359	674	451	551	620	336	87	505	0	361	172	0	63	585
TCGA-AJ-A3NE-10A-01D-A22A-09_UCEC	583	317	359	0	0	0	547	623	550	0	0	0	0	0	0	97	581
TCGA-AJ-A3NF-10A-01D-A22A-09_UCEC	694	0	0	356	682	453	552	626	458	0	0	0	0	0	42	7	585
TCGA-AJ-A3NG-10A-01D-A22A-09_UCEC	697	0	0	327	660	442	541	606	308	91	554	0	338	174	0	45	567
TCGA-AJ-A3NH-10A-01D-A22A-09_UCEC	696	0	0	374	665	470	554	635	550	0	0	0	0	0	52	3	591
TCGA-AJ-A3OJ-10A-01D-A22A-09_UCEC	685	0	0	337	641	365	521	615	322	91	413	0	323	171	0	38	577
TCGA-AJ-A3OK-10A-01D-A22A-09_UCEC	699	0	0	359	669	463	548	632	549	0	0	0	0	0	0	102	590
TCGA-AJ-A3OL-10A-01D-A22A-09_UCEC	691	306	331	340	681	365	554	638	545	0	612	556	0	0	0	98	587
TCGA-AJ-A3QS-10A-01D-A22A-09_UCEC	593	327	362	0	695	183	557	655	557	0	653	575	376	0	43	57	590
TCGA-AJ-A3TW-10A-01D-A22A-09_UCEC	577	291	353	0	402	138	539	586	414	0	419	512	0	0	13	29	574
TCGA-AJ-A5DV-10A-01D-A27P-09_UCEC	701	289	318	306	592	418	549	622	409	0	0	0	0	0	27	0	565
TCGA-AJ-A5DW-10A-01D-A27P-09_UCEC	680	299	337	322	624	446	517	499	331	0	595	0	354	178	0	64	589
TCGA-AK-3426-10A-01D-1251-10_KIRC	703	0	0	402	725	389	556	661	490	0	0	0	0	0	0	127	593
TCGA-AK-3427-10A-01D-0966-08_KIRC	681	254	274	294	594	386	531	649	468	0	619	0	300	138	39	1	579
TCGA-AK-3429-10A-01D-1251-10_KIRC	779	0	0	393	708	465	557	659	485	0	0	0	0	0	0	140	588
TCGA-AK-3430-10A-01D-1251-10_KIRC	683	0	0	389	694	384	542	658	444	108	619	0	358	174	0	38	568
TCGA-AK-3436-10A-01D-1251-10_KIRC	750	307	361	0	0	0	523	627	0	111	661	0	456	186	0	0	577
TCGA-AK-3440-10A-01D-0966-08_KIRC	751	251	280	290	596	380	533	668	464	85	644	0	381	139	0	83	582
TCGA-AK-3443-10A-01D-0966-08_KIRC	691	0	0	310	612	392	531	658	482	0	0	0	0	0	0	119	578
TCGA-AK-3444-10A-01D-0966-08_KIRC	753	257	265	297	596	389	534	667	482	0	0	0	0	0	0	126	577
TCGA-AK-3447-10A-01D-0966-08_KIRC	761	0	0	306	615	399	533	661	463	80	609	0	305	138	0	91	578
TCGA-AK-3451-10A-01D-1251-10_KIRC	795	0	0	402	716	468	563	681	584	113	0	0	0	0	50	0	594
TCGA-AK-3453-10A-01D-0966-08_KIRC	757	255	272	303	548	393	533	664	462	81	616	0	374	139	0	87	579
TCGA-AK-3455-10A-01D-0966-08_KIRC	599	261	273	0	0	0	531	658	483	0	0	0	0	0	32	79	579
TCGA-AK-3456-10A-01D-1251-10_KIRC	682	275	332	227	638	414	557	649	573	0	0	0	0	0	36	0	588
TCGA-AK-3458-10A-01D-1501-10_KIRC	677	266	334	373	705	429	559	654	349	110	649	527	0	177	0	33	574
TCGA-AK-3465-10A-01D-0966-08_KIRC	684	0	0	304	608	395	539	653	479	0	0	0	0	0	35	76	578
TCGA-AL-3466-10A-01D-1252-08_KIRP	685	0	0	310	616	404	535	657	488	0	0	0	0	0	38	89	581

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-AL-3467-10A-01D-1252-08_KIRP	763	0	0	306	612	396	535	664	484	0	0	0	0	0	0	184	580
TCGA-AL-3468-10A-01D-1252-08_KIRP	671	265	278	0	612	142	535	665	491	0	643	579	0	0	44	83	581
TCGA-AL-3472-10A-01D-1252-08_KIRP	688	254	271	303	595	387	536	661	485	0	0	0	0	0	33	87	579
TCGA-AL-3473-10A-01D-1252-08_KIRP	759	0	0	304	609	299	523	658	486	0	0	0	0	0	0	109	578
TCGA-AL-7173-10A-01D-2136-08_KIRP	679	246	257	281	550	277	526	650	460	0	0	0	0	0	28	65	573
TCGA-AL-A5DJ-10A-01D-A26P-10_KIRP	648	0	0	276	651	442	529	606	0	0	477	0	441	184	0	0	581
TCGA-AN-A04C-10A-01D-A047-09_BRCA	800	0	0	415	724	473	557	678	578	0	0	0	0	0	62	121	599
TCGA-AN-A0FY-10A-01D-A047-09_BRCA	801	0	0	406	723	476	561	677	585	0	0	0	0	0	58	123	598
TCGA-AN-A0XL-10A-01D-A10M-09_BRCA	699	306	344	378	714	374	559	661	573	0	635	540	0	0	0	96	581
TCGA-AN-A0XN-10A-01D-A10G-09_BRCA	799	321	377	385	729	382	562	674	584	0	648	580	0	0	61	110	598
TCGA-AN-A0XO-10A-01D-A10G-09_BRCA	555	259	338	0	379	179	534	622	265	103	634	451	271	145	15	0	557
TCGA-AN-A0XP-10A-01D-A10G-09_BRCA	698	100	81	382	710	463	556	649	571	0	0	322	0	0	0	141	592
TCGA-AN-A0XR-10A-01D-A117-09_BRCA	698	316	357	365	714	453	561	671	457	108	662	568	383	179	0	70	595
TCGA-AN-A0XS-10A-01D-A10G-09_BRCA	783	318	362	375	685	453	559	665	579	0	0	0	0	0	48	90	595
TCGA-AN-A0XT-10A-01D-A10G-09_BRCA	700	0	0	389	709	387	550	661	570	0	0	0	0	0	0	158	591
TCGA-AN-A0XU-10A-01D-A10G-09_BRCA	794	314	356	367	700	454	558	660	449	101	653	591	0	183	49	0	591
TCGA-AN-A0XV-10A-01D-A10G-09_BRCA	649	287	341	366	700	440	554	630	462	0	579	534	0	0	24	0	583
TCGA-AN-A0XW-10A-01D-A10G-09_BRCA	684	299	340	370	700	454	558	650	469	0	616	517	0	0	27	41	584
TCGA-AO-A03M-10A-01D-A10M-09_BRCA	700	322	366	385	702	464	559	665	0	108	667	555	460	187	0	0	596
TCGA-AO-A03N-10A-01D-A10M-09_BRCA	671	325	372	0	0	0	556	649	478	0	0	0	0	0	55	0	590
TCGA-AO-A03U-10A-01D-A10M-09_BRCA	613	0	0	383	693	377	533	638	454	106	591	0	352	178	0	27	580
TCGA-AO-A03V-10A-01D-A110-09_BRCA	782	0	0	388	699	461	560	656	454	106	632	0	377	177	0	68	592
TCGA-AO-A0JG-10A-01D-A099-09_BRCA	578	330	369	0	0	0	554	658	563	0	0	0	0	0	37	81	588
TCGA-AO-A124-10A-01D-A10M-09_BRCA	696	308	361	373	725	379	557	663	463	103	669	567	382	177	0	55	597
TCGA-AO-A125-10A-01D-A10M-09_BRCA	685	319	360	378	707	462	561	664	482	0	636	0	397	0	39	79	596
TCGA-AO-A126-10A-01D-A10M-09_BRCA	696	0	0	389	711	474	561	673	579	0	0	0	0	0	47	98	594
TCGA-AO-A128-10A-01D-A10M-09_BRCA	799	0	0	394	714	466	558	664	486	0	0	0	0	0	0	248	599
TCGA-AO-A129-10A-01D-A10M-09_BRCA	704	0	0	413	712	473	559	671	484	0	0	0	0	0	81	0	595
TCGA-AO-A12A-10A-01D-A110-09_BRCA	687	330	360	0	691	180	558	656	483	0	0	0	0	0	0	117	593
TCGA-AO-A12B-10A-01D-A10M-09_BRCA	799	324	359	381	696	459	558	647	470	0	635	543	0	186	0	79	595
TCGA-AO-A12D-10A-01D-A110-09_BRCA	800	0	0	400	728	477	560	674	472	0	0	0	0	0	0	204	599
TCGA-AO-A12E-10A-01D-A10M-09_BRCA	696	0	0	392	719	464	554	663	482	0	0	0	0	0	45	80	591
TCGA-AO-A12F-10A-01D-A110-09_BRCA	677	285	350	375	682	448	538	632	462	0	621	0	369	184	22	0	598
TCGA-AO-A12G-10A-01D-A10M-09_BRCA	728	251	296	353	673	341	553	641	471	0	0	0	0	0	33	0	579
TCGA-AO-A12H-10A-01D-A110-09_BRCA	796	0	357	238	695	456	563	676	476	105	660	0	457	187	43	2	598
TCGA-AO-A1KO-10A-01D-A13O-09_BRCA	681	291	342	214	655	365	557	649	553	0	0	0	0	0	26	61	590
TCGA-AO-A1KR-10A-01D-A142-09_BRCA	662	274	306	302	683	343	526	640	459	0	535	496	0	0	20	41	568
TCGA-AO-A1KT-10A-01D-A188-09_BRCA	599	327	355	0	671	177	558	657	570	0	0	0	0	0	44	74	589
TCGA-AP-A059-10A-01D-A122-09_UCEC	801	330	379	391	730	478	565	682	588	0	671	590	0	0	0	217	600
TCGA-AP-A05O-10A-01D-A122-09_UCEC	796	0	0	396	721	395	556	673	0	110	673	0	470	189	0	0	599
TCGA-AP-A0LE-10A-01D-A10B-09_UCEC	684	0	0	394	719	476	559	672	579	0	0	0	0	0	48	81	594
TCGA-AP-A0LF-10A-01D-A122-09_UCEC	703	330	371	388	705	384	547	663	461	0	660	0	461	188	0	92	596
TCGA-AP-A0LL-10A-01D-A10B-09_UCEC	704	0	0	385	703	469	560	661	581	0	0	0	0	0	0	132	596
TCGA-AP-A0LM-10A-01D-A122-09_UCEC	782	325	379	0	718	190	559	676	580	0	679	584	479	0	59	87	599
TCGA-AP-A0LP-10A-01D-A10B-09_UCEC	667	0	0	365	705	375	555	636	476	0	0	0	0	0	0	77	582
TCGA-AP-A0LQ-10A-01D-A10B-09_UCEC	700	334	380	0	718	189	563	674	0	109	682	597	0	193	0	0	600
TCGA-AP-A0LS-10B-01D-A14G-09_UCEC	670	299	323	322	595	430	531	560	407	0	551	0	340	165	27	1	580
TCGA-AP-A1DH-10A-01D-A135-09_UCEC	578	321	349	0	550	173	546	632	556	0	581	535	0	0	34	49	585
TCGA-AP-A1DK-10A-01D-A135-09_UCEC	680	0	0	351	667	330	509	566	314	0	0	0	0	162	0	51	569
TCGA-AP-A1DM-10A-01D-A135-09_UCEC	694	0	0	379	674	455	554	654	550	0	0	0	0	0	38	51	590
TCGA-AP-A1DO-10A-01D-A135-09_UCEC	696	305	339	332	682	458	553	634	420	91	627	541	371	171	34	1	593
TCGA-AP-A1DP-10A-01D-A135-09_UCEC	591	327	358	0	0	0	554	637	550	0	0	0	0	0	56	1	587
TCGA-AP-A1DQ-10A-01D-A135-09_UCEC	755	0	0	376	694	447	549	657	467	0	0	0	0	0	23	49	583
TCGA-AP-A1DR-10A-01D-A135-09_UCEC	558	311	345	0	593	338	552	620	455	0	565	0	357	0	29	40	586
TCGA-AP-A1DV-10A-01D-A135-09_UCEC	681	277	324	339	609	422	525	579	317	0	542	0	348	172	0	51	573
TCGA-AP-A1E0-10A-01D-A135-09_UCEC	689	0	0	341	653	451	545	518	451	0	0	0	0	0	0	74	587
TCGA-AP-A1E1-10A-01D-A135-09_UCEC	662	282	316	232	589	429	556	623	300	0	452	0	324	166	0	53	584
TCGA-AP-A1E3-10A-01D-A135-09_UCEC	666	0	0	351	658	450	547	599	0	96	594	0	376	180	0	0	588
TCGA-AP-A1E4-10A-01D-A135-09_UCEC	696	309	342	362	691	454	550	651	324	86	643	589	0	180	0	66	590
TCGA-AP-A3K1-10A-01D-A20S-09_UCEC	685	293	337	330	624	0	541	590	406	0	0	0	0	177	34	3	566
TCGA-AP-A5FX-10A-01D-A27P-09_UCEC	699	0	363	356	701	457	558	659	564	0	621	0	471	0	49	80	594
TCGA-AQ-A04H-10A-01D-A10M-09_BRCA	702	322	369	232	718	384	561	663	581	0	636	570	0	0	31	93	595
TCGA-AQ-A04L-10A-01D-A12J-09_BRCA	661	0	0	351	682	353	515	631	437	100	591	0	271	159	0	0	563
TCGA-AQ-A0Y5-10A-01D-A17G-09_BRCA	667	270	317	216	688	357	530	631	0	100	634	559	0	171	0	0	563
TCGA-AQ-A1H2-10A-01D-A13O-09_BRCA	679	0	0	382	703	382	547	665	442	106	632	0	374	174	0	54	596
TCGA-AQ-A1H3-10A-01D-A188-09_BRCA	675	0	0	378	689	446	537	638	325	101	603	0	363	158	0	42	583
TCGA-AQ-A54N-10A-01D-A25Q-09_BRCA	677	300	326	323	674	439	543	633	535	0	577	557	0	0	0	90	586
TCGA-AQ-A54O-10A-01D-A25Q-09_BRCA	699	0	0	362	710	465	560	663	455	98	550	0	444	0	44	52	587
TCGA-AR-A0TP-10A-01D-A099-09_BRCA	693	0	0	385	714	388	555	648	454	104	610	0	453	176	0	81	595
TCGA-AR-A0TQ-10A-01D-A099-09_BRCA	621	0	0	374	682	435	536	621	456	0	0	0	0	0	0	48	573
TCGA-AR-A0TR-10A-01D-A099-09_BRCA	572	321	365	0	663	176	551	650	346	103	642	534	372	178	0	67	587
TCGA-AR-A0TS-10A-01D-A110-09_BRCA	679	311	356	372	683	375	556	649	571	0	0	0	0	0	34	76	591
TCGA-AR-A0TT-10A-01D-A099-09_BRCA	800	0	0	395	721	471	562	664	584	0	0	0	0	0	44	83	593
TCGA-AR-A0TU-10A-01D-A10G-09_BRCA	654	0	0	376	691	459	542	639	332	104	583	0	349	171	0	23	580
TCGA-AR-A0TV-10A-01D-A099-09_BRCA	699	0	0	392	707	463	556	658	569	0	0	0	0	0	0	182	592
TCGA-AR-A0TW-10A-01D-A099-09_BRCA	569	0	0	357	624	363	501	578	298	100	446	0	332	166	0	17	532
TCGA-AR-A0TX-10A-01D-A099-09_BRCA	690	0	0	383	703	468	560	649	570	0	0	0	0	0	0	172	594
TCGA-AR-A0TY-10A-01D-A110-09_BRCA	802	0	0	413	728	479	559	681	579	106	669	0	467	190	85	0	598
TCGA-AR-A0TZ-10A-01D-A099-09_BRCA	795	0	0	401	729	387	551	663	481	0	0	0	0	188	0	81	585
TCGA-AR-A0U0-10A-01D-A10G-09_BRCA	690	0	0	381	691	449	552	640	469	0	0	0	0	0	35	60	593
TCGA-AR-A0U1-10A-01D-A110-09_BRCA	788	0	0	245	718	387	563	671	582	0	0	0	0	0	34	76	599
TCGA-AR-A0U2-10A-01D-A10G-09_BRCA	682	0	0	374	692	380	550	635	362	0	0	0	0	0	0	93	593
TCGA-AR-A0U3-10A-01D-A10G-09_BRCA	762	0	0	370	693	461	558	648	568	0	0	0	0	0	0	87	592
TCGA-AR-A0U4-10A-01D-A10G-09_BRCA	785	314	344	367	678	380	555	658	478	0	0	0	0	0	33	62	587
TCGA-AR-A1AH-10A-01D-A12B-09_BRCA	802	330	380	391	718	392	565	678	581	0	0	0	0	0	72	127	599
TCGA-AR-A1AI-10A-01D-A12Q-09_BRCA	803	320	375	390	713	466	563	684	572	112	675	0	469	187	0	117	597
TCGA-AR-A1AJ-10A-01D-A12Q-09_BRCA	797	0	0	398	718	473	560	674	586	0	0	0	0	0	68	130	597
TCGA-AR-A1AK-10A-01D-A12Q-09_BRCA	803	0	0	414	722	476	561	673	579	0	0	0	0	0	0	238	594
TCGA-AR-A1AL-10A-01D-A12Q-09_BRCA	800	333	369	389	708	462	561	674	584	0	0	0	0	0	50	109	597
TCGA-AR-A1AM-10A-01D-A22A-09_BRCA	560	301	308	0	151	47	544	599	444	0	0	0	0	26	0	35	579
TCGA-AR-A1AN-10A-01D-A12Q-09_BRCA	796	328	364	396	718	473	564	676	586	0	0	0	0	0	56	106	600
TCGA-AR-A1AO-10A-01D-A12Q-09_BRCA	801	326	0	387	724	395	561	671	586	0	0	0	0	0	0	242	597
TCGA-AR-A1AP-10A-01D-A12Q-09_BRCA	686	0	0	386	702	464	559	665	569	0	0	0	0	0	60	0	589
TCGA-AR-A1AQ-10A-01D-A12Q-09_BRCA	800	328	371	381	724	469	560	681	579	102	657	589	0	0	130	0	598
TCGA-AR-A1AR-10A-01D-A135-09_BRCA	801	323	370	391	699	473	565	677	565	107	664	0	462	185	0	146	600
TCGA-AR-A1AS-10A-01D-A12Q-09_BRCA	796	327	368	394	723	471	559	668	473	109	673	580	465	185	0	102	600

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-AR-A1AT-10A-01D-A12Q-09_BRCA	799	322	373	384	724	387	558	683	577	107	676	594	0	184	74	0	599
TCGA-AR-A1AU-10A-01D-A12Q-09_BRCA	798	0	0	397	721	472	561	674	580	0	0	0	0	0	90	1	598
TCGA-AR-A1AV-10A-01D-A12Q-09_BRCA	794	330	370	388	725	467	560	669	582	0	657	583	0	0	0	132	594
TCGA-AR-A1AW-10A-01D-A12Q-09_BRCA	779	0	0	416	704	0	537	644	470	0	0	0	0	181	0	40	584
TCGA-AR-A1AX-10A-01D-A12Q-09_BRCA	700	0	0	394	719	468	558	676	554	105	663	0	384	183	0	121	599
TCGA-AR-A1AY-10A-01D-A12Q-09_BRCA	702	0	0	389	716	382	548	665	558	0	0	0	0	0	0	137	595
TCGA-AR-A24H-10A-01D-A167-09_BRCA	775	305	363	354	672	374	557	644	461	0	0	0	0	0	65	0	590
TCGA-AR-A24K-10A-01D-A167-09_BRCA	656	0	0	341	659	414	531	500	399	0	0	0	0	0	0	50	553
TCGA-AR-A24L-10A-01D-A167-09_BRCA	699	0	0	390	702	455	555	665	452	103	621	0	365	183	43	2	583
TCGA-AR-A24M-10A-01D-A167-09_BRCA	677	0	0	352	660	450	548	616	451	0	0	0	0	0	0	74	559
TCGA-AR-A24N-10A-01D-A167-09_BRCA	686	297	344	346	689	456	543	643	466	0	607	539	0	0	0	105	586
TCGA-AR-A24O-10A-01D-A167-09_BRCA	651	283	323	337	689	433	541	639	456	0	595	512	0	0	24	48	573
TCGA-AR-A24P-10A-01D-A167-09_BRCA	683	295	330	337	624	355	549	639	459	0	0	0	0	0	25	43	575
TCGA-AR-A24Q-10A-01D-A167-09_BRCA	694	0	0	373	691	444	539	655	467	0	0	0	0	0	29	48	585
TCGA-AR-A24R-10A-01D-A167-09_BRCA	666	265	328	327	616	344	506	543	410	0	552	506	0	163	26	0	582
TCGA-AR-A24S-10A-01D-A167-09_BRCA	679	0	0	376	680	375	546	648	471	0	0	0	0	0	0	97	587
TCGA-AR-A24T-10A-01D-A167-09_BRCA	651	0	0	325	664	371	514	613	392	91	547	501	0	165	0	49	580
TCGA-AR-A24U-10A-01D-A167-09_BRCA	674	0	0	365	662	415	528	642	452	0	0	0	0	0	20	32	587
TCGA-AR-A24V-10A-01D-A167-09_BRCA	671	0	0	372	669	439	537	638	450	0	0	0	0	0	26	38	578
TCGA-AR-A24W-10A-01D-A167-09_BRCA	682	0	0	368	669	457	555	639	460	0	0	0	0	0	0	80	585
TCGA-AR-A24X-10A-01D-A167-09_BRCA	667	268	315	320	537	422	538	641	398	95	572	0	340	166	0	34	574
TCGA-AR-A24Z-10A-01D-A167-09_BRCA	668	0	0	371	674	452	532	630	451	0	0	0	0	0	0	82	563
TCGA-AR-A250-10A-01D-A167-09_BRCA	645	276	291	322	630	327	542	622	450	0	0	0	0	0	0	58	580
TCGA-AR-A251-10A-01D-A167-09_BRCA	670	0	0	365	673	422	548	638	454	0	0	0	0	0	0	57	577
TCGA-AR-A252-10A-01D-A167-09_BRCA	665	271	300	244	613	424	540	631	335	0	0	0	0	0	0	53	562
TCGA-AR-A254-10A-01D-A167-09_BRCA	689	0	0	368	664	448	547	629	442	0	0	0	0	0	0	67	581
TCGA-AR-A255-10A-01D-A167-09_BRCA	694	0	0	369	681	453	552	644	344	96	599	0	361	169	0	54	591
TCGA-AR-A256-10A-01D-A167-09_BRCA	662	265	341	337	687	352	534	653	468	0	587	507	0	0	0	80	585
TCGA-AR-A2LE-10A-01D-A17W-09_BRCA	682	298	349	354	668	0	553	615	446	0	0	0	0	171	35	0	552
TCGA-AR-A2LH-10A-01D-A18P-09_BRCA	661	0	0	363	676	373	523	638	451	0	0	0	0	0	25	42	585
TCGA-AR-A2LJ-10A-01D-A19Y-09_BRCA	628	258	278	283	557	383	534	585	388	0	448	0	294	158	0	37	567
TCGA-AR-A2LK-10A-01D-A17W-09_BRCA	689	0	0	387	691	369	552	646	453	0	0	0	0	0	0	102	586
TCGA-AR-A2LL-10A-01D-A17W-09_BRCA	670	0	0	370	689	455	542	637	434	100	585	0	357	177	0	47	583
TCGA-AR-A2LM-10A-01D-A17W-09_BRCA	702	316	370	370	708	456	557	669	569	0	641	580	0	0	42	78	590
TCGA-AR-A2LN-10A-01D-A18P-09_BRCA	684	0	0	379	696	375	543	647	570	0	0	0	0	0	0	110	594
TCGA-AR-A2LO-10A-01D-A18P-09_BRCA	696	0	0	370	700	369	553	642	564	0	0	0	0	0	32	56	587
TCGA-AR-A2LQ-10A-01D-A18P-09_BRCA	666	285	320	342	691	424	555	639	426	100	639	529	363	170	27	0	578
TCGA-AR-A2LR-10A-01D-A18P-09_BRCA	686	0	0	376	713	462	560	663	0	107	659	554	459	182	0	0	591
TCGA-AR-A5QM-10A-01D-A27P-09_BRCA	672	0	0	360	663	447	547	622	316	0	552	0	334	169	0	52	587
TCGA-AR-A5QN-10A-01D-A28E-09_BRCA	687	0	0	345	671	364	549	628	452	0	0	0	0	0	43	0	583
TCGA-AR-A5QP-10A-01D-A28E-09_BRCA	672	312	341	339	667	364	551	638	548	0	488	557	0	0	36	56	591
TCGA-AR-A5QQ-10A-01D-A28E-09_BRCA	680	0	0	369	679	445	548	615	553	0	0	0	0	0	0	77	586
TCGA-AS-3777-10A-01D-0966-08_KIRC	685	0	0	302	610	397	535	662	476	0	0	0	0	0	36	93	577
TCGA-AS-3778-10A-01D-0966-08_KIRC	679	0	0	301	594	292	522	646	480	0	0	0	0	0	0	118	578
TCGA-AT-A5NU-10A-01D-A28G-10_KIRP	655	168	339	244	539	363	545	622	354	0	0	0	0	0	0	96	581
TCGA-AU-3779-10A-01D-1719-10_COAD	698	0	0	404	703	462	554	647	475	0	0	0	0	0	0	107	593
TCGA-AU-6004-10A-01D-1719-10_COAD	656	0	0	352	635	377	512	588	426	0	0	0	0	0	0	36	558
TCGA-AW-A1PO-10A-01D-A159-09_UCEC	672	0	0	327	628	422	508	449	274	0	0	0	0	168	0	33	544
TCGA-AX-A06D-10A-01D-A122-09_UCEC	793	333	380	0	678	187	561	671	582	0	657	584	0	0	0	174	598
TCGA-AX-A06H-10A-01D-A122-09_UCEC	800	332	373	389	712	475	562	677	582	0	0	0	0	0	0	193	599
TCGA-AX-A06L-10A-01D-A122-09_UCEC	798	0	0	398	723	481	562	675	0	109	672	0	467	189	0	0	599
TCGA-AX-A0IS-10B-01D-A10M-09_UCEC	704	0	0	399	722	470	561	665	580	0	0	0	0	0	0	244	597
TCGA-AX-A0IU-10A-01D-A10B-09_UCEC	801	322	363	389	719	467	563	674	580	0	642	583	0	0	43	79	596
TCGA-AX-A0IZ-10A-01D-A122-09_UCEC	795	318	369	237	702	380	559	668	575	0	0	0	0	0	77	0	598
TCGA-AX-A1C4-10A-01D-A135-09_UCEC	680	287	321	169	655	354	548	617	0	90	642	554	340	178	0	1	585
TCGA-AX-A1C5-10A-01D-A135-09_UCEC	685	0	0	341	654	439	536	607	534	0	0	0	0	0	0	83	581
TCGA-AX-A1C7-10A-01D-A135-09_UCEC	690	0	0	391	698	455	544	652	477	0	0	0	0	0	24	50	584
TCGA-AX-A1C8-10A-01D-A135-09_UCEC	628	310	341	0	646	152	551	654	464	0	583	525	0	0	30	42	567
TCGA-AX-A1C9-10A-01D-A135-09_UCEC	687	288	318	322	595	426	532	561	426	0	584	0	344	171	28	0	578
TCGA-AX-A1CA-10A-01D-A135-09_UCEC	701	317	364	376	685	457	557	661	573	0	0	0	0	0	64	0	591
TCGA-AX-A1CC-10A-01D-A135-09_UCEC	631	0	0	354	661	442	549	614	433	0	0	0	0	0	10	15	544
TCGA-AX-A1CE-10A-01D-A135-09_UCEC	671	305	326	300	617	350	549	623	543	0	0	0	0	0	0	72	586
TCGA-AX-A1CN-10A-01D-A135-09_UCEC	681	297	338	317	605	338	547	622	452	0	0	0	0	0	0	106	590
TCGA-AX-A1CP-10A-01D-A135-09_UCEC	674	0	0	385	693	460	552	651	480	0	0	0	0	0	0	116	583
TCGA-AX-A2H7-10A-01D-A18P-09_UCEC	701	311	337	344	685	367	555	654	0	104	650	534	457	183	0	2	587
TCGA-AX-A2HF-10A-01D-A17D-09_UCEC	645	267	339	333	648	415	528	633	451	0	0	0	0	0	31	42	584
TCGA-AX-A2HG-10A-01D-A17D-09_UCEC	587	326	346	0	0	0	547	616	553	0	0	0	0	0	0	108	583
TCGA-AX-A2HH-10A-01D-A17D-09_UCEC	582	295	325	317	615	346	548	611	0	98	616	518	359	181	0	2	585
TCGA-AX-A2HJ-10A-01D-A17D-09_UCEC	680	0	0	348	656	455	546	623	440	0	0	0	0	0	42	2	577
TCGA-AX-A2HK-10A-01D-A17D-09_UCEC	670	280	310	315	585	434	552	615	530	0	0	0	0	0	29	44	586
TCGA-AX-A2IN-10A-01D-A17W-09_UCEC	687	304	304	312	590	340	545	626	443	0	0	0	0	0	35	38	576
TCGA-AX-A2IO-10A-01D-A17W-09_UCEC	704	0	0	372	661	462	555	646	440	89	600	0	373	177	40	3	583
TCGA-AX-A3FS-10A-01D-A22A-09_UCEC	661	0	0	347	645	354	538	612	427	0	0	0	0	0	0	55	578
TCGA-AX-A3FT-10A-01D-A22A-09_UCEC	695	0	0	367	657	456	548	620	443	0	0	0	0	0	0	90	575
TCGA-AX-A3FV-10A-01D-A22A-09_UCEC	674	290	318	281	592	343	539	591	537	0	0	0	0	0	28	49	579
TCGA-AX-A3FW-10A-01D-A22A-09_UCEC	697	0	0	350	672	456	542	625	533	0	0	0	0	0	0	94	584
TCGA-AX-A3FX-10A-01D-A22A-09_UCEC	688	0	0	347	671	373	542	634	538	0	0	0	0	0	0	103	589
TCGA-AX-A3FZ-10A-01D-A22A-09_UCEC	684	0	0	362	670	440	549	639	553	0	0	0	0	0	34	58	580
TCGA-AX-A3G1-10A-01D-A22A-09_UCEC	663	0	0	326	633	437	543	588	111	90	578	489	320	175	0	10	580
TCGA-AX-A3G3-10A-01D-A20S-09_UCEC	682	295	335	194	526	416	552	629	0	96	614	0	374	176	0	4	581
TCGA-AX-A3G4-10A-01D-A20S-09_UCEC	682	289	311	326	617	432	554	638	537	0	0	0	0	0	29	53	587
TCGA-AX-A3G6-10A-01D-A20S-09_UCEC	696	0	0	356	661	457	548	639	543	0	0	0	0	0	31	49	587
TCGA-AX-A3G7-10A-01D-A20S-09_UCEC	695	0	0	368	667	454	547	649	448	0	0	0	0	0	36	59	587
TCGA-AX-A3G8-10A-01D-A22A-09_UCEC	669	288	304	324	595	328	543	612	374	91	460	0	347	167	0	36	578
TCGA-AX-A3G9-10A-01D-A22A-09_UCEC	593	324	355	0	0	0	524	600	0	0	635	528	354	184	0	1	583
TCGA-AX-A3GB-10A-01D-A22A-09_UCEC	675	294	328	301	657	440	549	628	536	0	576	545	0	0	19	41	582
TCGA-AX-A3GI-10A-01D-A20S-09_UCEC	697	0	0	369	685	475	556	649	561	0	0	0	0	0	57	78	591
TCGA-AY-5543-10A-01D-1650-10_COAD	693	236	141	349	569	342	499	555	433	0	523	0	364	170	15	0	587
TCGA-AY-6197-10A-01D-1719-10_COAD	637	0	0	321	505	407	476	534	336	0	0	0	0	0	12	15	550
TCGA-AZ-4315-10A-01D-1408-10_COAD	681	0	0	378	682	457	548	641	468	0	0	0	0	0	0	78	590
TCGA-AZ-4323-10A-01D-1835-10_COAD	622	0	0	198	538	386	459	530	250	0	280	0	120	45	0	18	513
TCGA-AZ-4616-10A-01D-1835-10_COAD	675	0	0	360	636	273	435	557	313	0	0	0	0	157	0	30	535
TCGA-AZ-4681-10A-01D-1408-10_COAD	650	0	0	350	627	370	505	563	343	0	0	0	0	0	0	38	556
TCGA-AZ-4682-10A-01D-1408-10_COAD	578	0	0	205	441	388	470	501	0	88	510	0	289	144	0	0	553
TCGA-AZ-5403-10A-01D-1650-10_COAD	689	0	0	378	676	373	528	651	463	0	0	0	0	0	16	28	591
TCGA-B0-5399-10A-01D-1501-10_KIRC	797	13	51	420	727	395	554	678	589	0	0	0	0	0	29	95	599

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-B0-5698-10A-01D-1669-08_KIRC	598	262	276	0	0	0	534	655	489	0	0	0	0	0	30	65	574
TCGA-B1-5398-10A-01D-1589-08_KIRP	689	0	0	307	605	381	532	647	476	0	0	0	0	0	0	95	578
TCGA-B1-7332-10A-01D-2136-08_KIRP	680	248	272	190	609	321	532	643	475	0	610	573	0	0	40	3	575
TCGA-B1-A47M-10A-01D-A25F-10_KIRP	652	0	0	359	629	366	538	591	339	0	0	0	0	0	31	0	570
TCGA-B1-A47N-10A-01D-A25F-10_KIRP	679	269	236	341	664	351	531	624	369	0	365	492	0	0	0	103	575
TCGA-B1-A47O-10A-01D-A25F-10_KIRP	685	0	0	370	649	381	527	617	325	91	443	0	365	172	0	46	585
TCGA-B1-A654-10A-01D-A31X-10_KIRP	532	0	226	221	415	292	493	561	336	0	0	0	0	0	25	0	551
TCGA-B1-A655-10A-01D-A31X-10_KIRP	528	263	219	0	316	134	483	585	0	0	358	0	329	167	0	0	531
TCGA-B1-A656-10A-01D-A31X-10_KIRP	545	293	327	0	0	0	529	615	300	0	376	0	284	140	18	1	582
TCGA-B1-A657-10A-01D-A31X-10_KIRP	639	0	0	247	537	423	513	473	326	0	0	0	0	0	0	51	557
TCGA-B2-3923-10A-01D-1458-08_KIRC	601	263	281	0	0	0	534	653	477	0	0	0	0	0	46	0	578
TCGA-B2-3924-10A-01D-1458-08_KIRC	683	253	272	200	617	286	532	661	493	0	618	562	0	0	0	160	579
TCGA-B2-4098-10A-01D-1458-08_KIRC	688	0	0	310	609	298	526	655	482	0	0	0	0	0	0	118	578
TCGA-B2-4099-10A-01D-1458-08_KIRC	689	0	0	307	608	401	533	660	459	75	611	572	0	137	0	85	578
TCGA-B2-5633-10A-01D-1535-10_KIRC	802	0	0	421	728	395	554	676	583	0	0	0	0	0	0	167	599
TCGA-B2-5635-10A-01D-A270-10_KIRC	628	251	260	227	437	290	501	596	353	0	0	0	0	0	30	0	579
TCGA-B2-5636-10A-01D-1535-10_KIRC	697	0	0	398	719	454	559	672	485	107	0	0	0	0	0	101	593
TCGA-B2-5639-10A-01D-1535-10_KIRC	684	0	0	395	713	459	550	659	482	0	0	0	0	0	23	45	586
TCGA-B2-5641-10A-01D-1535-10_KIRC	760	0	0	394	714	387	551	660	473	0	0	0	0	0	16	44	594
TCGA-B2-A4SR-10A-01D-A25V-10_KIRC	688	0	0	395	679	446	548	631	367	0	0	0	0	0	27	61	594
TCGA-B3-3925-10A-01D-1458-08_KIRP	679	0	0	295	599	391	532	648	390	51	602	0	298	137	30	0	578
TCGA-B3-4103-10A-01D-1458-08_KIRP	689	0	0	312	608	292	524	663	484	0	0	0	0	0	0	111	579
TCGA-B3-4104-10A-01D-1458-08_KIRP	762	0	0	306	614	383	531	658	482	0	0	0	0	0	0	143	577
TCGA-B3-8121-10A-01D-2396-08_KIRP	682	0	264	282	607	375	531	639	469	0	597	0	317	0	38	0	574
TCGA-B4-5377-10A-01D-1501-10_KIRC	790	0	0	403	728	393	549	678	589	0	0	0	0	0	39	84	596
TCGA-B4-5378-10A-01D-1501-10_KIRC	683	0	0	397	714	463	554	658	577	0	0	0	0	0	43	0	592
TCGA-B4-5832-10A-01D-1669-08_KIRC	760	0	0	311	611	380	530	645	452	80	598	0	295	135	0	67	579
TCGA-B4-5834-10A-02D-1669-08_KIRC	673	249	265	286	556	378	532	641	487	0	0	0	0	0	0	141	576
TCGA-B4-5835-10A-01D-1669-08_KIRC	687	251	272	292	609	378	530	640	480	0	611	506	0	0	26	66	576
TCGA-B4-5836-10A-01D-1669-08_KIRC	686	258	0	285	615	367	532	653	445	80	589	0	297	134	0	71	577
TCGA-B4-5838-10A-01D-1669-08_KIRC	600	259	276	0	554	137	531	639	484	0	601	568	0	0	0	120	573
TCGA-B4-5843-10A-01D-1669-08_KIRC	680	0	0	310	605	382	531	637	486	0	0	0	0	0	0	108	577
TCGA-B4-5844-10A-01D-1669-08_KIRC	664	250	268	284	612	271	530	646	398	79	623	570	0	137	0	53	576
TCGA-B5-A0JN-10A-01D-A10O-09_UCEC	796	320	357	386	726	466	563	670	579	0	657	0	459	0	0	190	593
TCGA-B5-A0JS-10A-01D-A10O-09_UCEC	684	316	358	364	705	463	557	661	453	104	661	553	381	182	0	77	592
TCGA-B5-A0JT-10A-01D-A122-09_UCEC	701	0	0	408	715	469	563	662	576	0	0	0	0	0	0	217	601
TCGA-B5-A0JU-10A-01D-A14G-09_UCEC	696	307	339	346	681	469	552	641	552	0	580	0	393	0	63	0	587
TCGA-B5-A0JX-10B-01D-A14K-09_UCEC	690	291	346	319	607	371	545	632	452	0	0	0	0	0	0	87	584
TCGA-B5-A0JY-10A-01D-A10O-09_UCEC	699	0	0	393	712	464	557	666	575	0	0	0	0	0	0	175	593
TCGA-B5-A0K2-10A-01D-A10B-09_UCEC	798	330	368	379	698	463	559	660	465	105	656	0	384	185	0	87	598
TCGA-B5-A0K7-10A-02D-A10B-09_UCEC	787	315	352	368	685	457	559	648	471	0	0	0	0	0	0	103	594
TCGA-B5-A0K8-10B-01D-A14K-09_UCEC	657	287	334	352	706	364	535	634	416	106	633	501	357	171	24	1	590
TCGA-B5-A0K9-10A-02D-A10B-09_UCEC	797	0	0	400	718	476	561	660	574	0	0	0	0	0	0	216	593
TCGA-B5-A0KB-10A-01D-A14G-09_UCEC	674	0	0	347	694	438	556	650	532	95	547	0	317	0	49	41	582
TCGA-B5-A11E-10A-01D-A10M-09_UCEC	672	0	0	391	710	452	555	658	480	0	0	0	0	0	26	55	579
TCGA-B5-A11F-10A-01D-A10M-09_UCEC	799	326	371	389	723	387	560	673	464	107	676	594	0	190	0	137	598
TCGA-B5-A11G-10A-01D-A122-09_UCEC	801	0	0	393	719	474	561	671	583	0	0	0	0	0	81	119	599
TCGA-B5-A11H-10B-01D-A122-09_UCEC	702	322	371	387	725	476	563	673	572	105	676	598	0	186	0	116	595
TCGA-B5-A11I-10A-01D-A10M-09_UCEC	804	0	0	397	738	484	565	682	588	0	676	0	471	0	84	0	595
TCGA-B5-A11J-10A-01D-A122-09_UCEC	700	320	369	388	703	391	563	675	579	0	0	0	0	0	58	107	599
TCGA-B5-A11L-10A-01D-A13O-09_UCEC	688	308	343	325	619	429	553	641	414	99	603	0	363	181	37	2	587
TCGA-B5-A11M-10A-01D-A122-09_UCEC	799	325	373	255	703	461	562	677	570	109	660	0	463	186	0	110	599
TCGA-B5-A11N-10A-01D-A122-09_UCEC	703	0	0	398	717	473	560	669	585	0	0	0	0	0	0	259	599
TCGA-B5-A11O-10A-01D-A122-09_UCEC	796	0	0	397	719	392	562	679	584	0	0	0	0	0	63	124	599
TCGA-B5-A11P-10A-01D-A14G-09_UCEC	584	320	349	0	582	165	541	613	444	0	551	512	0	0	44	1	576
TCGA-B5-A11Q-10A-01D-A122-09_UCEC	800	0	0	395	712	475	563	672	581	0	0	0	0	0	63	109	594
TCGA-B5-A11R-10A-01D-A122-09_UCEC	798	0	0	389	714	475	559	671	582	0	0	0	0	0	0	189	600
TCGA-B5-A11S-10A-01D-A122-09_UCEC	800	337	374	380	722	389	561	679	582	0	663	589	0	0	69	132	599
TCGA-B5-A11U-10A-01D-A122-09_UCEC	700	0	0	391	685	480	562	669	579	0	0	0	0	0	0	234	596
TCGA-B5-A11V-10A-01D-A10M-09_UCEC	795	0	0	397	728	474	564	678	577	105	664	0	464	186	60	0	596
TCGA-B5-A11W-10A-01D-A122-09_UCEC	801	0	0	397	719	481	560	679	580	0	0	0	0	0	54	112	597
TCGA-B5-A11X-10A-01D-A10M-09_UCEC	703	319	366	236	718	385	560	666	582	0	660	588	0	0	64	115	594
TCGA-B5-A11Y-10A-01D-A10M-09_UCEC	800	335	375	392	732	393	563	675	588	0	671	591	0	0	0	325	601
TCGA-B5-A11Z-10A-01D-A10M-09_UCEC	800	329	0	385	707	470	566	677	479	108	666	593	0	190	70	0	597
TCGA-B5-A121-10A-01D-A122-09_UCEC	801	0	0	398	720	482	564	679	585	0	0	0	0	0	56	139	598
TCGA-B5-A1MR-10A-01D-A14G-09_UCEC	570	312	349	0	576	163	545	599	517	0	459	507	0	0	33	35	587
TCGA-B5-A1MS-10A-01D-A22A-09_UCEC	700	0	0	369	682	375	544	629	565	0	0	0	0	0	35	57	592
TCGA-B5-A1MU-10A-01D-A13O-09_UCEC	683	0	0	370	690	377	542	644	461	0	0	0	0	0	37	50	585
TCGA-B5-A1MV-10A-01D-A14G-09_UCEC	692	313	337	310	676	361	548	622	545	0	556	523	0	0	0	102	585
TCGA-B5-A1MW-10A-01D-A17D-09_UCEC	687	0	0	364	662	451	551	634	346	91	595	0	358	178	0	52	589
TCGA-B5-A1MX-10A-01D-A142-09_UCEC	688	0	0	369	662	453	546	638	551	0	0	0	0	0	37	59	589
TCGA-B5-A1MY-10A-01D-A142-09_UCEC	680	251	307	104	665	177	545	652	0	104	669	557	434	168	0	0	578
TCGA-B5-A1MZ-10A-01D-A142-09_UCEC	663	266	286	160	637	331	532	590	300	92	562	512	326	151	0	33	579
TCGA-B5-A1N2-10A-01D-A142-09_UCEC	643	279	162	315	611	414	521	599	403	0	561	0	358	170	19	0	576
TCGA-B5-A3F9-10A-01D-A22A-09_UCEC	696	0	0	375	678	457	552	637	548	0	0	0	0	0	0	115	585
TCGA-B5-A3FA-10A-01D-A19Y-09_UCEC	696	0	0	366	674	447	549	638	429	95	555	535	0	183	0	31	590
TCGA-B5-A3FB-10A-01D-A19Y-09_UCEC	694	0	343	105	678	183	548	622	545	0	630	525	463	0	50	1	588
TCGA-B5-A3FC-10A-01D-A22A-09_UCEC	699	0	0	226	706	473	557	647	570	0	0	0	0	0	68	73	596
TCGA-B5-A3FD-10A-01D-A19Y-09_UCEC	664	300	155	320	641	427	543	568	301	0	569	0	364	177	38	0	585
TCGA-B5-A3FH-10A-01D-A19Y-09_UCEC	683	304	348	340	577	436	555	627	450	0	0	0	0	0	0	91	589
TCGA-B5-A3S1-10A-01D-A22A-09_UCEC	556	257	275	212	449	406	550	600	425	0	0	0	0	0	26	32	567
TCGA-B5-A5OC-10A-01D-A27P-09_UCEC	692	297	323	95	607	362	552	606	407	0	578	0	354	0	0	61	554
TCGA-B5-A5OD-10A-01D-A31U-09_UCEC	661	0	0	359	637	454	544	608	538	0	0	0	0	0	48	0	583
TCGA-B5-A5OE-10A-01D-A31U-09_UCEC	661	0	0	342	674	449	552	640	549	0	0	0	0	0	0	99	588
TCGA-B6-A0I1-10A-01D-A21Q-09_BRCA	639	274	293	87	654	340	545	606	186	89	606	0	439	162	0	1	560
TCGA-B6-A0IH-10A-01D-A110-09_BRCA	794	0	0	399	715	479	557	666	582	0	0	0	0	0	0	148	595
TCGA-B6-A0RH-10A-01D-A110-09_BRCA	703	325	369	384	725	416	560	671	587	0	647	549	0	0	39	95	596
TCGA-B6-A0RL-10A-01D-A099-09_BRCA	698	320	367	125	695	181	560	663	465	103	659	0	486	185	36	1	595
TCGA-B6-A0RM-10A-01D-A099-09_BRCA	794	321	359	369	716	382	556	660	573	0	632	548	0	0	0	163	595
TCGA-B6-A0RN-10A-01D-A099-09_BRCA	698	322	0	379	687	461	558	669	579	0	0	0	0	0	47	75	592
TCGA-B6-A0RO-10A-01D-A099-09_BRCA	692	0	0	387	695	450	549	643	434	101	628	536	0	175	0	42	583
TCGA-B6-A0RP-10A-01D-A099-09_BRCA	686	0	0	375	713	381	554	639	474	0	0	0	0	0	0	70	583
TCGA-B6-A0RQ-10A-01D-A110-09_BRCA	701	0	0	402	716	466	559	669	470	105	658	0	465	182	0	101	596
TCGA-B6-A0RT-10A-01D-A099-09_BRCA	795	0	0	394	722	466	558	666	470	105	652	0	386	185	42	0	598
TCGA-B6-A0RU-10A-01D-A099-09_BRCA	696	0	0	374	710	384	555	657	451	103	618	545	0	181	0	74	587
TCGA-B6-A0RV-10A-01D-A099-09_BRCA	795	0	0	390	713	470	561	667	576	0	0	0	0	0	48	93	596

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-B6-A0WS-10A-01D-A110-09_BRCA	788	0	0	387	714	464	559	652	480	0	0	0	0	0	33	48	592
TCGA-B6-A0WT-10A-01D-A10G-09_BRCA	658	0	0	380	693	441	556	634	472	0	0	0	0	0	0	76	589
TCGA-B6-A0WV-10A-01D-A10G-09_BRCA	796	325	363	385	693	477	561	671	461	104	654	0	382	186	0	116	598
TCGA-B6-A0WW-10A-01D-A10G-09_BRCA	799	0	0	398	725	478	562	679	587	0	0	0	0	0	72	135	597
TCGA-B6-A0WX-10A-01D-A10G-09_BRCA	791	320	369	375	718	465	561	665	582	0	642	0	480	0	0	153	595
TCGA-B6-A0WY-10A-01D-A10G-09_BRCA	625	265	319	343	618	338	537	621	455	0	0	0	0	0	19	2	568
TCGA-B6-A0WZ-10A-01D-A10G-09_BRCA	657	0	0	386	698	460	557	660	476	0	0	0	0	0	45	0	578
TCGA-B6-A0X0-10A-01D-A110-09_BRCA	702	310	368	378	699	464	555	652	0	105	667	0	464	187	0	0	596
TCGA-B6-A0X1-10A-01D-A117-09_BRCA	567	312	362	0	697	186	557	648	472	0	638	586	0	0	0	103	584
TCGA-B6-A0X4-10A-01D-A10G-09_BRCA	605	0	0	365	653	365	520	632	460	0	0	0	0	0	13	29	557
TCGA-B6-A0X5-10A-01D-A10G-09_BRCA	550	310	353	0	628	164	542	635	433	103	647	513	335	168	0	0	576
TCGA-B6-A0X7-10A-01D-A10M-09_BRCA	790	334	374	0	714	188	560	677	576	103	678	593	460	186	0	115	598
TCGA-B6-A1KN-10A-01D-A188-09_BRCA	663	259	316	332	640	348	535	641	454	0	0	0	0	0	16	43	579
TCGA-B6-A2IU-10A-01D-A18P-09_BRCA	679	270	336	351	655	360	550	650	459	0	0	0	0	0	21	48	589
TCGA-B6-A3ZX-10A-01D-A23C-09_BRCA	684	0	0	351	648	443	547	642	541	0	0	0	0	0	30	35	584
TCGA-B6-A400-10A-01D-A23C-09_BRCA	689	0	0	355	677	455	554	637	538	0	0	0	0	0	53	5	581
TCGA-B6-A401-10A-01D-A23C-09_BRCA	697	301	309	360	681	449	548	634	424	96	611	516	438	175	34	1	590
TCGA-B6-A402-10A-01D-A23C-09_BRCA	659	296	342	334	667	453	553	631	463	0	542	519	0	0	27	39	591
TCGA-B6-A408-10A-01D-A243-09_BRCA	684	304	317	342	606	420	551	628	425	0	0	0	0	0	0	33	558
TCGA-B6-A409-10A-01D-A243-09_BRCA	687	0	0	199	623	439	551	614	457	0	538	0	367	0	37	5	583
TCGA-B6-A40B-10A-01D-A23C-09_BRCA	693	0	0	361	674	468	548	617	543	0	0	0	0	0	0	102	585
TCGA-B6-A40C-10A-01D-A23C-09_BRCA	573	283	304	132	576	336	549	622	519	0	0	0	0	0	0	64	569
TCGA-B7-5816-10A-01D-1600-08_STAD	753	254	267	299	594	285	531	648	476	0	0	0	0	0	0	116	578
TCGA-B7-5818-10A-01D-1600-08_STAD	675	247	267	290	620	285	531	655	486	0	621	562	0	0	0	103	578
TCGA-B7-A5TI-10A-01D-A31J-08_STAD	598	249	269	0	547	134	530	640	383	70	621	569	0	128	25	0	575
TCGA-B7-A5TJ-10A-01D-A31J-08_STAD	600	251	272	0	576	136	531	646	377	78	631	561	303	135	0	56	573
TCGA-B7-A5TK-10A-01D-A31J-08_STAD	682	0	0	302	574	378	526	625	458	0	0	0	0	0	0	69	575
TCGA-B7-A5TN-10A-01D-A31J-08_STAD	669	247	264	278	608	279	527	634	467	0	602	508	0	0	0	73	573
TCGA-B8-4146-10A-01D-1669-08_KIRC	687	253	270	289	621	394	531	644	484	0	609	570	0	0	0	99	579
TCGA-B8-4148-10A-01D-1251-10_KIRC	698	0	0	384	704	457	555	663	444	104	638	0	449	173	0	63	596
TCGA-B8-4151-10A-01D-1251-10_KIRC	787	295	359	379	678	424	548	654	487	0	0	0	0	0	24	61	588
TCGA-B8-4619-10A-01D-1251-10_KIRC	798	283	361	395	692	442	559	669	566	0	0	0	0	0	0	125	589
TCGA-B8-4620-10A-01D-1251-10_KIRC	673	0	0	392	702	461	558	666	584	0	0	0	0	0	23	69	595
TCGA-B8-4621-10A-01D-1501-10_KIRC	696	40	0	400	717	472	559	670	492	0	1	0	0	0	23	89	596
TCGA-B8-5158-10A-01D-1421-08_KIRC	690	0	0	310	623	388	535	669	485	0	0	0	0	0	0	164	580
TCGA-B8-5159-10A-01D-1421-08_KIRC	684	246	267	296	606	384	533	665	466	77	632	566	0	137	0	85	580
TCGA-B8-5162-10A-01D-1421-08_KIRC	756	250	263	289	597	371	531	649	367	73	611	0	294	135	0	70	579
TCGA-B8-5163-10A-01D-1421-08_KIRC	670	263	276	0	0	0	535	658	483	0	0	0	0	0	0	106	578
TCGA-B8-5164-10A-01D-1421-08_KIRC	763	254	269	298	542	389	537	662	469	77	610	0	370	139	0	79	579
TCGA-B8-5165-10A-01D-1421-08_KIRC	741	0	0	308	609	387	532	656	479	0	0	0	0	0	0	101	581
TCGA-B8-5545-10A-01D-1669-08_KIRC	684	0	0	308	611	389	535	648	488	0	0	0	0	0	33	72	577
TCGA-B8-5546-10A-01D-1535-10_KIRC	782	299	348	392	709	451	556	661	583	0	648	557	0	0	0	108	591
TCGA-B8-5549-10A-01D-1535-10_KIRC	751	0	0	384	710	381	537	646	450	110	597	0	374	173	0	47	578
TCGA-B8-5550-10A-01D-1535-10_KIRC	700	0	0	417	710	465	560	666	486	0	0	0	0	0	0	127	595
TCGA-B8-5551-10A-01D-1535-10_KIRC	792	0	0	400	716	468	563	666	482	0	0	0	0	0	35	0	595
TCGA-B8-5552-10A-01D-1669-08_KIRC	683	0	0	306	609	389	532	652	396	71	598	0	372	138	32	0	581
TCGA-B8-5553-10A-01D-1535-10_KIRC	794	0	0	420	719	395	559	670	586	0	0	0	0	0	51	0	597
TCGA-B8-A54D-10A-01D-A25V-10_KIRC	770	286	303	266	528	438	540	625	365	0	0	0	0	0	43	0	577
TCGA-B8-A54E-10A-01D-A25V-10_KIRC	679	261	284	254	541	186	541	594	362	0	426	488	0	0	22	48	571
TCGA-B8-A54F-10A-01D-A25V-10_KIRC	683	243	283	244	446	368	543	600	352	0	0	0	0	0	0	87	565
TCGA-B8-A54G-10A-01D-A25V-10_KIRC	664	0	280	246	461	431	528	605	357	0	0	0	0	0	31	57	585
TCGA-B9-4114-10A-01D-1252-08_KIRP	758	0	0	308	617	393	535	665	491	0	0	0	0	0	0	134	582
TCGA-B9-4115-10A-01D-1252-08_KIRP	693	32	82	309	616	394	536	650	486	0	81	0	97	10	51	2	577
TCGA-B9-4116-10A-01D-1252-08_KIRP	686	245	271	299	618	390	534	664	485	0	602	0	391	0	43	97	579
TCGA-B9-4117-10A-01D-1252-08_KIRP	678	239	254	271	606	374	520	606	372	0	631	0	393	136	30	0	576
TCGA-B9-4617-10A-01D-1252-08_KIRP	663	0	0	308	618	394	535	658	478	0	0	0	0	0	36	77	580
TCGA-B9-5155-10A-01D-1589-08_KIRP	705	251	263	288	592	279	513	616	376	0	610	0	296	137	0	69	577
TCGA-B9-5156-10A-01D-1589-08_KIRP	668	253	280	0	560	135	530	654	477	0	596	515	0	0	43	2	576
TCGA-B9-7268-10A-01D-2136-08_KIRP	686	245	255	283	600	362	529	655	476	70	606	508	0	0	29	61	575
TCGA-B9-A44B-10A-01D-A25F-10_KIRP	686	0	0	360	675	457	542	625	360	0	0	0	0	0	28	57	586
TCGA-B9-A5W7-10A-01D-A31X-10_KIRP	660	0	230	235	519	356	525	623	298	0	461	0	363	161	13	0	582
TCGA-B9-A5W8-10A-01D-A28G-10_KIRP	576	312	345	0	572	187	549	634	328	0	605	550	0	0	35	60	575
TCGA-B9-A5W9-10A-01D-A28G-10_KIRP	763	0	0	358	576	452	553	608	352	0	0	0	0	0	17	61	577
TCGA-B9-A69E-10A-01D-A31X-10_KIRP	654	165	236	246	512	412	510	599	307	0	437	399	301	157	0	38	569
TCGA-BA-4074-10A-01D-1434-08_HNSC	686	245	270	298	565	377	535	663	483	0	0	0	0	0	35	82	577
TCGA-BA-4075-10A-01D-1434-08_HNSC	688	0	0	309	604	385	531	640	484	0	0	0	0	0	50	1	579
TCGA-BA-4076-10A-01D-1434-08_HNSC	598	261	270	0	584	137	531	659	473	76	646	579	0	138	0	82	576
TCGA-BA-4077-10A-01D-1434-08_HNSC	683	251	262	291	611	286	533	650	475	0	591	567	0	0	43	1	576
TCGA-BA-4078-10A-01D-1434-08_HNSC	685	0	0	300	605	390	533	647	486	0	0	0	0	0	0	134	580
TCGA-BA-5149-10A-01D-1512-08_HNSC	752	254	273	295	591	383	534	665	484	0	0	0	0	0	36	83	575
TCGA-BA-5151-10A-01D-1434-08_HNSC	687	0	0	307	612	387	533	660	464	75	604	0	374	137	0	77	580
TCGA-BA-5152-10A-01D-1870-08_HNSC	751	254	267	285	588	382	537	656	456	81	608	0	370	135	0	72	576
TCGA-BA-5153-10A-01D-1434-08_HNSC	684	254	269	200	584	283	532	650	477	0	0	0	0	0	0	97	576
TCGA-BA-5555-10A-01D-1512-08_HNSC	753	253	266	288	612	385	530	649	475	0	597	513	0	0	46	2	577
TCGA-BA-5556-10A-01D-1512-08_HNSC	689	0	0	308	603	386	533	648	478	0	0	0	0	0	0	138	575
TCGA-BA-5557-10A-01D-1512-08_HNSC	684	0	0	305	596	396	534	659	480	0	0	0	0	0	33	66	577
TCGA-BA-5558-10A-01D-1512-08_HNSC	682	0	0	301	608	376	531	655	472	0	0	0	0	0	0	126	579
TCGA-BA-5559-10A-01D-1512-08_HNSC	687	0	0	302	600	288	522	652	447	73	533	0	295	136	0	66	573
TCGA-BA-6868-10A-01D-1912-08_HNSC	675	245	255	280	586	388	530	637	384	72	633	508	361	132	30	2	575
TCGA-BA-6869-10A-01D-1870-08_HNSC	759	253	266	293	584	383	533	654	483	0	0	0	0	0	38	69	575
TCGA-BA-6870-10A-01D-1870-08_HNSC	760	0	0	307	603	393	536	647	467	0	0	0	0	0	38	0	572
TCGA-BA-6871-10A-01D-1870-08_HNSC	683	0	0	308	609	393	533	647	484	0	0	0	0	0	0	96	579
TCGA-BA-6872-10A-01D-1870-08_HNSC	687	0	0	306	614	291	528	649	472	0	0	0	0	0	0	94	577
TCGA-BA-6873-10A-01D-1870-08_HNSC	760	0	0	314	617	399	529	644	402	79	605	0	294	137	0	65	576
TCGA-BA-7269-10A-01D-2013-08_HNSC	685	0	0	305	605	382	533	650	461	81	610	0	371	136	0	62	577
TCGA-BA-A4IF-10A-01D-A25Y-08_HNSC	755	247	261	284	605	379	534	639	479	0	584	512	0	0	0	129	581
TCGA-BA-A4IG-10A-01D-A25Y-08_HNSC	680	0	0	289	606	377	529	617	471	0	0	0	0	0	0	106	573
TCGA-BA-A4IH-10A-01D-A25Y-08_HNSC	684	0	0	296	575	281	523	637	459	0	0	0	0	0	0	110	579
TCGA-BA-A4II-10A-01D-A25Y-08_HNSC	658	241	260	281	602	275	527	639	466	0	578	503	0	0	27	65	576
TCGA-BA-A6D8-10A-01D-A31J-08_HNSC	685	0	0	299	601	386	531	633	460	0	0	0	0	0	37	0	575
TCGA-BA-A6DA-10A-01D-A31J-08_HNSC	672	0	0	298	597	377	522	618	470	0	0	0	0	0	0	120	573
TCGA-BA-A6DB-10A-01D-A30H-08_HNSC	755	255	271	292	595	381	535	651	482	0	622	570	0	0	0	136	579
TCGA-BA-A6DD-10A-01D-A31J-08_HNSC	679	231	259	273	548	360	530	625	465	0	0	0	0	0	22	51	572
TCGA-BA-A6DE-10A-01D-A31J-08_HNSC	680	0	0	291	590	282	520	641	376	63	588	0	294	135	0	57	569
TCGA-BA-A6DF-10A-01D-A30H-08_HNSC	689	0	0	306	614	389	531	643	0	85	630	0	386	142	0	0	577
TCGA-BA-A6DG-10A-01D-A30H-08_HNSC	680	250	267	296	596	377	536	649	454	73	614	0	369	137	0	79	579

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BA-A6DI-10A-01D-A30H-08_HNSC	678	249	260	279	574	380	531	641	455	80	599	0	368	138	0	66	576
TCGA-BA-A6DJ-10A-01D-A30H-08_HNSC	596	264	275	0	515	138	529	610	386	0	646	567	376	141	0	60	576
TCGA-BA-A6DL-10A-01D-A30H-08_HNSC	676	0	0	299	609	288	521	643	473	0	0	0	0	0	0	87	573
TCGA-BB-4217-10A-01D-2078-08_HNSC	680	0	0	297	595	361	530	629	461	0	0	0	0	0	31	0	571
TCGA-BB-4223-10A-01D-1434-08_HNSC	679	255	267	297	599	283	533	664	479	74	0	0	0	0	0	97	578
TCGA-BB-4224-10A-01D-1434-08_HNSC	683	0	0	306	603	400	532	654	466	83	613	0	372	141	0	80	573
TCGA-BB-4225-10A-01D-1434-08_HNSC	686	0	0	304	594	377	527	649	377	77	590	0	294	133	31	1	573
TCGA-BB-4227-10A-01D-1870-08_HNSC	762	254	263	284	584	384	534	643	490	0	0	0	0	0	33	74	574
TCGA-BB-4228-10A-01D-1434-08_HNSC	683	256	269	295	563	375	536	663	473	78	0	0	0	0	41	76	576
TCGA-BB-7861-10A-01D-2229-08_HNSC	684	0	0	308	606	388	530	638	406	0	0	0	0	0	0	78	577
TCGA-BB-7862-10A-01D-2229-08_HNSC	743	234	245	283	597	281	527	632	471	0	586	566	0	0	0	89	574
TCGA-BB-7863-10A-01D-2229-08_HNSC	599	259	275	0	596	141	531	642	383	83	643	575	298	138	30	0	574
TCGA-BB-7864-10A-01D-2229-08_HNSC	682	0	0	305	601	384	536	624	304	78	565	0	364	135	0	59	576
TCGA-BB-7866-10A-01D-2229-08_HNSC	681	0	0	306	605	380	533	645	480	0	0	0	0	0	36	57	577
TCGA-BB-7870-10A-01D-2229-08_HNSC	683	0	0	298	604	375	533	647	475	0	0	0	0	0	29	56	577
TCGA-BB-7871-10A-01D-2229-08_HNSC	661	241	256	274	515	278	528	645	476	0	0	0	0	0	26	61	578
TCGA-BB-7872-10A-01D-2229-08_HNSC	663	229	259	267	508	359	511	580	364	0	564	0	292	136	0	53	577
TCGA-BB-8596-10A-01D-2394-08_HNSC	670	243	0	280	548	369	525	606	374	0	533	0	358	128	0	60	571
TCGA-BB-8601-10A-01D-2394-08_HNSC	671	234	257	273	604	370	525	639	470	0	586	559	0	0	28	56	572
TCGA-BC-4073-10A-01D-A12Z-10_LIHC	647	163	149	241	531	300	530	581	331	0	312	337	0	0	8	0	542
TCGA-BC-A217-10A-01D-A152-10_LIHC	571	293	338	0	0	0	549	625	336	101	572	0	327	158	0	42	588
TCGA-BC-A3KF-10A-01D-A20W-10_LIHC	635	154	282	220	426	331	509	556	308	0	345	0	303	149	0	35	565
TCGA-BC-A3KG-10A-01D-A20W-10_LIHC	790	0	0	404	699	442	557	639	365	0	0	0	0	0	0	71	587
TCGA-BC-A5W4-10A-01D-A28X-10_LIHC	695	0	0	370	666	460	543	629	359	0	0	0	0	0	0	109	577
TCGA-BC-A69H-10A-01D-A30V-10_LIHC	534	274	315	0	0	0	516	613	312	0	349	0	304	157	14	0	545
TCGA-BC-A69I-10A-01D-A30V-10_LIHC	612	0	0	265	500	420	504	489	345	0	0	0	0	0	11	34	541
TCGA-BF-A1PU-10A-01D-A19A-08_SKCM	665	235	260	277	510	274	528	645	439	55	563	0	354	135	0	50	576
TCGA-BF-A1PV-10A-01D-A19A-08_SKCM	639	0	0	266	499	342	516	625	299	0	427	0	227	115	14	1	568
TCGA-BF-A1PX-10A-01D-A19A-08_SKCM	674	0	0	298	540	369	535	640	287	57	517	0	278	132	0	47	575
TCGA-BF-A1PZ-10A-01D-A19A-08_SKCM	593	257	265	0	479	117	530	643	459	0	503	472	0	0	15	44	577
TCGA-BF-A1Q0-10A-01D-A19A-08_SKCM	684	0	0	300	609	398	531	647	481	0	0	0	0	0	0	132	577
TCGA-BF-A3DJ-10A-02D-A20D-08_SKCM	669	250	239	277	603	371	535	642	470	0	596	551	0	0	27	58	575
TCGA-BF-A3DL-10A-02D-A20D-08_SKCM	642	245	253	280	573	280	535	651	468	0	0	0	0	0	28	62	573
TCGA-BF-A3DM-10A-02D-A20D-08_SKCM	679	0	0	289	593	374	527	646	464	0	0	0	0	0	0	87	575
TCGA-BF-A3DN-10A-01D-A20D-08_SKCM	661	237	258	279	602	281	527	637	477	0	593	516	0	0	0	122	579
TCGA-BF-A5EO-10A-01D-A27N-08_SKCM	685	0	0	296	605	381	530	634	380	59	591	0	361	136	0	53	573
TCGA-BF-A5EP-10A-01D-A27N-08_SKCM	682	0	0	302	596	386	536	642	464	0	0	0	0	0	0	73	579
TCGA-BF-A5EQ-10A-01D-A27N-08_SKCM	681	0	0	299	598	362	527	636	394	0	0	0	0	0	0	70	573
TCGA-BF-A5ER-10A-01D-A27N-08_SKCM	591	253	264	0	574	136	529	628	394	0	564	509	0	0	0	74	570
TCGA-BF-A5ES-10A-01D-A27N-08_SKCM	674	0	0	291	593	287	519	633	472	0	0	0	0	0	0	101	570
TCGA-BG-A0M0-10A-01D-A10B-09_UCEC	798	318	360	373	711	465	558	670	0	106	668	591	455	191	0	0	590
TCGA-BG-A0M3-10A-01D-A127-09_UCEC	652	0	0	383	690	360	523	613	430	0	0	0	0	161	0	40	537
TCGA-BG-A0M8-10A-01D-A10O-09_UCEC	787	0	0	391	712	467	556	668	578	0	0	0	0	0	46	87	594
TCGA-BG-A0M9-10A-01D-A10B-09_UCEC	678	309	355	380	702	456	556	648	367	0	624	542	0	0	0	115	595
TCGA-BG-A0MG-10A-01D-A10B-09_UCEC	685	300	349	358	670	362	550	645	470	0	0	0	0	0	30	61	592
TCGA-BG-A0MK-10A-01D-A19Y-09_UCEC	695	0	0	338	649	444	551	630	514	0	0	0	0	0	31	0	578
TCGA-BG-A0MQ-10A-02D-A10B-09_UCEC	700	0	0	383	715	461	554	662	462	102	642	0	460	184	0	76	594
TCGA-BG-A0MU-10A-02D-A10B-09_UCEC	778	0	0	390	705	473	558	666	482	0	0	0	0	0	0	117	595
TCGA-BG-A0RY-10A-02D-A10B-09_UCEC	586	325	367	0	0	0	555	664	571	0	0	0	0	0	47	74	587
TCGA-BG-A0VV-10A-01D-A122-09_UCEC	801	325	374	391	727	477	563	681	585	0	673	594	0	0	64	146	598
TCGA-BG-A0VW-10A-01D-A122-09_UCEC	795	326	370	389	723	471	560	674	573	0	660	588	0	0	0	150	598
TCGA-BG-A0VX-10A-01D-A122-09_UCEC	795	0	0	397	717	466	559	664	577	0	0	0	0	0	84	0	597
TCGA-BG-A0VZ-10A-02D-A117-09_UCEC	754	301	335	374	712	446	558	673	468	105	644	573	0	0	0	112	587
TCGA-BG-A0W1-10A-01D-A117-09_UCEC	703	335	374	387	711	472	561	678	577	110	671	0	469	189	0	152	598
TCGA-BG-A0YU-10A-01D-A10M-09_UCEC	792	0	0	395	709	465	556	664	0	106	665	587	455	187	0	0	593
TCGA-BG-A0YV-10A-01D-A10M-09_UCEC	796	314	366	384	703	467	556	648	469	0	651	0	462	181	0	105	595
TCGA-BG-A186-10A-01D-A12J-09_UCEC	792	321	380	0	0	0	557	668	581	0	0	0	0	0	87	1	598
TCGA-BG-A187-10A-01D-A12J-09_UCEC	701	0	0	411	727	475	558	671	564	109	669	548	460	181	44	0	597
TCGA-BG-A18A-10A-01D-A12J-09_UCEC	790	0	0	397	719	394	554	674	480	108	644	553	0	185	0	106	596
TCGA-BG-A18B-10A-01D-A12J-09_UCEC	799	0	0	388	719	390	561	668	477	105	655	0	456	184	0	120	597
TCGA-BG-A18C-10A-01D-A12J-09_UCEC	702	320	370	385	704	467	562	680	583	0	0	0	0	0	98	0	600
TCGA-BG-A220-10A-01D-A159-09_UCEC	693	0	0	361	641	464	550	635	533	0	0	0	0	0	27	41	582
TCGA-BG-A221-10A-01D-A159-09_UCEC	689	300	334	326	586	436	552	609	322	86	583	0	360	177	28	0	589
TCGA-BG-A222-10A-01D-A159-09_UCEC	680	0	0	373	665	443	551	605	522	0	0	0	0	0	0	108	582
TCGA-BG-A2AE-10A-01D-A16D-09_UCEC	698	302	355	375	691	450	560	659	462	107	631	0	382	182	0	79	592
TCGA-BG-A2L7-10A-01D-A18P-09_UCEC	591	324	349	0	658	179	554	623	547	0	615	581	0	0	51	1	589
TCGA-BG-A3PP-10A-01D-A22A-09_UCEC	691	306	347	318	681	451	552	605	451	0	536	507	0	0	0	98	583
TCGA-BH-A0AV-10A-01D-A110-09_BRCA	688	324	382	0	701	188	565	674	487	0	653	0	483	0	48	89	592
TCGA-BH-A0B0-10A-01D-A110-09_BRCA	701	319	367	386	704	383	544	646	474	0	650	0	382	185	0	105	592
TCGA-BH-A0B6-10A-01D-A19Y-09_BRCA	661	283	321	319	574	407	547	604	312	0	434	0	343	161	0	34	584
TCGA-BH-A0B7-10A-01D-A110-09_BRCA	800	0	0	418	721	472	563	668	581	0	0	0	0	0	0	244	598
TCGA-BH-A0BC-10A-01D-A099-09_BRCA	794	322	356	377	695	470	559	671	579	0	0	0	0	0	57	90	597
TCGA-BH-A0BG-10A-01D-A110-09_BRCA	687	67	5	272	358	443	541	654	452	0	0	0	0	0	0	53	581
TCGA-BH-A0BL-10A-01D-A110-09_BRCA	703	320	369	383	704	384	560	673	477	104	654	0	461	189	0	121	597
TCGA-BH-A0BO-10A-01D-A12B-09_BRCA	804	333	375	411	727	391	562	682	589	0	673	591	0	0	82	142	599
TCGA-BH-A0BP-10A-01D-A110-09_BRCA	795	327	373	387	729	390	559	679	583	0	661	589	0	0	70	165	600
TCGA-BH-A0BQ-10A-01D-A110-09_BRCA	697	319	371	375	687	461	557	669	360	104	660	0	459	179	0	90	594
TCGA-BH-A0BR-10A-01D-A110-09_BRCA	793	0	0	384	702	467	559	656	573	0	0	0	0	0	0	125	593
TCGA-BH-A0BW-10A-01D-A110-09_BRCA	704	0	0	400	727	480	565	675	583	0	0	111	0	0	46	82	600
TCGA-BH-A0C1-10A-01D-A12B-09_BRCA	799	329	374	393	707	384	561	675	573	106	664	0	467	186	0	123	591
TCGA-BH-A0C7-10A-01D-A110-09_BRCA	681	318	362	381	720	386	560	671	475	105	669	577	0	184	52	0	598
TCGA-BH-A0DE-10A-02D-A110-09_BRCA	679	0	0	386	703	444	558	641	462	0	0	0	0	0	0	81	588
TCGA-BH-A0DH-10A-01D-A099-09_BRCA	789	313	359	367	684	369	556	670	563	0	0	0	0	0	48	79	588
TCGA-BH-A0DL-10A-01D-A110-09_BRCA	801	326	374	387	706	390	562	676	484	105	665	0	463	187	62	0	598
TCGA-BH-A0DQ-10A-01D-A099-09_BRCA	692	307	356	365	673	455	556	630	467	0	0	0	0	0	0	112	592
TCGA-BH-A0DX-10A-02D-A110-09_BRCA	802	330	373	389	726	477	562	670	589	0	663	590	0	0	0	238	597
TCGA-BH-A0E9-10A-01D-A110-09_BRCA	694	0	0	384	703	462	557	655	561	0	0	0	0	0	0	117	590
TCGA-BH-A0EA-10A-01D-A110-09_BRCA	801	330	371	392	730	477	564	678	587	0	666	586	0	0	107	6	598
TCGA-BH-A0EI-10A-01D-A110-09_BRCA	784	0	0	388	710	387	548	671	575	0	0	0	0	0	47	91	597
TCGA-BH-A0H5-10A-01D-A110-09_BRCA	690	144	202	387	711	462	556	656	481	0	0	0	0	0	0	114	595
TCGA-BH-A0HI-10A-01D-A099-09_BRCA	699	324	364	378	720	389	558	666	471	107	667	540	460	183	0	92	596
TCGA-BH-A0HN-10A-01D-A099-09_BRCA	698	0	0	387	711	462	556	664	461	102	648	0	453	179	47	0	595
TCGA-BH-A0HP-10A-01D-A099-09_BRCA	691	0	0	385	707	464	559	662	574	0	0	0	0	0	0	143	593
TCGA-BH-A0RX-10A-01D-A099-09_BRCA	777	312	352	372	672	368	550	648	529	102	617	0	377	177	0	58	590
TCGA-BH-A0W4-10A-01D-A10G-09_BRCA	671	288	337	357	698	355	551	650	441	107	633	525	432	172	0	37	587
TCGA-BH-A0W5-10A-01D-A117-09_BRCA	687	0	0	385	698	466	558	654	455	99	636	0	378	181	0	76	589

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BH-A0W7-10A-01D-A110-09_BRCA	689	309	364	382	725	387	561	670	576	0	642	537	0	0	36	87	594
TCGA-BH-A0WA-10A-01D-A117-09_BRCA	700	322	363	379	689	459	561	665	469	103	642	0	454	188	0	102	593
TCGA-BH-A18G-10A-01D-A12B-09_BRCA	800	338	385	0	728	194	564	683	569	107	685	598	0	188	0	134	600
TCGA-BH-A18H-10A-01D-A12B-09_BRCA	794	325	359	379	715	473	559	671	578	0	655	592	0	0	59	100	597
TCGA-BH-A18I-10A-01D-A12B-09_BRCA	795	0	0	391	714	463	560	664	363	104	655	560	0	183	0	90	596
TCGA-BH-A201-10A-01D-A14K-09_BRCA	796	322	377	390	715	467	562	673	481	111	675	0	467	186	0	109	598
TCGA-BH-A202-10A-01D-A14K-09_BRCA	693	0	0	394	716	469	555	652	574	0	0	0	0	0	0	180	595
TCGA-BH-A28O-10A-01D-A22A-09_BRCA	694	0	0	363	682	449	553	653	464	87	532	534	0	0	0	87	591
TCGA-BH-A28Q-10A-01D-A16D-09_BRCA	693	0	0	379	699	380	537	645	360	0	0	0	0	0	0	87	591
TCGA-BH-A2L8-10A-01D-A18P-09_BRCA	688	0	0	377	693	456	553	640	465	0	0	0	0	0	0	96	584
TCGA-BH-A42T-10A-01D-A243-09_BRCA	637	272	263	179	634	329	544	619	432	0	403	499	0	0	35	1	571
TCGA-BH-A42U-10A-01D-A243-09_BRCA	691	0	0	359	663	450	552	629	543	0	0	0	0	0	41	42	590
TCGA-BH-A42V-10A-01D-A243-09_BRCA	673	0	0	339	632	439	545	602	435	0	0	0	0	0	18	33	574
TCGA-BH-A5IZ-10A-01D-A27P-09_BRCA	675	303	304	206	672	171	542	623	449	0	527	528	0	0	21	44	583
TCGA-BH-A5J0-10A-01D-A27P-09_BRCA	688	299	318	317	519	183	547	635	535	0	0	0	0	0	48	2	569
TCGA-BI-A0VR-10A-01D-A10S-08_CESC	682	0	0	299	603	385	529	657	472	0	0	0	0	0	31	64	575
TCGA-BI-A0VS-10A-01D-A10S-08_CESC	679	254	263	284	611	286	529	646	476	0	608	512	0	0	0	128	577
TCGA-BI-A20A-10A-01D-A14W-08_CESC	690	0	0	297	603	384	533	638	479	0	0	0	0	0	25	51	572
TCGA-BJ-A0YZ-10A-01D-A10S-08_THCA	760	0	0	304	609	384	529	646	480	0	0	0	0	0	0	146	578
TCGA-BJ-A0Z0-10A-01D-A10S-08_THCA	752	245	262	289	614	281	530	655	461	76	647	568	367	136	0	76	577
TCGA-BJ-A0Z2-10A-01D-A10S-08_THCA	686	0	0	300	619	385	533	655	480	0	0	0	0	0	35	81	577
TCGA-BJ-A0Z3-10A-01D-A13W-08_THCA	756	254	267	203	623	292	540	662	398	83	646	584	0	140	0	82	581
TCGA-BJ-A0Z9-10A-01D-A10S-08_THCA	679	248	274	294	609	382	531	651	483	0	592	572	0	0	0	142	576
TCGA-BJ-A0ZA-10A-02D-A10S-08_THCA	684	0	0	302	598	289	523	657	393	66	597	0	296	138	0	72	575
TCGA-BJ-A0ZB-10A-01D-A10S-08_THCA	679	247	271	286	585	288	521	637	462	0	621	0	366	137	0	66	578
TCGA-BJ-A0ZC-10A-01D-A13W-08_THCA	769	0	0	324	645	408	539	661	500	0	0	0	0	0	48	88	583
TCGA-BJ-A0ZE-10A-01D-A10S-08_THCA	684	0	0	307	609	382	531	652	471	0	0	0	0	0	0	94	575
TCGA-BJ-A0ZF-10A-01D-A10S-08_THCA	600	253	273	0	0	0	533	659	478	0	0	0	0	0	32	78	574
TCGA-BJ-A0ZG-10A-01D-A10S-08_THCA	686	0	0	305	609	385	532	650	460	78	610	0	364	135	0	80	576
TCGA-BJ-A0ZH-10A-01D-A10S-08_THCA	686	0	0	302	606	389	533	652	375	74	597	0	367	135	0	79	576
TCGA-BJ-A0ZJ-10A-01D-A10S-08_THCA	684	0	0	300	604	394	531	650	461	80	616	0	370	135	0	72	578
TCGA-BJ-A18Y-10A-01D-A13W-08_THCA	757	249	276	304	596	386	536	659	493	0	0	0	0	0	43	80	582
TCGA-BJ-A18Z-10A-01D-A13W-08_THCA	757	258	268	306	596	384	533	643	478	0	622	0	382	141	0	98	579
TCGA-BJ-A190-10A-01D-A13W-08_THCA	765	260	276	305	600	392	536	667	493	0	0	0	0	0	35	80	580
TCGA-BJ-A191-10A-01D-A13W-08_THCA	677	272	283	0	626	144	539	667	0	91	672	584	382	145	0	3	580
TCGA-BJ-A192-10A-01D-A13W-08_THCA	761	0	0	359	618	396	531	660	488	0	0	0	0	0	0	131	579
TCGA-BJ-A28R-10A-01D-A16O-08_THCA	689	0	0	305	609	390	535	656	454	79	598	0	376	138	0	73	577
TCGA-BJ-A28S-10A-01D-A19M-08_THCA	633	241	249	276	458	354	530	637	0	73	616	0	366	137	0	0	575
TCGA-BJ-A28T-10A-01D-A16O-08_THCA	670	252	271	294	520	285	532	648	490	0	0	0	0	0	33	78	578
TCGA-BJ-A28V-10A-01D-A19M-08_THCA	759	241	259	285	620	143	536	658	484	66	614	574	0	0	27	54	577
TCGA-BJ-A28W-10A-01D-A17V-08_THCA	648	241	258	260	606	283	528	634	453	74	616	561	299	134	0	69	578
TCGA-BJ-A28X-10A-01D-A22D-08_THCA	596	251	264	0	547	136	532	646	461	64	527	568	0	0	0	128	574
TCGA-BJ-A28Z-10A-01D-A16O-08_THCA	751	255	261	293	612	287	529	645	376	76	644	566	365	141	0	72	577
TCGA-BJ-A290-10A-01D-A17V-08_THCA	596	256	274	0	505	134	528	638	385	64	633	510	358	139	0	57	575
TCGA-BJ-A2N7-10A-01D-A18F-08_THCA	674	0	0	306	598	283	523	616	472	0	0	0	0	0	0	106	576
TCGA-BJ-A2N8-10A-01D-A18F-08_THCA	681	0	0	306	606	382	528	646	383	75	594	0	363	134	24	0	578
TCGA-BJ-A2N9-10A-01D-A18F-08_THCA	666	238	253	268	504	363	532	629	462	0	0	0	0	0	0	82	575
TCGA-BJ-A2NA-10A-01D-A19M-08_THCA	670	258	273	0	605	142	534	652	389	83	645	573	369	140	0	63	576
TCGA-BJ-A2P4-10A-01D-A18F-08_THCA	686	0	0	307	597	376	531	634	377	59	571	0	369	134	0	60	577
TCGA-BJ-A3EZ-10A-01D-A202-08_THCA	689	0	0	305	607	385	528	649	463	0	0	0	0	0	0	80	577
TCGA-BJ-A3F0-10A-01D-A202-08_THCA	642	234	260	280	506	366	529	645	469	0	0	0	0	0	33	56	576
TCGA-BJ-A3PR-10A-01D-A21Z-08_THCA	672	244	257	288	589	376	533	652	473	0	0	0	0	0	27	64	574
TCGA-BJ-A3PT-10A-01D-A21Z-08_THCA	681	242	259	289	582	281	530	649	477	0	0	0	0	0	28	70	574
TCGA-BJ-A3PU-10A-01D-A21Z-08_THCA	686	241	261	280	589	271	529	660	476	0	0	0	0	0	34	67	576
TCGA-BJ-A45C-10A-01D-A23U-08_THCA	740	240	252	277	610	295	534	641	470	0	571	0	309	0	0	62	572
TCGA-BJ-A45D-10A-01D-A23U-08_THCA	650	232	242	244	585	270	523	626	374	0	505	498	0	0	0	70	570
TCGA-BJ-A45E-10A-01D-A23U-08_THCA	668	223	234	259	562	362	522	623	16	79	627	490	295	132	0	3	569
TCGA-BJ-A45F-10A-01D-A23U-08_THCA	674	266	281	0	592	141	538	658	490	0	538	575	0	0	44	80	580
TCGA-BJ-A45G-10A-01D-A23U-08_THCA	673	241	266	184	608	283	528	653	449	74	631	568	0	134	0	67	575
TCGA-BJ-A45H-10A-01D-A23U-08_THCA	762	245	266	304	603	289	537	658	383	81	611	0	308	144	0	85	582
TCGA-BJ-A45I-10A-01D-A23U-08_THCA	681	0	0	296	597	392	529	650	459	0	0	0	0	0	0	80	576
TCGA-BJ-A45J-10A-01D-A23U-08_THCA	661	237	260	272	545	359	525	649	464	0	0	36	0	0	0	87	574
TCGA-BJ-A45K-10A-01D-A23U-08_THCA	684	0	0	281	580	367	524	612	390	0	0	0	0	0	0	95	571
TCGA-BJ-A4O8-10A-01D-A25A-08_THCA	640	234	257	279	493	352	516	624	388	0	0	0	0	0	25	50	571
TCGA-BJ-A4O9-10A-01D-A25A-08_THCA	669	0	0	277	552	372	510	617	293	0	492	0	275	118	0	53	573
TCGA-BK-A0CA-10A-02D-A272-09_UCEC	704	0	0	373	700	385	556	666	462	97	628	0	455	183	0	83	598
TCGA-BK-A0CC-10A-02D-A272-09_UCEC	691	0	0	332	629	445	543	614	534	0	0	0	0	0	24	37	582
TCGA-BK-A139-10A-01D-A272-09_UCEC	699	0	0	379	703	471	559	668	566	0	0	0	0	0	63	98	594
TCGA-BK-A13B-10A-01D-A22A-09_UCEC	688	0	316	198	679	416	550	637	552	0	565	0	370	0	33	44	579
TCGA-BK-A13C-10A-01D-A122-09_UCEC	800	0	0	400	730	481	560	676	584	0	0	0	0	0	58	140	599
TCGA-BK-A26L-10A-01D-A16D-09_UCEC	585	326	363	0	0	0	551	667	476	0	0	0	0	0	40	60	595
TCGA-BK-A4ZD-10A-01D-A27P-09_UCEC	696	304	165	316	521	429	521	470	407	0	476	0	363	169	0	51	580
TCGA-BK-A56F-10A-01D-A27P-09_UCEC	688	0	0	364	667	463	550	635	535	0	0	0	0	0	43	58	586
TCGA-BL-A0C8-10A-01D-A10S-08_BLCA	755	0	0	306	612	381	531	648	483	0	0	0	0	0	0	150	576
TCGA-BL-A13I-10A-01D-A271-08_BLCA	684	0	0	287	598	377	529	644	467	0	0	0	0	0	0	94	575
TCGA-BL-A13J-10A-01D-A271-08_BLCA	685	0	0	296	594	369	524	627	397	0	0	0	0	0	0	102	570
TCGA-BL-A5ZZ-10A-01D-A30H-08_BLCA	752	260	272	299	612	295	538	649	490	0	0	0	0	0	71	0	582
TCGA-BM-6198-10A-01D-1733-10_READ	557	297	301	0	608	172	530	597	0	101	469	435	353	169	0	0	583
TCGA-BR-6452-10A-01D-1800-08_STAD	688	0	0	310	608	375	529	626	382	0	0	0	0	132	0	61	572
TCGA-BR-6455-10A-01D-1800-08_STAD	677	248	270	288	593	285	535	660	464	83	622	0	374	134	0	64	575
TCGA-BR-6456-10A-01D-1800-08_STAD	682	255	260	292	569	376	532	644	479	0	0	0	0	0	0	122	576
TCGA-BR-6457-10A-01D-1800-08_STAD	688	247	258	291	608	386	530	644	480	0	607	565	0	0	0	124	576
TCGA-BR-6458-10A-01D-1800-08_STAD	684	0	0	304	598	393	532	653	450	70	595	0	298	131	0	66	577
TCGA-BR-6563-10A-01D-2053-08_STAD	685	240	259	269	602	367	532	644	440	74	630	569	0	131	28	0	575
TCGA-BR-6564-10A-01D-1882-08_STAD	687	0	0	303	612	388	535	655	476	0	0	0	0	0	35	81	577
TCGA-BR-6565-10A-01D-1800-08_STAD	690	242	261	285	553	366	534	652	479	0	0	0	0	0	30	62	574
TCGA-BR-6566-10A-01D-1800-08_STAD	680	249	276	284	571	378	535	651	473	68	588	0	363	0	0	91	573
TCGA-BR-6705-10A-01D-1882-08_STAD	692	0	0	305	618	387	531	645	488	0	0	0	0	0	0	89	578
TCGA-BR-6706-10A-01D-1882-08_STAD	673	252	269	299	593	285	532	652	470	0	0	0	0	0	0	105	580
TCGA-BR-6707-10A-01D-1882-08_STAD	597	262	280	0	594	137	531	619	465	0	651	570	375	137	0	79	582
TCGA-BR-6709-10A-01D-1882-08_STAD	741	255	266	293	564	378	533	650	484	0	0	0	0	0	0	98	580
TCGA-BR-6710-10A-01D-1882-08_STAD	687	253	266	287	612	381	532	653	481	0	620	567	0	0	0	141	574
TCGA-BR-6801-10A-01D-1882-08_STAD	681	252	273	294	596	281	531	662	486	0	0	0	0	0	38	69	577
TCGA-BR-6802-10A-01D-1882-08_STAD	680	253	267	291	513	0	533	636	0	74	611	0	369	142	0	1	572
TCGA-BR-6803-10A-01D-1882-08_STAD	763	0	0	305	606	383	529	653	466	75	616	0	368	140	0	62	577
TCGA-BR-6852-10A-01D-1882-08_STAD	678	253	265	288	617	379	534	649	399	79	645	575	0	139	0	73	575

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BR-7196-10A-01D-2053-08_STAD	597	250	262	0	502	134	532	629	461	0	595	557	0	0	0	72	571
TCGA-BR-7197-10A-01D-2201-08_STAD	755	255	258	298	589	380	533	658	462	83	616	569	0	138	0	77	575
TCGA-BR-7703-10A-01D-2053-08_STAD	650	232	249	278	568	349	529	643	467	0	0	0	0	0	0	70	577
TCGA-BR-7704-10A-01D-2053-08_STAD	669	232	249	256	551	270	526	644	383	63	589	527	0	134	0	60	577
TCGA-BR-7707-10A-01D-2053-08_STAD	595	249	259	0	19	0	532	649	471	0	0	0	0	0	26	61	574
TCGA-BR-7715-10A-01D-2053-08_STAD	683	221	242	279	609	362	532	638	462	0	534	514	0	0	0	117	570
TCGA-BR-7716-10A-01D-2053-08_STAD	670	234	242	279	505	349	530	634	461	0	0	0	0	0	0	67	575
TCGA-BR-7717-10A-01D-2053-08_STAD	685	0	0	295	594	371	527	643	374	76	579	0	343	126	0	52	575
TCGA-BR-7722-10A-01D-2201-08_STAD	737	229	241	280	569	359	531	649	462	0	0	0	0	0	0	89	577
TCGA-BR-7723-10A-01D-2053-08_STAD	649	238	263	272	509	271	531	652	378	81	624	0	377	133	0	60	572
TCGA-BR-7851-10A-01D-2201-08_STAD	728	243	236	287	605	254	531	665	468	0	623	564	0	0	28	59	578
TCGA-BR-7901-10A-01D-2201-08_STAD	715	229	243	277	519	350	525	629	384	0	595	0	342	133	0	60	575
TCGA-BR-7957-10A-01D-2201-08_STAD	726	223	241	280	609	363	532	655	454	0	602	517	0	0	30	68	577
TCGA-BR-7958-10A-01D-2340-08_STAD	681	255	266	293	576	0	529	625	0	80	615	0	367	139	0	0	575
TCGA-BR-7959-10A-01D-2340-08_STAD	689	0	0	315	620	389	526	656	479	0	0	0	0	0	0	96	577
TCGA-BR-8058-10A-01D-2340-08_STAD	632	214	230	255	549	347	512	614	439	0	471	485	0	0	0	60	571
TCGA-BR-8059-10A-01D-2340-08_STAD	760	0	0	305	600	389	535	648	486	0	0	0	0	0	0	133	577
TCGA-BR-8060-10A-01D-2340-08_STAD	689	0	0	359	613	397	530	644	462	76	598	0	369	135	0	71	578
TCGA-BR-8077-10A-01D-2340-08_STAD	763	0	0	308	617	396	533	651	449	76	623	574	0	137	0	66	576
TCGA-BR-8078-10A-01D-2340-08_STAD	759	0	0	304	612	280	521	636	457	0	0	0	0	138	0	70	572
TCGA-BR-8080-10A-01D-2340-08_STAD	752	0	0	292	613	375	522	639	453	66	504	0	373	139	26	0	575
TCGA-BR-8081-10A-01D-2340-08_STAD	755	0	0	314	611	390	536	651	484	0	0	0	0	0	0	146	577
TCGA-BR-8284-10A-01D-2340-08_STAD	690	0	0	307	616	387	536	652	455	81	622	0	373	137	0	77	578
TCGA-BR-8285-10A-01D-2340-08_STAD	594	258	271	0	0	0	531	647	391	73	612	0	362	135	38	0	579
TCGA-BR-8286-10A-01D-2340-08_STAD	687	252	267	197	619	285	536	658	492	0	623	568	0	0	41	70	575
TCGA-BR-8289-10A-01D-2340-08_STAD	686	45	54	296	602	276	513	610	459	0	99	235	0	133	0	41	572
TCGA-BR-8291-10A-01D-2340-08_STAD	578	210	219	207	469	261	524	614	344	0	498	0	270	128	0	21	575
TCGA-BR-8295-10A-01D-2340-08_STAD	687	0	0	309	612	385	531	646	481	0	0	0	0	0	0	97	576
TCGA-BR-8296-10A-01D-2340-08_STAD	688	0	0	301	608	393	533	654	481	0	0	0	0	0	32	78	579
TCGA-BR-8297-10A-01D-2340-08_STAD	660	0	0	269	559	241	487	549	283	0	0	0	0	119	0	40	537
TCGA-BR-8360-10A-01D-2340-08_STAD	668	264	271	0	616	138	533	662	487	0	642	576	0	0	38	77	575
TCGA-BR-8361-10A-01D-2340-08_STAD	678	253	0	297	597	281	531	651	464	82	619	0	368	136	0	75	575
TCGA-BR-8362-10A-01D-2340-08_STAD	680	237	253	184	605	278	527	649	462	0	590	502	0	0	25	58	571
TCGA-BR-8363-10A-01D-2341-08_STAD	666	246	265	273	605	276	526	648	468	0	594	560	0	0	29	63	573
TCGA-BR-8364-10A-01D-2341-08_STAD	591	245	259	0	552	134	524	608	0	74	623	568	261	135	0	0	569
TCGA-BR-8365-10A-01D-2341-08_STAD	596	262	271	0	610	137	535	645	465	79	654	578	0	137	0	68	577
TCGA-BR-8366-10A-01D-2341-08_STAD	673	251	266	293	594	380	534	657	458	77	622	0	366	138	0	79	577
TCGA-BR-8367-10A-01D-2341-08_STAD	684	244	264	289	609	377	533	651	484	0	607	513	0	0	0	141	579
TCGA-BR-8368-10A-01D-2341-08_STAD	762	0	0	305	614	395	533	657	486	0	0	0	0	0	0	102	578
TCGA-BR-8369-10A-01D-2341-08_STAD	682	0	0	293	595	376	529	637	479	0	0	0	0	0	0	80	573
TCGA-BR-8370-10A-01D-2341-08_STAD	682	248	269	303	611	139	529	639	459	0	632	512	0	139	37	0	575
TCGA-BR-8371-10A-01D-2341-08_STAD	685	251	265	303	618	287	532	661	482	0	619	564	0	0	34	80	576
TCGA-BR-8372-10A-01D-2341-08_STAD	687	0	0	304	612	388	533	646	486	0	0	0	0	0	0	146	579
TCGA-BR-8373-10A-01D-2341-08_STAD	690	0	0	311	618	388	533	650	478	0	0	0	0	0	0	92	578
TCGA-BR-8380-10A-01D-2341-08_STAD	659	0	0	282	553	364	499	595	282	56	509	0	263	129	0	42	565
TCGA-BR-8381-10A-01D-2394-08_STAD	685	0	0	297	595	278	514	606	373	0	0	0	0	137	0	59	573
TCGA-BR-8382-10A-01D-2394-08_STAD	667	246	260	290	600	370	530	632	471	0	596	503	0	0	0	101	574
TCGA-BR-8384-10A-01D-2394-08_STAD	684	231	261	278	610	380	529	638	452	73	631	568	0	132	0	63	572
TCGA-BR-8483-10A-01D-2394-08_STAD	673	244	262	296	605	378	531	658	481	75	599	510	0	0	34	64	572
TCGA-BR-8484-10A-01D-2394-08_STAD	687	0	0	305	610	380	528	636	461	0	0	0	0	0	0	88	573
TCGA-BR-8485-10A-01D-2394-08_STAD	676	239	264	187	614	281	529	648	377	77	644	568	0	139	0	61	571
TCGA-BR-8486-10A-01D-2394-08_STAD	678	247	260	292	609	132	513	617	455	0	614	513	0	135	28	4	571
TCGA-BR-8487-10A-01D-2394-08_STAD	596	257	274	0	132	0	530	642	471	0	0	0	0	0	35	3	573
TCGA-BR-8588-10A-01D-2394-08_STAD	677	235	256	287	600	278	525	643	473	0	589	557	0	0	0	117	577
TCGA-BR-8589-10A-01D-2394-08_STAD	593	250	272	0	574	136	531	637	480	0	615	563	0	0	0	118	575
TCGA-BR-8590-10A-01D-2394-08_STAD	657	244	265	286	587	280	528	641	466	0	0	0	0	0	0	121	576
TCGA-BR-8591-10A-01D-2394-08_STAD	689	0	0	303	603	394	533	653	489	0	98	0	0	0	39	72	575
TCGA-BR-8592-10A-01D-2394-08_STAD	591	194	214	211	463	324	506	596	335	57	473	0	242	120	0	31	571
TCGA-BR-8676-10A-01D-2394-08_STAD	680	246	261	278	613	373	531	652	477	0	592	512	0	0	29	55	573
TCGA-BR-8677-10A-01D-2394-08_STAD	685	250	264	288	597	278	528	648	454	80	587	0	367	135	31	3	575
TCGA-BR-8678-10A-01D-2394-08_STAD	684	0	0	302	607	372	532	651	466	0	35	46	0	0	29	63	579
TCGA-BR-8679-10A-01D-2394-08_STAD	669	245	265	291	566	279	532	649	471	0	0	0	0	0	26	69	576
TCGA-BR-8680-10A-01D-2394-08_STAD	688	248	269	291	611	380	533	655	476	80	624	519	111	74	32	62	577
TCGA-BR-8682-10A-01D-2394-08_STAD	747	249	263	274	590	375	529	645	151	84	630	59	376	138	0	8	574
TCGA-BR-8683-10A-01D-2394-08_STAD	675	241	267	295	579	377	531	635	478	0	0	0	0	0	0	83	572
TCGA-BR-8686-10A-01D-2394-08_STAD	588	245	253	0	0	0	524	614	378	0	0	0	0	0	0	53	571
TCGA-BR-8687-10A-01D-2394-08_STAD	687	0	0	302	599	384	532	655	479	75	0	0	0	0	33	67	578
TCGA-BR-8690-10A-01D-2394-08_STAD	675	245	267	290	577	276	529	649	450	82	605	0	299	133	0	77	575
TCGA-BR-A44T-10A-01D-A24F-08_STAD	635	226	238	266	532	267	521	626	454	0	0	0	0	0	28	54	568
TCGA-BR-A44U-10A-01D-A24F-08_STAD	673	248	261	283	584	379	532	643	471	0	0	0	0	0	40	0	576
TCGA-BR-A452-10A-01D-A25E-08_STAD	759	0	0	289	602	388	531	641	472	0	0	0	0	0	29	54	570
TCGA-BR-A453-10A-01D-A24F-08_STAD	680	0	0	298	595	378	530	638	474	0	0	0	0	0	0	113	575
TCGA-BR-A4CQ-10A-01D-A25E-08_STAD	647	245	264	274	608	375	529	639	378	69	635	571	0	136	0	69	574
TCGA-BR-A4CR-10A-01D-A24F-08_STAD	676	245	252	277	602	278	526	630	446	70	621	563	0	134	0	60	573
TCGA-BR-A4CS-10A-01D-A24F-08_STAD	651	248	269	277	575	0	514	610	447	0	0	0	0	133	33	1	564
TCGA-BR-A4IU-10A-01D-A25E-08_STAD	633	217	228	247	474	334	521	617	377	0	0	0	0	0	19	46	569
TCGA-BR-A4IV-10A-01D-A25E-08_STAD	680	249	275	280	566	371	535	656	447	85	632	0	376	134	33	5	576
TCGA-BR-A4IY-10A-01D-A25E-08_STAD	689	0	0	302	594	385	531	646	464	72	575	0	364	134	29	5	574
TCGA-BR-A4IZ-10A-01D-A25E-08_STAD	685	242	266	277	591	375	531	655	482	0	0	0	0	0	27	65	578
TCGA-BR-A4J1-10A-01D-A25E-08_STAD	669	236	254	285	580	373	531	634	387	72	592	0	284	132	28	2	574
TCGA-BR-A4J2-10A-01D-A25E-08_STAD	592	257	268	0	507	134	530	654	472	76	584	564	0	0	38	0	573
TCGA-BR-A4J4-10A-01D-A25E-08_STAD	684	0	0	298	605	396	533	643	378	74	591	561	0	135	36	0	575
TCGA-BR-A4J5-10A-01D-A25E-08_STAD	683	0	0	297	592	379	526	646	459	0	0	0	0	0	23	61	573
TCGA-BR-A4J6-10A-01D-A25E-08_STAD	663	241	259	288	579	274	531	646	476	0	0	0	0	0	0	73	577
TCGA-BR-A4J7-10A-01D-A25E-08_STAD	681	245	261	275	572	358	529	619	0	74	618	0	370	137	0	0	575
TCGA-BR-A4J8-10A-01D-A25E-08_STAD	684	0	0	298	601	382	529	646	473	0	0	0	0	0	0	82	577
TCGA-BR-A4J9-10A-01D-A25E-08_STAD	683	236	255	282	605	382	530	644	459	76	632	570	93	132	29	7	574
TCGA-BR-A4PD-10A-01D-A25E-08_STAD	588	251	275	0	595	138	533	636	440	64	642	570	0	130	32	0	575
TCGA-BR-A4PE-10A-01D-A25E-08_STAD	676	244	268	297	604	282	529	646	489	0	0	0	0	0	45	0	577
TCGA-BR-A4PF-10A-01D-A25E-08_STAD	685	0	0	299	596	377	530	632	377	63	534	511	0	129	0	65	572
TCGA-BR-A4QI-10A-01D-A25E-08_STAD	596	254	271	0	58	21	530	639	481	0	0	0	0	0	0	134	575
TCGA-BR-A4QL-10A-01D-A25E-08_STAD	596	250	269	0	554	136	523	633	47	73	633	570	356	137	0	7	576
TCGA-BR-A4QM-10A-01D-A25E-08_STAD	681	226	216	285	571	335	525	617	456	0	0	0	0	0	0	87	570
TCGA-BS-A0T9-10C-01D-A12J-09_UCEC	794	0	0	397	723	480	561	671	585	0	0	0	0	0	93	0	599
TCGA-BS-A0TA-10A-01D-A10B-09_UCEC	600	261	304	356	620	410	542	632	425	100	565	0	309	164	0	24	564
TCGA-BS-A0TC-10A-01D-A10B-09_UCEC	588	159	253	325	629	364	525	596	442	0	495	477	0	0	10	25	572

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BS-A0TD-10A-01D-A10B-09_UCEC	646	0	0	391	677	453	543	636	467	0	0	0	0	0	19	28	584
TCGA-BS-A0TE-10A-01D-A10B-09_UCEC	679	0	0	383	692	459	554	645	471	0	0	0	0	0	0	84	591
TCGA-BS-A0TG-10A-01D-A14K-09_UCEC	801	0	0	398	722	475	562	669	584	0	0	0	0	0	0	175	598
TCGA-BS-A0TI-10A-01D-A10B-09_UCEC	785	317	365	378	701	372	549	657	0	109	668	0	475	192	0	0	596
TCGA-BS-A0TJ-10A-01D-A10B-09_UCEC	702	0	0	419	726	472	561	670	583	0	0	0	0	0	0	180	595
TCGA-BS-A0U5-10A-01D-A10G-09_UCEC	695	0	0	392	721	474	555	664	0	108	669	0	460	184	0	0	592
TCGA-BS-A0U7-10A-01D-A10B-09_UCEC	687	318	363	375	710	458	555	656	569	0	619	571	0	0	0	151	594
TCGA-BS-A0U8-10A-01D-A10B-09_UCEC	697	317	356	360	706	382	556	656	354	100	654	584	376	181	0	81	593
TCGA-BS-A0U9-10A-01D-A10M-09_UCEC	698	325	362	389	722	463	559	667	582	0	648	584	0	0	48	100	595
TCGA-BS-A0UA-10A-01D-A122-09_UCEC	703	331	370	385	707	472	562	676	582	0	0	0	0	0	64	125	598
TCGA-BS-A0UF-10A-01D-A10B-09_UCEC	694	0	0	382	692	457	556	650	0	105	650	586	0	183	0	0	595
TCGA-BS-A0UJ-10A-01D-A127-09_UCEC	668	0	0	383	685	380	548	633	461	0	0	0	0	0	16	32	572
TCGA-BS-A0UL-10A-01D-A10G-09_UCEC	700	0	0	394	713	471	560	666	461	103	647	545	0	183	0	90	597
TCGA-BS-A0UM-10A-01D-A10B-09_UCEC	798	342	383	0	723	191	564	680	0	111	686	600	464	190	0	0	601
TCGA-BS-A0UT-10A-01D-A10B-09_UCEC	665	0	0	386	711	453	544	651	476	0	0	0	0	0	35	0	591
TCGA-BS-A0UV-10A-01D-A10B-09_UCEC	799	0	0	395	735	480	564	684	581	105	668	595	0	0	0	247	596
TCGA-BS-A0V4-10A-01D-A14G-09_UCEC	681	0	0	335	660	364	543	619	279	78	475	0	424	167	0	34	588
TCGA-BS-A0V6-10A-01D-A122-09_UCEC	701	0	0	397	716	480	565	678	588	0	0	0	0	0	69	115	599
TCGA-BS-A0V7-10A-01D-A122-09_UCEC	798	0	0	399	724	479	557	677	578	0	0	0	0	0	70	130	595
TCGA-BS-A0V8-10A-01D-A122-09_UCEC	703	0	0	415	719	482	561	678	585	0	0	0	0	0	73	125	597
TCGA-BS-A0VI-10A-01D-A14G-09_UCEC	585	319	359	0	0	0	552	636	413	92	572	522	0	174	32	0	584
TCGA-BS-A0WQ-10A-01D-A10G-09_UCEC	798	315	363	391	708	467	562	667	588	0	0	0	0	0	45	85	595
TCGA-BT-A0S7-10A-01D-A10S-08_BLCA	685	254	0	193	612	284	530	645	452	78	611	0	296	134	0	77	577
TCGA-BT-A0YX-10A-01D-A10S-08_BLCA	686	0	0	309	611	384	525	652	482	0	0	0	0	0	0	129	572
TCGA-BT-A2LB-10A-01D-A18F-08_BLCA	758	0	0	303	611	377	531	645	484	0	0	0	0	0	28	73	578
TCGA-BT-A2LD-10A-01D-A20D-08_BLCA	689	0	0	299	603	383	531	647	453	71	603	0	369	136	31	0	576
TCGA-BT-A3PH-10A-01D-A21Z-08_BLCA	595	257	271	0	595	135	533	646	474	0	611	512	0	0	0	85	576
TCGA-BT-A3PJ-10A-01D-A21Z-08_BLCA	595	256	266	0	600	136	531	654	370	75	643	572	363	133	0	70	577
TCGA-BT-A3PK-10A-01D-A21Z-08_BLCA	674	248	253	276	604	279	529	641	479	0	581	568	0	0	0	109	574
TCGA-BT-A42B-10A-01D-A23K-08_BLCA	675	269	287	0	615	141	537	663	496	0	632	575	0	0	44	100	582
TCGA-BT-A42C-10A-01D-A23K-08_BLCA	672	266	281	0	0	0	537	654	470	76	582	0	378	142	37	0	580
TCGA-BT-A42E-10A-01D-A23U-08_BLCA	589	247	264	0	540	125	527	632	385	0	555	497	0	0	28	50	572
TCGA-BT-A42F-10A-01D-A23U-08_BLCA	748	239	255	294	590	379	533	645	485	0	0	0	0	0	0	106	579
TCGA-BW-A5NO-10A-01D-A27I-10_LIHC	676	0	0	279	479	178	499	566	331	0	336	0	362	175	31	0	585
TCGA-BW-A5NP-10A-01D-A27I-10_LIHC	680	0	0	276	549	459	541	622	336	0	389	487	0	170	28	0	588
TCGA-BW-A5NQ-10A-01D-A27I-10_LIHC	660	0	0	372	661	438	529	619	358	0	0	0	0	0	23	45	575
TCGA-C4-A0EZ-10A-01D-A10S-08_BLCA	757	0	0	308	609	389	531	655	453	65	628	0	301	139	0	69	576
TCGA-C4-A0F0-10A-01D-A10S-08_BLCA	676	251	269	295	615	286	530	656	477	0	599	567	0	0	37	76	575
TCGA-C4-A0F1-10A-01D-A10S-08_BLCA	595	261	276	0	0	0	533	660	474	0	0	0	0	0	35	74	576
TCGA-C4-A0F6-10A-01D-A10S-08_BLCA	675	251	267	293	562	375	530	661	470	0	0	0	0	0	34	68	575
TCGA-C4-A0F7-10A-01D-A10S-08_BLCA	684	0	0	301	627	385	533	657	474	0	0	0	0	0	0	92	580
TCGA-C5-A0TN-10B-01D-A14W-08_CESC	692	0	0	295	599	385	529	625	400	0	0	0	0	0	28	1	574
TCGA-C5-A1BE-10A-01D-A13W-08_CESC	757	253	275	300	599	386	538	658	0	88	644	574	371	144	0	1	581
TCGA-C5-A1BF-10A-01D-A13W-08_CESC	757	0	0	322	630	299	528	665	493	0	0	0	0	0	29	81	579
TCGA-C5-A1BI-10A-01D-A13W-08_CESC	752	255	271	309	522	387	537	660	400	88	632	0	309	139	49	0	582
TCGA-C5-A1BJ-10A-01D-A13W-08_CESC	672	268	285	0	610	141	539	660	472	78	644	578	378	140	42	0	581
TCGA-C5-A1BK-10A-01D-A13W-08_CESC	763	260	270	301	628	400	538	660	496	0	619	570	0	0	57	0	582
TCGA-C5-A1BL-10A-01D-A13W-08_CESC	762	0	0	320	627	401	536	667	494	0	0	0	0	0	43	95	580
TCGA-C5-A1BM-10A-01D-A13W-08_CESC	762	253	272	294	600	394	537	654	492	0	0	0	0	0	54	1	579
TCGA-C5-A1BN-10A-01D-A14W-08_CESC	663	234	253	285	507	355	530	629	364	72	572	0	352	130	0	51	579
TCGA-C5-A1BQ-10A-01D-A20U-09_CESC	693	292	338	237	676	438	552	637	559	0	591	529	0	0	0	125	594
TCGA-C5-A1M5-10A-01D-A13W-08_CESC	670	269	280	0	0	0	538	661	493	0	0	0	0	0	32	72	582
TCGA-C5-A1M6-10A-01D-A13W-08_CESC	760	0	0	316	641	408	537	662	485	0	0	0	0	0	0	138	578
TCGA-C5-A1M7-10A-01D-A13W-08_CESC	745	252	268	289	567	387	534	653	485	0	0	0	0	0	61	0	582
TCGA-C5-A1M8-10A-01D-A13W-08_CESC	750	254	275	286	594	278	535	659	458	60	581	489	0	142	29	0	580
TCGA-C5-A1M9-10A-01D-A13W-08_CESC	763	0	0	325	635	411	534	658	490	0	0	0	0	0	0	183	580
TCGA-C5-A1ME-10A-01D-A13W-08_CESC	693	0	0	314	642	395	532	667	466	75	615	0	373	141	37	2	581
TCGA-C5-A1MF-10A-01D-A13W-08_CESC	767	0	0	321	630	401	535	665	496	0	0	0	0	0	0	161	582
TCGA-C5-A1MH-10A-01D-A14W-08_CESC	686	0	0	300	605	384	530	629	473	0	0	0	0	0	0	76	575
TCGA-C5-A1MI-10A-01D-A14W-08_CESC	662	229	269	270	549	368	523	642	382	76	578	0	294	133	0	48	575
TCGA-C5-A1MJ-10A-01D-A14W-08_CESC	674	242	256	289	599	366	528	650	464	73	520	502	0	0	25	64	575
TCGA-C5-A1MK-10A-01D-A14W-08_CESC	682	0	0	294	601	371	529	648	466	0	0	0	0	0	26	61	574
TCGA-C5-A1ML-10A-01D-A14W-08_CESC	683	0	0	300	578	394	527	633	382	75	530	0	290	134	0	61	575
TCGA-C5-A1MN-10A-01D-A14W-08_CESC	680	0	0	297	605	377	529	635	373	70	560	0	288	138	0	51	577
TCGA-C5-A1MP-10A-01D-A14W-08_CESC	659	242	248	284	576	366	528	627	466	0	583	508	0	0	32	0	572
TCGA-C5-A1MQ-10A-01D-A14W-08_CESC	645	230	219	270	569	362	526	618	0	77	639	560	292	140	0	0	574
TCGA-C5-A2LS-10A-01D-A22X-09_CESC	699	0	0	357	681	370	544	640	548	0	0	0	0	0	0	124	583
TCGA-C5-A2LT-10A-01D-A18J-09_CESC	682	284	289	114	505	336	543	531	436	0	0	0	0	0	0	67	582
TCGA-C5-A2LV-10A-01D-A18J-09_CESC	682	0	0	347	668	459	555	626	544	0	0	0	0	0	46	3	584
TCGA-C5-A2LX-10A-01D-A18J-09_CESC	686	0	0	366	677	466	550	530	443	0	0	0	0	0	0	88	577
TCGA-C5-A2LY-10A-01D-A18J-09_CESC	693	0	0	377	676	461	552	620	543	0	0	0	0	0	0	121	589
TCGA-C5-A2LZ-10B-01D-A20U-09_CESC	588	323	361	0	620	198	554	654	435	102	646	531	446	173	33	6	589
TCGA-C5-A2M1-10A-01D-A18J-09_CESC	683	0	0	334	657	366	529	602	390	0	411	0	311	163	0	33	584
TCGA-C5-A2M2-10A-01D-A18J-09_CESC	681	298	326	326	662	347	542	615	0	97	637	552	348	177	0	1	587
TCGA-C5-A3HD-10A-01D-A20U-09_CESC	691	0	0	358	665	450	547	639	554	0	0	0	0	0	34	51	589
TCGA-C5-A3HF-10A-01D-A20U-09_CESC	701	310	329	331	630	355	550	663	546	0	0	0	0	0	38	72	590
TCGA-C5-A3HL-10A-01D-A20U-09_CESC	690	0	14	367	685	466	553	642	435	90	598	0	365	173	0	59	594
TCGA-C8-A12K-10A-01D-A110-09_BRCA	684	0	0	383	700	467	554	658	476	0	0	0	0	0	41	77	590
TCGA-C8-A12L-10A-01D-A110-09_BRCA	801	0	0	400	720	483	563	677	484	0	0	0	0	0	79	0	599
TCGA-C8-A12M-10A-01D-A110-09_BRCA	780	331	380	0	0	0	564	660	0	112	668	592	0	192	0	0	596
TCGA-C8-A12N-10A-01D-A110-09_BRCA	696	0	0	391	703	468	562	673	581	0	0	0	0	0	56	97	595
TCGA-C8-A12O-10A-01D-A110-09_BRCA	794	0	0	384	708	470	557	653	574	0	0	0	0	0	63	0	592
TCGA-C8-A12P-10A-01D-A110-09_BRCA	799	0	0	419	731	480	560	677	482	109	665	0	468	188	66	0	598
TCGA-C8-A12Q-10A-01D-A110-09_BRCA	700	0	0	394	708	473	559	671	460	106	651	0	455	186	45	0	595
TCGA-C8-A12T-10A-01D-A110-09_BRCA	703	0	0	391	711	467	559	668	579	0	0	0	0	0	67	1	593
TCGA-C8-A12U-10A-01D-A110-09_BRCA	692	322	365	384	720	463	561	664	482	0	651	588	0	0	42	74	596
TCGA-C8-A12V-10A-01D-A110-09_BRCA	700	0	0	385	705	468	559	664	565	0	0	0	0	0	63	0	593
TCGA-C8-A12W-10A-01D-A110-09_BRCA	689	308	349	366	692	449	555	661	574	0	0	0	0	0	53	0	596
TCGA-C8-A12X-10A-01D-A110-09_BRCA	669	0	0	365	658	448	530	637	457	0	0	0	0	0	19	41	566
TCGA-C8-A12Y-10A-01D-A12B-09_BRCA	798	0	0	401	728	482	562	677	587	0	0	0	0	0	0	271	601
TCGA-C8-A12Z-10A-01D-A110-09_BRCA	793	0	0	392	711	471	558	666	577	0	0	0	0	0	0	173	596
TCGA-C8-A130-10A-01D-A110-09_BRCA	694	0	0	392	717	455	552	661	568	0	0	0	0	0	56	0	593
TCGA-C8-A131-10A-01D-A110-09_BRCA	795	0	0	398	722	480	560	670	578	0	0	0	0	0	62	103	595
TCGA-C8-A132-10A-01D-A110-09_BRCA	794	0	0	390	717	476	562	672	583	0	0	0	0	0	63	102	599
TCGA-C8-A133-10A-01D-A12B-09_BRCA	803	0	0	423	731	482	565	683	468	111	676	0	474	187	0	176	601
TCGA-C8-A134-10A-01D-A110-09_BRCA	703	320	369	382	719	468	560	663	572	0	644	582	0	0	78	0	596

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-C8-A135-10A-02D-A110-09_BRCA	802	0	0	396	724	482	564	677	580	0	0	0	0	0	137	0	598
TCGA-C8-A137-10A-02D-A110-09_BRCA	695	0	0	384	705	468	558	658	481	0	0	0	0	0	71	0	593
TCGA-C8-A138-10A-01D-A110-09_BRCA	648	278	312	349	676	448	544	647	426	99	641	512	344	159	19	0	574
TCGA-C8-A1HE-10A-01D-A13O-09_BRCA	651	0	0	357	671	432	532	622	440	0	0	0	0	0	0	66	570
TCGA-C8-A1HF-10A-01D-A135-09_BRCA	803	0	0	393	732	478	564	683	585	0	0	0	0	0	0	307	602
TCGA-C8-A1HG-10A-01D-A135-09_BRCA	803	337	372	395	709	473	565	682	586	0	0	0	0	0	80	155	602
TCGA-C8-A1HI-10A-01D-A135-09_BRCA	801	0	0	421	730	483	566	681	588	0	0	0	0	0	92	158	601
TCGA-C8-A1HJ-10A-01D-A13O-09_BRCA	664	0	0	367	686	437	556	628	409	99	582	514	0	166	0	33	576
TCGA-C8-A1HK-10A-01D-A13O-09_BRCA	632	242	299	314	598	409	518	622	447	0	0	0	0	0	0	49	584
TCGA-C8-A1HL-10A-01D-A135-09_BRCA	800	0	0	419	732	479	562	682	580	108	667	0	468	187	74	0	599
TCGA-C8-A1HM-10A-01D-A135-09_BRCA	801	0	0	402	725	469	562	682	577	106	669	594	0	185	91	0	600
TCGA-C8-A1HN-10A-01D-A135-09_BRCA	701	0	0	390	717	480	562	674	583	0	0	0	0	0	98	0	599
TCGA-C8-A1HO-10A-01D-A188-09_BRCA	690	0	0	386	706	466	557	661	573	0	0	0	0	0	40	73	595
TCGA-C8-A26V-10A-01D-A16D-09_BRCA	680	0	0	372	703	451	559	664	456	97	603	530	0	0	47	1	582
TCGA-C8-A26W-10A-01D-A16D-09_BRCA	686	0	0	391	701	466	554	660	453	105	631	0	450	177	42	3	592
TCGA-C8-A26X-10A-01D-A16D-09_BRCA	658	285	334	356	697	440	551	659	446	100	586	524	0	0	44	0	583
TCGA-C8-A26Y-10A-01D-A16D-09_BRCA	662	0	0	360	669	441	526	642	458	0	0	0	0	0	24	50	574
TCGA-C8-A26Z-10A-01D-A16D-09_BRCA	666	304	340	350	643	441	553	652	456	0	0	0	0	0	28	51	579
TCGA-C8-A273-10A-01D-A16D-09_BRCA	675	293	326	359	693	442	555	655	420	99	637	586	0	169	26	0	576
TCGA-C8-A274-10A-01D-A16D-09_BRCA	673	0	0	367	678	443	538	629	413	90	568	0	315	163	0	44	573
TCGA-C8-A275-10A-01D-A16D-09_BRCA	672	302	340	355	664	438	550	649	444	99	609	526	0	178	0	56	582
TCGA-C8-A278-10A-01D-A167-09_BRCA	688	0	0	365	673	365	545	643	319	99	574	0	348	169	0	37	586
TCGA-C8-A27A-10B-01D-A167-09_BRCA	666	0	0	356	661	428	549	624	325	99	560	0	334	156	21	0	556
TCGA-C8-A27B-10A-01D-A167-09_BRCA	648	0	0	303	623	361	546	604	332	0	0	0	0	0	34	1	542
TCGA-C8-A3M7-10A-01D-A21Q-09_BRCA	656	0	60	339	632	435	535	612	390	85	448	487	0	158	0	33	574
TCGA-C8-A3M8-10A-01D-A20S-09_BRCA	652	0	0	348	644	429	526	590	291	84	442	0	292	150	0	35	561
TCGA-C9-A47Z-10A-01D-A24F-08_HNSC	680	0	0	305	598	370	529	634	382	79	594	0	295	134	0	53	576
TCGA-C9-A480-10A-01D-A24F-08_HNSC	669	0	0	294	593	375	527	620	392	0	0	0	0	0	34	1	568
TCGA-CA-5796-10A-01D-1650-10_COAD	680	0	0	368	659	439	540	615	329	99	399	462	0	176	12	0	568
TCGA-CA-5797-10A-01D-1650-10_COAD	787	0	0	378	634	453	554	638	437	102	388	439	0	156	14	0	582
TCGA-CA-6716-10A-01D-1835-10_COAD	618	100	215	178	472	329	475	536	319	0	228	257	0	0	14	0	558
TCGA-CA-6719-10A-01D-1835-10_COAD	581	0	0	200	416	328	462	546	323	0	0	0	0	0	10	1	538
TCGA-CC-5258-10A-01D-A12Z-10_LIHC	658	0	0	367	623	358	528	624	350	0	0	0	0	0	18	0	585
TCGA-CC-5259-10A-01D-A20W-10_LIHC	671	0	0	365	666	455	548	616	355	0	0	0	0	0	39	0	575
TCGA-CC-5260-10B-01D-A12Z-10_LIHC	689	0	0	383	646	421	534	627	457	0	0	0	0	0	8	35	596
TCGA-CC-5261-10A-01D-A12Z-10_LIHC	681	0	0	378	624	423	534	619	433	99	388	0	323	174	0	21	576
TCGA-CC-5262-10B-01D-A12Z-10_LIHC	695	0	0	373	654	448	538	638	0	100	597	503	325	181	0	0	593
TCGA-CC-5263-10B-01D-A12Z-10_LIHC	664	0	0	367	639	431	554	611	454	0	0	0	0	0	8	33	580
TCGA-CC-5264-10A-01D-A12Z-10_LIHC	673	0	0	365	664	442	527	621	314	96	378	0	305	162	0	23	579
TCGA-CC-A123-10A-01D-A12Z-10_LIHC	673	0	0	378	632	432	531	619	324	94	500	0	300	153	0	32	574
TCGA-CC-A1HT-10A-01D-A12Z-10_LIHC	782	0	0	376	677	446	550	622	452	0	0	0	0	0	32	0	582
TCGA-CC-A3M9-10A-01D-A20W-10_LIHC	691	0	0	284	649	446	544	602	355	0	0	0	0	0	19	39	580
TCGA-CC-A3MA-10A-01D-A20W-10_LIHC	684	0	0	368	651	443	543	603	316	0	411	0	330	171	0	43	576
TCGA-CC-A3MB-10A-01D-A20W-10_LIHC	671	0	0	360	659	443	536	621	447	0	0	0	0	0	33	0	570
TCGA-CC-A3MC-10A-01D-A22F-10_LIHC	510	243	208	208	370	285	422	445	295	0	392	0	272	139	12	0	551
TCGA-CC-A5UC-10A-01D-A28X-10_LIHC	656	0	0	272	548	460	531	599	358	0	0	0	0	0	18	44	573
TCGA-CC-A5UD-10A-01D-A28X-10_LIHC	675	0	0	263	534	443	532	614	333	0	424	494	0	167	30	1	573
TCGA-CC-A5UE-10A-01D-A28X-10_LIHC	673	0	0	358	550	452	543	595	357	0	0	0	0	0	28	43	572
TCGA-CD-5798-10A-01D-1600-08_STAD	684	253	272	296	598	384	534	662	400	85	630	570	0	138	0	75	578
TCGA-CD-5799-10A-01D-1600-08_STAD	688	0	0	351	615	392	535	653	482	0	0	0	0	0	46	0	577
TCGA-CD-5800-10A-01D-1600-08_STAD	689	0	0	304	612	391	532	658	486	0	0	0	0	0	42	1	575
TCGA-CD-5801-10A-01D-1600-08_STAD	759	251	268	293	522	384	534	668	488	0	0	0	0	0	36	79	575
TCGA-CD-5802-10A-01D-1600-08_STAD	760	0	0	313	609	404	534	672	487	0	0	0	0	0	36	86	581
TCGA-CD-5803-10A-01D-1600-08_STAD	692	0	0	306	611	402	534	661	487	0	0	0	0	0	33	75	578
TCGA-CD-5804-10A-01D-2053-08_STAD	678	236	241	265	547	365	530	637	469	0	0	0	0	0	33	60	575
TCGA-CD-5813-10A-01D-1600-08_STAD	685	0	0	308	610	398	537	661	490	0	0	0	0	0	35	62	581
TCGA-CD-8524-10A-01D-2341-08_STAD	760	0	0	305	618	384	530	647	469	78	616	0	373	138	38	0	577
TCGA-CD-8525-10A-01D-2341-08_STAD	691	0	0	311	614	388	532	664	483	0	0	0	0	0	36	76	576
TCGA-CD-8526-10A-01D-2341-08_STAD	682	253	267	298	593	376	533	642	462	87	612	0	373	138	0	70	580
TCGA-CD-8527-10A-01D-2341-08_STAD	691	0	0	308	605	391	533	646	387	78	621	0	368	138	0	67	576
TCGA-CD-8528-10A-01D-2341-08_STAD	683	0	0	306	609	383	533	644	460	76	595	0	300	138	41	0	579
TCGA-CD-8529-10A-01D-2341-08_STAD	761	253	271	297	596	382	535	650	488	0	0	0	0	0	32	84	577
TCGA-CD-8530-10A-01D-2341-08_STAD	760	0	0	309	615	390	535	649	469	79	608	564	0	140	40	0	579
TCGA-CD-8531-10A-01D-2341-08_STAD	687	0	0	311	606	393	536	654	458	81	638	518	0	139	28	0	577
TCGA-CD-8532-10A-01D-2341-08_STAD	689	0	0	311	609	388	530	643	482	0	0	0	0	0	41	0	576
TCGA-CD-8533-10A-01D-2341-08_STAD	659	209	243	247	495	356	492	580	0	66	592	513	0	136	0	1	573
TCGA-CD-8534-10A-01D-2341-08_STAD	684	0	0	304	595	381	533	627	445	73	602	0	301	132	0	38	576
TCGA-CD-8535-10A-01D-2341-08_STAD	671	234	242	261	602	349	526	611	386	0	495	503	0	71	0	12	571
TCGA-CD-8536-10A-01D-2341-08_STAD	686	0	0	310	605	389	534	650	478	0	0	0	0	0	30	69	577
TCGA-CD-A486-10A-01D-A24F-08_STAD	644	239	249	267	593	275	523	628	374	74	611	496	290	132	0	53	578
TCGA-CD-A487-10A-01D-A24F-08_STAD	680	0	0	300	591	381	531	624	468	0	0	0	0	0	36	1	577
TCGA-CD-A489-10A-01D-A24F-08_STAD	684	0	0	290	588	379	527	633	373	71	580	503	0	131	27	2	571
TCGA-CD-A48A-10A-01D-A24F-08_STAD	683	0	0	294	601	379	533	644	471	0	0	0	0	0	31	64	576
TCGA-CD-A48C-10A-01D-A24F-08_STAD	681	0	0	296	598	379	526	642	471	0	0	0	0	0	29	60	573
TCGA-CD-A4MG-10A-01D-A25E-08_STAD	682	0	0	301	606	389	532	637	470	0	0	0	0	0	29	57	573
TCGA-CD-A4MH-10A-01D-A25E-08_STAD	678	237	255	263	600	352	530	637	382	60	628	501	358	132	25	3	572
TCGA-CD-A4MI-10A-01D-A25E-08_STAD	683	0	0	293	603	384	531	629	469	0	0	0	0	0	38	0	574
TCGA-CD-A4MJ-10A-01D-A25E-08_STAD	689	0	0	293	600	391	529	652	470	0	0	0	0	0	35	63	576
TCGA-CE-A13K-10A-01D-A10S-08_THCA	680	256	269	283	519	284	531	654	0	80	635	0	379	140	0	0	574
TCGA-CE-A27D-10A-01D-A17V-08_THCA	684	0	0	298	601	383	534	626	472	0	0	0	0	0	33	0	574
TCGA-CE-A3MD-10A-01D-A20C-08_THCA	595	260	276	0	568	131	535	664	480	76	593	572	0	0	32	68	579
TCGA-CE-A3ME-10A-01D-A20C-08_THCA	690	0	0	307	631	386	533	653	464	81	609	0	369	134	29	0	576
TCGA-CE-A481-10A-01D-A23U-08_THCA	676	220	220	271	489	350	493	595	0	60	615	507	276	133	0	3	570
TCGA-CE-A482-10A-01D-A23U-08_THCA	678	0	0	289	586	380	523	639	465	0	0	0	0	0	28	57	574
TCGA-CE-A483-10A-01D-A23U-08_THCA	750	242	266	298	596	286	536	656	472	74	610	571	0	142	0	71	580
TCGA-CE-A484-10A-01D-A23U-08_THCA	674	0	0	287	582	373	524	621	390	0	0	0	0	0	30	0	568
TCGA-CE-A485-10A-01D-A23U-08_THCA	634	230	242	258	585	346	529	640	371	72	600	517	0	129	25	0	570
TCGA-CF-A1HR-10A-01D-A13W-08_BLCA	763	0	0	323	627	406	538	659	486	0	0	0	0	0	52	0	582
TCGA-CF-A1HS-10A-01D-A13W-08_BLCA	671	268	286	0	0	0	537	664	495	0	0	0	0	0	36	84	580
TCGA-CF-A27C-10A-01D-A16O-08_BLCA	685	0	0	306	604	393	533	647	474	0	0	0	0	0	43	0	577
TCGA-CF-A3MF-10A-01D-A21A-08_BLCA	684	0	0	289	594	385	529	636	373	72	586	504	0	136	0	62	577
TCGA-CF-A3MG-10A-01D-A20D-08_BLCA	684	0	0	301	603	376	533	650	478	0	0	0	0	0	31	71	576
TCGA-CF-A3MH-10A-01D-A20D-08_BLCA	685	0	0	309	604	383	534	646	439	76	601	564	0	136	29	0	571
TCGA-CF-A3MI-10A-01D-A20D-08_BLCA	680	0	0	340	593	382	529	636	437	75	589	0	276	136	0	58	579
TCGA-CF-A47S-10A-01D-A23U-08_BLCA	674	229	245	283	498	360	528	621	377	67	585	0	282	131	26	1	574
TCGA-CF-A47T-10A-01D-A23U-08_BLCA	680	0	0	288	594	374	532	634	391	0	0	0	0	0	27	54	570

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CF-A47V-10A-01D-A23U-08_BLCA	664	235	254	277	577	367	528	635	371	68	516	0	298	133	28	2	573
TCGA-CF-A47W-10A-01D-A23U-08_BLCA	747	252	270	295	528	387	537	640	481	0	0	0	0	0	39	68	581
TCGA-CF-A47X-10A-01D-A23U-08_BLCA	652	228	247	254	588	360	528	645	385	61	519	493	0	0	23	49	572
TCGA-CF-A47Y-10A-01D-A23U-08_BLCA	762	0	0	318	641	406	534	651	487	0	0	0	0	0	64	0	582
TCGA-CF-A5U8-10A-01D-A289-08_BLCA	672	248	267	295	567	373	532	650	487	0	0	0	0	0	0	141	582
TCGA-CF-A5UA-10A-01D-A289-08_BLCA	757	0	0	305	614	397	534	657	479	0	0	0	0	0	45	0	578
TCGA-CG-4300-10A-01D-1158-08_STAD	763	244	262	292	593	382	538	652	490	0	0	0	0	0	0	119	578
TCGA-CG-4301-10A-01D-1158-08_STAD	761	249	274	203	619	290	534	664	492	0	611	574	0	0	34	73	583
TCGA-CG-4304-10A-01D-1158-08_STAD	764	0	0	314	618	407	536	656	494	0	0	0	0	0	0	159	581
TCGA-CG-4305-10A-01D-1158-08_STAD	754	253	266	289	614	396	537	654	455	79	639	516	376	139	0	69	578
TCGA-CG-4306-10A-01D-1158-08_STAD	687	0	0	305	614	398	533	648	458	81	607	0	297	140	0	74	579
TCGA-CG-4436-10A-01D-1158-08_STAD	688	0	0	308	611	400	536	658	475	79	616	0	371	138	0	85	581
TCGA-CG-4437-10A-01D-1800-08_STAD	688	0	0	296	602	375	529	628	458	0	0	0	0	134	0	57	576
TCGA-CG-4438-10A-01D-1158-08_STAD	692	0	0	359	620	390	533	654	492	0	0	0	0	0	0	171	581
TCGA-CG-4440-10A-01D-1158-08_STAD	759	0	0	307	609	382	535	654	410	0	0	0	0	0	0	110	579
TCGA-CG-4441-10A-01D-1800-08_STAD	754	0	0	303	610	383	530	646	456	74	578	0	365	135	0	73	573
TCGA-CG-4442-10A-01D-1158-08_STAD	686	253	261	290	619	386	534	659	490	0	622	571	0	0	30	70	579
TCGA-CG-4443-10A-01D-1158-08_STAD	757	0	0	353	619	374	533	648	477	0	0	0	0	0	0	126	580
TCGA-CG-4444-10A-01D-1158-08_STAD	600	260	280	0	587	142	534	653	489	0	621	573	0	0	50	1	578
TCGA-CG-4449-10A-01D-1158-08_STAD	763	250	272	303	627	395	536	655	494	0	635	521	0	0	0	169	584
TCGA-CG-4455-10A-01D-1158-08_STAD	765	0	0	318	620	396	535	651	493	0	0	0	0	0	0	159	580
TCGA-CG-4460-10A-01D-1158-08_STAD	686	0	0	310	612	389	533	654	482	0	0	0	0	0	0	132	579
TCGA-CG-4462-10A-01D-1158-08_STAD	691	0	0	313	623	401	538	659	491	0	0	0	0	0	0	126	579
TCGA-CG-4465-10A-01D-1158-08_STAD	601	258	278	0	0	0	533	663	402	78	616	0	306	141	36	1	582
TCGA-CG-4466-10A-01D-1158-08_STAD	761	0	0	316	620	404	534	664	496	0	0	0	0	0	0	141	581
TCGA-CG-4469-10A-01D-1158-08_STAD	761	0	0	313	619	392	532	656	470	77	615	0	366	137	0	88	581
TCGA-CG-4472-10A-01D-1158-08_STAD	759	0	0	313	614	294	526	651	457	73	624	0	375	139	0	71	579
TCGA-CG-4474-10A-01D-1158-08_STAD	691	250	264	294	597	388	535	663	495	0	0	0	0	0	0	168	583
TCGA-CG-4475-10A-01D-1158-08_STAD	675	267	279	0	623	144	536	665	473	74	656	585	0	139	36	0	579
TCGA-CG-4476-10A-01D-1158-08_STAD	763	0	0	310	619	391	531	658	482	0	0	0	0	0	33	88	581
TCGA-CG-4477-10A-01D-1158-08_STAD	673	264	281	0	0	0	536	651	483	0	0	0	0	0	0	114	581
TCGA-CG-5716-10A-01D-1800-08_STAD	682	0	0	304	609	378	528	648	476	0	0	0	0	0	28	73	575
TCGA-CG-5717-10A-01D-1600-08_STAD	760	0	0	307	614	398	534	665	488	0	0	0	0	0	33	70	577
TCGA-CG-5718-10A-01D-1600-08_STAD	761	0	0	308	618	385	534	655	458	79	606	0	380	139	0	91	577
TCGA-CG-5719-10A-01D-1600-08_STAD	689	249	273	299	596	0	532	643	475	0	0	0	0	139	0	73	572
TCGA-CH-5737-10A-01D-1576-08_PRAD	686	0	0	312	617	399	534	662	470	80	616	0	378	139	0	75	580
TCGA-CH-5738-10A-01D-1576-08_PRAD	665	258	280	0	606	142	532	659	467	77	659	578	0	139	0	79	577
TCGA-CH-5739-10A-01D-1576-08_PRAD	766	0	0	313	613	403	536	659	483	0	0	0	0	0	0	103	580
TCGA-CH-5740-10A-01D-1576-08_PRAD	677	255	266	289	590	282	533	659	470	84	622	0	372	137	0	88	577
TCGA-CH-5741-10A-01D-1576-08_PRAD	689	0	0	306	616	399	530	662	478	0	0	0	0	0	0	107	579
TCGA-CH-5743-10A-01D-1576-08_PRAD	762	0	0	306	612	395	535	668	494	0	0	0	0	0	0	116	581
TCGA-CH-5744-10A-01D-1576-08_PRAD	684	0	0	306	610	398	536	663	463	81	605	0	368	137	0	78	578
TCGA-CH-5745-10A-01D-1576-08_PRAD	689	0	0	311	618	392	534	657	480	0	0	0	0	0	44	3	578
TCGA-CH-5746-10A-01D-1576-08_PRAD	681	242	268	279	577	369	532	650	386	77	610	0	366	138	0	73	576
TCGA-CH-5748-10A-01D-1576-08_PRAD	761	260	270	302	619	393	533	656	4	85	662	578	379	142	0	4	579
TCGA-CH-5750-10A-01D-1576-08_PRAD	759	0	0	305	614	294	523	658	494	0	0	0	0	0	0	137	579
TCGA-CH-5751-10A-01D-1576-08_PRAD	690	0	0	350	616	397	534	658	489	0	0	0	0	0	0	166	577
TCGA-CH-5752-10A-01D-1576-08_PRAD	595	265	275	0	588	138	535	665	458	82	642	575	0	140	0	87	578
TCGA-CH-5753-10A-01D-1576-08_PRAD	756	0	0	312	615	402	535	655	493	0	0	0	0	0	0	178	577
TCGA-CH-5754-10A-01D-1576-08_PRAD	759	0	0	302	605	291	523	660	480	0	0	0	0	0	0	118	578
TCGA-CH-5788-10A-01D-1576-08_PRAD	758	0	0	312	619	398	536	662	495	0	0	0	0	0	0	157	580
TCGA-CH-5789-10A-01D-1576-08_PRAD	668	254	268	287	613	286	531	650	480	0	599	567	0	0	33	75	575
TCGA-CH-5790-10A-01D-1576-08_PRAD	684	254	269	199	594	284	535	658	476	0	0	0	0	0	0	110	578
TCGA-CH-5791-10A-01D-1576-08_PRAD	689	0	0	318	615	403	535	656	480	0	0	0	0	0	0	116	578
TCGA-CH-5792-10A-01D-1576-08_PRAD	685	0	0	305	605	393	532	663	480	0	0	0	0	0	30	74	577
TCGA-CH-5794-10A-01D-1577-08_PRAD	685	0	0	305	607	377	530	656	458	80	618	0	367	138	0	75	578
TCGA-CI-6621-10A-01D-1826-10_READ	646	0	0	347	589	345	501	588	343	0	0	0	0	0	13	29	567
TCGA-CI-6622-10A-01D-1826-10_READ	662	0	0	360	648	432	548	605	305	104	402	431	279	150	0	23	566
TCGA-CI-6624-10A-01D-1826-10_READ	647	0	0	341	624	407	503	598	421	0	0	0	0	0	0	66	571
TCGA-CK-4947-10A-01D-1650-10_COAD	690	0	0	389	677	439	543	624	343	100	554	0	334	167	0	39	587
TCGA-CK-4952-10A-01D-1719-10_COAD	648	150	235	189	431	312	520	539	313	0	318	0	296	148	0	14	555
TCGA-CK-5912-10A-01D-1650-10_COAD	588	320	353	0	0	0	494	577	430	0	571	0	352	172	0	34	585
TCGA-CK-5913-10A-01D-1650-10_COAD	780	170	273	341	607	408	533	612	455	0	0	0	0	0	11	25	576
TCGA-CK-5915-10A-01D-1650-10_COAD	675	0	0	375	647	436	532	593	314	96	313	0	306	158	0	32	590
TCGA-CK-5916-10A-01D-1650-10_COAD	632	0	0	344	589	353	520	551	332	0	0	0	0	0	0	44	566
TCGA-CL-5917-10A-01D-1657-10_READ	541	283	316	0	338	169	543	596	459	0	403	422	0	0	0	45	589
TCGA-CL-5918-10A-01D-1657-10_READ	678	166	204	351	449	414	493	562	329	0	402	0	247	160	0	28	593
TCGA-CM-4743-10A-01D-1719-10_COAD	799	317	337	361	649	365	520	609	349	0	586	0	445	183	0	54	591
TCGA-CM-4746-10A-01D-1408-10_COAD	614	0	0	322	433	333	459	556	316	0	0	0	0	0	7	19	530
TCGA-CM-4747-10A-01D-1408-10_COAD	594	0	0	229	397	384	455	429	320	0	0	0	0	0	0	30	552
TCGA-CM-4748-10A-01D-1408-10_COAD	595	0	0	276	473	332	452	454	236	0	219	0	162	113	0	20	519
TCGA-CM-4752-10A-01D-1408-10_COAD	627	0	0	207	495	379	484	559	224	0	289	0	137	136	0	29	542
TCGA-CM-5341-10A-01D-1408-10_COAD	611	0	0	209	308	314	421	481	217	0	75	0	195	43	6	0	526
TCGA-CM-5344-10A-01D-1719-10_COAD	700	314	343	370	656	434	551	654	476	0	0	0	0	0	35	47	596
TCGA-CM-5348-10A-01D-1719-10_COAD	787	0	0	375	697	460	556	648	562	0	0	0	0	0	23	55	594
TCGA-CM-5349-10A-01D-1719-10_COAD	793	293	363	361	712	375	554	644	358	100	633	539	447	181	0	49	599
TCGA-CM-5860-10A-01D-1650-10_COAD	699	0	0	381	664	430	529	619	0	103	582	0	364	186	0	0	588
TCGA-CM-5861-10A-01D-1650-10_COAD	671	299	346	0	0	0	516	626	446	0	0	0	0	0	17	39	585
TCGA-CM-5862-10A-01D-1650-10_COAD	558	298	319	0	437	141	482	583	439	0	340	425	0	0	32	0	583
TCGA-CM-5864-10A-01D-1650-10_COAD	647	149	214	294	600	355	507	588	429	0	304	444	0	0	0	49	566
TCGA-CM-5868-10A-01D-1650-10_COAD	494	259	236	0	301	117	484	518	328	0	164	243	0	0	7	13	550
TCGA-CM-6161-10A-01D-1650-10_COAD	678	230	305	219	653	340	551	630	461	0	508	468	0	0	0	58	585
TCGA-CM-6163-10A-01D-1650-10_COAD	665	0	0	358	571	373	501	597	309	88	385	0	321	141	0	24	575
TCGA-CM-6164-10A-01D-1650-10_COAD	667	280	311	357	617	373	559	638	474	0	0	0	0	0	0	60	586
TCGA-CM-6165-10A-01D-1650-10_COAD	574	317	338	0	0	0	553	637	461	0	0	0	0	0	26	0	585
TCGA-CM-6166-10A-01D-1650-10_COAD	682	0	0	360	644	432	525	607	320	92	356	0	307	163	0	26	571
TCGA-CM-6168-10A-01D-1650-10_COAD	628	149	313	218	411	293	496	503	308	0	413	0	267	151	0	24	565
TCGA-CM-6169-10A-01D-1650-10_COAD	648	0	0	351	597	373	513	619	342	0	0	0	0	0	9	26	563
TCGA-CM-6170-10A-01D-1650-10_COAD	682	0	0	364	587	417	536	630	415	0	0	0	0	0	13	23	576
TCGA-CM-6171-10A-01D-1650-10_COAD	569	298	343	0	0	0	533	634	455	0	0	0	0	0	34	0	585
TCGA-CM-6172-10A-01D-1650-10_COAD	686	136	233	299	505	279	528	623	315	76	420	0	236	149	0	25	591
TCGA-CM-6674-10A-01D-1835-10_COAD	659	0	0	340	581	361	491	594	354	0	0	0	0	0	0	49	567
TCGA-CM-6675-10A-01D-1835-10_COAD	666	0	250	210	613	332	521	601	424	0	353	0	268	0	17	23	566
TCGA-CM-6676-10A-01D-1835-10_COAD	679	200	246	214	628	414	510	551	342	0	294	445	0	0	0	44	570
TCGA-CM-6677-10A-01D-1835-10_COAD	559	277	327	0	0	0	527	624	351	0	0	0	0	0	0	70	576
TCGA-CM-6678-10A-01D-1835-10_COAD	664	0	0	336	608	422	490	589	325	92	374	0	305	144	0	29	563

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CM-6679-10A-01D-1835-10_COAD	673	227	289	338	624	436	501	571	319	0	384	0	319	170	0	33	581
TCGA-CN-4723-10A-01D-1434-08_HNSC	668	260	276	0	591	139	535	649	491	0	599	568	0	0	0	137	578
TCGA-CN-4725-10A-01D-1434-08_HNSC	689	0	0	305	608	388	530	653	479	0	0	0	0	0	0	100	575
TCGA-CN-4726-10A-01D-1434-08_HNSC	691	0	0	309	603	387	528	661	483	0	0	0	0	0	0	96	578
TCGA-CN-4727-10A-01D-1434-08_HNSC	684	0	0	301	604	381	528	660	479	0	0	0	0	0	38	86	572
TCGA-CN-4728-10A-01D-1434-08_HNSC	753	250	271	296	614	381	534	662	482	0	620	573	0	0	36	77	577
TCGA-CN-4729-10A-01D-1434-08_HNSC	689	0	0	307	631	392	532	649	477	0	0	0	0	0	0	144	579
TCGA-CN-4730-10A-01D-1434-08_HNSC	685	255	267	297	563	379	534	658	481	0	0	0	0	0	41	78	575
TCGA-CN-4731-10A-01D-1434-08_HNSC	687	247	261	295	614	380	534	657	484	0	584	568	0	0	0	138	580
TCGA-CN-4733-10A-01D-1870-08_HNSC	761	264	283	299	570	385	533	616	463	0	649	573	0	141	35	1	576
TCGA-CN-4734-10A-01D-1434-08_HNSC	679	252	270	288	621	390	532	660	485	0	606	519	0	0	37	79	578
TCGA-CN-4735-10A-01D-1434-08_HNSC	746	249	269	297	614	389	535	656	461	74	639	570	0	132	0	81	579
TCGA-CN-4736-10A-01D-1434-08_HNSC	755	259	271	288	562	391	535	651	491	0	0	0	0	0	42	87	579
TCGA-CN-4737-10A-01D-1434-08_HNSC	690	0	0	311	615	391	533	658	459	80	623	572	0	138	0	81	575
TCGA-CN-4738-10A-01D-1512-08_HNSC	677	251	264	294	561	284	531	654	480	0	0	0	0	0	31	77	575
TCGA-CN-4739-10A-01D-1512-08_HNSC	687	249	266	291	609	385	534	655	477	0	595	515	0	0	37	59	576
TCGA-CN-4740-10A-01D-1434-08_HNSC	685	253	259	290	614	381	533	654	481	0	612	566	0	0	38	71	577
TCGA-CN-4741-10A-01D-1434-08_HNSC	602	257	278	0	0	0	532	655	391	79	623	0	369	137	36	4	572
TCGA-CN-4742-10A-01D-1512-08_HNSC	758	0	0	302	605	392	533	653	381	76	590	0	360	135	26	3	573
TCGA-CN-5355-10A-01D-1434-08_HNSC	686	0	0	294	620	390	531	659	469	0	637	0	398	0	0	66	570
TCGA-CN-5356-10A-01D-1434-08_HNSC	753	0	0	298	603	286	523	639	406	0	0	0	0	0	0	119	577
TCGA-CN-5358-10A-01D-1512-08_HNSC	684	241	269	296	514	375	534	639	475	0	0	0	0	0	0	91	579
TCGA-CN-5359-10A-01D-1434-08_HNSC	686	0	0	307	606	389	537	661	476	81	0	0	0	0	48	3	573
TCGA-CN-5360-10A-01D-1434-08_HNSC	684	250	265	286	587	374	531	646	479	0	0	0	0	0	0	92	577
TCGA-CN-5361-10A-01D-1434-08_HNSC	684	248	269	297	614	383	534	655	481	0	614	568	0	0	0	147	580
TCGA-CN-5363-10A-01D-1434-08_HNSC	691	0	0	303	605	384	531	645	483	0	0	0	0	0	44	1	575
TCGA-CN-5364-10A-01D-1434-08_HNSC	688	0	0	303	607	288	522	654	472	0	0	0	0	0	0	104	579
TCGA-CN-5365-10A-01D-1434-08_HNSC	685	0	0	300	602	383	527	652	0	84	636	0	378	140	0	1	575
TCGA-CN-5366-10A-01D-1434-08_HNSC	682	0	0	305	600	391	531	656	388	78	598	534	0	134	0	72	578
TCGA-CN-5367-10A-01D-1434-08_HNSC	689	0	0	303	606	387	527	642	475	0	0	0	0	0	0	89	575
TCGA-CN-5369-10A-01D-1434-08_HNSC	685	0	0	304	603	290	525	642	471	0	0	0	0	0	0	99	580
TCGA-CN-5370-10A-01D-2013-08_HNSC	685	0	0	298	596	392	534	639	477	0	0	0	0	0	35	57	578
TCGA-CN-5373-10A-01D-1434-08_HNSC	681	0	0	301	599	382	530	649	473	0	0	0	0	0	48	0	576
TCGA-CN-5374-10A-01D-1434-08_HNSC	686	255	268	301	593	281	528	658	484	0	0	0	0	0	39	85	577
TCGA-CN-6010-10A-01D-1683-08_HNSC	672	237	248	279	542	360	526	634	467	0	0	0	0	0	0	79	577
TCGA-CN-6011-10A-01D-1683-08_HNSC	682	242	257	266	558	358	528	632	479	0	0	0	0	0	24	42	572
TCGA-CN-6012-10A-01D-1683-08_HNSC	659	231	261	175	599	285	533	639	479	0	518	509	0	0	23	59	577
TCGA-CN-6013-10A-01D-1683-08_HNSC	682	0	0	302	608	387	530	639	482	0	0	0	0	0	25	52	575
TCGA-CN-6016-10A-01D-1683-08_HNSC	685	238	256	278	588	367	527	635	373	63	615	505	276	133	27	0	575
TCGA-CN-6017-10A-01D-1683-08_HNSC	678	242	264	274	604	277	532	635	402	0	570	503	0	0	0	89	575
TCGA-CN-6018-10A-01D-1683-08_HNSC	671	0	0	296	601	385	530	643	469	0	0	0	0	0	23	51	572
TCGA-CN-6019-10A-01D-1683-08_HNSC	684	0	0	300	576	374	515	632	393	0	0	0	0	0	0	66	573
TCGA-CN-6020-10A-01D-1683-08_HNSC	674	237	251	180	606	308	535	640	472	0	522	494	0	0	28	53	573
TCGA-CN-6021-10A-01D-1683-08_HNSC	682	0	0	302	599	382	531	638	368	76	505	493	0	137	0	45	574
TCGA-CN-6022-10A-01D-1683-08_HNSC	682	0	0	304	606	385	532	638	450	72	578	0	292	138	0	64	577
TCGA-CN-6023-10A-01D-1683-08_HNSC	682	239	259	281	569	365	533	639	464	0	574	501	0	0	19	52	575
TCGA-CN-6024-10A-01D-1683-08_HNSC	677	0	0	298	595	390	537	644	436	74	588	0	286	130	0	53	574
TCGA-CN-6988-10A-01D-1912-08_HNSC	686	0	0	339	606	393	533	638	478	0	0	0	0	0	0	91	577
TCGA-CN-6989-10A-01D-1912-08_HNSC	750	251	273	288	522	372	534	653	486	0	0	0	0	0	30	67	580
TCGA-CN-6992-10A-01D-1912-08_HNSC	681	0	0	306	613	391	535	645	487	0	0	0	0	0	0	97	578
TCGA-CN-6994-10A-01D-1912-08_HNSC	661	239	259	281	586	283	531	637	391	62	633	574	0	137	0	65	577
TCGA-CN-6995-10A-01D-2013-08_HNSC	750	253	272	282	590	279	530	645	479	0	0	0	0	0	38	1	581
TCGA-CN-6996-10A-01D-1912-08_HNSC	680	248	268	280	339	0	521	614	393	0	592	565	0	135	0	57	578
TCGA-CN-6997-10A-01D-2013-08_HNSC	680	253	268	291	591	382	533	642	476	0	0	0	0	0	0	109	577
TCGA-CN-6998-10A-01D-2013-08_HNSC	679	249	269	288	614	385	535	656	479	0	536	521	0	0	29	76	576
TCGA-CN-A497-10A-01D-A24F-08_HNSC	670	235	251	182	510	280	532	641	473	0	0	0	0	0	30	55	570
TCGA-CN-A498-10A-01D-A24F-08_HNSC	674	0	0	295	597	281	519	634	467	0	0	0	0	0	0	114	574
TCGA-CN-A499-10A-01D-A24F-08_HNSC	684	0	0	300	594	377	525	633	370	72	521	0	289	130	0	55	572
TCGA-CN-A49A-10A-01D-A24F-08_HNSC	585	226	255	253	520	273	527	623	346	68	614	558	0	132	0	51	569
TCGA-CN-A49B-10A-01D-A24F-08_HNSC	670	0	0	296	593	372	525	625	460	0	0	0	0	0	32	3	571
TCGA-CN-A49C-10B-01D-A24F-08_HNSC	683	0	0	297	595	375	530	631	401	0	0	0	0	0	0	110	573
TCGA-CN-A63U-10A-01D-A30H-08_HNSC	674	248	268	292	598	286	534	648	475	0	0	0	0	0	0	98	578
TCGA-CN-A63W-10A-01D-A30H-08_HNSC	761	0	0	312	622	297	529	653	491	0	0	0	0	0	0	177	581
TCGA-CN-A63Y-10A-01D-A30H-08_HNSC	749	262	276	293	596	295	533	650	0	90	654	584	382	145	0	0	580
TCGA-CN-A640-10A-01D-A30H-08_HNSC	752	254	270	289	618	296	537	648	486	0	619	571	0	0	42	75	579
TCGA-CN-A641-10A-01D-A30H-08_HNSC	760	0	0	321	620	406	537	652	401	78	572	0	375	142	0	82	581
TCGA-CN-A642-10A-01D-A30H-08_HNSC	767	256	264	300	623	384	539	654	0	83	649	576	397	145	0	1	580
TCGA-CQ-5323-10A-01D-1683-08_HNSC	639	241	245	271	594	278	524	627	473	0	547	507	0	0	0	78	571
TCGA-CQ-5324-10A-01D-1683-08_HNSC	674	230	258	270	611	367	535	645	377	79	628	569	290	130	0	56	574
TCGA-CQ-5325-10A-01D-1683-08_HNSC	640	245	260	272	574	362	531	644	467	0	0	0	0	0	36	2	573
TCGA-CQ-5326-10A-01D-1870-08_HNSC	757	0	0	310	616	292	524	656	471	81	593	0	303	136	0	78	576
TCGA-CQ-5327-10A-01D-1683-08_HNSC	688	0	0	301	597	392	528	639	474	0	0	0	0	0	23	57	573
TCGA-CQ-5329-10A-01D-1683-08_HNSC	666	212	252	266	519	0	496	578	440	0	0	0	0	134	0	49	562
TCGA-CQ-5330-10A-01D-1683-08_HNSC	674	234	248	272	561	367	529	621	464	0	0	0	0	0	0	84	573
TCGA-CQ-5331-10A-01D-1870-08_HNSC	682	0	0	295	613	384	531	637	487	0	0	0	0	0	33	66	580
TCGA-CQ-5332-10A-01D-1683-08_HNSC	668	246	250	191	608	376	530	645	472	0	511	509	0	0	26	61	576
TCGA-CQ-5333-10A-01D-2394-08_HNSC	663	230	249	262	606	272	527	640	304	61	618	504	287	130	0	61	575
TCGA-CQ-5334-10A-01D-1683-08_HNSC	675	0	0	261	467	353	505	589	375	0	0	0	0	0	0	49	574
TCGA-CQ-6218-10A-01D-1912-08_HNSC	688	246	254	284	575	373	530	645	448	65	538	0	305	134	0	62	573
TCGA-CQ-6219-10A-01D-1912-08_HNSC	688	0	0	304	615	287	528	655	492	0	0	0	0	0	22	69	580
TCGA-CQ-6220-10A-01D-1912-08_HNSC	688	0	0	303	610	381	534	647	317	76	600	0	363	138	0	63	574
TCGA-CQ-6221-10A-01D-2078-08_HNSC	683	0	0	300	595	367	522	640	472	0	0	0	0	0	21	55	577
TCGA-CQ-6222-10A-01D-1912-08_HNSC	686	246	262	291	559	375	532	644	482	0	0	0	0	0	0	73	577
TCGA-CQ-6223-10A-01D-1912-08_HNSC	640	243	258	273	608	284	531	647	455	78	636	562	360	134	0	65	575
TCGA-CQ-6224-10A-01D-1912-08_HNSC	686	0	0	297	606	380	530	633	482	0	0	0	0	0	0	117	577
TCGA-CQ-6225-10A-01D-1912-08_HNSC	676	0	0	340	607	373	529	649	379	76	606	563	0	138	0	56	574
TCGA-CQ-6227-10A-01D-1912-08_HNSC	684	0	0	301	604	380	532	635	454	79	543	514	0	135	0	64	572
TCGA-CQ-6228-10A-01D-1912-08_HNSC	678	247	262	275	513	373	536	639	446	74	592	511	0	133	28	0	574
TCGA-CQ-6229-10A-01D-1912-08_HNSC	599	256	272	0	552	133	532	624	0	79	650	563	377	139	0	0	577
TCGA-CQ-7063-10A-01D-2394-08_HNSC	684	0	0	298	602	376	528	648	367	68	601	0	364	133	0	59	569
TCGA-CQ-7064-10A-01D-2394-08_HNSC	663	241	265	282	609	280	530	642	457	77	622	513	363	134	0	71	576
TCGA-CQ-7065-10A-01D-2078-08_HNSC	688	217	235	265	566	347	529	641	378	68	567	0	281	121	0	41	577
TCGA-CQ-7067-10A-01D-2229-08_HNSC	673	243	260	269	577	365	533	631	377	70	614	567	293	134	0	43	575
TCGA-CQ-7068-10A-01D-2078-08_HNSC	683	240	259	285	604	357	529	640	387	76	627	565	283	134	0	64	572
TCGA-CQ-7069-10A-01D-2394-08_HNSC	667	250	259	290	610	284	530	642	42	85	637	560	373	140	0	2	578
TCGA-CQ-7071-10A-01D-A30H-08_HNSC	761	0	0	318	618	407	536	654	490	0	0	0	0	0	0	143	581

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CQ-7072-10A-01D-A30H-08_HNSC	739	258	266	285	569	380	528	618	444	0	545	519	0	140	0	69	578
TCGA-CQ-A4C6-10A-01D-A25E-08_HNSC	676	0	0	285	605	378	528	639	0	83	626	554	371	135	0	1	570
TCGA-CQ-A4C7-10A-01D-A25E-08_HNSC	592	254	266	0	583	135	528	642	457	0	608	568	0	0	20	60	570
TCGA-CQ-A4C9-10A-01D-A25E-08_HNSC	679	239	251	281	608	368	528	632	441	73	620	566	0	132	0	50	573
TCGA-CQ-A4CA-10A-01D-A25E-08_HNSC	670	236	249	265	604	374	528	635	304	65	607	506	357	131	0	57	574
TCGA-CQ-A4CB-10A-01D-A25E-08_HNSC	680	0	0	283	584	277	526	621	458	0	0	0	0	0	0	99	569
TCGA-CQ-A4CD-10A-01D-A25E-08_HNSC	667	240	252	272	546	364	527	629	474	0	0	0	0	0	0	106	571
TCGA-CQ-A4CE-10A-01D-A25Y-08_HNSC	672	233	249	158	523	265	527	621	428	65	603	562	0	131	0	36	572
TCGA-CQ-A4CG-10A-01D-A25Y-08_HNSC	684	0	0	304	610	383	524	641	381	73	580	516	0	131	0	71	573
TCGA-CQ-A4CH-10A-01D-A25Y-08_HNSC	663	239	265	279	600	359	525	630	471	0	586	501	0	0	37	2	572
TCGA-CQ-A4CI-10A-01D-A25Y-08_HNSC	594	259	274	0	556	133	528	653	444	80	622	514	299	137	38	3	572
TCGA-CR-5243-10A-01D-1512-08_HNSC	672	231	256	277	497	276	526	643	358	60	561	0	274	127	0	44	577
TCGA-CR-5247-10A-01D-2013-08_HNSC	685	0	264	288	526	372	536	639	474	0	0	0	0	0	34	72	574
TCGA-CR-5248-10A-01D-2013-08_HNSC	687	0	0	300	607	380	526	618	400	0	0	0	0	0	0	85	578
TCGA-CR-5249-10A-01D-1512-08_HNSC	742	242	270	292	608	280	526	663	471	0	608	564	0	0	27	66	575
TCGA-CR-5250-10A-01D-1512-08_HNSC	752	253	270	297	621	383	535	660	487	0	600	569	0	0	69	0	580
TCGA-CR-6467-10A-01D-1870-08_HNSC	686	249	272	290	613	280	530	643	481	0	610	566	0	0	0	95	574
TCGA-CR-6470-10A-01D-1870-08_HNSC	686	0	0	292	606	291	531	641	454	64	607	0	303	135	31	0	579
TCGA-CR-6471-10A-01D-1870-08_HNSC	675	243	266	270	605	366	527	645	374	62	609	507	291	132	0	57	579
TCGA-CR-6472-10A-01D-1870-08_HNSC	686	0	0	302	606	382	533	656	376	82	606	0	303	136	0	65	573
TCGA-CR-6473-10A-01D-1870-08_HNSC	681	239	267	279	610	376	533	642	458	0	594	508	0	0	0	84	578
TCGA-CR-6474-10A-01D-1870-08_HNSC	680	255	265	300	581	374	522	623	452	0	609	0	367	135	0	67	575
TCGA-CR-6477-10A-01D-1870-08_HNSC	677	248	266	287	570	285	535	655	478	74	0	0	0	0	0	95	576
TCGA-CR-6478-10A-01D-1870-08_HNSC	684	0	0	304	616	388	531	648	461	76	529	0	375	135	0	63	579
TCGA-CR-6480-10A-01D-1870-08_HNSC	756	0	0	304	614	401	534	651	484	0	0	0	0	0	0	96	576
TCGA-CR-6481-10A-01D-1870-08_HNSC	681	250	269	277	580	385	535	642	478	0	0	0	0	0	48	0	577
TCGA-CR-6482-10A-01D-1870-08_HNSC	757	0	0	312	609	390	528	620	455	0	581	0	365	139	31	1	577
TCGA-CR-6484-10A-01D-1870-08_HNSC	757	0	0	306	615	381	534	651	482	0	0	0	0	0	38	63	579
TCGA-CR-6487-10A-01D-1870-08_HNSC	686	0	0	300	615	388	536	649	475	0	0	0	0	0	29	65	575
TCGA-CR-6488-10A-01D-2078-08_HNSC	637	231	234	272	566	343	526	632	456	0	568	507	0	0	19	47	573
TCGA-CR-6491-10A-01D-1870-08_HNSC	685	0	0	301	642	336	536	652	488	0	617	566	0	0	39	80	579
TCGA-CR-6492-10A-01D-2078-08_HNSC	634	240	254	262	490	362	524	633	397	0	0	0	0	0	20	37	576
TCGA-CR-6493-10A-01D-1870-08_HNSC	686	0	0	307	613	390	535	643	476	82	618	0	373	140	0	81	577
TCGA-CR-7364-10A-01D-2013-08_HNSC	688	0	0	307	615	387	529	657	488	0	0	0	0	0	34	72	577
TCGA-CR-7365-10A-01D-2013-08_HNSC	686	0	0	304	609	386	532	655	477	0	0	0	0	0	32	77	575
TCGA-CR-7367-10A-01D-2013-08_HNSC	598	259	276	0	0	0	531	636	478	0	0	0	0	0	45	0	576
TCGA-CR-7368-10A-01D-2129-08_HNSC	683	0	0	299	600	376	526	635	478	0	0	0	0	0	0	109	576
TCGA-CR-7369-10A-01D-2129-08_HNSC	682	245	259	296	596	284	529	645	483	0	0	0	0	0	0	124	576
TCGA-CR-7370-10A-01D-2129-08_HNSC	670	247	257	288	573	282	529	637	0	82	630	0	381	138	0	2	575
TCGA-CR-7371-10A-01D-2013-08_HNSC	686	0	0	296	609	381	533	651	442	78	599	0	369	136	0	74	574
TCGA-CR-7372-10A-01D-2013-08_HNSC	599	261	275	0	559	136	530	654	391	75	631	565	365	137	0	72	574
TCGA-CR-7373-10A-01D-2013-08_HNSC	682	250	267	288	588	379	527	619	471	0	584	0	365	135	0	72	575
TCGA-CR-7374-10A-01D-2013-08_HNSC	674	252	263	287	586	384	532	652	470	0	614	511	0	0	0	93	579
TCGA-CR-7376-10A-01D-2129-08_HNSC	592	254	269	0	0	0	532	644	468	0	0	0	0	0	26	55	571
TCGA-CR-7377-10A-01D-2013-08_HNSC	677	252	264	291	612	382	532	653	479	0	593	566	0	0	29	66	578
TCGA-CR-7379-10A-01D-2013-08_HNSC	671	257	138	291	582	380	533	653	457	74	591	0	371	137	24	0	576
TCGA-CR-7380-10A-01D-2013-08_HNSC	688	0	0	305	607	386	531	644	477	0	0	0	0	0	31	77	575
TCGA-CR-7382-10A-01D-2129-08_HNSC	687	0	0	297	589	381	529	641	406	0	0	0	0	0	29	51	574
TCGA-CR-7383-10A-01D-2129-08_HNSC	683	35	0	293	608	369	525	614	0	76	587	512	29	135	0	3	574
TCGA-CR-7385-10A-01D-2013-08_HNSC	669	243	268	287	562	282	532	641	475	0	0	0	0	0	0	132	577
TCGA-CR-7386-10A-01D-2013-08_HNSC	757	0	0	302	609	290	525	657	482	0	0	0	0	0	0	131	575
TCGA-CR-7388-10A-01D-2013-08_HNSC	685	251	272	290	612	381	530	647	376	73	635	573	0	139	0	69	575
TCGA-CR-7389-10A-01D-2013-08_HNSC	760	0	0	306	607	387	532	628	478	0	0	0	0	0	34	1	575
TCGA-CR-7390-10A-01D-2013-08_HNSC	687	0	0	302	605	383	529	651	486	0	0	0	0	0	28	79	575
TCGA-CR-7391-10A-01D-2013-08_HNSC	757	0	0	301	625	389	531	641	487	0	0	0	0	0	0	143	575
TCGA-CR-7392-10A-01D-2013-08_HNSC	759	0	0	308	629	390	531	649	473	0	0	0	0	0	0	93	574
TCGA-CR-7393-10A-01D-2013-08_HNSC	755	0	0	302	609	293	525	650	466	79	593	0	304	136	0	76	578
TCGA-CR-7394-10A-01D-2013-08_HNSC	688	0	0	303	598	389	532	638	477	0	0	0	0	0	0	127	580
TCGA-CR-7395-10A-01D-2013-08_HNSC	681	242	270	284	557	377	532	651	472	0	0	0	0	0	32	66	574
TCGA-CR-7397-10A-01D-2013-08_HNSC	683	247	270	295	614	378	533	645	454	75	636	576	0	137	32	0	578
TCGA-CR-7398-10A-01D-2013-08_HNSC	689	0	0	307	603	289	524	653	484	0	0	0	0	0	0	149	578
TCGA-CR-7399-10A-01D-2013-08_HNSC	688	0	0	307	608	389	530	648	484	0	0	0	0	0	0	133	580
TCGA-CR-7401-10A-01D-2013-08_HNSC	690	0	0	307	606	386	533	654	480	0	0	0	0	0	38	74	578
TCGA-CR-7402-10A-01D-2013-08_HNSC	673	247	270	289	605	380	533	654	453	82	639	562	368	137	29	0	576
TCGA-CR-7404-10A-01D-2129-08_HNSC	684	0	0	300	597	285	522	635	469	0	0	0	0	0	0	111	577
TCGA-CS-4938-10A-01D-1893-08_LGG	685	0	0	312	610	393	534	641	482	0	0	0	0	0	0	88	578
TCGA-CS-4941-10A-01D-1468-08_LGG	675	253	263	290	609	286	531	659	466	0	589	518	0	0	35	71	581
TCGA-CS-4942-10A-01D-1468-08_LGG	688	0	0	304	610	385	535	652	452	79	616	0	368	136	33	1	577
TCGA-CS-4943-10A-01D-1468-08_LGG	684	0	0	300	603	376	522	622	386	0	0	0	0	131	0	65	570
TCGA-CS-4944-10A-01D-1468-08_LGG	601	261	276	0	605	140	532	654	0	85	658	579	381	139	0	0	578
TCGA-CS-5390-10A-01D-1468-08_LGG	756	0	0	298	605	289	525	662	485	0	0	0	0	0	0	141	580
TCGA-CS-5393-10A-01D-1468-08_LGG	683	243	261	280	615	382	536	660	446	78	640	577	0	137	0	71	574
TCGA-CS-5394-10A-01D-1468-08_LGG	596	259	270	0	603	136	526	652	450	72	647	577	363	137	0	75	575
TCGA-CS-5395-10A-01D-1468-08_LGG	687	241	266	285	610	375	531	664	472	68	532	509	0	0	25	71	572
TCGA-CS-5396-10A-01D-1468-08_LGG	685	246	269	279	558	374	531	650	468	0	0	0	0	0	0	98	576
TCGA-CS-5397-10A-03D-1893-08_LGG	758	0	0	309	599	286	525	646	472	0	0	0	0	0	0	98	575
TCGA-CS-6186-10A-01D-2024-08_LGG	596	250	273	0	578	135	530	627	0	81	653	568	370	140	0	0	573
TCGA-CS-6188-10A-01D-1893-08_LGG	687	0	0	308	612	288	523	645	401	79	624	0	366	137	34	1	576
TCGA-CS-6290-10A-01D-1705-08_LGG	676	0	0	302	601	385	523	639	471	0	0	0	0	0	0	93	579
TCGA-CS-6665-10A-01D-1893-08_LGG	690	0	0	312	607	399	533	655	483	0	0	0	0	0	31	58	575
TCGA-CS-6666-10A-01D-1893-08_LGG	681	254	263	296	593	281	532	653	480	0	0	0	0	0	45	0	578
TCGA-CS-6667-10A-01D-2024-08_LGG	595	253	271	0	554	131	530	651	474	74	598	513	0	0	0	109	573
TCGA-CS-6668-10A-01D-1893-08_LGG	681	250	270	293	566	284	532	649	490	0	0	0	0	0	31	83	575
TCGA-CS-6669-10A-01D-1893-08_LGG	686	253	272	295	594	382	533	653	490	0	0	0	0	0	0	154	579
TCGA-CS-6670-10A-01D-1893-08_LGG	755	250	272	290	616	286	531	657	484	0	617	567	0	0	0	150	578
TCGA-CU-A0YO-10A-01D-A10S-08_BLCA	672	250	268	294	615	285	530	653	456	71	626	573	0	135	0	79	577
TCGA-CU-A0YR-10A-01D-A10S-08_BLCA	599	259	274	0	573	138	536	656	478	0	596	564	0	0	0	105	575
TCGA-CU-A3KJ-10A-01D-A21A-08_BLCA	689	236	236	255	593	356	528	638	465	0	568	507	0	0	0	80	577
TCGA-CU-A3QU-10B-01D-A22Z-08_BLCA	756	0	0	359	618	393	536	659	488	0	0	0	0	0	35	79	580
TCGA-CU-A3YL-10A-01D-A22Z-08_BLCA	762	251	264	296	571	388	534	656	490	0	0	0	0	0	0	127	579
TCGA-CU-A5W6-10A-01D-A289-08_BLCA	754	0	0	304	613	391	530	655	474	0	0	0	0	0	0	92	578
TCGA-CU-A72E-10A-01D-A339-08_BLCA	594	250	272	0	545	132	523	638	437	66	624	565	0	136	28	0	577
TCGA-CV-5430-10A-01D-1870-08_HNSC	684	0	0	302	601	384	532	640	0	82	633	0	376	140	0	0	579
TCGA-CV-5432-10A-01D-1870-08_HNSC	757	251	270	286	615	385	537	650	484	0	610	570	0	0	0	129	577
TCGA-CV-5434-10A-01D-1870-08_HNSC	599	263	281	0	519	139	531	615	473	0	646	570	373	139	42	0	578
TCGA-CV-5435-10A-01D-1870-08_HNSC	593	264	277	0	612	140	534	652	0	85	661	585	0	143	0	0	577

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CV-5436-10A-01D-1870-08_HNSC	741	246	0	297	610	287	536	644	459	63	627	0	366	136	31	0	578
TCGA-CV-5966-10A-01D-1870-08_HNSC	681	254	269	289	618	376	535	640	464	0	627	564	379	141	0	70	576
TCGA-CV-5970-10A-01D-1870-08_HNSC	683	252	260	282	617	388	535	654	480	0	609	516	0	0	31	63	576
TCGA-CV-6933-10A-01D-1912-08_HNSC	678	251	259	283	606	286	530	650	482	0	534	559	0	0	34	67	574
TCGA-CV-6934-10A-01D-1912-08_HNSC	683	0	0	300	603	386	532	633	470	0	0	0	0	0	0	127	572
TCGA-CV-6935-10A-01D-1912-08_HNSC	657	247	265	275	605	283	525	639	479	0	588	511	0	0	25	58	574
TCGA-CV-6936-10A-01D-1912-08_HNSC	757	0	0	298	600	285	524	635	388	80	600	0	298	134	27	0	578
TCGA-CV-6937-10A-01D-2013-08_HNSC	685	0	0	306	602	386	529	642	473	0	0	0	0	0	30	71	574
TCGA-CV-6938-10A-01D-1912-08_HNSC	673	246	266	287	608	386	531	640	456	79	634	499	367	138	0	55	578
TCGA-CV-6939-10A-01D-1912-08_HNSC	686	0	0	298	601	386	531	645	455	72	605	0	290	131	0	69	573
TCGA-CV-6940-10A-01D-1912-08_HNSC	680	251	259	284	611	378	534	643	461	66	637	564	303	137	0	60	577
TCGA-CV-6941-10A-01D-1912-08_HNSC	752	244	260	285	609	374	534	643	479	0	600	557	0	0	28	66	572
TCGA-CV-6942-10A-01D-2013-08_HNSC	688	0	0	299	602	391	533	640	455	77	579	0	370	132	33	1	575
TCGA-CV-6943-10A-01D-1912-08_HNSC	686	0	0	294	600	384	531	646	474	0	0	0	0	0	0	123	575
TCGA-CV-6945-10A-01D-1912-08_HNSC	597	255	272	0	583	137	530	636	387	70	636	574	0	137	0	65	572
TCGA-CV-6948-10A-01D-1912-08_HNSC	687	0	0	300	601	290	523	649	475	0	0	0	0	0	0	117	576
TCGA-CV-6950-10A-01D-1912-08_HNSC	677	237	264	290	615	377	534	643	392	73	623	563	0	137	0	71	577
TCGA-CV-6951-10A-01D-1912-08_HNSC	686	0	0	300	592	385	532	643	476	0	0	0	0	0	0	124	578
TCGA-CV-6952-10A-01D-1912-08_HNSC	644	243	252	270	603	377	531	630	364	71	619	576	0	129	0	59	573
TCGA-CV-6953-10A-01D-1912-08_HNSC	756	250	262	288	580	375	535	649	480	0	0	0	0	0	0	133	576
TCGA-CV-6954-10A-01D-1912-08_HNSC	685	0	0	305	595	390	533	636	479	0	0	0	0	0	0	133	580
TCGA-CV-6955-10A-01D-2013-08_HNSC	684	0	0	298	594	396	531	648	479	0	0	0	0	0	36	80	574
TCGA-CV-6956-10A-01D-2013-08_HNSC	686	0	0	299	608	389	531	644	470	0	0	0	0	0	29	68	576
TCGA-CV-6959-10A-01D-1912-08_HNSC	680	0	0	299	596	374	527	624	473	0	0	0	0	0	0	81	576
TCGA-CV-6960-10A-01D-2013-08_HNSC	683	0	0	300	603	381	532	645	470	0	0	0	0	0	36	62	574
TCGA-CV-6961-10A-01D-1912-08_HNSC	684	0	0	304	600	378	530	642	471	0	0	0	0	0	29	66	576
TCGA-CV-6962-10A-01D-1912-08_HNSC	675	0	257	294	574	376	534	642	476	0	584	0	385	0	29	64	574
TCGA-CV-7089-10A-01D-2013-08_HNSC	686	0	0	307	595	386	524	637	462	0	0	0	0	0	0	83	575
TCGA-CV-7090-10A-01D-2013-08_HNSC	598	252	273	0	0	0	528	622	376	0	589	565	0	136	0	70	575
TCGA-CV-7091-10A-01D-2013-08_HNSC	755	0	0	299	625	386	532	647	452	80	634	565	375	134	0	62	572
TCGA-CV-7095-10A-01D-2013-08_HNSC	686	0	0	299	604	379	530	646	480	0	0	0	0	0	0	116	578
TCGA-CV-7097-10A-01D-2013-08_HNSC	758	0	0	311	615	393	536	655	482	0	0	0	0	0	0	125	578
TCGA-CV-7099-10A-01D-2013-08_HNSC	682	242	271	295	621	284	534	651	445	78	639	561	301	140	0	57	581
TCGA-CV-7100-10A-01D-2013-08_HNSC	688	0	0	306	602	387	532	651	485	0	0	0	0	0	30	71	578
TCGA-CV-7101-10A-01D-2013-08_HNSC	685	252	273	191	620	284	532	648	466	79	646	564	369	137	33	2	578
TCGA-CV-7102-10A-01D-2013-08_HNSC	684	0	0	306	578	285	522	651	482	0	0	0	0	0	30	69	579
TCGA-CV-7103-10A-01D-2013-08_HNSC	597	259	273	0	0	0	530	648	390	70	594	0	374	137	0	64	575
TCGA-CV-7104-10A-01D-2013-08_HNSC	680	248	269	289	611	289	532	646	459	74	643	565	368	140	0	82	574
TCGA-CV-7177-10A-01D-2013-08_HNSC	681	248	273	198	609	283	526	632	0	60	643	564	367	138	0	1	571
TCGA-CV-7178-10A-01D-2013-08_HNSC	689	0	0	303	601	289	525	650	481	0	0	0	0	0	32	70	575
TCGA-CV-7180-10A-01D-2013-08_HNSC	693	0	0	304	610	383	534	654	483	0	0	0	0	0	39	76	576
TCGA-CV-7183-10A-01D-2013-08_HNSC	683	0	0	312	617	388	531	642	482	0	0	0	0	0	0	129	580
TCGA-CV-7235-10A-01D-2013-08_HNSC	760	252	275	287	618	376	534	650	486	0	610	512	0	0	0	105	576
TCGA-CV-7236-10A-01D-2013-08_HNSC	756	0	0	303	582	400	535	643	489	0	0	0	0	0	35	64	577
TCGA-CV-7238-10A-01D-2013-08_HNSC	689	0	0	309	613	386	532	653	476	0	0	0	0	0	35	77	573
TCGA-CV-7242-10A-01D-2013-08_HNSC	687	0	0	306	608	383	531	636	479	0	0	0	0	0	0	118	576
TCGA-CV-7243-10A-01D-2013-08_HNSC	672	255	265	291	562	282	532	652	477	0	0	0	0	0	30	71	576
TCGA-CV-7245-10A-01D-2013-08_HNSC	681	255	265	295	559	279	531	648	459	76	608	0	371	139	0	67	574
TCGA-CV-7247-10A-01D-2013-08_HNSC	689	0	0	303	598	381	533	641	481	0	0	0	0	0	0	129	577
TCGA-CV-7248-10A-01D-2013-08_HNSC	682	249	267	286	613	394	533	648	478	0	591	0	368	0	38	76	575
TCGA-CV-7250-10A-01D-2013-08_HNSC	689	0	0	301	607	292	533	646	479	0	0	0	0	0	0	137	576
TCGA-CV-7252-10A-01D-2013-08_HNSC	682	247	262	188	608	381	533	641	458	75	643	572	373	135	0	64	579
TCGA-CV-7253-10A-01D-2013-08_HNSC	597	261	278	0	582	136	532	640	480	0	541	565	0	0	0	77	577
TCGA-CV-7254-10A-01D-2013-08_HNSC	762	0	0	301	594	387	532	647	459	79	624	0	364	136	0	66	576
TCGA-CV-7255-10A-01D-2013-08_HNSC	666	238	264	288	558	280	534	654	489	0	0	0	0	0	33	61	574
TCGA-CV-7261-10A-01D-2013-08_HNSC	757	0	0	301	611	387	532	650	476	0	0	0	0	0	0	83	575
TCGA-CV-7263-10A-01D-2013-08_HNSC	753	253	274	288	609	328	532	652	399	75	635	567	366	137	0	71	571
TCGA-CV-7406-10A-01D-2078-08_HNSC	684	0	0	297	597	376	531	633	373	65	579	0	360	133	0	52	574
TCGA-CV-7407-10A-01D-2078-08_HNSC	683	0	0	296	598	376	528	632	384	70	559	0	286	136	0	43	573
TCGA-CV-7409-10A-01D-2229-08_HNSC	681	0	259	270	615	383	530	634	471	0	569	0	377	0	23	59	574
TCGA-CV-7410-10A-01D-2078-08_HNSC	657	247	259	268	498	280	523	626	475	0	0	0	0	0	29	54	575
TCGA-CV-7411-10A-01D-2078-08_HNSC	684	0	0	292	591	377	528	630	373	67	576	0	288	134	0	46	573
TCGA-CV-7413-10A-01D-2078-08_HNSC	680	0	0	295	587	365	527	636	360	62	504	0	289	131	0	52	573
TCGA-CV-7414-10A-01D-2078-08_HNSC	677	0	0	299	599	280	521	639	379	68	553	0	355	134	0	52	575
TCGA-CV-7415-10A-01D-2078-08_HNSC	598	249	268	0	0	0	523	646	375	76	579	0	284	130	20	2	578
TCGA-CV-7416-10A-01D-2078-08_HNSC	671	247	255	275	598	360	528	642	377	78	619	565	0	133	0	53	572
TCGA-CV-7418-10A-01D-2078-08_HNSC	676	0	261	188	600	274	529	626	463	0	580	0	308	0	24	55	572
TCGA-CV-7421-10A-01D-2078-08_HNSC	684	0	0	302	600	373	528	650	465	0	0	0	0	0	24	45	573
TCGA-CV-7422-10A-01D-2078-08_HNSC	685	0	0	302	597	377	531	627	474	0	0	0	0	0	0	83	578
TCGA-CV-7423-10A-01D-2078-08_HNSC	680	0	0	302	593	372	530	646	474	0	0	0	0	0	0	83	576
TCGA-CV-7424-10A-01D-2078-08_HNSC	683	0	0	297	587	379	531	639	389	73	564	0	289	134	27	1	576
TCGA-CV-7425-10A-01D-2078-08_HNSC	686	0	0	336	599	360	528	631	454	0	0	0	0	0	0	103	573
TCGA-CV-7427-10A-01D-2078-08_HNSC	683	234	245	274	534	345	530	636	463	0	0	0	0	0	0	92	573
TCGA-CV-7429-10A-01D-2129-08_HNSC	688	0	0	299	595	368	530	648	478	0	0	0	0	0	23	59	574
TCGA-CV-7430-10A-01D-2129-08_HNSC	683	0	0	307	598	379	529	638	474	0	0	0	0	0	0	107	572
TCGA-CV-7432-10A-01D-2129-08_HNSC	677	240	256	287	615	283	531	649	475	58	621	570	0	0	0	108	574
TCGA-CV-7433-10A-01D-2129-08_HNSC	666	236	254	277	573	277	527	645	476	0	0	0	0	0	28	61	573
TCGA-CV-7434-10A-01D-2129-08_HNSC	674	261	285	0	608	143	537	650	487	0	632	578	0	0	39	71	581
TCGA-CV-7435-10A-01D-2129-08_HNSC	592	255	270	0	592	137	530	634	383	76	643	569	295	134	0	53	575
TCGA-CV-7437-10A-01D-2129-08_HNSC	592	254	263	0	551	136	529	644	31	85	620	0	375	138	0	8	574
TCGA-CV-7438-10A-01D-2129-08_HNSC	676	0	0	300	602	375	529	637	384	73	519	0	281	135	0	56	572
TCGA-CV-7440-10A-01D-2129-08_HNSC	674	0	0	301	599	287	522	648	401	0	0	76	0	0	0	100	576
TCGA-CV-7446-10A-01D-2229-08_HNSC	684	246	261	273	577	368	532	646	382	78	592	0	353	132	0	64	575
TCGA-CV-7568-10A-01D-2229-08_HNSC	647	237	261	274	550	272	529	631	370	71	519	0	290	132	0	55	577
TCGA-CV-A45O-10A-01D-A24F-08_HNSC	684	240	251	271	562	361	528	621	462	0	0	0	0	0	0	82	572
TCGA-CV-A45P-10A-01D-A24F-08_HNSC	677	240	256	268	499	365	520	619	459	0	0	0	0	0	0	79	572
TCGA-CV-A45Q-10A-01D-A24F-08_HNSC	674	236	258	275	598	272	528	642	370	76	611	510	355	132	0	69	575
TCGA-CV-A45R-10A-01D-A24F-08_HNSC	762	0	0	358	626	407	538	655	490	0	0	0	0	0	64	1	579
TCGA-CV-A45T-10A-01D-A24F-08_HNSC	685	0	0	306	603	381	530	643	471	0	23	0	0	0	0	81	573
TCGA-CV-A45U-10A-01D-A24F-08_HNSC	684	256	265	281	594	373	532	647	465	0	0	0	0	0	0	75	571
TCGA-CV-A45V-10A-01D-A25E-08_HNSC	668	0	0	293	593	285	520	629	369	76	577	557	0	133	0	55	579
TCGA-CV-A45W-10A-01D-A25E-08_HNSC	661	237	262	282	554	273	525	645	469	0	0	0	0	0	32	60	573
TCGA-CV-A45X-10A-01D-A25E-08_HNSC	669	0	0	297	566	370	529	640	369	68	0	0	285	131	0	59	573
TCGA-CV-A45Y-10A-01D-A25E-08_HNSC	673	0	0	296	587	375	527	631	366	68	567	0	295	134	31	3	571
TCGA-CV-A45Z-10A-01D-A25E-08_HNSC	678	0	0	295	571	385	531	640	468	0	0	0	0	0	28	60	569
TCGA-CV-A460-10A-01D-A25E-08_HNSC	638	242	244	247	490	263	515	625	377	65	569	0	284	131	0	58	572

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CV-A461-10A-01D-A25Y-08_HNSC	683	9	0	303	601	378	528	636	465	0	0	0	0	0	0	83	576
TCGA-CV-A463-10A-01D-A25Y-08_HNSC	599	259	279	0	583	135	529	649	473	0	611	0	381	0	29	70	573
TCGA-CV-A464-10A-01D-A25Y-08_HNSC	681	252	267	286	608	380	532	641	481	0	597	564	0	0	0	85	575
TCGA-CV-A465-10A-01D-A25Y-08_HNSC	689	0	0	310	605	392	529	650	382	78	613	0	299	138	0	68	572
TCGA-CV-A468-10A-01D-A25Y-08_HNSC	634	230	260	278	596	350	528	631	466	0	547	494	0	0	27	61	575
TCGA-CV-A6JD-10A-01D-A31J-08_HNSC	681	0	0	299	579	370	528	636	383	65	571	0	292	132	0	59	574
TCGA-CV-A6JE-10A-01D-A31J-08_HNSC	672	242	262	258	501	268	528	634	461	0	0	0	0	0	24	49	571
TCGA-CV-A6JM-10A-01D-A31J-08_HNSC	664	233	246	274	561	360	529	634	467	0	0	0	0	0	0	73	573
TCGA-CV-A6JN-10A-01D-A31J-08_HNSC	589	257	271	0	596	136	528	641	454	74	637	571	0	133	29	0	571
TCGA-CV-A6JT-10A-01D-A31J-08_HNSC	661	241	253	270	571	365	533	636	469	0	0	0	0	0	27	49	575
TCGA-CV-A6JU-10A-01D-A31J-08_HNSC	672	233	243	264	594	365	519	624	377	64	619	496	287	131	0	58	572
TCGA-CV-A6JY-10A-01D-A31J-08_HNSC	677	241	260	277	601	275	527	630	456	0	590	559	0	0	0	82	573
TCGA-CV-A6JZ-10A-01D-A31J-08_HNSC	647	236	256	274	509	272	500	601	366	0	594	0	295	134	0	51	575
TCGA-CV-A6K0-10A-01D-A31J-08_HNSC	689	0	0	306	610	387	527	646	466	0	0	0	0	0	31	53	575
TCGA-CV-A6K1-10A-01D-A31J-08_HNSC	682	0	0	296	585	381	531	642	378	77	591	0	289	135	30	1	572
TCGA-CV-A6K2-10A-01D-A31J-08_HNSC	681	0	0	294	601	380	530	640	461	0	0	0	0	0	0	74	572
TCGA-CX-7082-10A-01D-2013-08_HNSC	691	0	0	310	617	290	523	653	492	0	0	0	0	0	0	129	580
TCGA-CX-7085-10A-01D-2013-08_HNSC	755	0	0	297	613	394	529	650	454	76	615	0	374	139	31	0	577
TCGA-CX-7086-10D-01D-2078-08_HNSC	682	0	0	294	586	371	528	641	440	0	0	0	0	0	0	48	568
TCGA-CX-7219-10A-01D-2013-08_HNSC	695	0	0	345	624	397	533	654	490	0	0	0	0	0	42	0	580
TCGA-CX-A4AQ-10A-01D-A25E-08_HNSC	681	0	0	291	601	283	527	624	399	0	0	0	0	0	0	73	573
TCGA-D1-A0ZN-10A-01D-A122-09_UCEC	698	0	0	391	713	474	559	668	470	104	652	0	458	185	63	0	599
TCGA-D1-A0ZO-10A-01D-A122-09_UCEC	795	0	0	413	719	480	565	675	585	0	0	0	0	0	0	177	600
TCGA-D1-A0ZP-10A-01D-A10M-09_UCEC	697	318	358	375	708	461	558	656	464	105	669	540	378	186	0	62	592
TCGA-D1-A0ZQ-10A-01D-A122-09_UCEC	800	329	375	390	726	395	561	681	483	105	677	594	0	187	65	0	599
TCGA-D1-A0ZR-10A-01D-A10M-09_UCEC	699	320	369	382	722	468	564	675	457	106	670	594	0	183	0	105	598
TCGA-D1-A0ZS-10A-01D-A122-09_UCEC	705	327	376	386	723	470	559	673	0	111	682	593	462	187	0	0	598
TCGA-D1-A0ZU-10A-01D-A10M-09_UCEC	703	322	370	387	720	388	560	662	584	0	654	558	0	0	0	161	598
TCGA-D1-A0ZV-10A-01D-A10M-09_UCEC	700	325	365	378	715	388	559	672	564	103	665	593	0	183	0	98	596
TCGA-D1-A0ZZ-10A-01D-A10M-09_UCEC	795	326	369	376	699	464	562	671	469	106	654	0	456	186	57	0	598
TCGA-D1-A101-10A-01D-A10M-09_UCEC	691	0	0	396	716	467	560	662	565	0	0	0	0	0	0	158	597
TCGA-D1-A102-10A-01D-A10M-09_UCEC	787	330	372	0	0	0	556	667	570	0	0	0	0	0	0	199	593
TCGA-D1-A103-10A-01D-A10M-09_UCEC	797	317	365	385	721	383	557	671	0	111	680	558	468	190	0	0	597
TCGA-D1-A15V-10A-01D-A122-09_UCEC	800	334	374	410	727	475	562	679	481	107	678	587	464	187	0	141	597
TCGA-D1-A15W-10A-01D-A122-09_UCEC	789	0	0	394	698	467	557	664	456	100	645	0	378	180	0	68	593
TCGA-D1-A15X-10A-01D-A122-09_UCEC	800	0	0	396	717	479	560	668	480	108	656	0	462	189	0	116	597
TCGA-D1-A15Z-10A-01D-A122-09_UCEC	698	0	0	398	717	479	561	670	582	0	0	0	0	0	0	144	593
TCGA-D1-A160-10A-01D-A122-09_UCEC	802	0	0	398	728	474	559	678	482	108	668	0	462	189	0	115	593
TCGA-D1-A161-10A-01D-A122-09_UCEC	797	321	369	382	704	388	562	673	570	106	662	0	388	183	0	126	597
TCGA-D1-A163-10A-01D-A12J-09_UCEC	799	0	0	397	723	481	558	664	582	0	0	0	0	0	0	210	599
TCGA-D1-A165-10A-01D-A12J-09_UCEC	703	0	0	399	713	471	562	678	476	110	662	0	387	182	0	95	596
TCGA-D1-A167-10A-01D-A12J-09_UCEC	702	325	372	392	714	387	561	682	589	0	0	0	0	0	67	169	601
TCGA-D1-A168-10A-01D-A12J-09_UCEC	699	0	0	394	711	478	561	671	465	111	634	0	386	183	0	91	592
TCGA-D1-A169-10A-01D-A12J-09_UCEC	698	341	378	0	713	191	560	674	473	105	679	593	0	188	0	134	599
TCGA-D1-A16B-10A-01D-A12J-09_UCEC	701	0	0	410	717	396	552	669	577	0	0	0	0	0	0	185	598
TCGA-D1-A16D-10A-01D-A12J-09_UCEC	802	0	0	416	726	476	563	679	585	0	0	0	0	0	69	150	596
TCGA-D1-A16E-10A-01D-A12J-09_UCEC	800	0	0	394	720	471	558	675	482	105	662	0	463	187	0	119	598
TCGA-D1-A16F-10A-01D-A12J-09_UCEC	702	0	0	399	722	481	563	679	582	0	0	0	0	0	0	263	602
TCGA-D1-A16G-10A-01D-A12J-09_UCEC	791	0	0	394	717	466	558	665	483	0	0	0	0	0	0	158	599
TCGA-D1-A16I-10A-01D-A12J-09_UCEC	792	320	368	382	715	387	559	669	577	0	654	587	0	0	0	143	592
TCGA-D1-A16J-10A-01D-A12J-09_UCEC	693	334	376	0	702	181	562	663	576	0	653	586	0	0	0	148	598
TCGA-D1-A16N-10A-01D-A12J-09_UCEC	801	0	0	421	726	482	564	678	578	109	668	0	466	190	0	141	598
TCGA-D1-A16O-10A-01D-A12J-09_UCEC	798	0	0	421	722	473	556	671	0	111	674	0	468	190	0	0	599
TCGA-D1-A16Q-10A-01D-A12J-09_UCEC	796	324	374	378	704	385	560	678	582	0	0	0	0	0	70	126	599
TCGA-D1-A16R-10A-01D-A12J-09_UCEC	799	0	0	419	733	484	561	679	588	0	0	0	0	0	0	309	597
TCGA-D1-A16S-10A-01D-A12J-09_UCEC	702	0	0	393	716	472	560	668	579	0	0	0	0	0	0	221	597
TCGA-D1-A16V-10A-01D-A12J-09_UCEC	700	321	358	375	699	462	560	664	578	0	0	0	0	0	0	175	596
TCGA-D1-A16X-10A-01D-A12J-09_UCEC	798	327	365	385	702	466	561	668	584	0	0	0	0	0	0	143	598
TCGA-D1-A16Y-10A-01D-A12J-09_UCEC	684	306	351	378	713	380	553	662	483	0	631	538	0	0	30	65	590
TCGA-D1-A174-10A-01D-A12J-09_UCEC	799	319	364	385	689	378	554	664	582	0	0	0	0	0	42	98	598
TCGA-D1-A175-10A-01D-A12J-09_UCEC	801	320	365	381	710	390	557	667	578	0	0	0	0	0	0	186	599
TCGA-D1-A176-10A-01D-A12J-09_UCEC	788	321	383	241	696	383	564	677	473	110	674	0	467	186	0	111	597
TCGA-D1-A177-10A-01D-A12J-09_UCEC	700	309	360	381	712	463	560	666	464	0	636	551	91	110	0	127	588
TCGA-D1-A179-10A-01D-A12J-09_UCEC	794	334	375	319	721	369	561	675	581	88	669	592	136	100	0	193	599
TCGA-D1-A17A-10A-01D-A12J-09_UCEC	792	0	0	398	717	457	556	643	475	0	0	0	0	185	0	77	579
TCGA-D1-A17B-10A-01D-A12J-09_UCEC	703	330	369	389	724	476	563	677	578	107	647	589	0	0	0	130	597
TCGA-D1-A17C-10A-01D-A12J-09_UCEC	796	330	369	236	702	390	561	676	477	110	663	0	462	187	0	116	597
TCGA-D1-A17D-10A-01D-A12J-09_UCEC	797	320	376	382	703	384	558	658	578	0	0	0	0	0	0	154	594
TCGA-D1-A17F-10A-01D-A12J-09_UCEC	795	0	0	399	723	466	557	671	468	106	660	136	458	181	0	89	597
TCGA-D1-A17H-10A-01D-A12J-09_UCEC	795	324	366	392	710	383	560	679	588	0	0	0	0	0	50	89	599
TCGA-D1-A17K-10A-01D-A12J-09_UCEC	803	327	373	390	709	392	561	669	486	107	657	0	464	183	0	124	599
TCGA-D1-A17L-10A-01D-A12J-09_UCEC	798	0	0	395	718	479	564	677	587	0	0	0	0	0	69	131	601
TCGA-D1-A17M-10A-01D-A12J-09_UCEC	802	0	0	420	726	469	561	680	585	0	0	0	0	0	58	122	599
TCGA-D1-A17N-10A-01D-A12J-09_UCEC	799	0	0	414	722	480	562	672	568	0	0	0	0	0	0	223	600
TCGA-D1-A17Q-10A-01D-A12J-09_UCEC	797	0	0	397	718	468	558	669	579	0	0	0	0	0	45	118	594
TCGA-D1-A17R-10A-01D-A12J-09_UCEC	801	0	0	418	722	474	561	679	586	0	0	0	0	0	69	126	599
TCGA-D1-A17S-10A-01D-A12J-09_UCEC	798	0	0	398	724	480	564	680	571	105	661	0	459	184	0	130	599
TCGA-D1-A17T-10A-01D-A12J-09_UCEC	801	329	373	386	729	394	562	669	586	0	663	585	0	0	0	266	598
TCGA-D1-A17U-10A-01D-A12J-09_UCEC	802	324	376	387	731	390	564	681	480	106	682	590	467	187	0	149	598
TCGA-D1-A1NS-10A-01D-A14G-09_UCEC	696	306	346	328	683	447	555	661	550	89	595	530	0	0	57	1	581
TCGA-D1-A1NU-10A-01D-A14G-09_UCEC	669	277	342	344	642	436	546	642	556	0	0	0	0	0	29	41	585
TCGA-D1-A1NX-10A-01D-A16D-09_UCEC	695	0	0	388	708	450	557	663	574	0	0	0	0	0	39	75	593
TCGA-D1-A1NY-10A-01D-A16D-09_UCEC	689	0	0	349	659	362	541	633	419	87	597	0	353	183	0	46	574
TCGA-D1-A1NZ-10A-01D-A14G-09_UCEC	686	0	0	348	656	444	546	628	454	0	0	0	0	0	0	74	586
TCGA-D1-A1O0-10A-01D-A17D-09_UCEC	694	0	0	353	671	460	550	635	552	0	0	0	0	0	30	52	586
TCGA-D1-A1O5-10A-01D-A14G-09_UCEC	664	288	321	292	602	329	542	524	351	0	0	0	0	0	0	74	583
TCGA-D1-A1O7-10A-01D-A14G-09_UCEC	695	0	0	351	645	438	544	621	429	0	0	0	0	0	36	45	573
TCGA-D1-A1O8-10A-01D-A14G-09_UCEC	671	0	0	336	638	454	544	610	280	79	450	0	356	170	0	41	585
TCGA-D1-A2G0-10A-01D-A17D-09_UCEC	698	0	0	365	672	466	555	654	559	0	0	0	0	0	41	64	588
TCGA-D1-A2G5-10A-01D-A17D-09_UCEC	693	0	0	358	661	372	541	645	306	83	572	0	346	177	0	60	584
TCGA-D1-A2G6-10A-01D-A17D-09_UCEC	578	311	342	0	523	165	543	606	404	81	607	548	0	160	35	0	578
TCGA-D1-A2G7-10A-01D-A17W-09_UCEC	659	302	321	225	594	417	550	627	533	0	0	0	0	0	33	44	581
TCGA-D1-A3DA-10A-01D-A20S-09_UCEC	699	296	320	317	520	444	548	642	555	0	0	0	0	0	30	66	589
TCGA-D1-A3DG-10A-01D-A19Y-09_UCEC	700	0	0	373	689	343	544	633	448	0	0	0	0	174	0	51	567
TCGA-D1-A3DH-10A-01D-A19Y-09_UCEC	653	289	318	345	611	347	550	621	323	81	565	0	343	180	0	35	582
TCGA-D1-A3JP-10B-01D-A22A-09_UCEC	696	302	324	312	610	347	553	651	560	0	0	0	0	0	37	51	586

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-D1-A3JQ-10B-01D-A22A-09_UCEC	692	0	0	368	681	447	547	647	545	0	0	0	0	0	36	48	584
TCGA-D3-A1Q1-10A-01D-A198-08_SKCM	762	0	0	309	604	386	534	641	0	80	631	0	378	138	0	1	574
TCGA-D3-A1Q3-10A-01D-A198-08_SKCM	680	0	0	293	568	375	528	627	394	0	0	0	0	0	35	0	575
TCGA-D3-A1Q4-10A-01D-A198-08_SKCM	683	0	0	279	602	384	533	638	468	0	0	0	0	0	33	56	572
TCGA-D3-A1Q5-10A-01D-A198-08_SKCM	677	0	0	293	575	381	531	633	461	0	0	0	0	0	34	0	572
TCGA-D3-A1Q6-10A-01D-A198-08_SKCM	739	240	253	265	543	357	529	636	369	0	519	0	293	130	0	58	577
TCGA-D3-A1Q7-10A-01D-A19A-08_SKCM	591	254	269	0	0	0	524	642	474	0	0	0	0	0	0	79	575
TCGA-D3-A1Q8-10A-01D-A19A-08_SKCM	656	239	256	285	604	279	529	645	456	67	622	575	0	134	0	58	572
TCGA-D3-A1Q9-10A-01D-A19A-08_SKCM	688	0	0	281	564	377	531	630	474	0	0	0	0	0	0	101	570
TCGA-D3-A1QA-10A-01D-A198-08_SKCM	683	251	266	290	589	376	530	641	476	0	0	0	0	0	0	89	579
TCGA-D3-A1QB-10A-01D-A19A-08_SKCM	682	0	0	300	607	380	530	646	0	75	548	0	374	139	0	3	577
TCGA-D3-A2J6-10A-01D-A19A-08_SKCM	688	0	0	297	600	373	519	606	0	62	587	0	294	138	0	0	573
TCGA-D3-A2J7-10A-01D-A198-08_SKCM	667	244	265	268	589	283	526	627	380	70	582	568	293	134	27	0	576
TCGA-D3-A2J8-10A-01D-A198-08_SKCM	669	252	264	277	570	277	531	639	482	0	0	0	0	0	0	121	577
TCGA-D3-A2J9-10A-01D-A198-08_SKCM	683	0	0	299	602	375	532	640	460	81	583	0	365	135	0	68	576
TCGA-D3-A2JA-10A-01D-A198-08_SKCM	672	246	258	272	547	373	528	625	462	0	0	0	0	0	0	76	573
TCGA-D3-A2JB-10A-01D-A198-08_SKCM	688	249	264	261	507	131	532	653	373	79	511	0	365	133	0	61	573
TCGA-D3-A2JC-10A-01D-A19A-08_SKCM	686	0	0	294	526	387	525	645	478	0	0	0	0	0	0	130	575
TCGA-D3-A2JD-10A-01D-A19A-08_SKCM	666	247	262	178	621	380	530	649	471	0	618	0	386	0	30	70	577
TCGA-D3-A2JF-10A-01D-A198-08_SKCM	687	0	0	283	597	383	530	635	469	0	0	0	0	0	26	53	578
TCGA-D3-A2JG-10A-01D-A198-08_SKCM	683	0	0	298	603	383	526	645	475	0	0	0	0	0	34	67	576
TCGA-D3-A2JH-10A-01D-A198-08_SKCM	678	241	258	286	553	367	530	644	472	0	0	0	0	0	31	61	571
TCGA-D3-A2JK-10A-01D-A198-08_SKCM	662	248	260	281	504	270	531	640	449	50	575	0	288	135	0	54	576
TCGA-D3-A2JL-10A-01D-A198-08_SKCM	594	256	272	0	502	129	525	625	449	66	589	563	0	135	0	52	575
TCGA-D3-A2JN-10A-01D-A198-08_SKCM	704	243	0	261	571	374	525	631	447	67	542	0	290	131	28	0	575
TCGA-D3-A2JO-10A-01D-A198-08_SKCM	665	253	272	0	549	131	532	649	0	80	631	573	295	135	0	1	577
TCGA-D3-A2JP-10A-01D-A19A-08_SKCM	672	242	264	276	609	373	531	652	378	78	622	558	297	136	30	0	573
TCGA-D3-A3BZ-10A-01D-A198-08_SKCM	679	247	267	275	507	381	529	637	0	81	633	0	369	139	0	1	573
TCGA-D3-A3C1-10A-01D-A198-08_SKCM	664	243	256	283	572	374	532	640	470	0	522	560	0	0	0	113	574
TCGA-D3-A3C3-10A-01D-A19A-08_SKCM	640	240	253	245	569	266	521	637	452	66	624	571	0	125	0	39	579
TCGA-D3-A3C6-10A-01D-A198-08_SKCM	687	0	0	293	597	389	529	645	475	0	0	0	0	0	25	67	574
TCGA-D3-A3C7-10A-01D-A198-08_SKCM	590	228	261	264	507	264	532	632	380	61	527	0	283	135	25	1	571
TCGA-D3-A3C8-10A-01D-A19A-08_SKCM	682	236	239	279	488	339	529	644	474	0	0	0	0	0	17	54	575
TCGA-D3-A3CB-10A-01D-A198-08_SKCM	675	0	0	286	573	340	522	633	384	0	0	0	0	0	0	68	577
TCGA-D3-A3CC-10A-01D-A19A-08_SKCM	601	261	273	0	0	0	530	638	473	0	0	0	0	0	0	90	574
TCGA-D3-A3CE-10A-01D-A19A-08_SKCM	592	252	271	0	0	0	534	635	473	0	0	0	0	0	35	72	574
TCGA-D3-A3CF-10A-01D-A198-08_SKCM	591	249	271	0	0	0	529	626	461	0	0	0	0	0	25	50	575
TCGA-D3-A3ML-10A-01D-A21A-08_SKCM	668	243	237	159	596	258	531	652	460	57	519	480	0	0	34	1	573
TCGA-D3-A3MO-10A-01D-A21A-08_SKCM	684	244	256	279	601	378	532	646	387	74	636	575	0	135	0	70	575
TCGA-D3-A3MR-10A-01D-A21A-08_SKCM	684	0	0	304	602	287	529	651	480	0	0	0	0	0	0	133	577
TCGA-D3-A3MU-10A-01D-A21A-08_SKCM	739	246	262	295	607	281	532	658	485	0	619	570	0	0	28	66	579
TCGA-D3-A3MV-10A-01D-A21A-08_SKCM	754	0	0	301	610	288	530	650	371	77	597	0	366	136	0	81	578
TCGA-D3-A51E-10A-01D-A25O-08_SKCM	675	0	0	292	597	365	527	622	387	0	0	0	0	0	0	68	573
TCGA-D3-A51F-10A-01D-A25O-08_SKCM	656	223	238	242	490	351	522	624	367	0	0	0	0	0	0	57	571
TCGA-D3-A51G-10A-01D-A25O-08_SKCM	668	0	0	287	588	284	520	630	299	72	517	0	284	132	0	59	573
TCGA-D3-A51H-10A-01D-A25O-08_SKCM	683	0	0	287	603	377	529	634	370	72	579	559	277	131	0	48	574
TCGA-D3-A51J-10A-01D-A25O-08_SKCM	676	224	250	275	546	365	528	618	449	0	0	0	0	0	35	0	569
TCGA-D3-A51K-10A-01D-A25O-08_SKCM	681	0	0	289	590	375	530	637	462	0	0	0	0	0	23	47	571
TCGA-D3-A51N-10A-01D-A25O-08_SKCM	675	0	0	279	567	368	529	627	464	0	0	0	0	0	0	86	574
TCGA-D3-A51R-10A-01D-A25O-08_SKCM	637	216	241	167	555	261	525	608	292	64	592	480	275	128	0	37	570
TCGA-D3-A51T-10A-01D-A25O-08_SKCM	652	229	244	263	488	270	529	634	390	0	0	0	0	0	0	88	572
TCGA-D3-A5GL-10A-01D-A27N-08_SKCM	679	0	0	295	583	284	511	630	455	0	0	0	0	0	0	99	570
TCGA-D3-A5GN-10A-01D-A27N-08_SKCM	675	239	254	281	602	371	528	654	464	78	607	557	0	0	23	53	573
TCGA-D3-A5GO-10A-01D-A27N-08_SKCM	682	235	250	188	504	278	535	645	386	76	533	0	302	132	30	0	574
TCGA-D3-A5GR-10A-01D-A27N-08_SKCM	672	238	255	257	549	351	528	635	449	0	0	0	0	0	0	71	572
TCGA-D3-A5GS-10A-01D-A27N-08_SKCM	679	0	0	299	603	283	520	637	475	0	0	0	0	0	0	114	573
TCGA-D3-A5GT-10A-01D-A30X-08_SKCM	645	233	255	275	581	276	524	639	464	0	591	560	0	0	0	99	574
TCGA-D3-A5GU-10A-01D-A27N-08_SKCM	692	0	0	303	601	379	527	628	469	0	0	0	0	0	0	114	571
TCGA-D5-5537-10A-01D-1924-10_COAD	558	0	0	313	500	307	460	514	290	0	0	0	0	0	0	26	541
TCGA-D5-5538-10A-02D-1650-10_COAD	674	0	0	383	684	442	532	643	445	86	554	0	345	169	16	0	576
TCGA-D5-6529-10A-01D-1771-10_COAD	672	164	174	324	561	300	513	590	348	0	0	0	0	0	8	28	555
TCGA-D5-6531-10A-01D-1719-10_COAD	638	230	155	240	560	353	491	608	303	0	517	326	298	150	0	37	574
TCGA-D5-6532-10A-01D-1719-10_COAD	590	314	353	0	0	0	547	634	374	0	0	0	0	0	0	90	593
TCGA-D5-6533-10A-01D-1719-10_COAD	687	0	0	391	701	461	547	644	465	0	0	0	0	0	0	84	592
TCGA-D5-6534-10A-01D-1924-10_COAD	638	192	174	204	629	319	486	568	287	0	430	523	0	146	0	25	561
TCGA-D5-6535-10A-01D-1719-10_COAD	795	0	0	385	695	378	547	645	559	0	0	0	0	0	30	54	589
TCGA-D5-6536-10A-01D-1719-10_COAD	691	0	0	389	695	385	554	657	471	0	0	0	0	0	0	113	595
TCGA-D5-6538-10A-01D-1719-10_COAD	680	271	302	256	601	398	531	610	363	0	0	0	0	0	0	60	590
TCGA-D5-6539-10A-01D-1719-10_COAD	679	0	0	366	673	435	524	624	327	92	448	0	329	170	0	26	580
TCGA-D5-6540-10A-01D-1719-10_COAD	690	0	0	371	666	461	557	622	458	0	0	0	0	0	0	61	588
TCGA-D5-6541-10A-01D-1719-10_COAD	700	0	0	382	688	454	549	652	462	0	0	0	0	0	32	50	589
TCGA-D5-6898-10A-01D-1924-10_COAD	678	0	0	357	616	358	506	590	346	0	0	0	0	0	23	26	586
TCGA-D5-6920-10A-01D-1924-10_COAD	680	0	0	377	626	414	522	610	354	0	0	0	0	0	0	73	581
TCGA-D5-6922-10A-01D-1924-10_COAD	663	0	0	348	611	437	514	583	308	82	355	0	310	146	0	23	554
TCGA-D5-6924-10A-01D-1924-10_COAD	621	100	0	204	459	306	495	538	296	0	381	0	216	118	0	26	561
TCGA-D5-6926-10A-01D-1924-10_COAD	630	0	0	239	575	323	459	562	317	0	0	0	0	0	0	30	557
TCGA-D5-6927-10A-01D-1924-10_COAD	692	0	0	342	631	407	497	597	428	0	0	0	0	0	0	32	551
TCGA-D5-6928-10A-01D-1924-10_COAD	510	264	298	0	444	134	505	555	270	0	393	393	228	148	0	16	547
TCGA-D5-6929-10A-01D-1924-10_COAD	656	203	182	112	615	303	489	577	290	96	424	462	0	128	0	21	567
TCGA-D5-6930-10A-01D-1924-10_COAD	608	0	0	214	539	285	471	520	314	0	0	0	0	0	5	11	555
TCGA-D5-6931-10A-01D-1924-10_COAD	444	193	198	0	432	148	448	483	231	0	387	466	0	100	0	0	510
TCGA-D5-6932-10A-01D-1924-10_COAD	626	114	167	192	370	358	486	537	330	0	0	0	0	0	0	42	542
TCGA-D5-7000-10A-01D-1924-10_COAD	462	96	92	91	239	183	361	475	0	93	354	0	308	157	0	0	498
TCGA-D6-6515-10A-01D-1870-08_HNSC	666	263	281	0	603	142	533	648	480	0	637	574	0	0	25	71	576
TCGA-D6-6516-10A-01D-1870-08_HNSC	688	0	0	307	605	386	532	632	487	0	0	0	0	0	0	129	578
TCGA-D6-6517-10A-01D-1870-08_HNSC	685	0	0	299	613	394	536	636	478	0	0	0	0	0	26	59	579
TCGA-D6-6823-10A-01D-1912-08_HNSC	758	0	0	308	603	386	531	651	472	0	0	0	0	0	0	110	579
TCGA-D6-6824-10A-01D-1912-08_HNSC	759	0	0	299	608	285	525	645	469	0	0	0	0	0	0	94	575
TCGA-D6-6825-10A-01D-1912-08_HNSC	677	249	253	257	578	278	530	649	483	0	0	0	0	0	0	116	582
TCGA-D6-6826-10A-01D-1912-08_HNSC	692	0	0	308	610	394	534	656	474	70	613	0	369	138	0	62	576
TCGA-D6-6827-10A-01D-1912-08_HNSC	688	0	0	302	611	391	536	646	487	0	0	0	0	0	0	121	578
TCGA-D6-8568-10A-01D-2394-08_HNSC	747	243	264	291	615	137	516	618	0	80	632	516	347	142	0	0	573
TCGA-D6-8569-10A-01D-2394-08_HNSC	667	246	262	291	551	274	529	633	475	0	0	0	0	0	0	124	572
TCGA-D6-A4Z9-10A-01D-A25E-08_HNSC	686	0	0	299	571	379	525	634	472	0	0	0	0	0	0	76	573
TCGA-D6-A4ZB-10A-01D-A25E-08_HNSC	685	0	0	293	590	374	530	633	382	65	588	0	355	133	30	4	574
TCGA-D6-A6EK-10A-01D-A31J-08_HNSC	682	0	0	298	597	287	523	646	446	67	594	475	0	133	29	1	576

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-D6-A6EM-10A-01D-A31J-08_HNSC	675	241	0	276	604	372	525	638	384	64	584	0	362	130	0	53	573
TCGA-D6-A6EN-10A-01D-A31J-08_HNSC	587	249	265	0	0	0	525	636	467	0	0	0	0	0	23	52	572
TCGA-D6-A6EO-10A-01D-A31J-08_HNSC	656	134	259	284	543	278	503	613	434	0	586	0	352	133	0	58	574
TCGA-D6-A6EP-10A-01D-A31J-08_HNSC	679	0	0	292	596	384	529	642	385	67	567	0	363	135	27	1	573
TCGA-D6-A6EQ-10A-01D-A31J-08_HNSC	665	242	254	286	572	271	526	651	476	0	0	0	0	0	27	60	570
TCGA-D6-A6ES-10A-01D-A31J-08_HNSC	682	0	0	297	598	379	530	623	0	78	631	507	289	137	0	1	575
TCGA-D7-5577-10A-01D-1600-08_STAD	688	0	0	309	613	392	537	661	493	0	0	0	0	0	0	148	573
TCGA-D7-5578-10A-01D-1600-08_STAD	758	246	273	295	609	382	532	654	480	0	608	571	0	0	0	104	578
TCGA-D7-5579-10A-01D-1600-08_STAD	598	262	268	0	592	136	535	657	475	84	623	0	371	140	27	0	581
TCGA-D7-6518-10A-01D-1800-08_STAD	689	0	0	301	608	385	534	652	458	68	604	0	367	135	34	0	578
TCGA-D7-6519-10A-01D-1800-08_STAD	595	258	269	0	598	139	533	633	0	84	658	573	377	140	0	1	576
TCGA-D7-6520-10A-01D-1800-08_STAD	688	0	0	300	611	386	532	648	445	75	603	0	372	138	0	51	577
TCGA-D7-6521-10A-01D-1800-08_STAD	691	0	0	305	611	382	532	644	461	70	610	0	363	137	0	69	573
TCGA-D7-6522-10A-01D-1800-08_STAD	691	0	0	306	603	386	529	644	473	0	0	0	0	0	0	92	574
TCGA-D7-6524-10A-01D-1800-08_STAD	761	0	0	297	602	381	530	651	476	0	0	0	0	0	0	121	577
TCGA-D7-6525-10A-01D-1800-08_STAD	689	0	0	298	606	385	531	647	481	0	0	0	0	0	29	67	577
TCGA-D7-6526-10A-01D-1800-08_STAD	681	252	267	287	609	286	534	644	485	0	617	516	0	0	31	72	574
TCGA-D7-6527-10A-01D-1800-08_STAD	684	0	0	304	606	288	524	642	479	0	0	0	0	0	0	98	574
TCGA-D7-6528-10A-01D-1800-08_STAD	688	0	0	307	602	389	532	644	393	76	585	0	366	135	0	78	574
TCGA-D7-6815-10A-01D-1882-08_STAD	687	0	0	309	610	392	532	635	467	0	0	0	0	0	0	97	575
TCGA-D7-6817-10A-01D-1882-08_STAD	684	253	268	295	638	289	530	652	462	78	649	569	378	136	0	74	579
TCGA-D7-6818-10A-01D-1882-08_STAD	764	0	0	310	617	384	532	650	485	0	0	0	0	0	0	102	579
TCGA-D7-6820-10A-01D-1882-08_STAD	691	0	0	305	614	393	533	658	489	0	0	0	0	0	0	155	579
TCGA-D7-6822-10A-01D-1882-08_STAD	690	0	0	309	609	397	531	650	462	77	606	0	373	140	30	0	578
TCGA-D7-8570-10A-01D-2341-08_STAD	762	0	0	308	609	397	534	648	481	0	0	0	0	0	34	71	577
TCGA-D7-8572-10A-01D-2341-08_STAD	686	248	262	290	613	279	530	647	476	0	624	563	0	0	45	0	577
TCGA-D7-8573-10A-01D-2341-08_STAD	683	247	269	291	616	386	529	643	0	82	654	573	373	138	0	0	577
TCGA-D7-8574-10A-01D-2341-08_STAD	762	0	0	303	604	388	531	648	474	0	0	0	0	0	0	93	580
TCGA-D7-8575-10A-01D-2341-08_STAD	688	0	0	306	623	394	537	654	461	87	649	578	364	139	33	0	575
TCGA-D7-8576-10A-01D-2341-08_STAD	687	115	138	299	604	376	527	625	388	0	217	261	0	132	0	66	572
TCGA-D7-8578-10A-01D-2341-08_STAD	755	250	267	302	611	379	532	657	484	0	597	564	0	0	0	139	577
TCGA-D7-8579-10A-01D-2341-08_STAD	761	252	262	291	586	378	532	644	480	0	0	0	0	0	0	127	575
TCGA-D7-A4YT-10A-01D-A25E-08_STAD	687	0	0	300	604	383	530	644	461	76	606	0	296	134	0	68	577
TCGA-D7-A4YU-10A-01D-A25E-08_STAD	669	238	259	280	579	365	529	619	450	0	587	0	364	133	0	60	576
TCGA-D7-A4YV-10A-01D-A25E-08_STAD	759	0	0	304	605	392	531	643	483	0	0	0	0	0	0	125	577
TCGA-D7-A4YX-10A-01D-A25E-08_STAD	597	258	273	0	574	137	534	638	474	0	600	560	0	0	33	64	573
TCGA-D7-A4YY-10A-01D-A25E-08_STAD	677	245	253	284	579	365	528	636	478	0	0	0	0	0	0	114	574
TCGA-D7-A4Z0-10A-01D-A25E-08_STAD	682	0	0	301	601	381	532	649	474	0	0	0	0	0	33	66	578
TCGA-D7-A6ET-10A-01D-A32N-08_STAD	688	0	0	307	606	383	530	651	472	0	0	0	0	0	34	67	574
TCGA-D7-A6EV-10A-01D-A31J-08_STAD	678	243	268	282	585	279	529	646	476	0	0	0	0	0	24	60	576
TCGA-D7-A6EX-10A-01D-A31J-08_STAD	686	0	0	296	598	381	530	645	458	0	0	0	0	0	0	72	572
TCGA-D7-A6EY-10A-01D-A31J-08_STAD	671	242	0	286	606	280	532	627	307	72	598	0	359	135	0	56	573
TCGA-D7-A6EZ-10A-01D-A31J-08_STAD	682	251	262	286	601	379	529	641	384	78	628	554	293	133	0	52	575
TCGA-D7-A6F0-10A-01D-A31J-08_STAD	662	237	253	283	596	276	519	631	374	72	634	505	356	136	0	47	574
TCGA-D7-A6F2-10A-01D-A31J-08_STAD	591	255	270	0	580	135	529	644	384	68	631	566	0	129	29	0	575
TCGA-D7-A747-10A-21D-A33W-08_STAD	673	234	261	276	603	282	527	647	461	60	628	506	298	133	0	67	575
TCGA-D7-A748-10A-21D-A32N-08_STAD	687	0	0	297	609	290	531	649	464	69	617	0	368	137	0	71	578
TCGA-D7-A74A-10A-21D-A32N-08_STAD	599	264	273	0	605	143	533	648	480	0	646	576	0	0	38	0	572
TCGA-D7-A74B-10A-01D-A33W-08_STAD	675	241	250	289	601	376	534	653	462	69	578	564	0	0	24	56	573
TCGA-D8-A13Y-10A-01D-A110-09_BRCA	782	319	361	383	694	380	556	660	472	105	652	0	457	181	0	86	591
TCGA-D8-A13Z-10A-01D-A110-09_BRCA	771	278	326	247	403	379	551	635	438	0	0	0	0	0	0	53	569
TCGA-D8-A140-10A-01D-A110-09_BRCA	703	328	368	389	724	384	560	672	478	107	670	592	0	190	0	117	598
TCGA-D8-A141-10A-01D-A110-09_BRCA	691	0	0	396	713	470	560	661	485	0	0	0	0	0	0	188	596
TCGA-D8-A142-10A-01D-A110-09_BRCA	797	0	0	393	709	460	557	678	583	0	0	0	0	0	42	84	597
TCGA-D8-A143-10A-01D-A110-09_BRCA	684	310	354	373	621	450	561	666	461	106	643	0	380	187	0	66	594
TCGA-D8-A145-10A-01D-A110-09_BRCA	797	0	0	397	722	466	560	668	574	0	0	0	0	0	0	127	593
TCGA-D8-A146-10A-01D-A110-09_BRCA	688	295	350	374	672	368	559	648	463	0	0	0	0	0	0	109	588
TCGA-D8-A147-10A-01D-A110-09_BRCA	696	0	0	396	713	465	557	671	459	103	644	0	457	183	0	104	595
TCGA-D8-A1J8-10A-01D-A13O-09_BRCA	792	0	0	388	708	469	554	646	567	0	0	0	0	0	0	150	586
TCGA-D8-A1J9-10A-01D-A13O-09_BRCA	669	0	0	371	682	455	554	647	459	0	0	0	0	0	0	104	593
TCGA-D8-A1JB-10A-01D-A13O-09_BRCA	658	267	316	324	642	422	546	618	445	0	0	0	0	0	0	63	588
TCGA-D8-A1JC-10A-01D-A13O-09_BRCA	689	0	0	377	687	466	554	655	562	0	0	0	0	0	0	123	588
TCGA-D8-A1JD-10A-01D-A13O-09_BRCA	789	0	0	387	705	461	553	648	474	0	0	0	0	0	0	162	589
TCGA-D8-A1JE-10A-01D-A188-09_BRCA	524	288	345	0	607	158	535	632	410	98	590	524	0	162	0	27	550
TCGA-D8-A1JF-10A-01D-A17G-09_BRCA	666	317	365	0	677	176	556	658	349	103	650	583	0	178	0	68	585
TCGA-D8-A1JG-10A-01D-A13O-09_BRCA	679	291	340	337	675	445	555	658	456	96	582	518	0	0	29	40	578
TCGA-D8-A1JH-10A-01D-A13O-09_BRCA	677	308	347	355	660	428	552	650	460	0	0	0	0	0	0	99	596
TCGA-D8-A1JI-10A-01D-A13O-09_BRCA	577	323	363	0	686	180	541	659	435	98	659	589	0	181	36	0	587
TCGA-D8-A1JJ-10A-01D-A14K-09_BRCA	697	306	371	383	718	467	559	667	577	0	655	559	0	0	54	116	594
TCGA-D8-A1JK-10A-01D-A13O-09_BRCA	670	263	344	321	671	345	537	635	427	95	624	548	0	159	0	34	581
TCGA-D8-A1JL-10A-01D-A188-09_BRCA	696	0	0	385	703	383	547	656	476	0	0	0	0	0	0	169	590
TCGA-D8-A1JM-10A-01D-A188-09_BRCA	692	0	0	386	704	460	556	650	564	0	0	0	0	0	0	107	589
TCGA-D8-A1JN-10A-01D-A13O-09_BRCA	665	0	0	369	673	444	538	649	451	0	0	0	0	0	19	46	573
TCGA-D8-A1JP-10A-01D-A13O-09_BRCA	684	0	0	394	705	459	555	660	464	104	638	0	377	180	0	72	594
TCGA-D8-A1JS-10A-01D-A13O-09_BRCA	677	0	0	373	698	454	553	649	464	0	0	0	0	0	0	112	593
TCGA-D8-A1JT-10A-01D-A13O-09_BRCA	666	0	0	365	687	451	555	638	460	0	0	0	0	0	19	33	573
TCGA-D8-A1JU-10A-01D-A188-09_BRCA	647	283	336	0	427	148	536	600	295	0	523	479	255	146	9	1	562
TCGA-D8-A1X5-10A-01D-A14G-09_BRCA	635	0	0	370	679	451	525	601	353	0	0	0	0	0	0	59	560
TCGA-D8-A1X6-10A-01D-A14K-09_BRCA	693	290	358	354	705	451	553	645	445	107	649	514	356	174	0	54	576
TCGA-D8-A1X7-10A-01D-A14K-09_BRCA	665	0	0	365	678	337	504	483	320	0	0	0	0	161	0	40	582
TCGA-D8-A1X9-10A-01D-A17G-09_BRCA	649	275	318	340	679	371	538	640	451	0	554	505	0	0	26	25	569
TCGA-D8-A1XA-10A-01D-A14G-09_BRCA	696	0	0	375	685	459	555	648	442	96	621	0	367	168	37	0	591
TCGA-D8-A1XB-10A-01D-A14G-09_BRCA	683	0	0	376	689	446	546	649	468	0	0	0	0	0	0	120	591
TCGA-D8-A1XC-10A-01D-A14G-09_BRCA	657	0	0	339	653	423	530	633	430	0	0	0	0	0	11	29	563
TCGA-D8-A1XF-10A-01D-A14G-09_BRCA	693	0	0	371	666	435	538	661	526	0	0	0	0	0	19	35	585
TCGA-D8-A1XG-10A-01D-A14G-09_BRCA	686	287	347	352	691	454	549	639	459	0	612	524	0	0	39	61	586
TCGA-D8-A1XK-10A-01D-A14K-09_BRCA	590	325	370	0	683	180	554	633	460	0	645	589	0	179	37	0	592
TCGA-D8-A1XL-10A-01D-A14K-09_BRCA	693	0	0	385	704	389	557	664	458	107	645	0	453	181	0	93	592
TCGA-D8-A1XM-10A-01D-A14K-09_BRCA	682	0	0	384	703	465	558	659	448	102	640	0	452	180	0	77	589
TCGA-D8-A1XO-10A-01D-A14K-09_BRCA	580	326	365	0	682	178	548	636	349	0	658	539	373	177	0	71	594
TCGA-D8-A1XQ-10A-01D-A14K-09_BRCA	689	0	0	393	709	475	560	668	482	0	0	0	0	0	0	165	594
TCGA-D8-A1XR-10A-01D-A14K-09_BRCA	794	320	367	381	725	386	560	664	569	0	645	576	0	0	0	152	594
TCGA-D8-A1XS-10A-01D-A14K-09_BRCA	671	0	0	369	669	434	542	633	445	0	0	0	0	0	32	1	564
TCGA-D8-A1XT-10A-01D-A14K-09_BRCA	679	334	374	0	0	0	559	660	479	0	0	0	0	0	0	188	597
TCGA-D8-A1XU-10A-01D-A14K-09_BRCA	699	0	0	380	696	466	558	650	478	0	0	0	0	0	0	173	589
TCGA-D8-A1XV-10A-01D-A14K-09_BRCA	700	315	357	370	699	460	557	657	455	104	661	533	444	182	0	90	595

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-D8-A1XW-10A-01D-A14K-09_BRCA	596	330	373	0	0	0	559	651	571	0	0	0	0	0	0	130	593
TCGA-D8-A1XY-10A-01D-A14K-09_BRCA	690	0	0	389	699	452	558	652	478	0	0	0	0	0	0	114	594
TCGA-D8-A1XZ-10A-01D-A14K-09_BRCA	700	314	363	374	708	378	559	667	573	0	638	549	0	0	51	86	592
TCGA-D8-A1Y0-10A-01D-A14K-09_BRCA	681	294	334	342	640	438	550	639	442	0	0	0	0	0	0	71	581
TCGA-D8-A1Y1-10A-01D-A14K-09_BRCA	657	271	329	325	635	340	549	637	439	0	0	0	0	0	0	75	587
TCGA-D8-A1Y2-10A-01D-A159-09_BRCA	665	0	0	358	660	445	526	631	446	0	0	0	0	0	0	17	575
TCGA-D8-A1Y3-10A-01D-A159-09_BRCA	693	309	342	361	659	363	553	650	477	0	0	0	0	0	34	50	592
TCGA-D8-A27E-10A-01D-A16D-09_BRCA	679	283	336	347	687	438	557	658	454	98	584	516	0	0	0	76	591
TCGA-D8-A27F-10A-01D-A16D-09_BRCA	659	0	0	369	675	458	543	630	423	102	595	0	350	175	0	40	583
TCGA-D8-A27G-10A-01D-A16D-09_BRCA	691	288	334	370	691	446	554	653	457	98	646	536	368	161	0	52	592
TCGA-D8-A27H-10A-01D-A16D-09_BRCA	696	306	347	346	654	359	540	635	472	0	0	0	0	0	0	105	585
TCGA-D8-A27I-10A-02D-A16D-09_BRCA	657	288	325	331	676	360	546	638	445	0	582	520	0	0	0	76	558
TCGA-D8-A27K-10A-01D-A16D-09_BRCA	688	0	0	378	702	457	552	644	473	0	0	0	0	0	0	124	590
TCGA-D8-A27L-10A-01D-A16D-09_BRCA	691	299	367	365	684	442	559	663	451	103	653	0	457	172	0	68	591
TCGA-D8-A27M-10A-01D-A16D-09_BRCA	656	0	0	367	673	426	530	625	301	92	577	471	0	168	0	36	563
TCGA-D8-A27N-10A-01D-A16D-09_BRCA	543	317	360	0	644	176	546	636	427	99	628	533	0	164	23	0	584
TCGA-D8-A27P-10A-01D-A16D-09_BRCA	672	0	0	369	687	432	515	588	435	0	0	0	0	174	0	57	563
TCGA-D8-A27R-10A-01D-A16D-09_BRCA	687	0	0	377	689	450	540	648	460	0	0	0	0	0	0	96	594
TCGA-D8-A27T-10A-01D-A16D-09_BRCA	674	290	345	357	640	419	551	635	465	0	0	0	0	0	0	86	586
TCGA-D8-A27V-10A-01D-A17D-09_BRCA	642	268	290	326	630	413	533	633	432	0	0	0	0	0	20	19	572
TCGA-D8-A27W-10A-01D-A16D-09_BRCA	699	0	0	379	694	451	554	653	470	0	0	0	0	0	0	96	586
TCGA-D8-A3Z5-10A-01D-A243-09_BRCA	674	264	297	230	610	404	540	600	443	0	0	0	0	0	0	83	586
TCGA-D8-A3Z6-10A-01D-A23C-09_BRCA	694	296	304	297	598	438	554	618	444	0	0	0	0	0	0	77	576
TCGA-D8-A4Z1-10A-01D-A25Q-09_BRCA	687	0	0	361	656	451	549	632	534	0	0	0	0	0	0	68	576
TCGA-D9-A148-10A-01D-A19A-08_SKCM	680	0	0	293	600	389	532	645	478	0	0	0	0	0	0	97	578
TCGA-D9-A149-10A-01D-A198-08_SKCM	683	0	0	304	600	380	532	639	473	0	0	0	0	0	36	61	576
TCGA-D9-A1JW-10A-01D-A19A-08_SKCM	675	236	246	269	492	347	534	639	468	0	0	0	0	0	0	104	575
TCGA-D9-A1JX-10A-01D-A19A-08_SKCM	673	243	257	277	549	371	531	637	483	0	0	0	0	0	0	97	580
TCGA-D9-A1X3-10A-01D-A199-08_SKCM	687	0	0	295	518	363	530	645	451	65	558	0	293	137	0	62	575
TCGA-D9-A3Z1-10A-01D-A23B-08_SKCM	684	247	267	288	557	371	531	642	437	72	596	0	358	134	0	66	577
TCGA-D9-A3Z3-10A-01D-A23B-08_SKCM	691	0	0	294	600	372	531	634	478	0	0	0	0	0	0	116	575
TCGA-D9-A3Z4-10A-01D-A23B-08_SKCM	683	249	267	294	614	382	530	642	455	77	641	567	365	138	0	73	576
TCGA-D9-A4Z2-10A-01D-A24R-08_SKCM	590	245	267	0	499	130	530	634	463	0	571	504	0	0	0	53	569
TCGA-D9-A4Z3-10A-01D-A25O-08_SKCM	672	0	0	289	582	374	522	619	458	0	0	0	0	0	0	83	573
TCGA-D9-A4Z5-10A-01D-A25O-08_SKCM	667	239	242	254	587	351	523	621	352	0	613	558	0	133	0	43	570
TCGA-D9-A4Z6-10A-01D-A25O-08_SKCM	667	244	254	272	552	266	527	627	392	0	0	0	0	0	35	0	570
TCGA-D9-A6E9-10A-01D-A30X-08_SKCM	672	248	257	272	540	354	532	629	464	0	0	0	0	0	0	67	573
TCGA-D9-A6EA-10A-01D-A30X-08_SKCM	663	242	258	264	600	276	521	643	473	0	588	558	0	0	27	55	573
TCGA-D9-A6EC-10A-01D-A30X-08_SKCM	682	241	250	286	548	357	532	645	480	0	0	0	0	0	0	71	580
TCGA-D9-A6EG-10A-01D-A32N-08_SKCM	680	248	268	282	612	138	513	634	390	0	602	559	0	136	31	0	572
TCGA-DA-A1HV-10A-01D-A198-08_SKCM	678	0	0	299	572	366	523	640	468	0	0	0	0	0	22	56	574
TCGA-DA-A1HW-10A-01D-A19A-08_SKCM	637	248	255	169	550	365	532	630	399	0	0	0	0	0	0	106	570
TCGA-DA-A1HY-10A-01D-A19A-08_SKCM	669	0	0	299	595	280	519	642	475	0	0	0	0	0	0	91	573
TCGA-DA-A1I0-10B-01D-A20D-08_SKCM	679	243	252	288	610	373	530	653	485	0	594	516	0	0	28	67	576
TCGA-DA-A1I1-10A-01D-A198-08_SKCM	590	257	271	0	0	0	531	636	379	69	563	0	352	134	0	49	573
TCGA-DA-A1I2-10A-01D-A19A-08_SKCM	654	214	233	245	563	352	530	637	296	65	597	568	0	128	0	35	579
TCGA-DA-A1I4-10A-01D-A198-08_SKCM	673	248	262	279	560	275	522	611	311	0	580	0	364	134	0	74	577
TCGA-DA-A1I5-10A-01D-A199-08_SKCM	661	245	246	255	596	364	535	635	464	0	523	500	0	0	0	98	579
TCGA-DA-A1I7-10A-01D-A199-08_SKCM	685	0	0	306	603	393	536	646	0	83	623	0	382	142	0	0	578
TCGA-DA-A1I8-10A-01D-A199-08_SKCM	689	0	0	292	607	375	526	648	406	65	506	510	0	0	0	71	576
TCGA-DA-A1IA-10A-01D-A198-08_SKCM	682	0	0	300	599	367	528	641	479	0	0	0	0	0	26	48	576
TCGA-DA-A1IB-10A-01D-A198-08_SKCM	663	235	258	96	497	132	530	619	461	0	491	499	0	0	30	0	575
TCGA-DA-A1IC-10A-01D-A199-08_SKCM	662	250	259	277	588	370	533	645	379	82	504	0	368	135	27	0	581
TCGA-DA-A3F2-10A-01D-A20D-08_SKCM	686	0	0	294	578	378	532	651	391	67	575	0	291	136	0	54	577
TCGA-DA-A3F3-10A-01D-A20D-08_SKCM	759	0	0	303	606	375	532	645	446	80	585	0	362	136	0	63	576
TCGA-DA-A3F5-10A-01D-A20D-08_SKCM	681	247	253	277	588	375	535	651	461	81	623	0	368	133	0	65	575
TCGA-DA-A3F8-10A-01D-A20D-08_SKCM	682	0	0	305	595	374	528	654	407	0	0	0	0	0	0	78	578
TCGA-DB-5270-10A-01D-1468-08_LGG	668	237	262	194	514	280	529	656	399	0	0	0	0	0	33	75	578
TCGA-DB-5273-10A-01D-1468-08_LGG	687	0	0	300	608	395	534	657	479	0	0	0	0	0	38	78	578
TCGA-DB-5274-10A-01D-1468-08_LGG	690	0	0	300	609	389	531	651	479	0	0	0	0	0	0	115	577
TCGA-DB-5275-10A-01D-1468-08_LGG	757	0	0	305	606	390	530	654	381	76	611	0	366	139	0	76	572
TCGA-DB-5276-10A-01D-1468-08_LGG	658	246	260	277	581	279	529	659	470	0	0	0	0	0	32	77	578
TCGA-DB-5277-10A-01D-1468-08_LGG	678	252	261	291	612	377	531	648	476	0	608	570	0	0	50	1	575
TCGA-DB-5278-10A-01D-1468-08_LGG	684	0	0	299	602	289	524	647	457	77	600	0	295	137	0	75	577
TCGA-DB-5279-10A-01D-1468-08_LGG	688	0	0	307	606	384	535	645	477	0	0	0	0	0	0	139	578
TCGA-DB-5280-10A-01D-1468-08_LGG	688	0	0	304	606	401	528	643	476	0	0	0	0	0	0	104	576
TCGA-DB-5281-10A-01D-1468-08_LGG	680	246	268	288	608	380	531	650	473	0	603	515	0	0	0	91	580
TCGA-DB-A4X9-10A-01D-A26K-08_LGG	762	0	0	316	610	402	535	649	484	0	0	0	0	0	0	150	580
TCGA-DB-A4XA-10A-01D-A26K-08_LGG	661	244	249	285	566	282	529	642	400	0	0	0	0	0	35	2	576
TCGA-DB-A4XB-10A-01D-A26K-08_LGG	673	236	254	274	571	374	530	626	371	65	616	500	286	130	0	57	572
TCGA-DB-A4XC-10A-01D-A26K-08_LGG	597	253	273	0	541	133	534	646	445	84	611	565	0	131	0	43	575
TCGA-DB-A4XD-10A-01D-A27N-08_LGG	758	0	0	311	618	390	531	645	481	0	0	0	0	0	0	95	578
TCGA-DB-A4XE-10A-01D-A27N-08_LGG	686	0	0	305	604	291	531	650	484	0	0	0	0	0	0	144	580
TCGA-DB-A4XF-10A-01D-A27N-08_LGG	746	252	263	289	596	381	536	644	473	0	0	0	0	0	0	99	577
TCGA-DB-A4XG-10A-01D-A27N-08_LGG	673	244	260	291	554	284	529	646	474	0	0	0	0	0	30	69	577
TCGA-DB-A4XH-10A-01D-A27N-08_LGG	681	249	263	285	558	376	536	643	481	0	0	0	0	0	0	146	575
TCGA-DB-A64L-10A-01D-A29Q-08_LGG	652	234	242	276	604	276	528	634	379	71	617	557	293	133	30	0	575
TCGA-DB-A64O-10A-01D-A29Q-08_LGG	668	0	0	308	613	389	531	643	474	0	0	0	0	0	0	146	576
TCGA-DB-A64P-10A-01D-A29Q-08_LGG	748	241	265	190	515	290	534	639	472	0	0	0	0	0	0	152	578
TCGA-DB-A64Q-10A-01D-A29Q-08_LGG	763	0	0	340	609	390	530	643	475	0	0	0	0	0	0	141	577
TCGA-DB-A64R-10A-01D-A29Q-08_LGG	686	0	0	338	597	383	533	642	474	0	0	0	0	0	0	101	576
TCGA-DB-A64S-10A-01D-A29Q-08_LGG	683	0	0	297	602	381	523	641	478	0	0	0	0	0	34	59	578
TCGA-DB-A64U-10A-01D-A29Q-08_LGG	647	251	259	287	560	285	530	635	366	75	576	0	367	135	0	71	576
TCGA-DB-A64V-10A-01D-A29Q-08_LGG	652	251	272	286	567	378	534	654	483	0	0	0	0	0	41	76	576
TCGA-DB-A64W-10A-01D-A29Q-08_LGG	762	0	0	309	612	395	535	644	485	0	0	0	0	0	0	114	580
TCGA-DB-A64X-10A-01D-A29Q-08_LGG	754	252	271	196	542	288	534	651	486	0	579	570	0	0	0	117	581
TCGA-DB-A75K-10A-01D-A329-08_LGG	680	0	0	297	602	365	525	632	465	0	0	0	0	0	0	98	574
TCGA-DB-A75L-10A-01D-A329-08_LGG	677	0	0	294	598	376	529	636	463	0	0	0	0	0	23	54	570
TCGA-DB-A75M-10A-01D-A329-08_LGG	668	231	255	262	500	269	524	618	464	0	0	0	0	0	0	90	574
TCGA-DB-A75O-10A-01D-A329-08_LGG	632	239	257	270	598	271	528	630	359	76	633	570	0	129	19	0	571
TCGA-DB-A75P-10A-01D-A329-08_LGG	682	243	251	266	495	349	534	628	0	79	620	0	381	140	0	0	571
TCGA-DC-4745-10A-01D-1733-10_READ	673	0	0	361	660	376	527	624	349	0	0	0	0	0	0	70	585
TCGA-DC-4749-10A-01D-1733-10_READ	687	0	0	357	668	450	532	590	339	0	390	0	309	169	14	0	580
TCGA-DC-5337-10A-01D-1657-10_READ	682	175	237	338	532	298	536	611	330	100	538	0	298	169	0	21	574
TCGA-DC-5869-10A-01D-1657-10_READ	675	168	279	346	621	333	528	618	336	93	574	414	318	172	0	20	570
TCGA-DC-6154-10A-01D-1924-10_READ	628	0	0	333	532	419	487	555	325	0	0	0	0	0	0	48	544

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DC-6155-10A-01D-1657-10_READ	668	0	0	392	652	435	541	641	0	102	597	510	311	185	0	0	582
TCGA-DC-6157-10A-01D-1657-10_READ	571	257	324	0	546	167	529	616	448	0	367	464	0	0	0	50	587
TCGA-DC-6158-10A-01D-1657-10_READ	665	173	301	349	651	318	529	637	451	0	466	502	0	0	0	38	587
TCGA-DC-6681-10A-01D-1826-10_READ	634	0	0	340	608	424	483	577	276	0	360	0	230	134	0	25	561
TCGA-DC-6682-10A-01D-1826-10_READ	646	123	273	206	632	403	514	582	432	0	379	454	0	0	0	45	568
TCGA-DC-6683-10A-01D-1826-10_READ	653	0	0	350	515	359	486	578	298	87	296	0	301	108	0	37	558
TCGA-DD-A113-10A-01D-A12Z-10_LIHC	698	245	271	353	655	353	531	637	465	0	425	526	0	0	24	36	588
TCGA-DD-A114-10A-01D-A12Z-10_LIHC	689	0	0	383	672	456	542	640	443	0	0	0	0	0	0	44	587
TCGA-DD-A115-10A-01D-A12Z-10_LIHC	684	0	0	372	674	442	535	606	469	0	0	0	0	0	0	79	585
TCGA-DD-A116-10A-01D-A12Z-10_LIHC	644	0	0	355	598	413	511	575	434	0	0	0	0	0	14	20	563
TCGA-DD-A119-10A-01D-A12Z-10_LIHC	681	272	293	343	611	423	543	627	448	0	0	0	0	0	15	41	591
TCGA-DD-A11A-10A-01D-A12Z-10_LIHC	606	0	0	236	606	369	531	603	330	0	327	421	0	0	14	0	573
TCGA-DD-A11B-10A-01D-A12Z-10_LIHC	579	301	333	0	0	0	514	575	0	92	613	501	350	184	0	0	578
TCGA-DD-A1EA-10A-01D-A12Z-10_LIHC	613	144	250	212	408	316	508	554	419	0	0	0	0	0	18	0	555
TCGA-DD-A1EB-10A-01D-A12Z-10_LIHC	633	0	0	340	609	393	500	548	273	95	304	0	245	140	0	12	544
TCGA-DD-A1ED-10A-01D-A152-10_LIHC	686	273	282	341	652	420	528	629	302	98	481	556	0	150	0	38	587
TCGA-DD-A1EE-10A-01D-A12Z-10_LIHC	633	0	0	329	583	350	487	562	421	0	0	0	0	0	8	15	544
TCGA-DD-A1EF-10A-01D-A12Z-10_LIHC	615	141	229	199	533	301	489	546	332	0	0	0	0	0	0	29	551
TCGA-DD-A1EG-10A-01D-A20W-10_LIHC	576	287	309	0	531	175	519	595	301	89	507	555	290	161	18	0	575
TCGA-DD-A1EH-10A-01D-A12Z-10_LIHC	518	237	290	0	367	137	424	408	0	90	534	479	203	165	0	0	552
TCGA-DD-A1EJ-10A-01D-A152-10_LIHC	599	137	169	0	282	287	456	399	472	0	0	0	0	0	0	80	570
TCGA-DD-A1EK-10A-01D-A20W-10_LIHC	690	0	0	370	652	384	529	625	361	0	0	0	0	0	19	37	587
TCGA-DD-A1EL-10A-01D-A152-10_LIHC	697	272	329	214	669	355	533	629	454	0	523	501	0	0	26	43	580
TCGA-DD-A4NF-10A-01D-A27I-10_LIHC	676	289	285	266	677	444	548	632	354	0	447	0	363	0	0	80	555
TCGA-DD-A4NG-10A-01D-A27I-10_LIHC	688	0	0	360	649	447	544	616	334	0	386	0	338	177	0	69	579
TCGA-DD-A4NH-10A-01D-A27I-10_LIHC	660	252	268	258	534	432	535	624	370	0	376	492	0	0	47	0	574
TCGA-DD-A4NI-10A-01D-A27I-10_LIHC	675	0	0	274	506	438	543	610	351	0	0	0	0	0	27	58	579
TCGA-DD-A4NJ-10A-01D-A27I-10_LIHC	681	269	280	265	481	444	544	609	364	0	0	0	0	0	0	87	585
TCGA-DD-A4NK-10A-01D-A28X-10_LIHC	682	256	289	256	518	430	551	616	360	0	0	0	0	0	0	117	581
TCGA-DD-A4NN-10A-01D-A28X-10_LIHC	668	0	0	268	551	373	530	590	312	0	411	0	354	171	0	59	579
TCGA-DD-A4NO-10A-01D-A28X-10_LIHC	560	239	302	233	545	363	541	599	328	0	477	534	0	162	0	34	577
TCGA-DD-A4NP-10A-01D-A28X-10_LIHC	648	0	0	255	499	440	534	582	272	0	416	440	0	159	0	35	555
TCGA-DD-A4NQ-10A-01D-A28X-10_LIHC	573	303	335	0	508	174	543	581	337	0	432	489	0	0	26	56	565
TCGA-DD-A4NR-10A-01D-A30V-10_LIHC	503	105	310	196	426	236	493	479	208	0	394	0	295	138	0	21	552
TCGA-DD-A4NS-10A-01D-A30V-10_LIHC	518	170	194	221	374	307	398	366	282	0	323	0	227	137	0	25	541
TCGA-DD-A4NV-10A-01D-A30V-10_LIHC	490	151	240	117	469	319	490	470	344	0	0	0	0	0	15	30	554
TCGA-DE-A0XZ-10A-01D-A17V-08_THCA	675	257	266	289	590	282	530	647	465	76	543	564	0	137	30	0	575
TCGA-DE-A0Y2-10A-01D-A10S-08_THCA	671	242	272	290	591	280	528	657	478	0	0	0	0	0	34	84	576
TCGA-DE-A0Y3-10A-01D-A10S-08_THCA	678	243	263	281	582	376	530	646	471	0	0	0	0	0	40	1	576
TCGA-DE-A2OL-10A-01D-A18F-08_THCA	595	256	269	0	552	134	531	637	472	0	532	520	0	0	35	0	577
TCGA-DE-A3KN-10A-01D-A20C-08_THCA	686	0	0	346	604	383	531	649	476	0	0	0	0	0	40	1	578
TCGA-DE-A4M8-10A-01D-A25A-08_THCA	678	0	0	292	595	381	526	630	445	0	0	0	0	0	0	111	575
TCGA-DE-A4M9-10A-01D-A25A-08_THCA	671	0	0	286	513	280	522	620	384	0	0	0	0	0	21	38	568
TCGA-DE-A4MA-10A-01D-A25A-08_THCA	667	0	0	284	588	365	526	620	295	53	504	0	285	121	0	50	574
TCGA-DE-A4MB-10A-01D-A25A-08_THCA	720	252	269	292	622	293	535	657	488	0	597	574	0	0	37	72	582
TCGA-DE-A4MC-10A-01D-A25A-08_THCA	752	232	252	291	582	372	538	656	413	0	380	0	202	121	31	63	580
TCGA-DF-A2KN-10A-01D-A17W-09_UCEC	694	0	0	362	659	369	537	638	444	0	0	0	0	0	0	117	590
TCGA-DF-A2KR-10A-01D-A17W-09_UCEC	673	0	0	358	658	427	544	610	434	0	0	0	0	0	33	44	583
TCGA-DF-A2KS-10A-01D-A18P-09_UCEC	684	304	335	343	685	465	555	650	557	0	590	543	0	0	39	67	588
TCGA-DF-A2KU-10A-01D-A17W-09_UCEC	567	271	307	305	610	420	549	621	533	0	0	0	0	0	21	45	585
TCGA-DF-A2KV-10A-01D-A17W-09_UCEC	684	0	0	352	671	445	546	625	404	86	549	0	345	178	0	53	579
TCGA-DF-A2KY-10A-01D-A20S-09_UCEC	692	298	303	327	603	425	554	609	406	95	562	544	0	170	0	45	581
TCGA-DF-A2KZ-10A-01D-A20S-09_UCEC	686	302	307	313	605	347	548	617	543	0	0	0	0	0	0	79	584
TCGA-DF-A2L0-10A-01D-A17W-09_UCEC	667	0	0	351	655	346	515	494	324	0	0	0	0	170	0	41	553
TCGA-DG-A2KH-10A-01D-A22X-09_CESC	700	297	335	314	688	444	552	643	412	98	595	558	0	175	0	52	591
TCGA-DG-A2KJ-10A-01D-A18J-09_CESC	696	291	317	202	607	358	545	632	543	0	0	0	0	0	34	49	579
TCGA-DG-A2KK-10A-01D-A17W-09_CESC	694	0	0	375	680	452	556	633	450	92	614	0	433	177	0	66	593
TCGA-DG-A2KL-10A-01D-A17W-09_CESC	698	0	0	364	696	466	559	647	0	102	646	574	460	184	0	1	592
TCGA-DG-A2KM-10A-01D-A17W-09_CESC	699	0	0	361	677	455	553	627	554	0	0	0	0	0	0	92	591
TCGA-DH-5140-10A-01D-1468-08_LGG	689	254	270	299	592	389	535	654	478	0	0	0	0	0	0	104	581
TCGA-DH-5141-10A-01D-1468-08_LGG	687	0	0	307	605	398	532	659	463	81	635	0	373	138	41	1	576
TCGA-DH-5142-10A-01D-1468-08_LGG	599	260	274	0	590	137	535	658	482	0	618	574	0	0	36	64	578
TCGA-DH-5143-10A-01D-1468-08_LGG	682	255	273	289	616	287	533	662	482	0	626	0	0	0	39	89	580
TCGA-DH-5144-10A-01D-1468-08_LGG	689	0	0	305	609	291	525	665	485	0	0	0	0	0	44	84	576
TCGA-DH-A669-10A-01D-A31J-08_LGG	681	0	0	301	593	380	526	629	468	0	0	0	0	0	0	114	573
TCGA-DH-A66B-10A-01D-A29Q-08_LGG	763	0	0	316	621	396	536	654	491	0	0	0	0	0	0	155	580
TCGA-DH-A66D-10A-01D-A31J-08_LGG	681	0	0	304	592	383	529	637	0	82	624	0	373	138	0	0	575
TCGA-DH-A66F-10A-01D-A29Q-08_LGG	761	0	0	310	612	390	530	648	458	74	535	0	377	138	0	84	579
TCGA-DH-A66G-10A-01D-A31J-08_LGG	685	0	0	299	604	377	527	642	466	0	0	0	0	0	0	116	572
TCGA-DI-A0WH-10B-01D-A12J-09_UCEC	800	0	0	415	725	472	563	672	582	0	0	0	0	0	0	222	599
TCGA-DI-A1BU-10A-01D-A135-09_UCEC	673	277	304	280	635	320	545	605	432	0	387	503	0	0	20	29	574
TCGA-DI-A1BY-10A-01D-A135-09_UCEC	690	296	317	317	619	428	554	643	404	89	587	0	357	171	0	55	589
TCGA-DI-A1C3-10A-01D-A135-09_UCEC	691	0	0	345	655	458	551	620	448	0	0	0	0	0	0	83	581
TCGA-DI-A2QT-10A-01D-A19Y-09_UCEC	664	282	324	341	634	437	548	631	460	0	0	0	0	0	44	1	581
TCGA-DJ-A13L-10A-01D-A21Z-08_THCA	663	241	265	283	585	277	532	639	391	79	608	0	357	135	0	60	577
TCGA-DJ-A13M-10A-01D-A10S-08_THCA	754	249	271	297	616	381	533	661	456	76	633	570	368	135	0	83	577
TCGA-DJ-A13O-10A-01D-A10S-08_THCA	671	255	264	290	596	373	536	657	462	76	537	0	300	137	0	69	578
TCGA-DJ-A13P-10A-01D-A10S-08_THCA	674	253	269	294	588	283	532	666	478	0	0	0	0	0	37	83	576
TCGA-DJ-A13R-10A-01D-A10S-08_THCA	679	243	260	288	614	378	531	657	482	0	591	560	0	0	0	138	579
TCGA-DJ-A13S-10A-01D-A10S-08_THCA	684	0	0	310	606	385	531	662	482	0	0	0	0	0	34	78	578
TCGA-DJ-A13T-10A-01D-A10S-08_THCA	688	251	269	298	588	378	532	657	461	73	618	0	364	135	0	73	575
TCGA-DJ-A13U-10A-01D-A10S-08_THCA	682	253	267	284	589	366	534	651	457	82	614	0	376	135	32	0	577
TCGA-DJ-A13V-10A-01D-A10S-08_THCA	755	0	0	310	610	392	531	648	480	0	0	0	0	0	0	140	577
TCGA-DJ-A13W-10A-01D-A10S-08_THCA	681	251	271	294	614	288	532	654	480	0	610	519	0	0	0	106	576
TCGA-DJ-A13X-10A-01D-A10S-08_THCA	596	261	280	0	565	138	532	647	468	74	640	566	370	140	35	0	578
TCGA-DJ-A1QD-10A-01D-A14W-08_THCA	653	240	252	270	557	271	507	605	0	74	630	0	369	141	0	0	574
TCGA-DJ-A1QE-10A-01D-A14W-08_THCA	670	238	266	276	546	282	530	636	450	76	575	0	290	139	0	61	577
TCGA-DJ-A1QF-10A-01D-A14W-08_THCA	592	258	280	0	555	132	532	648	363	80	640	515	379	136	30	0	576
TCGA-DJ-A1QG-10A-01D-A14W-08_THCA	595	257	270	0	586	134	513	581	311	0	621	502	286	138	0	54	576
TCGA-DJ-A1QH-10A-01D-A14W-08_THCA	679	0	0	297	598	383	528	634	477	0	0	0	0	0	0	72	579
TCGA-DJ-A1QI-10A-01D-A14W-08_THCA	595	257	282	0	0	0	528	645	380	76	590	0	279	136	21	0	574
TCGA-DJ-A1QL-10A-01D-A14W-08_THCA	672	230	247	279	603	361	535	648	385	80	622	514	0	136	24	1	574
TCGA-DJ-A1QM-10A-01D-A14W-08_THCA	687	0	0	305	604	373	531	644	376	77	565	0	291	133	0	52	577
TCGA-DJ-A1QN-10A-01D-A14W-08_THCA	640	234	254	282	601	278	529	629	448	70	624	510	290	133	0	52	576
TCGA-DJ-A1QO-10A-01D-A14W-08_THCA	671	0	0	300	592	287	520	639	476	0	0	0	0	0	24	49	577
TCGA-DJ-A1QQ-10A-01D-A14W-08_THCA	671	242	248	271	593	368	533	644	469	0	578	564	0	0	0	72	578

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DJ-A2PN-10A-01D-A19M-08_THCA	684	0	0	300	608	295	529	658	487	0	0	0	0	0	29	71	576
TCGA-DJ-A2PO-10A-01D-A19M-08_THCA	681	0	0	305	635	376	530	646	413	0	0	0	0	0	0	109	577
TCGA-DJ-A2PP-10A-01D-A19M-08_THCA	743	249	258	279	586	278	531	642	460	76	612	0	367	138	34	2	578
TCGA-DJ-A2PQ-10A-01D-A18F-08_THCA	681	240	261	276	607	282	532	637	443	74	625	578	0	133	0	60	574
TCGA-DJ-A2PR-10A-01D-A19M-08_THCA	676	244	261	284	548	369	521	608	454	0	597	0	369	135	0	62	576
TCGA-DJ-A2PS-10A-01D-A18F-08_THCA	688	249	262	287	591	382	529	613	458	0	598	0	366	137	34	0	577
TCGA-DJ-A2PT-10A-01D-A18F-08_THCA	679	0	0	298	605	380	530	642	372	75	605	0	366	135	0	62	573
TCGA-DJ-A2PU-10A-01D-A19M-08_THCA	665	240	261	285	569	358	530	653	477	0	0	0	0	0	0	110	574
TCGA-DJ-A2PV-10A-01D-A19M-08_THCA	687	0	0	305	610	387	534	649	486	0	0	0	0	0	0	96	577
TCGA-DJ-A2PW-10A-01D-A19M-08_THCA	680	0	0	312	612	382	528	650	414	0	0	0	0	0	0	95	577
TCGA-DJ-A2PX-10A-01D-A18F-08_THCA	685	0	0	301	598	390	530	631	478	0	0	0	0	0	0	125	575
TCGA-DJ-A2PY-10A-01D-A18F-08_THCA	688	0	0	298	597	380	529	638	479	0	0	0	0	0	0	91	571
TCGA-DJ-A2PZ-10A-01D-A18F-08_THCA	683	0	0	296	599	390	527	626	375	76	575	0	364	136	0	71	576
TCGA-DJ-A2Q0-10A-01D-A202-08_THCA	671	236	257	278	535	366	531	632	463	0	0	0	0	0	0	75	576
TCGA-DJ-A2Q1-10A-01D-A19M-08_THCA	686	239	254	289	611	385	532	639	409	0	608	513	0	0	0	104	575
TCGA-DJ-A2Q2-10A-01D-A19M-08_THCA	665	233	258	286	611	349	532	648	409	0	595	503	0	0	17	44	579
TCGA-DJ-A2Q3-10A-01D-A18F-08_THCA	669	252	264	296	613	381	533	633	477	0	0	0	0	0	0	89	577
TCGA-DJ-A2Q4-10A-01D-A18F-08_THCA	674	248	256	278	585	368	529	642	460	65	586	0	359	138	0	73	575
TCGA-DJ-A2Q5-10A-01D-A18F-08_THCA	756	0	0	301	600	395	533	648	485	0	0	0	0	0	33	59	574
TCGA-DJ-A2Q6-10A-01D-A18F-08_THCA	683	0	0	305	610	377	531	637	475	0	0	0	0	0	29	58	576
TCGA-DJ-A2Q7-10A-01D-A18F-08_THCA	682	0	0	302	613	401	531	652	451	69	591	0	291	137	0	72	570
TCGA-DJ-A2Q8-10A-01D-A18F-08_THCA	648	244	255	278	577	373	534	645	472	0	0	0	0	0	30	64	574
TCGA-DJ-A2Q9-10A-01D-A18F-08_THCA	680	0	0	296	604	376	531	637	454	59	582	0	363	135	34	0	576
TCGA-DJ-A2QA-10A-01D-A18F-08_THCA	688	0	0	297	574	386	530	639	467	0	0	0	0	0	38	0	577
TCGA-DJ-A2QB-10A-01D-A19M-08_THCA	752	248	258	282	577	371	534	651	479	0	0	0	0	0	34	65	577
TCGA-DJ-A2QC-10A-01D-A18F-08_THCA	667	239	260	276	581	371	531	629	474	0	0	0	0	0	0	86	576
TCGA-DJ-A3UK-10A-01D-A22D-08_THCA	595	252	269	0	544	137	534	659	380	80	632	564	0	131	22	0	579
TCGA-DJ-A3UM-10A-01D-A22D-08_THCA	686	0	0	296	608	386	530	648	480	0	0	0	0	0	32	66	578
TCGA-DJ-A3UN-10A-01D-A22D-08_THCA	689	0	0	303	608	389	532	642	457	73	586	0	361	130	28	0	576
TCGA-DJ-A3UO-10A-01D-A22D-08_THCA	638	235	253	269	568	0	526	619	361	0	0	0	0	136	0	61	566
TCGA-DJ-A3UP-10A-01D-A22D-08_THCA	686	0	0	298	603	383	532	647	0	87	630	0	374	138	0	0	574
TCGA-DJ-A3UQ-10A-01D-A22D-08_THCA	685	0	0	301	606	387	529	651	466	0	0	0	0	0	29	62	573
TCGA-DJ-A3UR-10A-01D-A22D-08_THCA	684	0	0	297	604	383	531	652	388	74	600	0	366	136	33	0	578
TCGA-DJ-A3US-10A-01D-A22D-08_THCA	678	0	0	290	597	374	531	640	368	62	602	0	291	134	29	0	576
TCGA-DJ-A3UT-10A-01D-A22D-08_THCA	680	0	0	301	597	381	522	636	384	75	573	0	364	129	0	55	575
TCGA-DJ-A3UU-10A-01D-A22D-08_THCA	656	251	263	286	567	380	531	643	441	80	617	563	0	137	0	68	574
TCGA-DJ-A3UV-10A-01D-A22D-08_THCA	667	0	0	292	601	288	522	638	463	0	0	0	0	0	27	64	577
TCGA-DJ-A3UW-10A-01D-A22D-08_THCA	649	245	262	288	551	275	531	640	386	69	600	565	0	132	29	0	577
TCGA-DJ-A3UX-10A-01D-A22D-08_THCA	686	0	0	302	603	288	522	654	449	74	602	531	0	138	0	74	579
TCGA-DJ-A3UY-10A-01D-A22D-08_THCA	757	0	0	302	599	382	533	641	473	0	0	0	0	0	37	1	574
TCGA-DJ-A3UZ-10A-01D-A22Z-08_THCA	759	0	0	303	611	391	534	646	472	0	0	0	0	0	26	63	575
TCGA-DJ-A3V0-10A-01D-A22Z-08_THCA	757	260	268	297	610	394	539	657	472	79	656	578	377	138	0	68	581
TCGA-DJ-A3V2-10A-01D-A22Z-08_THCA	636	233	242	253	485	268	526	614	350	0	511	0	286	127	0	49	570
TCGA-DJ-A3V3-10A-01D-A22Z-08_THCA	587	246	251	0	553	134	525	628	361	63	598	490	289	132	23	0	571
TCGA-DJ-A3V4-10A-01D-A22Z-08_THCA	678	245	249	285	590	371	531	639	474	0	0	0	0	0	0	125	577
TCGA-DJ-A3V5-10A-01D-A22Z-08_THCA	667	230	247	263	590	367	524	615	374	77	610	514	286	133	0	43	569
TCGA-DJ-A3V6-10A-01D-A22Z-08_THCA	762	0	0	311	624	300	536	652	490	0	0	0	0	0	66	0	580
TCGA-DJ-A3V7-10A-01D-A23K-08_THCA	683	244	257	287	588	373	536	639	404	0	0	0	0	0	0	81	577
TCGA-DJ-A3V8-10A-01D-A23K-08_THCA	682	0	0	307	599	379	528	644	451	74	615	0	351	135	29	4	577
TCGA-DJ-A3V9-10A-01D-A23K-08_THCA	678	0	0	302	604	389	532	646	480	0	0	0	0	0	33	69	573
TCGA-DJ-A3VA-10A-01D-A23K-08_THCA	671	250	255	294	594	382	532	637	395	79	631	564	301	132	0	75	574
TCGA-DJ-A3VB-10A-01D-A23K-08_THCA	685	0	0	305	610	379	532	651	479	0	0	0	0	0	0	127	578
TCGA-DJ-A3VD-10A-01D-A23K-08_THCA	747	241	260	282	628	378	539	660	468	85	649	585	0	138	29	0	579
TCGA-DJ-A3VE-10A-01D-A23K-08_THCA	673	245	268	290	559	273	528	647	388	81	610	0	296	135	0	65	572
TCGA-DJ-A3VF-10A-01D-A23K-08_THCA	680	243	261	280	591	360	529	645	405	0	0	0	3	0	0	118	574
TCGA-DJ-A3VG-10A-01D-A23K-08_THCA	686	250	266	286	601	384	532	652	480	0	610	567	0	0	36	73	575
TCGA-DJ-A3VI-10A-01D-A23K-08_THCA	677	241	259	286	588	272	517	617	385	0	609	4	294	133	27	2	575
TCGA-DJ-A3VJ-10A-01D-A23K-08_THCA	595	261	272	0	134	0	534	651	474	0	35	2	0	0	0	84	573
TCGA-DJ-A3VK-10A-01D-A23K-08_THCA	592	255	266	0	604	137	528	645	464	0	633	569	0	0	0	75	572
TCGA-DJ-A3VL-10A-01D-A23K-08_THCA	683	237	257	192	606	280	529	637	455	75	638	506	295	131	21	1	572
TCGA-DJ-A3VM-10A-01D-A23K-08_THCA	685	0	0	306	604	383	530	635	470	0	0	0	0	0	0	84	572
TCGA-DJ-A4UL-10A-01D-A25A-08_THCA	650	222	238	260	555	350	523	606	374	0	489	485	0	0	0	83	565
TCGA-DJ-A4UP-10A-01D-A25A-08_THCA	662	233	260	261	503	270	487	592	301	0	549	0	291	133	0	48	574
TCGA-DJ-A4UQ-10A-01D-A25A-08_THCA	763	0	0	357	618	394	533	651	486	0	0	0	0	0	48	0	581
TCGA-DJ-A4UR-10A-01D-A25A-08_THCA	748	258	276	302	629	391	536	650	496	0	618	570	0	0	0	174	580
TCGA-DJ-A4UT-10A-01D-A25A-08_THCA	639	222	245	235	512	268	516	605	284	0	584	482	258	117	0	49	560
TCGA-DJ-A4UW-10A-01D-A25A-08_THCA	673	0	0	282	560	368	527	598	378	0	0	0	0	0	31	4	570
TCGA-DJ-A4V0-10A-01D-A25A-08_THCA	678	0	0	285	555	368	513	618	459	0	0	0	0	0	29	3	572
TCGA-DJ-A4V2-10A-01D-A25A-08_THCA	678	0	0	284	567	376	526	633	390	0	0	0	0	0	23	54	575
TCGA-DJ-A4V4-10A-01D-A25A-08_THCA	589	230	237	247	596	353	526	615	460	0	500	498	0	0	25	42	568
TCGA-DJ-A4V5-10A-01D-A25A-08_THCA	660	234	261	261	532	351	523	623	301	68	513	0	286	129	0	50	572
TCGA-DK-A1A3-10A-01D-A13W-08_BLCA	763	262	270	305	579	383	532	638	445	0	613	0	377	140	0	75	582
TCGA-DK-A1A5-10A-01D-A13W-08_BLCA	690	0	0	309	620	404	533	664	483	0	0	0	0	0	0	116	579
TCGA-DK-A1A6-10A-01D-A13W-08_BLCA	759	256	274	299	562	381	539	658	490	0	0	0	0	0	46	0	581
TCGA-DK-A1A7-10A-01D-A13W-08_BLCA	764	243	273	308	628	379	540	663	489	0	595	578	0	0	42	79	580
TCGA-DK-A1AA-10A-01D-A13W-08_BLCA	745	241	268	310	593	286	535	653	485	0	0	0	0	0	59	0	581
TCGA-DK-A1AB-10A-01D-A13W-08_BLCA	688	244	263	306	622	389	539	668	488	76	642	580	0	0	0	122	579
TCGA-DK-A1AC-10A-01D-A13W-08_BLCA	592	250	274	0	585	137	534	648	485	0	581	501	0	0	21	67	581
TCGA-DK-A1AD-10A-01D-A13W-08_BLCA	762	0	0	366	630	398	539	667	503	0	0	0	0	0	0	164	582
TCGA-DK-A1AE-10A-01D-A13W-08_BLCA	745	251	0	287	624	383	536	647	392	71	564	0	364	142	0	85	581
TCGA-DK-A1AF-10A-01D-A13W-08_BLCA	588	255	266	0	0	0	0	0	0	0	613	0	379	144	0	1	581
TCGA-DK-A1AG-10A-01D-A13W-08_BLCA	689	37	53	301	599	372	533	643	410	0	59	143	0	0	0	99	577
TCGA-DK-A2HX-10A-01D-A18F-08_BLCA	686	0	0	299	594	378	527	643	467	0	0	0	0	0	0	83	576
TCGA-DK-A2I1-10A-01D-A17V-08_BLCA	679	245	258	280	595	274	532	654	482	0	0	0	0	0	23	56	579
TCGA-DK-A2I2-10A-01D-A17V-08_BLCA	677	250	260	286	567	368	534	652	482	0	0	0	0	0	23	67	575
TCGA-DK-A2I4-10A-01D-A21A-08_BLCA	595	230	249	262	591	355	530	631	361	66	539	521	0	129	26	0	573
TCGA-DK-A2I6-10A-01D-A18F-08_BLCA	679	0	0	303	574	372	524	643	468	0	0	0	0	0	26	53	577
TCGA-DK-A3IK-10A-01D-A21A-08_BLCA	685	0	0	292	600	391	531	638	474	0	0	0	0	0	0	125	575
TCGA-DK-A3IL-10A-01D-A20D-08_BLCA	749	246	256	282	543	280	519	620	448	0	606	569	0	134	0	66	577
TCGA-DK-A3IM-10A-01D-A20D-08_BLCA	687	0	0	304	607	380	531	652	466	0	0	0	0	0	29	65	578
TCGA-DK-A3IN-10A-01D-A20D-08_BLCA	680	248	256	295	636	287	530	657	387	81	645	570	365	132	0	70	577
TCGA-DK-A3IQ-10A-01D-A20D-08_BLCA	654	226	256	285	599	275	527	634	303	76	620	505	275	136	0	46	574
TCGA-DK-A3IS-10A-01D-A21A-08_BLCA	678	246	254	268	507	368	530	637	474	0	0	0	0	0	27	75	576
TCGA-DK-A3IT-10A-01D-A20D-08_BLCA	682	0	0	302	604	375	532	649	483	0	0	0	0	0	36	73	578
TCGA-DK-A3IU-10A-01D-A20D-08_BLCA	680	0	0	289	607	286	531	661	481	0	0	0	0	0	25	68	577
TCGA-DK-A3IV-10A-01D-A21A-08_BLCA	688	0	0	299	602	389	530	641	393	75	601	0	360	135	0	75	579

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DK-A3WW-10A-01D-A23K-08_BLCA	666	247	262	289	605	282	532	642	466	80	634	563	364	133	0	57	577
TCGA-DK-A3WX-10A-01D-A22Z-08_BLCA	688	0	0	316	614	393	530	652	393	77	610	0	374	139	0	76	581
TCGA-DK-A3WY-10A-01D-A22Z-08_BLCA	750	248	280	295	605	383	534	650	473	80	606	0	377	138	47	0	581
TCGA-DK-A3X1-10A-01D-A22Z-08_BLCA	748	252	276	296	571	290	537	656	395	82	571	0	370	139	0	84	581
TCGA-DK-A3X2-10A-01D-A22Z-08_BLCA	763	249	272	312	638	391	538	653	490	59	614	576	0	0	46	98	580
TCGA-DK-A6AV-10A-01D-A30H-08_BLCA	761	0	0	320	621	408	537	645	482	0	0	0	0	0	33	66	581
TCGA-DK-A6AW-10A-01D-A30H-08_BLCA	754	255	277	303	626	293	536	658	0	86	659	586	386	144	0	0	579
TCGA-DK-A6B0-10A-01D-A31J-08_BLCA	666	242	253	283	571	267	528	623	472	0	0	0	0	0	0	82	574
TCGA-DK-A6B1-10A-01D-A30H-08_BLCA	765	0	0	308	626	406	536	656	490	0	0	0	0	0	0	163	581
TCGA-DK-A6B2-10A-01D-A30H-08_BLCA	671	266	285	0	607	144	537	654	470	85	661	587	305	136	0	102	583
TCGA-DK-A6B5-10A-01D-A31J-08_BLCA	669	235	253	274	601	364	530	627	363	63	619	506	357	129	0	55	574
TCGA-DK-A6B6-10A-01D-A30H-08_BLCA	751	256	262	295	618	396	537	652	461	77	644	573	380	139	0	81	581
TCGA-DM-A0X9-10A-01D-A152-10_COAD	671	0	0	345	502	415	497	603	334	0	0	0	0	0	0	41	551
TCGA-DM-A0XD-10A-01D-A152-10_COAD	671	227	270	304	647	436	515	584	353	0	366	498	0	0	0	65	582
TCGA-DM-A0XF-10A-01D-A152-10_COAD	603	123	123	181	397	194	489	562	0	94	394	0	324	163	0	0	575
TCGA-DM-A1D0-10A-01D-A152-10_COAD	649	223	251	232	460	292	415	503	299	0	341	0	321	145	0	26	560
TCGA-DM-A1D4-10A-01D-A152-10_COAD	666	0	0	355	618	360	489	594	319	0	391	0	302	157	0	25	580
TCGA-DM-A1D6-10A-01D-A152-10_COAD	670	0	0	365	645	434	528	609	341	0	0	0	0	0	0	56	578
TCGA-DM-A1D7-10A-01D-A152-10_COAD	672	0	0	330	618	351	510	585	333	0	0	0	0	0	0	42	562
TCGA-DM-A1D8-10A-01D-A152-10_COAD	645	138	295	332	679	366	530	626	427	94	539	511	0	0	13	33	566
TCGA-DM-A1D9-10A-01D-A152-10_COAD	665	0	0	348	638	352	487	605	309	97	391	0	285	153	15	0	568
TCGA-DM-A1DA-10A-01D-A152-10_COAD	677	0	0	343	623	427	484	580	342	0	0	0	0	0	28	0	574
TCGA-DM-A1DB-10A-01D-A152-10_COAD	749	0	0	359	637	401	501	588	342	0	0	0	0	0	13	24	571
TCGA-DM-A1HA-10A-01D-A152-10_COAD	649	0	0	337	559	405	469	585	315	0	0	0	0	0	16	0	557
TCGA-DM-A285-10A-01D-A16V-10_COAD	527	227	299	0	0	0	490	561	338	0	0	0	0	0	23	0	541
TCGA-DM-A28C-10A-01D-A16V-10_COAD	662	207	199	304	318	306	501	553	339	0	0	0	0	0	11	26	554
TCGA-DM-A28E-10A-01D-A16V-10_COAD	638	128	225	190	570	401	468	573	421	0	288	261	0	0	11	28	560
TCGA-DM-A28F-10A-01D-A16V-10_COAD	647	0	0	343	537	392	490	565	422	0	0	0	0	0	0	39	564
TCGA-DM-A28G-10A-01D-A16V-10_COAD	553	261	295	0	488	146	502	582	343	0	311	345	0	0	16	23	560
TCGA-DM-A28H-10A-01D-A16V-10_COAD	638	0	0	297	559	335	456	549	270	80	274	0	226	103	10	0	549
TCGA-DM-A28K-10A-01D-A16V-10_COAD	607	121	165	165	295	275	485	573	314	0	0	0	0	0	0	36	517
TCGA-DO-A1JZ-10A-01D-A13W-08_THCA	766	259	271	309	648	399	535	664	477	85	658	521	376	141	42	0	580
TCGA-DO-A1K0-10A-01D-A13W-08_THCA	760	0	0	310	619	296	525	669	493	0	0	0	0	0	29	80	581
TCGA-DO-A2HM-10B-01D-A22D-08_THCA	675	242	262	278	608	374	532	653	385	76	635	563	365	134	33	0	574
TCGA-DQ-5624-10A-01D-1870-08_HNSC	686	0	0	301	607	385	530	640	485	0	0	0	0	0	30	57	580
TCGA-DQ-5625-10A-01D-1870-08_HNSC	684	0	0	301	609	392	535	634	476	0	0	0	0	0	0	101	579
TCGA-DQ-5629-10A-01D-1870-08_HNSC	687	0	0	305	612	399	535	650	480	0	0	0	0	0	0	104	578
TCGA-DQ-5630-10A-01D-1870-08_HNSC	665	246	271	302	610	390	534	652	461	78	644	566	303	136	0	75	577
TCGA-DQ-5631-10A-01D-1870-08_HNSC	760	0	0	311	611	290	523	649	384	81	604	0	298	139	38	1	576
TCGA-DQ-7588-10B-01D-2078-08_HNSC	648	228	238	271	539	358	527	635	460	0	0	0	0	0	24	52	572
TCGA-DQ-7589-10C-01D-2229-08_HNSC	687	0	0	303	624	393	536	653	475	69	593	513	0	0	0	110	576
TCGA-DQ-7590-10D-01D-2229-08_HNSC	761	0	0	307	608	380	532	635	481	0	0	0	0	0	0	96	578
TCGA-DQ-7591-10A-01D-2078-08_HNSC	677	0	0	283	594	375	526	625	0	82	612	0	367	133	0	1	574
TCGA-DQ-7592-10A-01D-2078-08_HNSC	676	239	251	273	509	277	528	629	399	0	0	0	0	0	0	116	571
TCGA-DQ-7593-10D-01D-2229-08_HNSC	643	244	261	288	610	285	533	639	475	0	537	570	0	0	0	93	577
TCGA-DQ-7594-10D-01D-2229-08_HNSC	677	236	266	278	609	378	532	647	448	73	627	571	0	136	0	60	575
TCGA-DQ-7595-10D-01D-2229-08_HNSC	680	0	0	288	606	292	527	634	478	0	0	0	0	0	0	108	578
TCGA-DQ-7596-10D-01D-2229-08_HNSC	687	0	0	298	598	384	535	624	478	0	0	0	0	0	0	85	578
TCGA-DR-A0ZL-10A-01D-A10S-08_CESC	684	0	0	301	600	392	531	646	479	0	0	0	0	0	49	1	577
TCGA-DR-A0ZM-10A-01D-A10S-08_CESC	681	0	0	304	598	286	520	649	460	0	0	0	0	0	0	98	577
TCGA-DS-A0VK-10A-01D-A10S-08_CESC	670	246	268	287	593	284	534	649	483	0	0	0	0	0	0	150	579
TCGA-DS-A0VL-10A-01D-A10S-08_CESC	681	0	0	303	606	395	530	649	481	0	0	0	22	0	0	149	576
TCGA-DS-A0VM-10A-01D-A10S-08_CESC	682	0	0	302	608	382	530	659	472	0	0	0	0	0	29	66	578
TCGA-DS-A0VN-10A-01D-A10S-08_CESC	669	250	262	93	595	134	529	626	0	73	638	562	368	140	0	1	578
TCGA-DS-A1OA-10A-01D-A16Y-08_CESC	744	0	0	297	572	371	528	634	468	0	0	0	0	0	31	58	577
TCGA-DS-A1OB-10A-01D-A14W-08_CESC	686	0	0	309	599	374	532	640	469	0	0	0	0	0	0	94	574
TCGA-DS-A1OC-10A-01D-A14W-08_CESC	684	25	0	300	597	386	529	643	479	0	0	0	0	0	0	13	577
TCGA-DS-A1OD-10A-01D-A14W-08_CESC	680	0	0	297	605	380	532	637	471	0	0	0	0	0	33	70	577
TCGA-DS-A3LQ-10A-01D-A21Q-09_CESC	675	0	0	361	660	461	552	629	536	0	0	0	0	0	38	42	584
TCGA-DS-A5RQ-10A-01D-A28E-09_CESC	703	307	336	338	651	363	552	633	452	0	0	0	0	0	0	128	593
TCGA-DT-5265-10A-01D-1826-10_READ	657	143	179	319	434	309	499	582	433	0	0	0	0	0	13	29	567
TCGA-DU-5847-10A-01D-1705-08_LGG	587	248	268	0	548	134	521	638	380	72	606	511	0	132	0	47	576
TCGA-DU-5849-10A-01D-1705-08_LGG	590	244	244	276	600	355	524	634	467	0	544	508	0	0	34	1	576
TCGA-DU-5851-10A-01D-1893-08_LGG	687	0	0	303	609	293	526	639	481	0	0	0	0	0	0	142	574
TCGA-DU-5852-10A-01D-1705-08_LGG	675	0	0	299	588	378	524	643	400	0	0	0	0	0	22	49	577
TCGA-DU-5853-10A-01D-1893-08_LGG	758	0	0	299	611	287	531	656	480	0	0	0	0	0	31	79	577
TCGA-DU-5854-10A-01D-1705-08_LGG	659	0	0	286	595	382	530	634	461	0	0	0	0	0	36	1	571
TCGA-DU-5855-10A-01D-1705-08_LGG	593	251	270	0	597	139	528	633	380	73	628	575	0	134	20	0	576
TCGA-DU-5870-10A-01D-1705-08_LGG	682	0	0	291	600	284	524	644	474	0	0	0	0	0	20	41	574
TCGA-DU-5871-10A-01D-1705-08_LGG	587	253	266	0	563	133	530	631	0	85	637	490	302	140	0	0	575
TCGA-DU-5872-10A-01D-1705-08_LGG	677	239	261	270	503	363	526	638	382	76	546	0	292	134	22	0	576
TCGA-DU-5874-10A-01D-1705-08_LGG	747	0	0	302	520	274	515	608	386	0	0	0	0	135	0	51	569
TCGA-DU-6392-10A-01D-1705-08_LGG	670	237	248	274	603	280	520	639	477	0	574	507	0	0	22	45	578
TCGA-DU-6393-10A-01D-1705-08_LGG	664	248	244	275	549	281	528	637	469	0	0	0	0	0	21	55	575
TCGA-DU-6394-10A-01D-1705-08_LGG	676	248	251	186	567	274	531	636	390	0	0	0	0	0	0	80	576
TCGA-DU-6395-10A-01D-1705-08_LGG	593	254	266	0	594	141	528	637	362	72	635	571	0	136	0	54	574
TCGA-DU-6396-10A-01D-1705-08_LGG	686	0	0	301	606	378	522	641	378	62	589	0	295	137	0	46	573
TCGA-DU-6397-10A-01D-1705-08_LGG	597	256	270	0	541	133	529	628	380	70	618	511	286	134	0	55	572
TCGA-DU-6399-10A-01D-1705-08_LGG	686	0	0	291	592	383	527	636	388	69	556	499	0	138	24	0	574
TCGA-DU-6400-10A-01D-1705-08_LGG	685	0	0	293	600	370	520	629	466	0	0	0	0	0	0	68	572
TCGA-DU-6401-10A-01D-1705-08_LGG	673	235	258	265	597	362	530	633	440	78	623	498	289	137	18	0	575
TCGA-DU-6402-10A-01D-1705-08_LGG	657	234	252	284	567	262	520	626	468	0	0	0	0	0	32	0	576
TCGA-DU-6403-10A-01D-1705-08_LGG	748	232	245	291	600	271	527	628	467	0	565	496	0	0	20	36	578
TCGA-DU-6404-10A-01D-1705-08_LGG	662	0	0	301	588	371	520	636	315	75	583	0	284	134	0	55	577
TCGA-DU-6405-10A-01D-1705-08_LGG	633	232	238	279	559	269	528	635	379	69	511	494	0	134	0	51	574
TCGA-DU-6406-10A-01D-1705-08_LGG	682	0	0	297	595	389	529	643	292	76	576	0	297	133	0	45	575
TCGA-DU-6407-10A-01D-1705-08_LGG	673	245	251	270	565	350	530	650	465	0	0	0	0	0	32	52	573
TCGA-DU-6408-10A-01D-1705-08_LGG	681	0	0	299	590	384	520	630	461	0	0	0	0	0	0	104	572
TCGA-DU-6410-10A-01D-1893-08_LGG	693	250	263	285	622	389	535	652	0	92	656	576	0	141	0	0	576
TCGA-DU-6542-10A-01D-1893-08_LGG	741	251	268	285	592	386	532	653	459	74	614	0	374	139	33	0	577
TCGA-DU-7006-10A-01D-2024-08_LGG	686	0	0	295	600	288	521	638	382	63	585	0	358	130	0	60	578
TCGA-DU-7007-10A-01D-2024-08_LGG	677	251	265	284	601	284	529	637	452	56	640	570	0	135	0	63	577
TCGA-DU-7008-10A-01D-2024-08_LGG	673	244	265	288	584	278	519	612	381	0	546	0	294	133	0	59	575
TCGA-DU-7009-10A-01D-2024-08_LGG	671	236	252	276	604	367	532	660	386	81	612	507	292	131	17	2	575
TCGA-DU-7010-10A-01D-2024-08_LGG	683	0	0	302	603	384	530	641	410	0	0	0	0	0	33	53	574
TCGA-DU-7011-10A-01D-2024-08_LGG	685	226	257	268	578	356	525	639	461	0	0	0	0	0	0	77	571

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DU-7012-10A-01D-2024-08_LGG	677	0	0	339	598	381	528	628	477	0	0	0	0	0	33	2	577
TCGA-DU-7013-10A-01D-2024-08_LGG	674	245	262	284	586	372	533	641	484	0	0	112	0	0	0	119	573
TCGA-DU-7014-10A-01D-2024-08_LGG	685	0	0	294	597	371	533	636	479	0	0	0	0	0	22	57	576
TCGA-DU-7015-10B-01D-2024-08_LGG	691	0	0	300	611	386	534	645	469	78	595	570	0	0	36	4	572
TCGA-DU-7018-10A-01D-2024-08_LGG	658	243	257	276	580	278	530	647	472	0	0	0	0	0	23	62	573
TCGA-DU-7019-10A-01D-2024-08_LGG	677	233	252	271	560	357	529	638	463	0	0	0	0	0	22	70	574
TCGA-DU-7290-10A-01D-2024-08_LGG	683	0	0	289	590	289	519	646	470	0	0	0	0	0	0	109	578
TCGA-DU-7292-10A-01D-2024-08_LGG	668	256	271	0	581	134	529	639	392	0	595	511	0	0	0	79	573
TCGA-DU-7294-10A-01D-2024-08_LGG	685	0	0	300	592	374	528	638	471	0	0	0	0	0	0	108	575
TCGA-DU-7298-10A-01D-2024-08_LGG	676	246	254	272	599	369	530	644	475	0	586	501	0	0	0	105	576
TCGA-DU-7299-10A-01D-2024-08_LGG	677	0	0	289	600	384	535	641	376	65	572	0	290	130	0	59	575
TCGA-DU-7300-10A-01D-2086-08_LGG	663	239	258	264	491	350	527	637	457	0	0	0	0	0	0	79	575
TCGA-DU-7301-10A-01D-2086-08_LGG	681	0	0	303	597	381	528	644	471	0	0	0	0	0	0	118	572
TCGA-DU-7302-10A-01D-2086-08_LGG	666	242	257	281	547	278	531	647	470	0	0	0	0	0	26	65	575
TCGA-DU-7304-10A-01D-2086-08_LGG	689	0	0	305	597	376	529	643	0	79	628	528	356	138	0	0	574
TCGA-DU-7306-10A-01D-2086-08_LGG	684	0	0	303	600	383	529	646	476	0	0	0	0	0	0	117	576
TCGA-DU-7309-10A-01D-2086-08_LGG	595	253	262	0	0	0	532	653	478	0	0	0	0	0	30	65	576
TCGA-DU-8158-10A-01D-2253-08_LGG	684	0	0	303	609	378	533	652	463	79	600	0	297	133	0	79	576
TCGA-DU-8161-10A-01D-2253-08_LGG	682	250	260	292	579	376	533	646	456	77	579	0	370	135	0	69	576
TCGA-DU-8162-10A-01D-2253-08_LGG	688	0	0	309	616	393	534	655	482	0	0	0	0	0	0	122	579
TCGA-DU-8163-10A-01D-2253-08_LGG	664	243	243	251	603	355	530	624	433	64	618	569	0	130	0	62	571
TCGA-DU-8164-10A-01D-2253-08_LGG	685	0	0	297	593	379	533	651	385	0	602	567	0	137	0	59	577
TCGA-DU-8165-10A-01D-2253-08_LGG	688	0	0	302	595	379	530	632	313	71	596	0	369	132	0	70	573
TCGA-DU-8166-10A-01D-2253-08_LGG	686	0	0	304	608	283	531	644	405	0	0	0	0	0	39	0	573
TCGA-DU-8167-10A-01D-2253-08_LGG	660	245	259	283	611	282	532	653	475	0	604	566	0	0	34	76	577
TCGA-DU-8168-10A-01D-2253-08_LGG	673	254	263	288	585	277	532	652	394	75	616	0	362	138	0	75	580
TCGA-DU-A5TP-10A-01D-A289-08_LGG	741	257	266	292	605	283	532	643	470	0	0	0	0	0	0	110	578
TCGA-DU-A5TR-10A-01D-A289-08_LGG	763	0	0	310	609	396	534	644	448	79	591	0	388	139	0	74	579
TCGA-DU-A5TS-10A-01D-A289-08_LGG	687	0	0	312	614	376	533	650	479	0	0	0	0	0	43	61	577
TCGA-DU-A5TT-10A-01D-A289-08_LGG	758	0	0	308	606	391	534	651	0	83	638	0	385	140	0	0	578
TCGA-DU-A5TU-10A-01D-A289-08_LGG	746	250	260	273	608	384	534	640	451	76	627	558	372	135	0	65	577
TCGA-DU-A5TW-10A-01D-A289-08_LGG	677	246	260	285	608	383	534	634	477	0	601	0	301	0	0	129	577
TCGA-DU-A5TY-10A-01D-A289-08_LGG	595	259	276	0	557	134	534	643	448	81	623	563	284	139	0	74	578
TCGA-DU-A6S2-10A-01D-A329-08_LGG	679	0	0	297	588	372	528	622	456	0	0	0	0	0	25	48	572
TCGA-DU-A6S3-10A-01D-A329-08_LGG	673	0	0	301	593	363	526	621	375	0	513	0	284	134	17	0	572
TCGA-DU-A6S6-10A-01D-A329-08_LGG	586	252	265	0	0	0	528	639	377	60	515	0	282	130	0	37	574
TCGA-DU-A6S7-10A-01D-A329-08_LGG	681	0	0	296	597	360	520	633	457	0	0	0	0	0	16	52	572
TCGA-DU-A6S8-10A-01D-A329-08_LGG	592	251	262	0	567	139	522	630	0	79	646	580	292	140	0	0	575
TCGA-DU-A76L-10A-01D-A329-08_LGG	594	234	229	277	598	267	526	636	299	64	614	510	0	132	0	44	571
TCGA-DU-A76O-10A-01D-A329-08_LGG	593	253	270	0	0	0	533	638	484	0	0	0	0	0	37	0	574
TCGA-DU-A76R-10A-01D-A329-08_LGG	590	232	244	254	496	264	512	632	391	0	0	0	0	0	26	42	572
TCGA-DV-5565-10A-01D-1535-10_KIRC	784	0	0	419	727	464	560	671	0	112	664	0	457	182	0	0	599
TCGA-DV-5566-10A-01D-1535-10_KIRC	799	0	0	418	716	467	555	667	479	111	667	0	457	181	0	70	594
TCGA-DV-5568-10A-01D-1535-10_KIRC	705	305	370	393	704	459	559	672	477	114	649	0	455	183	23	0	597
TCGA-DV-5569-10A-01D-1535-10_KIRC	667	0	0	375	682	440	548	656	456	104	595	0	349	176	14	0	574
TCGA-DV-5573-10A-01D-1535-10_KIRC	679	0	0	365	679	427	539	640	454	0	0	0	0	0	15	43	576
TCGA-DV-5574-10A-01D-1535-10_KIRC	670	0	0	374	675	455	555	651	462	0	0	0	0	0	20	45	590
TCGA-DV-5575-10A-01D-1535-10_KIRC	674	276	348	367	644	430	545	637	465	0	0	0	0	0	0	72	589
TCGA-DV-5576-10A-01D-1535-10_KIRC	673	0	0	361	687	435	554	648	456	0	0	0	0	0	15	45	581
TCGA-DV-A4VX-10A-01D-A25V-10_KIRC	678	0	0	267	641	444	548	600	355	0	0	0	0	0	29	49	566
TCGA-DV-A4VZ-10A-01D-A25V-10_KIRC	664	0	278	138	609	452	544	614	463	0	458	0	363	0	26	48	582
TCGA-DV-A4W0-10A-01D-A25V-10_KIRC	688	290	309	127	670	444	546	620	365	0	452	0	345	0	30	65	574
TCGA-DW-5560-10A-01D-1589-08_KIRP	685	0	0	305	594	377	533	635	471	0	0	0	0	0	29	63	573
TCGA-DW-5561-10A-01D-1589-08_KIRP	688	0	0	305	602	392	534	649	476	0	0	0	0	0	0	97	577
TCGA-DW-7834-10A-01D-2136-08_KIRP	683	246	261	292	584	277	533	653	470	0	0	0	0	0	33	63	573
TCGA-DW-7836-10A-01D-2136-08_KIRP	681	0	0	293	612	287	530	646	485	0	0	0	0	0	0	134	574
TCGA-DW-7837-10A-01D-2136-08_KIRP	684	0	0	298	601	377	531	640	476	0	0	0	0	0	39	66	576
TCGA-DW-7838-10A-01D-2136-08_KIRP	689	0	0	308	615	382	532	649	487	0	0	0	0	0	0	132	575
TCGA-DW-7839-10A-01D-2136-08_KIRP	688	0	0	299	611	297	528	647	477	0	0	0	0	0	0	151	575
TCGA-DW-7840-10A-01D-2136-08_KIRP	597	244	270	0	598	136	526	637	474	0	636	562	384	0	43	2	574
TCGA-DW-7841-10A-01D-2136-08_KIRP	688	247	262	288	611	372	531	649	477	0	598	560	0	0	29	64	579
TCGA-DW-7842-10A-01D-2136-08_KIRP	684	0	0	303	601	381	529	640	458	68	604	0	295	136	0	71	572
TCGA-DW-7963-10C-01D-A28G-10_KIRP	557	260	271	248	658	425	546	618	349	0	395	516	0	0	31	0	572
TCGA-DX-A1KU-10A-01D-A24N-09_SARC	689	291	323	198	608	358	552	618	545	0	0	0	0	0	0	75	584
TCGA-DX-A1KW-10A-01D-A24N-09_SARC	677	0	0	325	639	439	545	499	517	0	0	0	0	0	17	25	578
TCGA-DX-A1KX-10A-01D-A24N-09_SARC	678	0	0	361	665	440	547	631	489	89	435	0	343	175	33	1	583
TCGA-DX-A1KY-10A-01D-A24N-09_SARC	695	24	0	365	681	386	547	648	553	0	0	32	0	0	0	104	594
TCGA-DX-A1KZ-10A-01D-A24N-09_SARC	683	292	327	301	647	449	546	613	347	0	533	531	0	0	0	70	579
TCGA-DX-A1L0-10A-01D-A24N-09_SARC	688	0	0	368	663	377	542	525	551	0	0	0	0	0	0	106	591
TCGA-DX-A1L1-10A-01D-A24N-09_SARC	581	291	329	306	573	353	552	633	426	96	535	0	357	173	35	2	582
TCGA-DX-A1L2-10A-01D-A24N-09_SARC	694	301	322	317	615	435	550	639	441	0	0	0	0	0	0	86	587
TCGA-DX-A1L3-10A-01D-A24N-09_SARC	697	0	0	340	666	365	547	601	346	88	594	0	347	162	0	41	587
TCGA-DX-A1L4-10A-01D-A26G-09_SARC	670	0	0	335	632	443	549	623	410	97	380	0	315	154	0	33	580
TCGA-DX-A23R-10A-01D-A26G-09_SARC	695	308	318	241	615	433	537	506	311	0	580	0	420	176	0	39	585
TCGA-DX-A23T-10A-01D-A26G-09_SARC	566	264	282	240	438	390	527	598	303	0	426	0	338	161	0	38	585
TCGA-DX-A23U-10A-01D-A26G-09_SARC	565	317	345	0	25	48	549	627	399	89	438	0	335	166	29	4	575
TCGA-DX-A23V-10A-01D-A29N-09_SARC	663	286	295	320	667	437	549	620	446	0	438	479	0	0	0	73	586
TCGA-DX-A23Y-10A-01D-A27P-09_SARC	676	296	350	300	615	354	551	619	316	97	576	0	344	176	0	48	587
TCGA-DX-A240-10A-01D-A27P-09_SARC	683	0	0	366	660	459	547	627	417	92	550	0	337	167	0	43	583
TCGA-DX-A2IZ-10A-01D-A21Q-09_SARC	679	307	333	337	625	350	553	645	550	0	0	0	0	0	36	66	583
TCGA-DX-A2J0-10A-01D-A21Q-09_SARC	686	0	0	346	667	454	545	511	452	0	0	0	0	0	0	93	589
TCGA-DX-A2J1-10A-01D-A21Q-09_SARC	700	0	0	362	675	467	557	637	551	0	0	0	0	0	44	64	586
TCGA-DX-A2J4-10A-01D-A21Q-09_SARC	697	303	345	322	686	377	547	644	427	94	635	524	444	176	0	58	584
TCGA-DX-A3LS-10A-01D-A21Q-09_SARC	698	0	0	369	660	447	549	638	316	92	541	0	332	169	0	50	583
TCGA-DX-A3LT-10A-01D-A21Q-09_SARC	666	299	317	321	608	361	549	630	542	0	0	0	0	0	34	53	584
TCGA-DX-A3LU-10A-01D-A21Q-09_SARC	671	287	309	299	572	416	532	474	408	0	465	0	347	154	0	42	572
TCGA-DX-A3LW-10A-01D-A21Q-09_SARC	586	325	351	0	0	0	548	634	460	0	0	0	0	0	0	101	590
TCGA-DX-A3LY-10B-01D-A27P-09_SARC	586	312	341	0	508	171	549	630	309	90	620	580	0	169	0	39	579
TCGA-DX-A3M1-10A-01D-A22A-09_SARC	693	0	0	370	671	463	553	653	0	103	621	0	453	183	0	1	580
TCGA-DX-A3M2-10A-01D-A22A-09_SARC	695	0	0	355	683	448	550	633	544	0	0	0	0	0	0	111	584
TCGA-DX-A3U5-10A-01D-A22A-09_SARC	673	277	317	314	608	438	550	621	546	0	0	0	0	0	0	75	580
TCGA-DX-A3U6-10A-01D-A29N-09_SARC	585	289	328	301	611	415	544	517	463	0	0	0	0	0	0	80	585
TCGA-DX-A3U7-10A-01D-A29N-09_SARC	558	0	0	335	623	356	533	609	389	86	411	0	351	172	0	37	579
TCGA-DX-A3U8-10A-01D-A29N-09_SARC	681	0	0	336	660	370	545	631	550	0	0	0	0	0	0	97	581
TCGA-DX-A3U9-10A-01D-A307-09_SARC	694	287	334	207	603	346	547	636	435	99	521	0	363	163	28	0	586
TCGA-DX-A3UA-10A-01D-A307-09_SARC	676	283	316	311	617	423	551	630	394	91	556	0	360	163	0	54	586

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DX-A3UB-10A-01D-A307-09_SARC	528	0	0	333	638	359	528	564	434	0	0	0	0	0	0	87	581
TCGA-DX-A3UC-10A-01D-A307-09_SARC	529	307	329	0	473	160	533	598	436	0	430	497	0	0	22	32	575
TCGA-DX-A3UD-10A-01D-A307-09_SARC	681	314	335	198	634	355	555	641	560	0	0	0	0	0	40	60	589
TCGA-DX-A3UE-10A-01D-A307-09_SARC	542	280	310	288	573	324	512	527	382	0	463	496	0	165	0	43	578
TCGA-DX-A3UF-10A-01D-A307-09_SARC	693	0	0	379	682	457	553	651	566	0	0	0	0	0	52	63	593
TCGA-DX-A48J-10A-01D-A307-09_SARC	578	324	357	0	666	354	557	619	430	94	631	558	440	175	34	0	586
TCGA-DX-A48K-10A-01D-A307-09_SARC	652	0	0	352	652	456	540	632	528	0	0	0	0	0	38	41	589
TCGA-DX-A48L-10A-01D-A307-09_SARC	674	0	0	309	637	435	545	613	0	99	551	0	437	179	0	0	580
TCGA-DX-A48O-10A-01D-A307-09_SARC	674	297	322	327	683	447	544	644	547	0	562	553	0	0	38	50	589
TCGA-DX-A48P-10A-01D-A307-09_SARC	584	322	355	0	675	187	554	639	433	96	643	580	360	172	0	49	588
TCGA-DX-A48R-10A-01D-A307-09_SARC	703	326	355	370	707	468	556	665	569	0	626	583	0	0	62	81	593
TCGA-DX-A48U-10A-01D-A307-09_SARC	694	317	349	341	648	457	558	650	569	0	0	0	0	0	50	66	588
TCGA-DX-A48V-10A-01D-A307-09_SARC	700	319	353	366	679	381	555	660	578	0	0	0	0	0	0	165	596
TCGA-DX-A6B7-10A-01D-A307-09_SARC	566	326	353	0	639	173	555	635	555	0	556	522	0	0	0	88	591
TCGA-DX-A6B8-10A-01D-A307-09_SARC	698	328	357	353	704	462	555	654	564	0	594	582	0	0	0	153	588
TCGA-DX-A6BA-10A-01D-A307-09_SARC	700	0	0	379	697	466	557	659	574	0	0	0	0	0	0	125	593
TCGA-DX-A6BF-10A-01D-A307-09_SARC	700	0	0	382	709	477	557	647	560	0	0	0	0	0	0	165	587
TCGA-DX-A6BG-10A-01D-A307-09_SARC	694	0	0	386	699	472	553	650	565	0	0	0	0	0	0	147	592
TCGA-DX-A6BH-10A-01D-A307-09_SARC	691	318	355	349	708	380	557	674	565	105	608	558	0	0	56	73	589
TCGA-DX-A6BK-10A-01D-A307-09_SARC	701	321	360	363	707	465	557	659	561	0	621	586	0	0	0	120	592
TCGA-DY-A0XA-10A-01D-A152-10_READ	685	253	293	346	663	361	537	622	324	94	583	517	318	156	0	47	578
TCGA-DY-A1DC-10A-01D-A152-10_READ	682	239	300	113	661	359	539	623	334	97	569	540	0	162	0	34	575
TCGA-DY-A1DD-10A-01D-A152-10_READ	663	276	315	344	553	404	487	470	0	98	468	0	349	172	0	0	574
TCGA-DY-A1DF-10A-01D-A152-10_READ	763	220	264	312	644	343	540	599	445	0	361	471	0	0	0	82	585
TCGA-DY-A1DG-10A-01D-A152-10_READ	538	263	302	0	531	131	526	602	309	95	443	530	0	158	0	28	553
TCGA-DY-A1H8-10A-01D-A152-10_READ	620	112	95	195	282	172	478	546	254	0	311	0	156	127	0	17	547
TCGA-DZ-6133-10A-01D-1962-08_KIRP	688	0	0	301	617	392	532	654	487	0	0	0	0	0	38	84	576
TCGA-DZ-6134-10A-01D-1962-08_KIRP	760	0	0	319	616	399	535	650	477	0	0	0	0	0	0	108	577
TCGA-DZ-6135-10A-01D-1962-08_KIRP	762	256	267	294	588	385	535	647	471	78	613	0	366	135	0	81	575
TCGA-E1-5302-10A-01D-1468-08_LGG	691	256	270	301	616	388	532	663	482	0	607	575	0	0	44	92	577
TCGA-E1-5303-10A-01D-1468-08_LGG	691	0	0	308	634	397	535	662	463	88	650	577	372	137	0	87	579
TCGA-E1-5304-10A-01D-1468-08_LGG	762	0	0	309	616	290	525	666	466	83	631	110	304	140	0	74	576
TCGA-E1-5305-10A-01D-1893-08_LGG	755	0	0	305	608	291	523	652	484	0	0	0	0	0	29	70	576
TCGA-E1-5307-10A-01D-1893-08_LGG	598	263	267	0	589	139	535	653	466	76	607	0	374	136	30	0	578
TCGA-E1-5311-10A-01D-1468-08_LGG	692	0	0	303	612	399	532	654	484	0	0	0	0	0	0	160	575
TCGA-E1-5318-10A-01D-1468-08_LGG	688	0	0	308	617	391	530	662	462	77	618	0	378	137	0	74	579
TCGA-E1-5319-10A-01D-1893-08_LGG	686	0	0	307	612	390	533	643	475	0	0	0	0	0	0	158	576
TCGA-E1-5322-10A-01D-1468-08_LGG	686	0	0	303	606	296	530	665	464	79	624	0	368	137	0	94	579
TCGA-E2-A105-10A-01D-A10M-09_BRCA	663	0	0	382	700	458	555	645	476	0	0	0	0	0	22	48	592
TCGA-E2-A107-10A-01D-A10M-09_BRCA	703	0	0	405	728	477	564	666	582	0	0	0	0	0	0	216	597
TCGA-E2-A108-10A-01D-A10M-09_BRCA	703	0	0	395	710	481	562	666	584	0	0	0	0	0	0	150	597
TCGA-E2-A109-10A-01D-A10M-09_BRCA	702	320	362	383	703	381	560	659	485	0	0	0	0	0	0	230	596
TCGA-E2-A10A-10A-01D-A110-09_BRCA	803	0	0	414	728	481	563	676	583	0	0	0	0	0	0	112	596
TCGA-E2-A10B-10A-01D-A10M-09_BRCA	796	0	0	420	729	465	561	671	585	0	0	0	0	0	41	105	598
TCGA-E2-A10C-10A-01D-A10M-09_BRCA	700	0	0	411	709	466	558	657	483	0	0	0	0	0	0	133	592
TCGA-E2-A10F-10A-01D-A10M-09_BRCA	683	322	370	0	707	190	558	661	453	106	670	593	0	185	29	0	592
TCGA-E2-A14N-10A-01D-A135-09_BRCA	805	0	0	420	731	485	565	684	585	110	670	0	465	189	0	178	602
TCGA-E2-A14O-10A-01D-A110-09_BRCA	688	0	0	389	705	385	548	664	569	0	0	0	0	0	51	93	587
TCGA-E2-A14P-10A-01D-A12B-09_BRCA	804	0	0	403	730	472	564	679	575	107	662	0	466	187	76	0	594
TCGA-E2-A14Q-10A-01D-A12B-09_BRCA	673	0	0	379	693	377	546	660	464	0	0	0	0	0	0	87	583
TCGA-E2-A14R-10A-01D-A110-09_BRCA	794	0	0	395	724	395	554	675	476	109	655	0	462	184	0	91	598
TCGA-E2-A14S-10A-01D-A12B-09_BRCA	796	325	369	388	725	475	565	674	583	0	663	587	0	0	0	196	600
TCGA-E2-A14T-10A-01D-A110-09_BRCA	704	0	0	419	729	475	561	680	482	107	675	0	466	187	0	173	600
TCGA-E2-A14U-10A-01D-A22A-09_BRCA	582	312	343	0	501	163	545	623	395	0	617	493	341	173	24	0	587
TCGA-E2-A14V-10A-01D-A12B-09_BRCA	802	320	374	387	724	478	565	666	584	0	667	592	0	0	0	248	600
TCGA-E2-A14W-10A-01D-A12B-09_BRCA	797	0	0	402	725	479	565	680	587	0	0	0	0	0	109	135	600
TCGA-E2-A14X-10A-01D-A110-09_BRCA	797	330	378	0	709	185	560	671	489	0	675	0	491	186	75	1	598
TCGA-E2-A14Y-10A-01D-A12B-09_BRCA	799	329	371	381	723	478	562	671	580	0	667	588	0	0	0	235	598
TCGA-E2-A14Z-10A-01D-A110-09_BRCA	677	319	344	368	712	376	559	662	479	0	630	544	0	0	0	112	591
TCGA-E2-A150-10A-01D-A12B-09_BRCA	799	0	0	400	728	478	564	680	578	109	668	0	471	189	77	0	603
TCGA-E2-A152-10A-01D-A12B-09_BRCA	699	308	361	385	714	458	557	663	0	110	678	586	452	186	0	0	597
TCGA-E2-A153-10A-01D-A12B-09_BRCA	800	328	375	389	708	475	564	680	581	0	0	0	0	0	0	203	598
TCGA-E2-A154-10A-01D-A110-09_BRCA	702	0	0	393	713	465	560	667	482	0	0	0	0	0	50	92	597
TCGA-E2-A155-10A-01D-A12B-09_BRCA	594	333	380	0	0	0	559	676	581	0	0	0	0	0	82	0	600
TCGA-E2-A156-10A-01D-A12B-09_BRCA	798	324	369	236	726	392	563	673	371	103	675	583	461	185	0	105	598
TCGA-E2-A158-10A-01D-A12B-09_BRCA	798	331	374	391	714	388	562	682	585	0	0	0	0	0	76	136	600
TCGA-E2-A159-10A-01D-A110-09_BRCA	799	331	375	391	725	479	564	679	585	104	664	589	0	0	99	0	598
TCGA-E2-A15A-10A-01D-A12B-09_BRCA	800	0	0	399	725	395	556	680	587	0	0	0	0	0	0	200	603
TCGA-E2-A15C-10A-01D-A12B-09_BRCA	703	0	0	391	723	469	562	672	469	104	663	0	460	188	56	0	598
TCGA-E2-A15D-10A-01D-A110-09_BRCA	803	0	0	400	729	395	555	682	584	0	0	0	0	0	77	160	600
TCGA-E2-A15E-10A-01D-A12B-09_BRCA	699	325	369	375	719	385	559	670	575	0	658	587	0	0	61	101	595
TCGA-E2-A15F-10A-01D-A110-09_BRCA	694	316	361	380	697	464	559	666	462	106	640	0	453	184	0	101	597
TCGA-E2-A15G-10A-01D-A12B-09_BRCA	704	0	0	396	725	396	557	676	586	0	0	0	0	0	0	212	596
TCGA-E2-A15H-10A-01D-A12B-09_BRCA	799	0	0	399	731	480	560	678	583	0	0	0	0	0	61	127	600
TCGA-E2-A15I-10A-01D-A135-09_BRCA	801	0	0	418	727	483	562	681	572	105	671	0	467	191	0	151	601
TCGA-E2-A15J-10A-01D-A12Q-09_BRCA	697	316	371	380	681	456	559	665	566	0	0	0	0	0	0	90	597
TCGA-E2-A15K-10A-01D-A12Q-09_BRCA	799	0	0	397	720	476	562	680	479	109	659	0	463	185	65	0	595
TCGA-E2-A15L-10A-01D-A12B-09_BRCA	804	336	377	392	684	478	563	680	589	0	0	0	0	0	71	171	600
TCGA-E2-A15M-10A-01D-A12B-09_BRCA	804	0	0	417	731	482	562	678	588	0	0	0	0	0	0	308	600
TCGA-E2-A15O-10A-01D-A110-09_BRCA	689	335	376	0	0	0	560	642	541	0	644	0	462	186	0	100	598
TCGA-E2-A15P-10A-01D-A110-09_BRCA	698	317	363	233	708	378	556	666	579	0	647	548	0	0	53	78	597
TCGA-E2-A15R-10A-01D-A110-09_BRCA	701	0	0	390	715	479	562	674	375	106	656	0	463	188	0	132	594
TCGA-E2-A15S-10A-01D-A110-09_BRCA	796	331	371	387	705	386	560	675	571	107	667	0	465	187	0	126	595
TCGA-E2-A15T-10A-01D-A110-09_BRCA	801	333	379	388	710	477	562	676	584	0	0	0	0	0	73	144	598
TCGA-E2-A1AZ-10A-01D-A12Q-09_BRCA	701	0	0	391	713	386	555	675	572	0	0	0	0	0	0	169	598
TCGA-E2-A1B0-10A-01D-A12Q-09_BRCA	800	332	365	385	696	464	560	671	474	103	668	0	460	183	0	117	598
TCGA-E2-A1B1-10A-01D-A12Q-09_BRCA	698	313	365	380	708	466	558	666	461	101	664	589	0	186	0	82	595
TCGA-E2-A1B4-10A-01D-A12Q-09_BRCA	795	0	0	397	721	475	561	672	570	0	0	0	0	0	0	215	600
TCGA-E2-A1B5-10A-01D-A12Q-09_BRCA	699	0	0	393	712	465	560	660	484	0	0	0	0	0	0	130	594
TCGA-E2-A1B6-10A-01D-A12Q-09_BRCA	799	314	369	392	731	388	563	676	586	0	666	584	0	0	54	94	599
TCGA-E2-A1BC-10A-01D-A12Q-09_BRCA	772	332	379	0	716	188	561	673	372	106	676	596	0	184	0	113	597
TCGA-E2-A1BD-10A-01D-A12Q-09_BRCA	703	0	0	416	722	477	565	672	579	0	0	0	0	0	0	173	599
TCGA-E2-A1IE-10A-01D-A13O-09_BRCA	695	0	359	358	666	451	557	648	470	0	0	0	0	0	0	113	594
TCGA-E2-A1IF-10A-01D-A142-09_BRCA	675	275	320	345	675	350	520	650	440	0	584	507	0	0	24	45	571
TCGA-E2-A1IG-10A-01D-A142-09_BRCA	666	0	0	373	679	438	545	639	331	92	568	502	0	174	0	55	588
TCGA-E2-A1IH-10A-01D-A13O-09_BRCA	699	318	364	233	680	376	556	660	567	0	0	0	0	0	42	93	592

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-E2-A1II-10A-01D-A142-09_BRCA	553	289	335	0	616	146	536	631	443	0	566	494	0	0	25	35	580
TCGA-E2-A1IJ-10A-01D-A142-09_BRCA	665	0	0	370	663	432	547	627	415	101	590	0	348	171	0	34	568
TCGA-E2-A1IK-10A-01D-A142-09_BRCA	666	280	320	343	693	373	537	629	472	0	597	515	0	0	0	104	587
TCGA-E2-A1IL-10A-01D-A14G-09_BRCA	679	283	341	215	674	363	542	647	453	98	634	0	370	175	0	52	586
TCGA-E2-A1IN-10A-01D-A188-09_BRCA	670	328	365	0	694	182	556	649	0	106	662	584	0	185	0	0	589
TCGA-E2-A1IO-10A-01D-A142-09_BRCA	674	274	329	328	635	345	543	647	451	0	0	0	0	0	27	43	576
TCGA-E2-A1L6-10A-01D-A13O-09_BRCA	623	0	0	356	673	423	515	626	444	0	0	0	0	0	11	39	580
TCGA-E2-A1L7-10A-01D-A142-09_BRCA	653	0	0	374	671	443	534	633	320	100	587	0	322	154	0	46	572
TCGA-E2-A1L8-10A-01D-A13O-09_BRCA	679	0	0	385	694	461	559	654	562	0	0	0	0	0	49	0	595
TCGA-E2-A1L9-10A-01D-A188-09_BRCA	699	311	364	375	711	468	559	660	453	104	661	562	0	183	0	96	593
TCGA-E2-A1LA-10A-01D-A142-09_BRCA	667	0	0	370	670	448	536	637	533	0	0	0	0	0	22	43	564
TCGA-E2-A2P5-10B-01D-A19Y-09_BRCA	664	0	0	345	649	436	550	622	315	92	555	0	319	171	0	41	576
TCGA-E2-A2P6-10B-01D-A19Y-09_BRCA	639	0	0	347	628	439	536	596	293	83	383	0	326	168	0	41	575
TCGA-E2-A3DX-10A-01D-A20S-09_BRCA	648	0	0	315	625	421	533	507	67	84	561	0	359	166	0	8	571
TCGA-E2-A56Z-10A-01D-A29N-09_BRCA	683	310	353	345	682	368	550	648	556	0	594	534	0	0	41	56	588
TCGA-E2-A570-10A-01D-A29N-09_BRCA	703	307	340	345	617	182	554	650	557	0	0	0	0	0	47	56	582
TCGA-E2-A572-10B-01D-A31U-09_BRCA	560	292	341	0	0	0	551	612	462	0	0	0	0	0	32	46	574
TCGA-E2-A573-10A-01D-A29N-09_BRCA	690	0	0	350	645	447	545	637	449	0	0	0	0	0	36	53	578
TCGA-E2-A574-10A-01D-A29N-09_BRCA	690	0	0	206	683	359	551	633	439	0	0	0	0	0	36	49	588
TCGA-E2-A576-10B-01D-A31U-09_BRCA	680	0	0	368	672	369	552	636	500	0	0	0	0	0	48	0	576
TCGA-E3-A3DY-10A-01D-A20C-08_THCA	688	0	0	303	616	383	525	647	484	0	0	0	0	0	0	120	573
TCGA-E3-A3DZ-10A-01D-A20C-08_THCA	681	247	262	196	578	282	531	626	396	0	0	0	0	0	0	74	575
TCGA-E3-A3E0-10A-01D-A20C-08_THCA	688	258	261	297	590	375	534	657	464	81	617	0	368	136	33	0	581
TCGA-E3-A3E1-10A-01D-A20C-08_THCA	758	248	263	284	590	383	531	651	458	75	605	0	379	134	34	1	576
TCGA-E3-A3E2-10A-01D-A20C-08_THCA	683	0	0	298	614	288	529	653	458	74	577	0	359	130	0	62	575
TCGA-E3-A3E3-10A-01D-A20C-08_THCA	759	0	0	300	597	386	531	653	380	83	598	0	365	136	0	71	576
TCGA-E3-A3E5-10A-01D-A20C-08_THCA	598	250	273	0	567	136	533	651	478	0	591	514	0	0	30	61	575
TCGA-E5-A2PC-10B-01D-A202-08_BLCA	681	0	0	301	590	375	527	639	468	0	0	0	0	0	0	91	575
TCGA-E5-A4TZ-10B-01D-A31J-08_BLCA	685	0	0	297	602	289	531	645	390	70	606	0	297	138	30	0	576
TCGA-E5-A4U1-10B-01D-A31J-08_BLCA	686	252	264	283	553	279	531	639	485	0	0	0	0	0	0	88	575
TCGA-E6-A1LX-10A-01D-A14G-09_UCEC	675	0	0	359	659	442	543	621	441	0	0	0	0	0	26	44	580
TCGA-E6-A1LZ-10A-01D-A142-09_UCEC	684	0	0	366	704	446	547	647	439	101	644	523	362	180	34	0	583
TCGA-E6-A1M0-10A-01D-A142-09_UCEC	660	294	333	323	519	433	552	642	549	0	0	0	0	0	37	52	583
TCGA-E6-A2P8-10B-01D-A19Y-09_UCEC	686	302	331	338	672	366	551	645	557	0	508	538	0	0	37	52	581
TCGA-E6-A2P9-10B-01D-A19Y-09_UCEC	679	0	0	346	657	448	540	531	459	0	0	0	0	0	0	70	585
TCGA-E7-A3X6-10A-01D-A22Z-08_BLCA	752	0	0	316	639	397	531	643	481	0	0	0	0	0	0	111	581
TCGA-E7-A3Y1-10A-01D-A22Z-08_BLCA	762	0	0	354	610	388	534	652	0	86	634	0	397	141	0	0	579
TCGA-E7-A4IJ-10A-01D-A26K-08_BLCA	664	231	249	259	573	362	533	638	457	61	522	502	0	0	32	2	573
TCGA-E7-A4XJ-10A-01D-A26K-08_BLCA	678	0	0	306	599	388	530	624	472	0	0	0	0	0	37	1	573
TCGA-E7-A519-10A-01D-A26K-08_BLCA	679	0	0	291	586	359	526	632	469	0	0	0	0	0	0	78	575
TCGA-E7-A541-10A-01D-A26K-08_BLCA	683	0	0	294	560	387	534	628	379	60	509	0	289	132	0	52	576
TCGA-E7-A5KE-10A-01D-A289-08_BLCA	761	0	0	303	569	381	533	644	401	76	590	0	295	136	27	0	576
TCGA-E7-A5KF-10A-01D-A289-08_BLCA	763	0	0	310	600	397	531	646	389	79	596	0	375	138	0	87	579
TCGA-E7-A677-10A-01D-A30H-08_BLCA	758	0	0	357	623	406	538	655	484	82	585	0	381	141	38	0	582
TCGA-E7-A678-10A-01D-A30H-08_BLCA	761	0	0	315	629	402	539	658	487	0	0	0	0	0	44	99	582
TCGA-E7-A6ME-10B-01D-A329-08_BLCA	682	0	0	304	604	387	533	639	405	0	0	0	0	0	25	46	577
TCGA-E7-A6MF-10B-01D-A329-08_BLCA	682	0	0	299	595	383	524	633	380	76	564	0	289	134	0	37	579
TCGA-E7-A7DU-10A-01D-A329-08_BLCA	659	226	239	274	549	356	531	636	466	0	0	0	0	0	19	44	570
TCGA-E7-A7DV-10A-01D-A339-08_BLCA	594	259	262	0	0	0	534	630	306	72	567	0	292	133	0	51	574
TCGA-E8-A242-10A-01D-A16O-08_THCA	681	251	269	296	616	286	534	652	481	0	623	569	0	0	36	80	576
TCGA-E8-A2EA-10A-01D-A17V-08_THCA	671	255	0	296	567	287	526	620	387	0	624	0	371	139	0	71	578
TCGA-E8-A2JQ-10A-01D-A19M-08_THCA	681	0	0	295	600	379	526	646	479	0	0	0	0	0	0	105	573
TCGA-E8-A3X7-10A-01D-A22Z-08_THCA	589	249	262	0	581	134	522	638	454	0	606	559	0	0	24	44	572
TCGA-E8-A413-10A-01D-A23K-08_THCA	593	257	272	0	0	0	531	646	32	82	642	0	377	139	0	0	577
TCGA-E8-A414-10A-01D-A23K-08_THCA	689	0	0	304	604	390	532	654	457	77	618	507	6	134	26	0	573
TCGA-E8-A415-10A-01D-A23K-08_THCA	686	0	36	294	596	386	533	641	472	0	27	59	0	0	32	65	572
TCGA-E8-A416-10A-01D-A23K-08_THCA	679	0	0	299	600	373	530	647	469	0	64	0	47	0	28	52	575
TCGA-E8-A417-10A-01D-A23K-08_THCA	687	0	0	305	610	377	519	642	476	0	0	35	0	0	0	112	577
TCGA-E8-A418-10A-01D-A23K-08_THCA	754	252	261	308	602	285	531	656	473	0	0	0	0	0	32	68	576
TCGA-E8-A419-10A-01D-A23K-08_THCA	760	0	42	302	607	384	529	650	460	76	616	79	370	136	0	65	576
TCGA-E8-A432-10A-01D-A23K-08_THCA	756	235	259	289	569	378	535	653	463	77	591	0	363	138	33	0	579
TCGA-E8-A433-10A-01D-A23K-08_THCA	685	248	264	289	584	373	531	644	395	81	612	0	301	136	0	64	573
TCGA-E8-A434-10A-01D-A23K-08_THCA	685	249	274	294	587	373	536	658	476	0	0	0	3	0	34	69	577
TCGA-E8-A436-10A-01D-A23U-08_THCA	588	242	257	0	38	0	511	583	0	63	585	0	367	134	0	1	571
TCGA-E8-A437-10A-01D-A23U-08_THCA	666	234	245	270	593	368	529	633	462	0	510	501	0	0	26	59	576
TCGA-E8-A438-10B-01D-A23U-08_THCA	631	238	246	248	525	274	524	628	362	60	599	505	279	131	0	65	571
TCGA-E8-A44K-10A-01D-A23U-08_THCA	682	241	256	281	570	362	528	646	468	0	0	0	0	0	32	55	567
TCGA-E8-A44M-10A-01D-A23U-08_THCA	684	0	0	293	589	374	533	637	464	0	0	0	0	0	27	55	571
TCGA-E9-A1N3-10A-01D-A159-09_BRCA	651	243	291	226	506	328	512	606	428	0	0	0	0	0	0	43	567
TCGA-E9-A1N4-10A-01D-A14K-09_BRCA	790	325	0	375	722	384	558	673	575	0	0	0	0	0	54	97	594
TCGA-E9-A1N5-10A-01D-A14G-09_BRCA	661	279	303	326	607	405	532	617	317	94	582	0	342	164	0	30	556
TCGA-E9-A1N8-10A-01D-A142-09_BRCA	659	0	0	343	653	408	492	483	317	0	0	0	0	163	0	34	532
TCGA-E9-A1N9-10A-01D-A14G-09_BRCA	679	280	325	334	686	356	549	634	0	100	649	527	443	183	0	0	586
TCGA-E9-A1NA-10A-01D-A142-09_BRCA	659	276	281	224	655	162	502	590	0	0	609	498	340	178	0	1	536
TCGA-E9-A1NC-10A-01D-A159-09_BRCA	651	0	0	363	690	377	542	639	458	0	0	0	0	0	18	46	580
TCGA-E9-A1NE-10A-01D-A14K-09_BRCA	589	329	373	0	685	180	557	668	458	104	661	546	376	182	46	0	597
TCGA-E9-A1NF-10A-01D-A14G-09_BRCA	694	303	350	372	673	451	559	663	473	0	0	0	0	0	0	101	591
TCGA-E9-A1NG-10A-01D-A14K-09_BRCA	682	0	0	373	678	451	553	648	462	0	0	0	0	0	27	45	588
TCGA-E9-A1NI-10A-01D-A17G-09_BRCA	677	296	0	365	684	444	531	634	448	0	631	0	378	180	37	0	594
TCGA-E9-A1QZ-10A-01D-A167-09_BRCA	665	273	308	353	621	407	540	628	432	0	0	0	0	0	20	37	577
TCGA-E9-A1R0-10A-01D-A16D-09_BRCA	685	310	361	369	628	462	556	662	352	100	639	0	449	182	0	66	592
TCGA-E9-A1R2-10A-01D-A14G-09_BRCA	650	282	344	344	652	440	554	654	427	99	603	502	0	176	0	51	589
TCGA-E9-A1R3-10A-01D-A14K-09_BRCA	569	316	374	0	673	179	559	655	483	0	643	531	0	0	32	69	592
TCGA-E9-A1R4-10A-01D-A14G-09_BRCA	690	0	0	377	693	469	555	651	442	94	627	526	0	179	43	0	589
TCGA-E9-A1R5-10A-01D-A14K-09_BRCA	698	0	0	389	708	471	558	665	0	105	672	0	464	189	0	1	597
TCGA-E9-A1R6-10A-01D-A14G-09_BRCA	673	0	0	378	688	464	546	654	465	0	0	0	0	0	34	68	576
TCGA-E9-A1R7-10A-01D-A14K-09_BRCA	668	272	310	232	587	302	525	624	430	0	0	0	0	0	17	38	583
TCGA-E9-A1RA-10A-01D-A14G-09_BRCA	675	0	0	367	678	441	554	635	448	0	0	0	0	0	19	32	583
TCGA-E9-A1RB-10A-01D-A159-09_BRCA	570	318	364	0	654	175	554	646	432	96	644	574	0	179	32	0	583
TCGA-E9-A1RC-10A-01D-A159-09_BRCA	681	303	343	360	699	442	550	648	445	96	644	549	0	179	0	56	589
TCGA-E9-A1RD-10A-01D-A159-09_BRCA	680	0	0	382	691	454	554	651	474	0	0	0	0	0	0	128	593
TCGA-E9-A1RE-10A-01D-A159-09_BRCA	630	146	302	246	489	329	532	617	445	0	0	0	0	0	0	15	548
TCGA-E9-A1RF-10A-01D-A159-09_BRCA	590	331	368	0	673	181	557	668	568	0	630	575	0	0	37	64	594
TCGA-E9-A1RG-10A-01D-A14G-09_BRCA	648	257	325	321	561	392	537	518	437	0	0	0	0	0	33	0	577
TCGA-E9-A1RH-10A-01D-A167-09_BRCA	669	0	0	370	685	380	544	633	460	0	0	0	0	0	0	107	586
TCGA-E9-A1RI-10A-01D-A167-09_BRCA	557	313	358	0	0	0	549	656	466	0	0	0	0	0	21	49	583

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-E9-A226-10A-01D-A159-09_BRCA	694	295	343	347	689	450	556	653	339	95	639	526	365	177	0	44	583
TCGA-E9-A227-10A-01D-A159-09_BRCA	531	296	353	0	650	178	529	590	392	99	631	529	329	158	0	29	549
TCGA-E9-A228-10A-01D-A159-09_BRCA	657	0	0	359	647	353	517	622	312	91	564	0	304	164	0	19	561
TCGA-E9-A229-10B-01D-A159-09_BRCA	570	315	362	0	661	171	549	651	464	0	602	524	0	0	30	71	578
TCGA-E9-A22A-10A-01D-A159-09_BRCA	663	0	0	381	648	352	529	642	436	0	0	0	0	0	0	30	562
TCGA-E9-A22B-10A-01D-A159-09_BRCA	674	307	345	362	664	371	553	654	0	102	647	560	365	183	0	1	592
TCGA-E9-A22D-10A-01D-A159-09_BRCA	687	304	347	359	673	449	555	651	551	0	0	0	0	0	0	99	593
TCGA-E9-A22E-10A-01D-A159-09_BRCA	644	0	0	338	627	357	449	445	270	0	0	0	0	146	0	29	518
TCGA-E9-A22G-10A-01D-A159-09_BRCA	643	0	0	362	651	421	517	633	445	0	0	0	0	0	0	52	588
TCGA-E9-A22H-10A-01D-A17G-09_BRCA	566	0	0	346	639	430	526	595	407	0	0	0	0	0	10	14	541
TCGA-E9-A243-10A-01D-A17G-09_BRCA	689	0	0	376	713	463	555	659	477	0	0	0	0	0	34	69	594
TCGA-E9-A244-10A-01D-A167-09_BRCA	646	0	0	348	669	426	545	642	305	92	587	498	276	147	0	29	576
TCGA-E9-A245-10A-01D-A16D-09_BRCA	693	0	0	372	701	371	546	660	340	98	606	0	356	173	0	40	584
TCGA-E9-A247-10A-01D-A167-09_BRCA	542	298	295	0	379	126	522	617	251	0	501	477	292	161	0	25	561
TCGA-E9-A248-10A-01D-A167-09_BRCA	647	255	282	188	565	318	516	624	437	0	0	0	0	0	0	48	558
TCGA-E9-A249-10A-01D-A167-09_BRCA	669	0	3	346	655	360	513	617	428	0	0	0	0	0	0	71	572
TCGA-E9-A24A-10A-01D-A167-09_BRCA	679	0	0	377	676	444	547	641	459	0	0	0	0	0	0	72	583
TCGA-E9-A295-10A-01D-A16D-09_BRCA	685	274	330	343	684	451	544	633	460	0	612	515	0	0	27	36	585
TCGA-E9-A2JS-10A-01D-A17W-09_BRCA	592	316	360	0	0	0	552	659	562	0	0	0	0	0	30	69	581
TCGA-E9-A2JT-10A-01D-A18P-09_BRCA	683	291	330	350	653	353	538	650	462	0	0	0	0	0	20	47	595
TCGA-E9-A3HO-10A-02D-A20S-09_BRCA	574	302	340	0	0	0	549	620	420	0	0	0	0	0	0	33	563
TCGA-E9-A3Q9-10A-01D-A21Q-09_BRCA	591	327	354	0	663	177	554	656	431	102	633	585	0	179	0	60	595
TCGA-E9-A3QA-10A-01D-A22A-09_BRCA	670	276	311	214	494	414	551	607	531	0	0	0	0	0	33	40	586
TCGA-E9-A3X8-10B-01D-A22X-09_BRCA	593	317	315	0	651	173	553	633	535	0	607	572	0	0	0	84	578
TCGA-E9-A54X-10A-01D-A25Q-09_BRCA	676	263	297	212	487	425	547	623	433	0	0	0	0	0	0	67	585
TCGA-E9-A54Y-10A-01D-A25Q-09_BRCA	585	324	348	0	606	176	551	648	331	91	635	588	0	172	0	65	592
TCGA-E9-A5FK-10A-01D-A27P-09_BRCA	690	290	332	238	656	365	547	616	446	0	567	522	0	0	46	1	582
TCGA-E9-A5FL-10A-01D-A27P-09_BRCA	698	310	344	335	634	448	553	634	549	0	0	0	0	0	0	93	587
TCGA-E9-A5UO-10A-01D-A28E-09_BRCA	693	305	352	336	620	360	548	625	554	0	0	0	0	0	0	113	590
TCGA-E9-A5UP-10A-01D-A28E-09_BRCA	696	0	0	372	687	453	551	655	516	84	597	511	0	172	0	68	588
TCGA-E9-A6HE-10A-01D-A31U-09_BRCA	682	314	336	338	652	449	558	632	458	0	0	0	0	0	0	84	584
TCGA-EA-A1QS-10A-01D-A22X-09_CESC	696	0	0	367	687	363	537	598	539	0	0	0	0	180	0	64	579
TCGA-EA-A1QT-10A-01D-A14W-08_CESC	690	0	0	303	602	366	531	643	369	66	563	0	291	138	0	44	574
TCGA-EA-A3HQ-10A-01D-A20U-09_CESC	698	313	337	326	618	359	551	626	554	0	0	0	0	0	0	124	585
TCGA-EA-A3HR-10A-01D-A20U-09_CESC	693	0	0	368	683	452	548	654	556	0	0	0	0	0	41	63	592
TCGA-EA-A3HS-10B-01D-A20U-09_CESC	589	322	364	0	625	174	558	646	325	0	611	582	0	173	0	60	584
TCGA-EA-A3HT-10A-01D-A21Q-09_CESC	695	304	336	336	675	458	552	641	330	96	639	539	363	176	0	57	586
TCGA-EA-A3HU-10B-01D-A20U-09_CESC	589	327	363	0	649	176	556	655	554	0	598	0	0	0	46	59	590
TCGA-EA-A3QD-10A-01D-A22X-09_CESC	702	294	330	346	682	445	551	645	513	90	637	579	0	175	0	57	586
TCGA-EA-A3QE-10A-01D-A21Q-09_CESC	686	299	337	348	608	429	553	639	528	0	0	0	0	0	0	95	588
TCGA-EA-A3Y4-10A-01D-A243-09_CESC	699	0	0	362	678	447	557	640	446	0	0	0	0	0	0	101	585
TCGA-EA-A410-10A-01D-A243-09_CESC	669	0	0	356	655	456	548	626	449	0	0	0	0	0	0	108	582
TCGA-EA-A411-10A-01D-A243-09_CESC	586	327	355	0	0	0	544	623	541	0	0	0	0	0	0	96	587
TCGA-EA-A439-10A-01D-A243-09_CESC	688	0	0	365	684	466	554	644	415	83	615	0	347	180	0	45	584
TCGA-EA-A43B-10A-01D-A243-09_CESC	698	310	325	312	624	438	549	626	399	0	477	0	363	177	0	55	584
TCGA-EA-A44S-10A-01D-A26G-09_CESC	583	317	360	0	120	72	549	622	437	0	0	0	0	0	0	85	586
TCGA-EA-A4BA-10A-01D-A26G-09_CESC	697	311	333	332	686	363	552	635	539	0	611	533	0	0	0	81	587
TCGA-EA-A50E-10A-01D-A26G-09_CESC	691	0	0	347	668	447	551	611	538	0	0	0	0	0	32	5	589
TCGA-EA-A556-10A-01D-A26G-09_CESC	697	48	0	367	671	457	551	640	550	0	12	0	0	0	0	77	579
TCGA-EA-A5FO-10A-01D-A28E-09_CESC	679	0	0	351	667	378	538	621	539	0	0	0	0	0	0	119	586
TCGA-EA-A5O9-10A-01D-A28E-09_CESC	794	319	354	168	611	360	556	656	398	90	510	0	344	168	39	0	584
TCGA-EA-A5ZD-10A-01D-A28E-09_CESC	680	0	0	358	681	454	548	638	550	0	0	0	0	0	57	0	590
TCGA-EA-A5ZE-10A-01D-A28E-09_CESC	697	0	0	361	672	459	549	625	547	0	0	0	0	0	59	1	588
TCGA-EA-A5ZF-10A-01D-A28E-09_CESC	694	0	0	383	650	353	555	646	429	92	603	520	0	170	43	0	590
TCGA-EB-A1NK-10A-01D-A198-08_SKCM	662	227	242	165	486	250	526	614	467	0	0	0	0	0	17	43	574
TCGA-EB-A24C-10A-01D-A199-08_SKCM	594	250	254	0	529	125	531	644	460	0	491	509	0	0	16	54	573
TCGA-EB-A24D-10A-01D-A199-08_SKCM	596	247	269	0	585	138	534	633	467	0	592	560	0	0	26	49	577
TCGA-EB-A299-10A-01D-A199-08_SKCM	665	238	260	259	505	359	528	624	466	0	0	0	0	0	0	79	575
TCGA-EB-A3HV-10B-01D-A21A-08_SKCM	686	246	252	274	573	365	532	647	474	0	0	0	0	0	0	80	574
TCGA-EB-A3XB-10B-01D-A23B-08_SKCM	684	0	0	299	591	383	529	638	384	77	619	561	0	135	0	59	571
TCGA-EB-A3XC-10A-01D-A23B-08_SKCM	679	247	267	294	611	287	530	650	485	0	621	568	0	0	33	74	576
TCGA-EB-A3XD-10A-01D-A23B-08_SKCM	595	251	270	0	0	0	518	633	460	0	0	0	0	0	24	60	573
TCGA-EB-A3XE-10A-01D-A23B-08_SKCM	682	0	0	304	600	284	525	643	480	0	0	0	0	0	0	78	574
TCGA-EB-A3XF-10A-01D-A23B-08_SKCM	756	0	0	306	600	374	529	646	388	77	590	509	0	136	0	56	572
TCGA-EB-A3Y6-10A-01D-A23B-08_SKCM	688	251	266	295	606	138	527	633	462	0	621	515	0	133	33	5	573
TCGA-EB-A3Y7-10A-01D-A23B-08_SKCM	686	240	245	287	559	366	532	633	463	0	0	26	0	0	0	75	572
TCGA-EB-A41A-10A-01D-A24R-08_SKCM	586	248	260	0	569	135	522	612	463	0	608	559	0	0	0	88	572
TCGA-EB-A41B-10A-01D-A24R-08_SKCM	681	238	258	284	601	377	531	637	378	63	627	514	0	133	28	1	573
TCGA-EB-A42Y-10A-01D-A24R-08_SKCM	682	247	265	280	585	274	530	651	475	0	0	0	0	0	31	63	573
TCGA-EB-A42Z-10A-01D-A24R-08_SKCM	687	248	257	288	606	377	529	636	472	0	580	565	0	0	0	73	575
TCGA-EB-A430-10A-01D-A24R-08_SKCM	676	238	261	279	586	277	530	639	462	0	0	0	0	0	0	74	575
TCGA-EB-A431-10A-01D-A25O-08_SKCM	662	218	239	250	522	344	523	627	391	0	0	0	0	0	0	82	571
TCGA-EB-A44N-10A-01D-A25O-08_SKCM	662	234	261	258	484	355	528	616	388	0	0	0	0	0	0	69	571
TCGA-EB-A44O-10A-01D-A25O-08_SKCM	668	230	245	274	593	358	525	617	451	0	553	502	0	0	0	65	570
TCGA-EB-A44P-10A-01D-A25O-08_SKCM	763	262	283	309	613	300	539	661	481	81	631	0	391	141	0	124	582
TCGA-EB-A44Q-10A-01D-A25O-08_SKCM	677	0	0	288	588	384	529	619	387	0	0	0	0	0	28	0	574
TCGA-EB-A44R-10A-01D-A25O-08_SKCM	633	208	246	256	519	344	524	608	368	59	613	497	276	126	23	0	572
TCGA-EB-A4IQ-10A-01D-A25O-08_SKCM	678	0	0	290	578	378	525	623	463	0	0	0	0	0	18	41	574
TCGA-EB-A4IS-10A-01D-A25O-08_SKCM	589	243	260	0	0	0	527	630	459	0	0	0	0	0	22	46	572
TCGA-EB-A4OY-10A-01D-A25O-08_SKCM	593	215	235	163	590	274	526	622	386	0	513	553	0	0	0	59	575
TCGA-EB-A4OZ-10A-01D-A25O-08_SKCM	586	245	259	0	529	129	524	621	363	72	580	489	288	127	23	0	571
TCGA-EB-A4P0-10A-01D-A25O-08_SKCM	588	246	264	0	491	128	528	631	460	0	495	494	0	0	16	34	571
TCGA-EB-A4XL-10A-01D-A27N-08_SKCM	679	0	0	294	594	377	529	635	466	0	0	0	0	0	0	101	572
TCGA-EB-A51B-10A-01D-A27N-08_SKCM	668	242	259	277	601	371	531	630	443	69	616	571	0	136	0	55	574
TCGA-EB-A550-10A-01D-A27N-08_SKCM	663	237	252	274	511	272	529	639	470	0	0	0	0	0	0	125	574
TCGA-EB-A551-10A-01D-A27N-08_SKCM	679	0	0	301	594	365	516	616	378	54	574	497	0	132	0	48	573
TCGA-EB-A553-10A-01D-A27N-08_SKCM	593	256	274	0	576	134	530	646	385	79	621	567	0	132	30	0	577
TCGA-EB-A57M-10A-01D-A30X-08_SKCM	674	0	0	289	569	382	532	634	471	0	0	0	0	0	27	39	575
TCGA-EB-A5FP-10A-01D-A27N-08_SKCM	680	245	260	282	585	371	528	645	376	70	586	0	364	130	0	61	572
TCGA-EB-A5KH-10A-01D-A27N-08_SKCM	686	0	0	288	594	378	527	624	449	64	570	0	284	132	0	50	571
TCGA-EB-A5SE-10A-01D-A30X-08_SKCM	682	0	0	299	593	383	531	637	468	0	0	0	0	0	0	109	575
TCGA-EB-A5SF-10A-01D-A30X-08_SKCM	665	0	0	292	594	276	508	632	464	0	0	0	0	0	0	71	571
TCGA-EB-A5SG-10A-01D-A30X-08_SKCM	672	234	246	280	571	264	523	637	307	63	587	0	287	133	0	56	575
TCGA-EB-A5SH-10A-01D-A30X-08_SKCM	677	0	0	286	585	366	530	637	399	0	0	0	0	0	0	90	571
TCGA-EB-A5UL-10A-01D-A30X-08_SKCM	677	246	259	286	557	0	0	0	0	0	579	0	289	141	0	0	572
TCGA-EB-A5UM-10A-01D-A30X-08_SKCM	678	237	246	276	556	365	534	638	467	0	0	0	0	0	23	59	575

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EB-A5UN-10A-01D-A30X-08_SKCM	681	0	0	295	586	382	526	635	439	60	520	0	356	132	0	45	569
TCGA-EB-A5VU-10A-01D-A32N-08_SKCM	686	0	0	350	611	386	534	655	476	0	0	0	0	0	0	95	579
TCGA-EB-A5VV-10A-01D-A32N-08_SKCM	685	254	268	289	616	284	532	663	453	82	642	563	301	141	38	0	575
TCGA-EB-A6L9-10A-01D-A32N-08_SKCM	758	0	0	302	604	387	535	652	461	78	624	0	366	136	31	0	577
TCGA-EB-A6QY-10B-01D-A32N-08_SKCM	676	256	274	293	619	284	532	656	470	75	649	572	366	137	34	0	578
TCGA-EB-A6QZ-10B-01D-A32N-08_SKCM	687	0	0	302	610	390	533	648	482	0	0	0	0	0	0	139	576
TCGA-EB-A6R0-10B-01D-A32N-08_SKCM	684	240	267	295	615	380	532	661	487	0	614	512	0	0	28	75	574
TCGA-EC-A1NJ-10A-01D-A14G-09_UCEC	666	293	325	220	674	432	551	628	546	0	514	535	0	0	44	0	583
TCGA-EC-A1QX-10A-01D-A16D-09_UCEC	687	281	292	315	599	446	544	621	448	0	0	0	0	0	0	83	580
TCGA-EC-A24G-10A-01D-A16D-09_UCEC	700	311	339	331	681	368	548	633	430	98	630	589	0	181	38	0	582
TCGA-ED-A459-10A-01D-A25V-10_LIHC	682	279	319	272	507	432	553	626	362	0	0	0	0	0	33	73	570
TCGA-ED-A4XI-10A-01D-A25V-10_LIHC	687	241	280	260	533	448	549	617	361	0	0	0	0	0	43	1	583
TCGA-ED-A5KG-10A-01D-A27I-10_LIHC	656	0	0	266	634	460	542	608	356	0	0	0	0	0	22	56	569
TCGA-ED-A627-10B-01D-A30V-10_LIHC	523	134	118	182	310	381	488	480	287	0	289	0	240	156	0	15	553
TCGA-ED-A66X-10A-01D-A30V-10_LIHC	496	0	0	253	450	392	482	461	315	0	0	0	0	0	0	51	550
TCGA-ED-A66Y-10A-01D-A30V-10_LIHC	521	192	243	222	528	408	501	568	348	0	308	439	0	0	22	0	544
TCGA-EE-A17X-10A-01D-A199-08_SKCM	754	242	255	283	585	366	533	641	476	0	0	0	0	0	33	0	577
TCGA-EE-A17Y-10B-01D-A198-08_SKCM	676	0	0	303	595	385	528	642	463	0	0	0	0	0	34	0	580
TCGA-EE-A17Z-10A-01D-A198-08_SKCM	682	204	230	216	579	299	521	647	469	0	504	509	0	0	0	60	578
TCGA-EE-A180-10B-01D-A21A-08_SKCM	686	238	254	287	561	368	529	661	488	0	0	0	0	0	27	70	575
TCGA-EE-A181-10A-01D-A198-08_SKCM	690	0	0	306	608	386	530	637	480	0	0	0	0	0	0	110	573
TCGA-EE-A182-10A-01D-A198-08_SKCM	751	245	262	184	517	277	534	646	380	67	558	0	366	134	0	60	576
TCGA-EE-A183-10A-01D-A198-08_SKCM	683	0	0	293	597	377	526	638	382	70	579	0	360	130	0	55	573
TCGA-EE-A184-10B-01D-A198-08_SKCM	686	0	0	301	610	381	530	645	487	0	0	0	0	0	0	100	579
TCGA-EE-A185-10A-01D-A198-08_SKCM	730	241	257	276	557	276	531	643	478	0	0	0	0	0	36	0	576
TCGA-EE-A20B-10A-01D-A198-08_SKCM	661	233	247	277	597	278	532	645	477	0	576	491	0	0	28	59	577
TCGA-EE-A20C-10A-01D-A198-08_SKCM	686	0	0	308	605	390	533	641	472	0	0	0	0	0	0	89	580
TCGA-EE-A20F-10A-01D-A198-08_SKCM	691	0	0	301	608	387	532	659	490	0	0	0	0	0	31	66	580
TCGA-EE-A20H-10A-01D-A199-08_SKCM	672	241	250	272	596	337	530	648	474	0	509	563	0	0	20	32	578
TCGA-EE-A20I-10A-01D-A198-08_SKCM	680	242	246	273	573	355	535	650	478	0	0	0	0	0	21	46	577
TCGA-EE-A29A-10A-01D-A198-08_SKCM	671	242	260	288	610	371	532	648	479	0	525	566	0	0	0	107	577
TCGA-EE-A29B-10A-01D-A199-08_SKCM	686	0	0	302	605	384	531	643	477	0	0	0	0	0	0	121	575
TCGA-EE-A29C-10A-01D-A199-08_SKCM	681	0	0	308	611	286	524	657	467	82	611	570	43	138	0	83	579
TCGA-EE-A29D-10A-01D-A199-08_SKCM	677	246	263	274	560	280	533	642	457	62	596	0	297	135	25	2	576
TCGA-EE-A29E-10A-01D-A199-08_SKCM	684	0	0	300	596	395	534	641	385	65	578	0	362	136	0	63	575
TCGA-EE-A29G-10A-01D-A198-08_SKCM	689	0	0	294	606	384	531	640	487	0	0	0	0	0	0	105	580
TCGA-EE-A29H-10A-01D-A199-08_SKCM	670	228	250	285	532	347	535	632	384	75	557	0	287	130	0	51	578
TCGA-EE-A29L-10A-01D-A198-08_SKCM	674	0	0	289	591	369	527	639	480	0	0	0	0	0	0	102	577
TCGA-EE-A29M-10A-01D-A198-08_SKCM	760	0	0	302	610	394	533	645	480	0	0	0	0	0	0	131	580
TCGA-EE-A29N-10A-01D-A199-08_SKCM	688	0	0	305	607	383	532	648	478	0	0	0	0	0	0	96	577
TCGA-EE-A29P-10A-01D-A199-08_SKCM	669	233	256	282	560	348	530	649	476	0	0	0	0	0	23	59	579
TCGA-EE-A29Q-10A-01D-A199-08_SKCM	592	250	263	0	494	131	529	633	438	74	591	544	275	129	0	49	574
TCGA-EE-A29R-10A-01D-A199-08_SKCM	689	0	0	297	573	290	526	635	481	0	0	0	0	0	0	94	580
TCGA-EE-A29S-10A-01D-A199-08_SKCM	680	0	0	302	600	370	535	644	477	0	0	0	0	0	16	43	578
TCGA-EE-A29T-10A-01D-A199-08_SKCM	756	247	257	291	584	289	533	654	487	0	0	0	0	0	0	129	575
TCGA-EE-A29V-10A-01D-A199-08_SKCM	664	228	256	255	535	361	534	632	376	64	517	0	277	132	0	34	577
TCGA-EE-A29W-10A-01D-A198-08_SKCM	679	0	0	306	582	369	531	644	385	0	570	0	293	131	0	56	576
TCGA-EE-A29X-10A-01D-A198-08_SKCM	688	253	266	279	603	359	535	649	440	82	631	511	294	138	0	57	580
TCGA-EE-A2A0-10A-01D-A198-08_SKCM	673	0	0	332	583	363	527	627	458	0	0	0	0	0	20	36	574
TCGA-EE-A2A1-10A-01D-A199-08_SKCM	674	0	0	295	523	380	527	638	379	67	531	0	280	131	0	56	576
TCGA-EE-A2A2-10A-01D-A198-08_SKCM	595	259	275	0	554	128	534	656	392	82	623	516	294	134	0	59	580
TCGA-EE-A2A5-10A-01D-A199-08_SKCM	752	0	0	300	605	378	529	647	483	0	0	0	0	0	0	105	579
TCGA-EE-A2A6-10A-01D-A199-08_SKCM	682	0	0	298	607	389	530	642	470	0	0	0	0	0	0	113	577
TCGA-EE-A2GB-10A-01D-A199-08_SKCM	686	0	0	294	594	374	533	639	484	0	0	0	0	0	0	76	575
TCGA-EE-A2GC-10A-01D-A199-08_SKCM	684	243	266	290	560	280	530	648	396	72	614	0	303	138	0	73	575
TCGA-EE-A2GD-10A-01D-A198-08_SKCM	682	0	0	307	602	367	530	638	478	0	0	0	0	0	0	110	580
TCGA-EE-A2GE-10A-01D-A198-08_SKCM	682	0	0	301	607	379	528	635	474	0	0	0	0	0	35	0	575
TCGA-EE-A2GH-10A-01D-A198-08_SKCM	674	240	261	278	587	271	530	624	454	0	0	0	0	0	0	69	575
TCGA-EE-A2GI-10A-01D-A198-08_SKCM	596	259	277	0	0	0	533	640	476	0	0	0	0	0	39	0	579
TCGA-EE-A2GJ-10A-01D-A198-08_SKCM	677	0	0	279	588	373	530	647	366	65	512	0	327	130	0	34	578
TCGA-EE-A2GK-10A-01D-A198-08_SKCM	677	0	0	297	604	289	522	640	431	76	567	0	359	137	0	69	575
TCGA-EE-A2GL-10A-01D-A198-08_SKCM	636	244	256	266	586	275	532	648	477	65	518	503	0	0	23	51	574
TCGA-EE-A2GM-10A-01D-A198-08_SKCM	687	0	0	289	604	368	534	654	476	0	0	0	0	0	22	52	580
TCGA-EE-A2GN-10A-01D-A198-08_SKCM	675	248	258	191	596	283	534	649	478	0	579	568	0	0	24	53	579
TCGA-EE-A2GO-10A-01D-A198-08_SKCM	597	235	235	262	428	356	525	643	380	52	508	0	343	134	22	2	578
TCGA-EE-A2GP-10A-01D-A199-08_SKCM	667	0	0	280	569	382	532	640	305	63	543	0	280	131	22	0	570
TCGA-EE-A2GR-10A-01D-A199-08_SKCM	675	232	222	243	569	329	528	641	304	76	573	504	262	126	0	34	570
TCGA-EE-A2GS-10A-01D-A199-08_SKCM	653	0	0	267	548	274	510	622	386	0	0	0	0	0	0	58	580
TCGA-EE-A2GT-10A-01D-A199-08_SKCM	684	0	0	307	609	382	531	654	396	77	611	0	363	133	0	63	574
TCGA-EE-A2GU-10A-01D-A198-08_SKCM	681	240	260	275	555	368	534	635	475	0	0	0	0	0	27	67	578
TCGA-EE-A2M5-10A-01D-A199-08_SKCM	663	207	243	268	585	331	530	626	360	57	536	569	0	132	0	38	574
TCGA-EE-A2M6-10A-01D-A199-08_SKCM	663	0	0	275	585	281	523	631	458	0	0	0	0	0	0	64	580
TCGA-EE-A2M7-10A-01D-A199-08_SKCM	683	0	0	307	600	381	532	643	480	0	0	0	0	0	0	120	573
TCGA-EE-A2M8-10A-01D-A198-08_SKCM	646	233	253	265	596	354	529	625	433	0	583	509	288	131	0	51	577
TCGA-EE-A2MC-10A-01D-A199-08_SKCM	686	0	0	295	598	374	530	648	477	0	0	0	0	0	15	37	577
TCGA-EE-A2MD-10A-01D-A199-08_SKCM	638	239	259	264	557	279	526	628	0	83	592	0	379	138	0	0	576
TCGA-EE-A2ME-10A-01D-A199-08_SKCM	685	0	0	296	589	285	523	637	376	75	529	0	363	130	0	54	577
TCGA-EE-A2MF-10B-01D-A21A-08_SKCM	683	0	0	296	596	383	528	640	464	0	0	0	0	0	0	77	573
TCGA-EE-A2MG-10A-01D-A199-08_SKCM	659	246	263	283	510	365	532	646	479	0	0	0	0	0	0	94	578
TCGA-EE-A2MH-10A-01D-A199-08_SKCM	665	0	0	291	581	342	521	626	392	0	0	0	0	0	11	24	575
TCGA-EE-A2MI-10A-01D-A199-08_SKCM	682	0	0	301	575	371	528	637	460	0	0	0	0	0	0	79	576
TCGA-EE-A2MJ-10A-01D-A199-08_SKCM	673	0	0	287	591	370	529	633	393	0	0	0	0	0	0	66	577
TCGA-EE-A2MK-10A-01D-A198-08_SKCM	644	227	239	222	586	218	527	613	274	0	613	563	0	127	0	37	571
TCGA-EE-A2ML-10A-01D-A199-08_SKCM	617	172	177	229	415	267	506	621	374	0	0	0	0	0	16	30	571
TCGA-EE-A2MM-10A-01D-A198-08_SKCM	692	0	0	302	608	288	524	649	452	70	580	0	346	134	21	0	578
TCGA-EE-A2MN-10A-01D-A199-08_SKCM	685	0	0	287	561	380	523	634	466	0	0	0	0	0	0	80	574
TCGA-EE-A2MP-10A-01D-A199-08_SKCM	665	236	240	259	575	277	528	642	465	0	526	499	0	0	18	48	572
TCGA-EE-A2MQ-10A-01D-A199-08_SKCM	757	0	0	300	613	376	530	644	482	0	0	0	0	0	34	68	576
TCGA-EE-A2MR-10A-01D-A198-08_SKCM	683	0	0	296	605	290	526	639	488	0	0	0	0	0	0	100	581
TCGA-EE-A2MS-10A-01D-A199-08_SKCM	596	258	271	0	598	141	532	631	386	0	624	520	0	131	31	0	575
TCGA-EE-A2MT-10A-01D-A199-08_SKCM	681	0	0	293	584	372	532	638	403	0	0	0	0	0	0	78	571
TCGA-EE-A2MU-10A-01D-A198-08_SKCM	681	0	0	297	578	373	528	634	469	0	0	0	0	0	0	75	575
TCGA-EE-A3AA-10A-01D-A198-08_SKCM	683	0	0	302	603	391	536	651	390	75	535	0	361	135	0	83	578
TCGA-EE-A3AB-10A-01D-A198-08_SKCM	674	0	0	298	606	289	525	649	486	0	0	0	0	0	0	114	579
TCGA-EE-A3AC-10A-01D-A198-08_SKCM	757	0	0	311	614	396	534	652	445	81	609	0	358	139	0	61	579
TCGA-EE-A3AD-10A-01D-A198-08_SKCM	675	0	0	305	579	286	525	650	480	0	0	0	0	0	0	105	576

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EE-A3AE-10A-01D-A198-08_SKCM	691	0	0	304	605	383	528	647	484	0	0	0	0	0	31	73	577
TCGA-EE-A3AF-10A-01D-A198-08_SKCM	686	0	0	288	594	285	528	635	470	0	0	0	0	0	34	65	574
TCGA-EE-A3AG-10A-01D-A198-08_SKCM	662	244	251	271	587	358	532	639	0	81	600	497	364	136	0	0	575
TCGA-EE-A3AH-10A-01D-A198-08_SKCM	591	250	261	0	510	120	524	632	466	0	495	472	0	0	0	78	577
TCGA-EE-A3J3-10A-01D-A20D-08_SKCM	676	255	259	293	615	281	529	641	465	79	640	507	357	134	0	65	575
TCGA-EE-A3J4-10A-01D-A20D-08_SKCM	683	0	0	302	595	371	528	652	480	0	0	0	0	0	28	60	575
TCGA-EE-A3J5-10A-01D-A20D-08_SKCM	687	0	0	293	603	373	533	660	474	60	0	0	0	0	0	118	578
TCGA-EE-A3J7-10A-01D-A20D-08_SKCM	685	0	0	306	606	288	523	662	474	0	0	0	0	0	32	68	576
TCGA-EE-A3J8-10A-01D-A20D-08_SKCM	680	247	252	287	611	374	531	652	470	0	599	517	0	0	36	62	576
TCGA-EE-A3JA-10A-01D-A20D-08_SKCM	677	0	0	294	564	378	533	643	479	0	0	0	0	0	0	115	577
TCGA-EE-A3JB-10A-01D-A21A-08_SKCM	691	0	0	309	609	390	534	661	484	0	0	0	0	0	0	105	578
TCGA-EE-A3JD-10A-01D-A20D-08_SKCM	682	0	0	303	569	370	533	652	481	0	0	0	0	0	31	59	576
TCGA-EE-A3JE-10A-01D-A20D-08_SKCM	683	0	0	300	589	379	529	628	474	0	0	0	0	0	0	106	574
TCGA-EE-A3JH-10A-01D-A21A-08_SKCM	686	0	0	302	605	383	532	652	451	75	599	0	362	134	0	61	579
TCGA-EE-A3JI-10A-01D-A21A-08_SKCM	690	249	259	274	613	379	533	666	478	81	615	565	0	0	27	67	574
TCGA-EF-5830-10A-01D-1657-10_READ	681	0	0	405	670	447	536	630	461	0	0	0	0	0	0	62	590
TCGA-EI-6506-10A-01D-1733-10_READ	665	236	240	198	560	406	537	599	336	87	423	0	307	152	9	0	583
TCGA-EI-6507-10A-01D-1733-10_READ	678	260	0	341	651	416	555	605	334	91	413	0	326	163	0	23	586
TCGA-EI-6508-10A-01D-1733-10_READ	558	287	318	0	523	162	515	627	397	82	458	494	337	149	10	0	581
TCGA-EI-6509-10A-01D-1733-10_READ	657	155	263	321	556	322	521	606	436	0	0	0	0	0	0	50	572
TCGA-EI-6510-10A-01D-1733-10_READ	652	148	265	330	618	407	512	602	318	0	395	505	0	154	0	16	562
TCGA-EI-6511-10A-01D-1733-10_READ	696	159	289	350	653	314	547	613	437	0	325	440	0	0	0	50	586
TCGA-EI-6512-10A-01D-1733-10_READ	676	230	259	335	570	354	531	585	450	0	0	0	0	0	0	55	584
TCGA-EI-6513-10A-01D-1733-10_READ	674	153	280	225	477	0	485	521	306	0	0	0	0	167	17	1	543
TCGA-EI-6514-10A-01D-1733-10_READ	658	0	0	351	636	435	509	596	433	0	0	0	0	0	0	50	579
TCGA-EI-6881-10A-01D-1924-10_READ	546	239	304	0	406	151	498	585	413	0	354	433	0	0	12	23	558
TCGA-EI-6882-10A-01D-1924-10_READ	636	211	180	220	510	407	506	583	0	102	473	505	268	171	0	0	557
TCGA-EI-6883-10A-01D-1924-10_READ	626	0	0	327	575	407	484	561	275	0	257	368	0	109	0	14	539
TCGA-EI-6884-10A-01D-1924-10_READ	600	53	0	104	542	251	458	547	246	0	263	0	188	132	0	16	524
TCGA-EI-6885-10A-01D-1924-10_READ	623	194	208	167	429	315	514	571	333	0	0	0	0	0	0	47	567
TCGA-EI-6917-10A-01D-1924-10_READ	635	0	0	327	587	398	493	558	333	0	0	0	0	0	0	29	532
TCGA-EI-7002-10A-01D-1924-10_READ	648	0	0	327	464	408	484	545	320	0	0	0	0	0	9	18	537
TCGA-EI-7004-10A-01D-1924-10_READ	619	0	0	241	635	359	481	546	292	0	357	0	300	138	0	15	554
TCGA-EJ-5494-10A-01D-1577-08_PRAD	690	251	270	298	611	381	533	663	487	0	607	519	0	0	0	142	581
TCGA-EJ-5495-10A-01D-1577-08_PRAD	762	0	0	315	610	406	535	665	481	83	624	0	376	140	47	2	581
TCGA-EJ-5496-10A-01D-1577-08_PRAD	689	0	0	314	612	395	534	659	491	0	0	0	0	0	0	157	577
TCGA-EJ-5497-10A-01D-1577-08_PRAD	690	0	0	312	620	388	532	659	460	76	627	0	367	139	0	76	579
TCGA-EJ-5498-10A-01D-1577-08_PRAD	688	0	0	311	615	400	531	658	477	0	0	0	0	0	0	116	582
TCGA-EJ-5499-10A-01D-1577-08_PRAD	689	0	0	313	613	293	523	660	482	0	0	0	0	0	0	109	579
TCGA-EJ-5501-10A-01D-1577-08_PRAD	666	257	279	0	0	0	531	658	478	0	0	0	0	0	53	2	579
TCGA-EJ-5502-10A-01D-1577-08_PRAD	686	0	0	314	610	392	533	664	473	0	0	0	0	0	31	64	578
TCGA-EJ-5503-10A-01D-1577-08_PRAD	591	260	276	0	0	0	530	648	479	0	0	0	0	0	52	3	576
TCGA-EJ-5504-10A-01D-1577-08_PRAD	596	261	285	0	491	137	535	657	489	0	607	572	0	0	37	81	578
TCGA-EJ-5505-10A-01D-1577-08_PRAD	758	0	0	303	616	392	534	653	489	0	0	0	0	0	0	135	579
TCGA-EJ-5506-10A-01D-1577-08_PRAD	679	0	0	304	601	290	524	657	483	0	0	0	0	0	34	72	576
TCGA-EJ-5507-10A-01D-1577-08_PRAD	761	0	0	306	616	295	524	661	492	0	0	0	0	0	0	169	577
TCGA-EJ-5508-10A-01D-1577-08_PRAD	689	0	0	310	616	403	536	663	478	77	623	0	376	137	0	84	578
TCGA-EJ-5509-10A-01D-1577-08_PRAD	682	247	259	275	608	359	531	649	459	0	599	567	0	0	0	112	577
TCGA-EJ-5510-10A-01D-1577-08_PRAD	680	0	0	304	609	274	507	633	449	0	0	0	0	137	0	73	578
TCGA-EJ-5511-10A-01D-1577-08_PRAD	690	139	276	294	598	384	537	658	477	0	0	0	0	0	36	2	574
TCGA-EJ-5512-10A-01D-1577-08_PRAD	685	260	272	300	623	389	534	664	0	86	650	570	381	141	0	3	581
TCGA-EJ-5514-10A-01D-1577-08_PRAD	749	256	273	300	621	386	534	659	499	0	623	575	0	0	44	86	578
TCGA-EJ-5515-10A-01D-1577-08_PRAD	683	261	269	295	622	386	534	662	486	0	620	570	0	0	34	77	581
TCGA-EJ-5516-10A-01D-1577-08_PRAD	686	0	0	304	634	400	532	653	492	0	0	0	0	0	0	158	576
TCGA-EJ-5517-10A-01D-1577-08_PRAD	745	258	273	298	623	295	532	658	455	83	652	573	0	142	0	84	578
TCGA-EJ-5518-10A-01D-1577-08_PRAD	690	248	268	294	587	380	531	647	479	0	0	0	0	0	39	74	576
TCGA-EJ-5519-10A-01D-1577-08_PRAD	599	262	279	0	593	138	533	652	472	81	648	575	304	137	0	93	580
TCGA-EJ-5521-10A-01D-1577-08_PRAD	683	252	266	298	596	383	537	655	462	76	611	577	0	135	0	76	578
TCGA-EJ-5522-10A-01D-1577-08_PRAD	753	256	269	300	613	293	530	660	464	74	652	576	376	139	0	80	580
TCGA-EJ-5524-10A-01D-1577-08_PRAD	692	0	0	312	618	406	536	655	497	0	0	0	0	0	0	167	577
TCGA-EJ-5525-10A-01D-1577-08_PRAD	756	254	271	301	623	292	535	662	484	0	620	571	0	0	50	2	579
TCGA-EJ-5526-10A-01D-1577-08_PRAD	685	0	0	303	614	393	532	667	459	80	620	0	367	140	0	82	576
TCGA-EJ-5527-10A-01D-1577-08_PRAD	685	256	267	301	619	389	531	659	0	88	659	580	373	142	0	4	579
TCGA-EJ-5530-10A-01D-1577-08_PRAD	680	0	0	303	602	392	530	652	403	0	0	0	0	0	0	105	578
TCGA-EJ-5531-10A-01D-1577-08_PRAD	756	245	259	290	607	374	534	654	484	0	609	512	0	0	0	124	579
TCGA-EJ-5532-10A-01D-1577-08_PRAD	596	255	268	0	0	0	530	639	469	0	635	0	302	135	0	64	577
TCGA-EJ-5542-10A-01D-1577-08_PRAD	689	57	0	309	627	395	534	662	488	0	0	0	0	0	39	76	579
TCGA-EJ-7115-10A-01D-2114-08_PRAD	684	0	0	297	600	381	526	638	480	0	0	0	0	0	0	122	575
TCGA-EJ-7123-10A-01D-1961-08_PRAD	691	0	0	305	580	290	524	656	491	0	0	0	0	0	0	126	578
TCGA-EJ-7125-10A-01D-1961-08_PRAD	686	0	0	313	616	392	531	645	478	0	0	0	0	0	0	114	577
TCGA-EJ-7218-10A-01D-A329-08_PRAD	674	246	257	280	565	361	532	636	484	0	0	0	0	0	0	104	581
TCGA-EJ-7312-10A-01D-A329-08_PRAD	676	238	247	260	603	357	530	618	472	0	574	556	0	0	0	58	569
TCGA-EJ-7314-10A-01D-2114-08_PRAD	594	257	274	0	0	0	532	642	400	0	0	0	0	0	0	82	572
TCGA-EJ-7315-10A-01D-2114-08_PRAD	684	243	266	283	611	365	532	649	0	88	653	575	360	140	0	1	577
TCGA-EJ-7317-10A-01D-2114-08_PRAD	685	0	0	305	601	381	531	643	469	0	0	0	0	0	0	107	578
TCGA-EJ-7318-10A-01D-A329-08_PRAD	682	224	252	275	532	348	528	618	467	0	0	0	0	0	0	75	574
TCGA-EJ-7321-10A-01D-2260-08_PRAD	684	242	251	280	606	383	535	646	386	0	592	0	294	0	0	60	570
TCGA-EJ-7325-10A-01D-A329-08_PRAD	672	253	265	288	593	373	532	657	477	0	0	0	0	0	0	99	576
TCGA-EJ-7327-10A-01D-2114-08_PRAD	680	0	0	200	588	287	530	647	469	0	0	0	0	0	33	62	575
TCGA-EJ-7328-10A-01D-2114-08_PRAD	685	0	0	298	577	378	529	651	446	75	524	0	360	130	0	56	573
TCGA-EJ-7330-10A-01D-2114-08_PRAD	591	255	273	0	590	136	530	654	458	74	645	570	56	134	31	6	574
TCGA-EJ-7331-10A-01D-2114-08_PRAD	674	246	260	186	617	379	532	661	484	0	597	569	0	0	28	72	577
TCGA-EJ-7781-10A-01D-2114-08_PRAD	595	261	278	0	559	135	531	650	462	68	638	564	366	134	31	4	577
TCGA-EJ-7782-10A-01D-2114-08_PRAD	681	249	258	295	609	286	532	643	474	0	568	560	0	0	36	0	573
TCGA-EJ-7783-10A-01D-2114-08_PRAD	683	246	238	277	413	0	528	640	475	0	0	0	0	0	0	93	577
TCGA-EJ-7784-10A-01D-2114-08_PRAD	690	0	0	299	597	386	529	646	470	0	0	0	0	0	0	92	576
TCGA-EJ-7785-10A-01D-2114-08_PRAD	679	0	0	292	608	379	530	644	308	64	576	0	296	131	0	52	575
TCGA-EJ-7786-10A-01D-2114-08_PRAD	678	0	0	305	595	286	522	651	385	75	606	0	275	138	0	57	574
TCGA-EJ-7788-10A-01D-2114-08_PRAD	673	243	246	284	609	361	535	649	374	74	622	576	0	132	32	0	577
TCGA-EJ-7789-10A-01D-2114-08_PRAD	687	240	255	289	557	323	532	653	476	0	0	0	0	0	34	62	572
TCGA-EJ-7791-10A-01D-2115-08_PRAD	754	0	0	306	600	285	524	654	479	0	0	0	0	0	0	151	576
TCGA-EJ-7792-10A-01D-2115-08_PRAD	684	0	0	302	611	287	521	653	455	70	605	0	366	133	37	0	578
TCGA-EJ-7793-10A-01D-2260-08_PRAD	756	0	0	304	607	383	530	650	373	77	617	0	364	135	0	69	578
TCGA-EJ-7794-10A-01D-2115-08_PRAD	660	242	236	281	485	264	515	616	308	0	526	0	287	129	0	60	576
TCGA-EJ-7797-10A-01D-2260-08_PRAD	670	244	254	277	600	375	534	649	389	75	605	567	0	136	0	57	572
TCGA-EJ-8468-10A-01D-2395-08_PRAD	679	249	264	291	614	377	532	650	385	69	638	574	0	136	0	64	577

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EJ-8469-10A-01D-2395-08_PRAD	687	0	0	302	604	376	530	655	479	0	0	0	0	0	0	128	577
TCGA-EJ-8470-10A-01D-2395-08_PRAD	760	0	0	316	639	397	531	655	468	77	624	0	376	138	37	1	576
TCGA-EJ-8472-10A-01D-2395-08_PRAD	688	0	0	298	599	383	532	646	473	0	0	0	0	0	33	65	571
TCGA-EJ-8474-10A-01D-2395-08_PRAD	691	0	0	307	600	388	532	645	459	74	609	0	297	135	30	0	574
TCGA-EJ-A46B-10A-01D-A25A-08_PRAD	670	244	255	283	600	279	534	648	466	0	578	511	0	0	26	63	572
TCGA-EJ-A46D-10A-01D-A25A-08_PRAD	682	0	0	308	612	380	532	656	477	0	0	0	0	0	32	67	575
TCGA-EJ-A46E-10A-01D-A25A-08_PRAD	682	241	260	277	607	377	533	652	466	0	534	567	0	0	27	68	576
TCGA-EJ-A46F-10A-01D-A25A-08_PRAD	682	246	262	284	564	369	534	649	478	0	0	0	0	0	0	95	575
TCGA-EJ-A46G-10A-01D-A26K-08_PRAD	599	228	244	250	494	342	520	622	390	0	0	0	0	0	32	2	574
TCGA-EJ-A46H-10A-01D-A26K-08_PRAD	682	0	0	302	589	387	524	626	462	0	0	0	0	0	25	41	578
TCGA-EJ-A46I-10A-01D-A26K-08_PRAD	649	0	0	275	547	367	514	629	375	0	0	0	0	0	0	84	567
TCGA-EJ-A65B-10A-01D-A30H-08_PRAD	770	0	0	324	626	398	536	665	495	0	0	0	0	0	44	101	580
TCGA-EJ-A65D-10A-01D-A30H-08_PRAD	762	258	276	189	595	290	538	654	495	0	0	0	0	0	0	167	581
TCGA-EJ-A65E-10A-01D-A29Q-08_PRAD	672	241	259	191	604	368	534	642	407	0	537	567	0	0	29	51	578
TCGA-EJ-A65F-10A-01D-A30X-08_PRAD	649	234	243	268	596	275	523	636	466	0	518	508	0	0	24	52	570
TCGA-EJ-A65G-10A-01D-A29Q-08_PRAD	745	253	267	294	590	283	531	645	480	0	0	0	0	0	0	109	577
TCGA-EJ-A65J-10A-01D-A30X-08_PRAD	681	0	0	299	577	365	523	641	421	64	578	0	367	134	24	0	575
TCGA-EJ-A65M-10A-01D-A29Q-08_PRAD	667	0	274	293	617	389	537	643	474	0	576	0	392	0	0	107	577
TCGA-EJ-A6RA-10A-01D-A33W-08_PRAD	682	0	0	296	580	383	530	641	367	72	592	0	292	133	0	53	572
TCGA-EJ-A6RC-10A-01D-A329-08_PRAD	595	244	275	0	534	133	533	629	468	0	596	504	0	0	0	98	572
TCGA-EJ-A7NF-10A-01D-A33W-08_PRAD	682	0	0	297	586	358	522	632	463	0	0	0	0	0	0	85	570
TCGA-EJ-A7NG-10A-01D-A33W-08_PRAD	684	238	252	269	604	373	528	638	378	71	622	570	0	136	0	56	573
TCGA-EJ-A7NH-10A-01D-A33W-08_PRAD	683	0	0	293	591	379	532	649	465	0	0	0	0	0	0	122	576
TCGA-EJ-A7NM-10A-01D-A33W-08_PRAD	660	224	249	258	499	271	529	629	380	70	528	0	286	133	25	0	571
TCGA-EJ-A7NN-10A-01D-A33W-08_PRAD	685	0	0	290	585	381	530	640	459	0	0	0	0	0	0	75	575
TCGA-EK-A2GZ-10A-01D-A17W-09_CESC	589	315	356	0	0	0	556	628	550	0	0	0	0	0	52	1	590
TCGA-EK-A2H0-10A-01D-A17W-09_CESC	699	0	0	382	692	465	552	662	560	0	0	0	0	0	39	78	593
TCGA-EK-A2H1-10A-01D-A17W-09_CESC	690	0	0	365	665	375	544	643	552	0	0	0	0	0	43	80	591
TCGA-EK-A2IP-10A-01D-A17W-09_CESC	698	0	0	364	682	459	550	643	557	0	0	0	0	0	0	101	587
TCGA-EK-A2PG-10A-01D-A18J-09_CESC	690	290	338	174	614	386	547	627	419	94	582	0	340	179	28	1	585
TCGA-EK-A2PI-10A-01D-A18J-09_CESC	587	321	356	0	0	0	552	646	548	0	0	0	0	0	43	57	586
TCGA-EK-A2PK-10A-01D-A18J-09_CESC	685	302	344	192	627	355	545	640	537	0	0	0	0	0	37	51	585
TCGA-EK-A2PL-10A-01D-A18J-09_CESC	582	309	357	0	602	167	541	617	539	0	464	516	0	0	31	47	582
TCGA-EK-A2PM-10A-01D-A18J-09_CESC	691	0	0	355	665	454	548	638	540	0	0	0	0	0	34	52	583
TCGA-EK-A2R7-10A-01D-A18J-09_CESC	694	0	0	357	638	454	550	631	325	0	502	0	333	168	39	1	577
TCGA-EK-A2R8-10A-01D-A18J-09_CESC	696	304	340	181	618	351	541	590	414	0	0	0	0	0	32	2	572
TCGA-EK-A2R9-10A-01D-A18J-09_CESC	590	318	351	0	601	172	546	628	420	94	632	536	359	177	30	0	589
TCGA-EK-A2RA-10A-01D-A18J-09_CESC	678	287	307	298	609	343	551	639	408	0	552	0	347	161	0	53	587
TCGA-EK-A2RB-10A-01D-A18J-09_CESC	694	288	321	325	672	365	549	642	432	92	622	544	352	176	0	57	589
TCGA-EK-A2RC-10A-01D-A18J-09_CESC	661	0	0	342	667	367	535	621	438	0	0	0	0	0	0	73	583
TCGA-EK-A2RD-10A-01D-A20U-09_CESC	687	0	0	365	649	451	550	619	546	0	0	0	0	0	0	80	584
TCGA-EK-A2RE-10A-01D-A18J-09_CESC	680	0	0	338	646	354	541	611	451	0	0	0	0	0	0	70	590
TCGA-EK-A2RJ-10A-01D-A18J-09_CESC	679	285	320	181	651	349	548	636	381	93	609	584	0	174	0	53	582
TCGA-EK-A2RK-10A-01D-A18J-09_CESC	667	0	0	340	672	370	535	617	456	0	0	0	0	0	0	40	586
TCGA-EK-A2RL-10A-01D-A18J-09_CESC	582	313	353	0	606	175	554	645	414	99	594	528	351	150	0	44	583
TCGA-EK-A2RN-10A-01D-A20U-09_CESC	684	0	0	355	668	458	551	634	545	0	0	0	0	0	30	51	589
TCGA-EK-A2RO-10A-01D-A18J-09_CESC	690	300	319	336	625	349	549	632	560	0	0	0	0	0	0	124	580
TCGA-EK-A3GK-10A-01D-A20U-09_CESC	685	277	314	232	566	433	553	637	400	97	545	0	349	173	36	1	590
TCGA-EK-A3GM-10A-01D-A20U-09_CESC	689	284	333	318	610	336	514	591	402	0	524	0	340	169	0	49	581
TCGA-EK-A3GN-10A-01D-A20U-09_CESC	695	271	311	299	651	451	552	609	308	92	603	513	338	168	0	44	579
TCGA-EL-A3CL-10A-01D-A19M-08_THCA	682	0	0	297	606	289	524	632	472	0	0	0	0	0	0	91	581
TCGA-EL-A3CM-10A-01D-A19M-08_THCA	680	0	0	299	598	367	527	627	469	0	0	0	0	0	0	74	575
TCGA-EL-A3CN-10A-01D-A20C-08_THCA	597	255	268	0	0	0	531	628	390	81	634	0	379	139	0	63	576
TCGA-EL-A3CO-10A-01D-A19M-08_THCA	752	245	263	299	613	380	538	644	473	0	608	569	0	0	0	139	577
TCGA-EL-A3CP-10A-01D-A19M-08_THCA	749	240	249	193	607	140	527	640	407	0	568	505	0	0	25	54	577
TCGA-EL-A3CR-10A-01D-A202-08_THCA	679	0	0	304	605	371	528	655	470	0	0	0	0	0	30	65	570
TCGA-EL-A3CS-10A-01D-A19M-08_THCA	758	0	0	300	606	381	533	633	480	0	0	0	0	0	0	91	578
TCGA-EL-A3CT-10A-01D-A202-08_THCA	687	0	0	302	599	385	529	646	459	70	611	0	292	134	0	62	576
TCGA-EL-A3CU-10A-01D-A19M-08_THCA	673	243	254	270	610	369	530	643	479	0	530	555	0	0	28	36	575
TCGA-EL-A3CV-10A-01D-A19M-08_THCA	678	242	262	286	508	377	525	643	407	0	0	0	0	0	35	5	578
TCGA-EL-A3CW-10A-01D-A19M-08_THCA	679	242	254	286	585	366	534	652	485	0	0	0	0	0	21	62	576
TCGA-EL-A3CX-10A-01D-A19M-08_THCA	688	0	0	297	599	384	531	639	462	0	0	0	0	0	26	48	574
TCGA-EL-A3CY-10A-01D-A19M-08_THCA	685	0	0	299	601	380	532	650	479	0	0	0	0	0	28	69	574
TCGA-EL-A3CZ-10A-01D-A19M-08_THCA	758	0	0	311	606	394	534	637	473	0	0	0	0	0	0	129	579
TCGA-EL-A3D0-10A-01D-A202-08_THCA	689	0	0	296	598	285	522	644	392	71	579	0	363	133	28	1	575
TCGA-EL-A3D1-10A-01D-A19M-08_THCA	736	243	261	278	591	368	513	615	43	74	619	0	383	140	0	3	576
TCGA-EL-A3D4-10A-01D-A19M-08_THCA	680	0	0	310	609	378	533	637	478	0	0	0	0	0	19	74	572
TCGA-EL-A3D5-10A-01D-A202-08_THCA	673	247	264	290	565	282	528	640	385	76	593	0	361	132	0	66	575
TCGA-EL-A3D6-10A-01D-A202-08_THCA	685	0	0	295	598	385	530	653	458	77	580	508	0	132	31	0	574
TCGA-EL-A3GO-10A-01D-A202-08_THCA	669	251	266	288	564	377	530	657	480	0	0	0	0	0	35	59	571
TCGA-EL-A3GP-10A-01D-A202-08_THCA	594	253	270	0	587	134	528	630	457	0	640	512	362	132	0	66	577
TCGA-EL-A3GQ-10A-01D-A202-08_THCA	681	242	255	282	561	369	533	649	475	0	0	0	0	0	27	57	576
TCGA-EL-A3GR-10A-01D-A202-08_THCA	682	253	266	287	583	373	535	656	485	0	0	0	0	0	33	74	574
TCGA-EL-A3GS-10A-01D-A20C-08_THCA	681	247	247	290	581	380	532	652	483	0	0	0	0	0	29	77	577
TCGA-EL-A3GV-10A-01D-A21A-08_THCA	684	0	0	298	573	386	531	639	368	71	586	0	287	131	0	56	575
TCGA-EL-A3GW-10A-01D-A202-08_THCA	597	256	262	0	572	133	531	648	373	77	608	0	358	133	0	61	571
TCGA-EL-A3GX-10A-01D-A202-08_THCA	757	248	267	299	584	381	533	654	379	75	592	0	296	136	0	63	574
TCGA-EL-A3GY-10A-01D-A202-08_THCA	686	0	0	305	605	381	530	646	391	74	578	0	296	136	0	71	575
TCGA-EL-A3H3-10A-01D-A202-08_THCA	682	251	258	280	581	373	530	639	475	0	0	0	0	0	0	113	573
TCGA-EL-A3H4-10A-01D-A202-08_THCA	683	0	0	200	599	317	534	651	488	0	618	0	384	0	30	64	577
TCGA-EL-A3H5-10A-01D-A202-08_THCA	599	259	270	0	597	136	530	654	455	76	650	566	296	135	29	1	572
TCGA-EL-A3H8-10A-01D-A20C-08_THCA	681	0	0	347	605	379	530	645	0	82	628	0	376	140	0	2	575
TCGA-EL-A4KG-10A-01D-A25A-08_THCA	627	226	251	186	545	338	521	618	457	0	0	0	0	0	20	48	571
TCGA-EL-A4KH-10A-01D-A25A-08_THCA	681	0	0	297	558	360	523	623	394	0	0	0	0	0	0	102	570
TCGA-EL-A4KI-10A-01D-A25A-08_THCA	676	0	0	289	566	370	525	622	358	55	512	0	284	134	0	53	575
TCGA-EM-A1CS-10A-01D-A13W-08_THCA	766	249	273	296	570	288	536	662	497	0	0	0	0	0	43	89	580
TCGA-EM-A1CT-10A-01D-A13W-08_THCA	764	0	0	317	622	298	527	662	473	78	623	0	385	140	46	0	580
TCGA-EM-A1CU-10A-02D-A13W-08_THCA	756	254	270	302	614	392	538	657	493	0	611	569	0	0	46	94	580
TCGA-EM-A1CV-10A-01D-A13W-08_THCA	672	267	280	0	581	138	529	651	474	77	632	582	0	141	32	1	578
TCGA-EM-A1CW-10A-01D-A13W-08_THCA	760	254	268	304	615	394	537	667	498	0	0	0	0	0	0	139	582
TCGA-EM-A1YA-10A-01D-A14W-08_THCA	687	0	0	292	597	367	531	635	385	68	580	0	295	138	25	1	571
TCGA-EM-A1YB-10A-01D-A14W-08_THCA	681	0	0	285	592	288	517	638	403	0	0	0	0	0	0	96	575
TCGA-EM-A22I-10A-01D-A17V-08_THCA	679	250	266	291	588	287	530	647	467	75	620	0	370	136	33	1	575
TCGA-EM-A22J-10A-01D-A17V-08_THCA	685	0	273	285	610	381	532	654	478	0	615	0	383	0	27	65	577
TCGA-EM-A22K-10A-01D-A17V-08_THCA	756	0	0	296	602	380	529	622	471	0	0	0	0	0	30	58	577
TCGA-EM-A22L-10A-01D-A17V-08_THCA	663	244	259	284	551	359	530	642	470	0	0	0	0	0	27	63	575

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EM-A22M-10A-01D-A17V-08_THCA	687	242	266	273	602	375	532	636	378	66	617	563	365	134	0	57	576
TCGA-EM-A22N-10A-01D-A17V-08_THCA	685	0	0	300	601	376	530	642	471	0	0	0	0	0	27	61	576
TCGA-EM-A22O-10A-01D-A17V-08_THCA	690	0	0	310	612	399	534	651	463	80	613	0	371	140	34	0	574
TCGA-EM-A22P-10A-01D-A19M-08_THCA	682	0	0	310	610	385	528	652	478	0	0	0	0	0	24	69	576
TCGA-EM-A22Q-10A-01D-A17V-08_THCA	680	254	264	293	611	376	530	641	0	83	650	505	383	139	0	0	574
TCGA-EM-A2CJ-10A-01D-A17V-08_THCA	597	253	278	0	562	135	525	610	385	0	636	568	0	136	29	0	575
TCGA-EM-A2CK-10A-01D-A17V-08_THCA	673	244	253	282	583	275	528	633	469	0	582	566	0	0	38	0	578
TCGA-EM-A2CL-10A-01D-A17V-08_THCA	599	260	278	0	0	0	533	641	467	79	627	0	372	135	0	68	577
TCGA-EM-A2CM-10A-01D-A17V-08_THCA	689	0	0	305	597	383	529	643	470	0	0	0	0	0	35	65	573
TCGA-EM-A2CN-10B-01D-A19M-08_THCA	686	0	0	307	607	386	531	652	481	0	0	0	0	0	0	102	576
TCGA-EM-A2CO-10A-01D-A19M-08_THCA	683	0	0	302	608	290	520	628	482	0	0	0	0	0	0	100	581
TCGA-EM-A2CP-10A-01D-A17V-08_THCA	678	0	0	295	594	378	531	625	389	0	0	0	0	0	20	62	575
TCGA-EM-A2CQ-10A-01D-A17V-08_THCA	686	0	0	302	601	386	534	639	476	0	0	0	0	0	32	61	581
TCGA-EM-A2CR-10A-01D-A17V-08_THCA	654	241	256	273	601	365	529	636	385	60	626	570	0	130	24	0	574
TCGA-EM-A2CS-10A-01D-A19M-08_THCA	671	235	248	272	547	360	529	644	465	0	0	0	0	0	29	57	572
TCGA-EM-A2CT-10A-01D-A17V-08_THCA	656	244	261	269	570	371	533	643	469	0	0	0	0	0	35	49	575
TCGA-EM-A2CU-10A-01D-A17V-08_THCA	636	252	257	284	504	284	528	642	467	0	0	0	0	0	0	85	578
TCGA-EM-A2OV-10A-01D-A202-08_THCA	688	0	0	306	596	388	530	644	473	0	0	0	0	0	43	2	573
TCGA-EM-A2OW-10A-01D-A202-08_THCA	687	0	0	311	610	383	531	647	470	0	0	0	0	0	0	95	574
TCGA-EM-A2OX-10A-01D-A202-08_THCA	593	257	273	0	0	0	533	654	478	0	0	0	0	0	26	63	575
TCGA-EM-A2OY-10A-01D-A202-08_THCA	745	0	0	304	607	286	521	638	456	78	618	0	365	136	0	53	577
TCGA-EM-A2OZ-10A-01D-A202-08_THCA	687	0	0	303	603	389	531	648	471	0	0	0	0	0	33	61	575
TCGA-EM-A2P0-10A-01D-A202-08_THCA	685	0	0	304	611	382	532	641	459	75	592	0	296	136	0	68	573
TCGA-EM-A2P1-10A-01D-A202-08_THCA	677	249	265	277	582	371	531	649	450	72	603	0	286	137	0	60	579
TCGA-EM-A2P2-10A-01D-A202-08_THCA	690	0	0	306	611	386	533	641	467	0	0	0	0	0	0	90	577
TCGA-EM-A2P3-10A-01D-A202-08_THCA	688	0	0	300	598	388	532	653	471	0	0	0	0	0	33	73	578
TCGA-EM-A3AI-10A-01D-A202-08_THCA	679	248	264	185	613	281	532	657	488	0	610	563	0	0	30	69	573
TCGA-EM-A3AJ-10A-01D-A202-08_THCA	672	238	258	287	588	281	532	643	477	0	0	0	0	0	0	122	577
TCGA-EM-A3AK-10A-01D-A202-08_THCA	680	250	264	288	577	371	529	638	404	0	0	0	0	0	0	90	574
TCGA-EM-A3AL-10A-01D-A202-08_THCA	681	245	256	284	588	363	531	649	471	0	0	0	0	0	0	80	578
TCGA-EM-A3AN-10A-01D-A202-08_THCA	687	0	0	306	609	389	526	644	476	0	0	0	0	0	0	90	575
TCGA-EM-A3AO-10A-01D-A202-08_THCA	688	0	0	305	600	380	533	650	471	0	0	0	0	0	31	70	575
TCGA-EM-A3AP-10A-01D-A20C-08_THCA	670	0	0	281	581	278	513	635	388	0	0	0	0	0	21	40	576
TCGA-EM-A3AQ-10A-01D-A20C-08_THCA	687	0	0	305	609	394	529	659	465	77	617	0	368	133	35	3	573
TCGA-EM-A3AR-10A-01D-A20C-08_THCA	686	0	0	307	614	392	535	652	484	0	0	0	0	0	0	153	574
TCGA-EM-A3FJ-10A-01D-A21A-08_THCA	666	243	239	286	572	360	531	644	398	0	0	0	0	0	29	60	578
TCGA-EM-A3FK-10A-01D-A21A-08_THCA	672	242	243	261	559	367	533	633	465	0	0	0	0	0	0	91	578
TCGA-EM-A3FL-10A-01D-A21A-08_THCA	648	245	259	267	567	269	530	648	445	74	522	0	288	137	31	1	577
TCGA-EM-A3FM-10A-01D-A21A-08_THCA	677	0	0	270	605	283	530	651	375	53	587	0	272	128	29	0	574
TCGA-EM-A3FN-10A-01D-A21A-08_THCA	666	246	249	281	598	379	534	655	459	80	649	514	380	132	0	77	574
TCGA-EM-A3FO-10A-01D-A21A-08_THCA	673	245	245	280	509	367	533	649	471	0	0	0	0	0	28	70	575
TCGA-EM-A3FP-10A-01D-A21A-08_THCA	682	0	0	298	591	387	536	647	385	67	573	0	365	131	32	0	576
TCGA-EM-A3FQ-10A-01D-A21A-08_THCA	742	246	261	277	549	276	528	651	482	0	0	0	0	0	35	68	578
TCGA-EM-A3FR-10A-01D-A21Z-08_THCA	671	246	257	289	585	370	533	644	474	0	0	0	0	0	35	1	576
TCGA-EM-A3O3-10A-01D-A21Z-08_THCA	682	249	264	281	575	270	529	652	391	81	618	564	0	135	32	1	574
TCGA-EM-A3O6-10A-01D-A21Z-08_THCA	686	0	0	304	600	290	522	643	388	83	607	0	364	136	0	53	576
TCGA-EM-A3O7-10A-01D-A21Z-08_THCA	599	260	268	0	590	136	532	639	472	0	621	572	0	0	36	0	578
TCGA-EM-A3O8-10A-01D-A21Z-08_THCA	593	260	271	0	586	137	534	649	465	79	644	563	369	135	35	0	574
TCGA-EM-A3O9-10A-01D-A21Z-08_THCA	594	256	272	0	595	137	532	657	386	79	644	577	0	133	0	71	575
TCGA-EM-A3OA-10A-01D-A21Z-08_THCA	675	245	264	293	506	371	531	641	470	0	0	0	0	0	35	0	574
TCGA-EM-A3OB-10A-01D-A21Z-08_THCA	597	263	273	0	602	136	534	652	481	0	633	571	0	0	32	73	575
TCGA-EM-A3SU-10A-01D-A22Z-08_THCA	595	244	264	0	454	129	530	614	0	78	627	506	365	136	0	0	571
TCGA-EM-A3SX-10A-01D-A22Z-08_THCA	594	245	260	0	0	0	527	624	395	0	0	0	0	0	21	40	574
TCGA-EM-A3SY-10A-01D-A22Z-08_THCA	678	0	0	287	548	371	524	608	382	0	0	0	0	0	0	55	554
TCGA-EM-A3SZ-10A-01D-A22Z-08_THCA	746	0	0	292	584	362	526	630	459	0	0	0	0	0	0	75	573
TCGA-EM-A4FF-10A-01D-A25A-08_THCA	688	0	0	318	607	299	528	649	481	0	0	0	0	0	51	0	581
TCGA-EM-A4FH-10A-01D-A25A-08_THCA	655	237	249	263	568	360	527	631	384	0	0	0	0	0	30	50	571
TCGA-EM-A4FK-10A-01D-A25A-08_THCA	587	247	264	0	0	0	511	607	374	0	0	0	0	0	25	36	570
TCGA-EM-A4FM-10A-01D-A25A-08_THCA	591	248	263	0	461	125	506	561	0	55	619	493	297	136	0	0	569
TCGA-EM-A4FN-10A-01D-A25A-08_THCA	592	248	270	0	542	133	525	626	373	60	606	511	0	133	0	58	568
TCGA-EM-A4FO-10A-01D-A25A-08_THCA	667	0	0	279	578	273	516	623	379	54	521	0	280	130	20	4	566
TCGA-EM-A4FQ-10A-01D-A25A-08_THCA	680	235	246	265	598	365	524	634	399	0	570	554	0	0	0	106	572
TCGA-EM-A4FR-10A-01D-A25A-08_THCA	681	0	0	292	560	370	529	646	455	57	0	0	0	0	25	61	569
TCGA-EM-A4FU-10A-01D-A25A-08_THCA	665	0	0	288	595	374	523	639	471	0	0	0	0	0	30	55	574
TCGA-EM-A4FV-10A-01D-A25A-08_THCA	651	223	243	244	564	368	516	633	358	0	569	491	265	128	15	6	572
TCGA-EM-A4G1-10A-01D-A25A-08_THCA	658	229	243	257	570	360	516	614	381	0	499	535	0	0	0	94	573
TCGA-EO-A1Y5-10A-01D-A159-09_UCEC	660	0	0	372	683	451	557	645	440	99	616	0	357	168	0	46	590
TCGA-EO-A1Y7-10A-01D-A159-09_UCEC	693	0	0	365	681	463	551	527	356	0	0	0	0	0	0	90	587
TCGA-EO-A1Y8-10A-01D-A159-09_UCEC	662	0	0	386	710	461	553	659	474	0	0	0	0	0	0	109	590
TCGA-EO-A22U-10B-01D-A17W-09_UCEC	676	282	298	217	491	418	545	612	451	0	0	0	0	0	33	40	579
TCGA-EO-A22X-10A-01D-A17W-09_UCEC	694	303	334	331	600	433	552	627	440	0	0	0	0	0	0	89	591
TCGA-EO-A22Y-10A-01D-A17W-09_UCEC	696	302	340	313	637	358	545	626	438	0	0	0	0	0	0	100	584
TCGA-EO-A2CG-10A-01D-A17W-09_UCEC	694	310	346	337	678	444	555	639	0	96	654	532	454	181	0	1	581
TCGA-EO-A2CH-10A-01D-A17W-09_UCEC	677	289	292	306	593	428	544	628	446	0	0	0	0	0	0	79	576
TCGA-EO-A3AS-10A-01D-A19Y-09_UCEC	586	323	361	0	659	181	547	642	341	95	637	587	357	180	40	3	583
TCGA-EO-A3AU-10A-01D-A19Y-09_UCEC	695	0	0	346	647	462	541	608	332	0	0	0	0	0	0	65	580
TCGA-EO-A3AV-10A-01D-A19Y-09_UCEC	696	0	0	367	678	452	552	641	552	0	0	0	0	0	27	69	591
TCGA-EO-A3AY-10A-01D-A19Y-09_UCEC	678	281	316	339	626	439	556	633	466	0	0	0	0	0	0	76	584
TCGA-EO-A3AZ-10A-01D-A19Y-09_UCEC	575	322	356	0	0	0	545	641	547	0	0	0	0	0	21	39	579
TCGA-EO-A3B0-10A-01D-A19Y-09_UCEC	588	283	333	310	680	447	540	633	536	0	561	520	0	0	36	47	584
TCGA-EO-A3B1-10A-01D-A19Y-09_UCEC	700	292	343	326	637	436	549	637	331	93	594	0	358	166	0	54	584
TCGA-EO-A3KU-10A-01D-A22A-09_UCEC	668	0	0	352	659	450	546	644	537	0	0	0	0	0	23	47	583
TCGA-EO-A3KW-10A-01D-A22A-09_UCEC	668	296	306	332	680	452	553	663	535	92	561	513	0	0	35	51	581
TCGA-EO-A3KX-10A-01D-A22A-09_UCEC	671	0	0	345	642	450	544	585	311	89	516	0	335	166	0	38	573
TCGA-EO-A3L0-10A-01D-A22A-09_UCEC	677	290	328	311	502	430	510	498	312	0	574	0	353	168	0	61	587
TCGA-EP-A12J-10A-01D-A12Z-10_LIHC	627	134	218	295	581	283	505	526	323	0	258	367	0	0	7	9	547
TCGA-EP-A26S-10A-01D-A16V-10_LIHC	760	0	0	318	638	366	492	556	362	99	309	0	252	152	0	30	539
TCGA-EP-A2KA-10A-01D-A183-10_LIHC	795	242	314	226	548	355	538	607	367	0	0	0	0	0	12	48	590
TCGA-EP-A2KB-10A-01D-A183-10_LIHC	677	264	293	353	593	363	527	627	455	0	0	0	0	0	0	98	576
TCGA-EP-A2KC-10A-01D-A20W-10_LIHC	581	281	353	0	667	189	544	618	321	0	480	510	361	0	28	39	578
TCGA-EP-A3JL-10A-01D-A20W-10_LIHC	697	0	0	368	646	447	530	616	359	0	0	0	0	0	27	37	585
TCGA-EP-A3RK-10A-01D-A22F-10_LIHC	624	145	213	224	301	273	495	471	335	0	0	0	0	0	0	52	554
TCGA-EQ-5647-10A-01D-1600-08_STAD	757	0	0	304	615	291	530	659	483	0	0	0	0	0	0	99	580
TCGA-EQ-8122-10A-01D-2341-08_STAD	690	0	0	309	619	389	533	656	484	0	0	0	0	0	0	152	580
TCGA-EQ-A4SO-10A-01D-A25E-08_STAD	682	0	0	295	599	381	533	638	367	70	570	0	292	131	34	0	572
TCGA-ER-A193-10A-01D-A199-08_SKCM	673	244	259	281	604	370	534	648	487	0	517	561	0	0	0	104	579

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-ER-A194-10A-01D-A199-08_SKCM	685	0	0	300	605	376	523	638	471	0	0	0	0	0	30	60	577
TCGA-ER-A195-10A-01D-A198-08_SKCM	682	240	252	280	562	366	531	647	385	64	567	0	294	138	0	60	577
TCGA-ER-A196-10A-01D-A199-08_SKCM	673	243	270	286	589	278	529	639	478	0	0	0	0	0	27	72	576
TCGA-ER-A197-10A-01D-A199-08_SKCM	675	249	261	281	587	372	528	647	382	62	624	562	295	134	22	0	574
TCGA-ER-A198-10A-01D-A198-08_SKCM	679	0	0	293	563	385	529	632	374	69	551	0	287	133	16	0	576
TCGA-ER-A199-10A-01D-A199-08_SKCM	644	224	227	249	497	257	524	615	394	0	0	0	0	0	0	74	580
TCGA-ER-A19A-10A-01D-A199-08_SKCM	677	0	0	300	595	369	533	628	465	0	0	0	0	0	0	76	575
TCGA-ER-A19B-10A-01D-A198-08_SKCM	635	241	236	251	484	342	526	630	463	0	0	0	0	0	17	40	576
TCGA-ER-A19C-10A-01D-A198-08_SKCM	669	213	230	250	569	329	529	626	375	58	614	566	0	133	0	35	575
TCGA-ER-A19D-10A-01D-A199-08_SKCM	593	228	255	264	600	362	524	635	367	58	608	552	287	134	0	52	574
TCGA-ER-A19E-10A-01D-A199-08_SKCM	684	0	0	288	602	381	529	638	466	0	0	0	0	0	0	97	573
TCGA-ER-A19F-10A-01D-A198-08_SKCM	677	0	0	298	593	377	527	633	476	0	0	0	0	0	0	98	575
TCGA-ER-A19G-10A-01D-A198-08_SKCM	652	240	234	258	612	368	529	644	0	81	644	572	283	140	0	1	573
TCGA-ER-A19H-10A-01D-A198-08_SKCM	597	235	241	263	597	262	519	639	463	0	510	566	0	0	0	66	579
TCGA-ER-A19J-10A-01D-A198-08_SKCM	594	259	275	0	528	129	534	635	486	0	588	514	0	0	26	57	578
TCGA-ER-A19K-10A-01D-A199-08_SKCM	597	252	267	0	0	0	529	635	460	66	516	0	294	133	0	67	577
TCGA-ER-A19L-10A-01D-A199-08_SKCM	668	0	0	276	563	367	527	622	306	0	492	0	280	132	0	41	575
TCGA-ER-A19M-10A-01D-A23B-08_SKCM	758	245	266	294	609	382	534	656	387	77	641	565	360	136	32	4	578
TCGA-ER-A19N-10A-01D-A199-08_SKCM	671	0	0	294	595	369	531	640	377	0	504	0	271	132	0	43	579
TCGA-ER-A19O-10A-01D-A199-08_SKCM	591	257	257	0	0	0	532	618	470	0	0	0	0	0	12	41	577
TCGA-ER-A19P-10A-01D-A198-08_SKCM	685	0	0	305	603	377	531	635	386	66	569	0	285	135	18	0	575
TCGA-ER-A19Q-10A-01D-A199-08_SKCM	593	257	276	0	511	135	533	642	469	0	531	511	0	0	36	76	577
TCGA-ER-A19S-10A-01D-A198-08_SKCM	681	243	262	174	608	282	532	638	475	0	577	563	0	0	0	128	576
TCGA-ER-A19T-10A-01D-A19A-08_SKCM	644	245	235	263	576	349	529	641	398	0	566	492	0	0	0	80	579
TCGA-ER-A19W-10A-01D-A23B-08_SKCM	756	254	266	282	613	276	533	649	480	0	609	563	0	0	28	75	576
TCGA-ER-A1A1-10A-01D-A199-08_SKCM	682	234	257	269	556	349	530	643	478	0	0	0	0	0	36	62	578
TCGA-ER-A2NB-10A-01D-A198-08_SKCM	590	223	247	238	527	272	520	627	366	59	605	516	0	129	0	49	574
TCGA-ER-A2NC-10A-01D-A199-08_SKCM	680	243	257	282	609	379	529	645	378	65	619	570	0	135	0	62	575
TCGA-ER-A2ND-10A-01D-A198-08_SKCM	641	248	262	283	602	275	531	633	481	0	568	505	0	0	0	124	579
TCGA-ER-A2NE-10A-01D-A198-08_SKCM	673	239	255	270	602	366	530	636	481	0	551	557	0	0	0	85	578
TCGA-ER-A2NF-10A-01D-A19A-08_SKCM	673	0	0	296	605	289	522	642	443	70	576	0	297	137	30	2	575
TCGA-ER-A2NG-10A-01D-A198-08_SKCM	594	248	267	0	487	118	528	642	450	0	531	498	0	0	20	52	573
TCGA-ER-A2NH-10A-01D-A198-08_SKCM	668	241	258	278	510	277	530	642	473	0	0	0	0	0	0	81	580
TCGA-ER-A3ES-10A-01D-A20D-08_SKCM	687	0	0	303	600	381	533	640	473	0	0	0	0	0	39	1	579
TCGA-ER-A3ET-10A-01D-A20D-08_SKCM	664	248	254	282	607	282	528	637	475	0	609	508	0	0	28	54	576
TCGA-ER-A3EV-10A-01D-A20D-08_SKCM	688	0	0	301	601	386	529	639	474	0	0	0	0	0	0	85	575
TCGA-ER-A3PL-10A-01D-A23B-08_SKCM	686	0	0	311	618	390	531	649	394	80	592	0	374	138	0	67	578
TCGA-ER-A42H-10A-01D-A24R-08_SKCM	687	0	0	298	604	389	531	643	473	0	0	0	0	0	0	123	576
TCGA-ER-A42K-10A-01D-A24R-08_SKCM	680	0	0	296	609	375	523	642	445	72	607	0	354	137	0	66	574
TCGA-ER-A42L-10A-01D-A24R-08_SKCM	683	0	0	296	603	374	525	635	462	0	0	0	0	0	0	73	572
TCGA-ET-A25G-10A-01D-A16O-08_THCA	689	257	258	291	588	381	532	639	484	0	0	0	0	0	0	136	580
TCGA-ET-A25I-10A-01D-A16O-08_THCA	680	244	266	292	590	375	535	661	485	68	0	0	0	0	0	102	577
TCGA-ET-A25K-10A-01D-A16O-08_THCA	684	253	269	289	566	283	521	629	0	76	642	519	365	141	0	0	580
TCGA-ET-A25O-10A-01D-A17V-08_THCA	680	0	0	298	616	384	533	658	464	70	581	563	0	0	30	56	579
TCGA-ET-A25R-10A-01D-A16O-08_THCA	685	0	0	297	599	287	522	641	474	0	0	0	0	0	0	123	579
TCGA-ET-A2MZ-10A-01D-A19M-08_THCA	746	242	266	283	591	286	530	648	486	0	0	0	0	0	26	76	574
TCGA-ET-A2N0-10A-01D-A18F-08_THCA	761	0	0	296	598	380	530	647	367	73	524	0	356	133	0	55	578
TCGA-ET-A2N1-10A-01D-A18F-08_THCA	680	238	252	271	588	368	530	625	467	0	554	508	0	0	0	84	574
TCGA-ET-A2N3-10A-01D-A23K-08_THCA	759	0	0	310	613	292	525	652	393	70	604	0	366	137	0	73	581
TCGA-ET-A2N4-10A-01D-A19M-08_THCA	683	246	265	282	613	370	527	645	486	0	591	509	0	0	0	111	578
TCGA-ET-A39I-10A-01D-A19M-08_THCA	672	248	257	285	581	258	528	634	484	0	0	0	0	0	0	109	574
TCGA-ET-A39J-10A-01D-A19M-08_THCA	658	244	251	281	572	356	520	640	475	0	0	0	0	0	27	2	577
TCGA-ET-A39K-10A-01D-A19M-08_THCA	686	0	0	304	601	391	530	649	389	79	589	0	298	135	0	55	577
TCGA-ET-A39L-10A-01D-A19M-08_THCA	760	0	0	300	617	391	533	639	482	0	0	0	0	0	0	96	579
TCGA-ET-A39M-10A-01D-A19M-08_THCA	737	134	258	276	602	277	528	636	373	74	631	511	358	129	0	61	573
TCGA-ET-A39N-10A-01D-A19M-08_THCA	737	240	252	287	523	281	525	645	417	0	0	0	0	0	25	51	575
TCGA-ET-A39O-10A-01D-A19M-08_THCA	687	0	0	303	620	395	537	650	482	0	0	0	0	0	22	52	579
TCGA-ET-A39P-10A-01D-A19M-08_THCA	754	243	260	188	605	275	532	642	482	0	590	510	0	0	21	57	577
TCGA-ET-A39R-10A-01D-A19M-08_THCA	686	246	269	294	595	285	534	654	391	76	628	0	374	135	0	76	578
TCGA-ET-A39S-10A-01D-A19M-08_THCA	744	0	0	306	607	289	525	645	481	0	0	0	0	0	29	50	580
TCGA-ET-A39T-10A-01D-A19M-08_THCA	676	233	251	272	564	348	532	638	402	0	0	0	0	0	0	95	577
TCGA-ET-A3BN-10A-01D-A19M-08_THCA	753	0	0	307	602	393	534	649	394	81	602	0	368	138	0	47	581
TCGA-ET-A3BO-10A-01D-A19M-08_THCA	675	254	268	283	556	282	530	647	489	0	0	0	0	0	35	69	581
TCGA-ET-A3BP-10A-01D-A19M-08_THCA	688	0	0	295	608	290	526	652	458	74	582	0	365	135	0	56	578
TCGA-ET-A3BQ-10A-01D-A202-08_THCA	688	0	0	303	604	391	529	656	479	0	0	0	0	0	0	81	577
TCGA-ET-A3BS-10A-01D-A202-08_THCA	679	241	262	284	590	379	534	647	441	75	601	0	365	130	0	74	572
TCGA-ET-A3BT-10A-01D-A19M-08_THCA	687	0	0	304	603	390	529	651	478	0	0	0	0	0	27	56	576
TCGA-ET-A3BU-10A-01D-A19M-08_THCA	672	247	263	281	579	365	533	650	390	80	590	565	0	131	0	73	577
TCGA-ET-A3BV-10A-01D-A19M-08_THCA	688	0	0	308	609	392	531	649	410	0	0	0	0	0	0	123	576
TCGA-ET-A3BW-10A-01D-A19M-08_THCA	687	0	0	306	610	394	534	646	480	0	0	0	0	0	0	96	578
TCGA-ET-A3BX-10A-01D-A19M-08_THCA	686	0	0	306	613	291	523	643	468	0	0	0	0	0	0	93	574
TCGA-ET-A3DO-10A-01D-A19M-08_THCA	735	237	261	281	545	365	533	650	394	71	604	0	363	136	21	0	572
TCGA-ET-A3DQ-10A-01D-A19M-08_THCA	688	0	0	300	618	385	529	638	482	0	0	0	0	0	0	113	576
TCGA-ET-A3DR-10A-01D-A19M-08_THCA	765	0	0	309	620	394	534	663	491	0	0	0	0	0	0	118	580
TCGA-ET-A3DS-10A-01D-A19M-08_THCA	596	259	275	0	565	134	532	638	479	0	609	510	0	0	40	3	576
TCGA-ET-A3DT-10A-01D-A19M-08_THCA	596	252	270	0	0	0	534	644	448	73	584	0	291	136	24	0	575
TCGA-ET-A3DU-10A-01D-A19M-08_THCA	595	256	280	0	119	0	534	651	484	0	0	0	0	0	54	1	578
TCGA-ET-A40P-10A-01D-A23K-08_THCA	689	0	0	297	608	396	533	656	460	78	615	0	300	139	0	77	578
TCGA-ET-A40Q-10A-01D-A23K-08_THCA	766	0	0	323	646	409	540	659	495	0	0	0	0	0	46	97	582
TCGA-ET-A40R-10A-01D-A23K-08_THCA	691	257	276	306	625	388	533	662	498	0	643	575	0	0	0	174	581
TCGA-ET-A40S-10A-01D-A23K-08_THCA	678	250	261	292	597	284	528	652	477	0	0	0	0	0	31	72	577
TCGA-ET-A40T-10A-01D-A23K-08_THCA	689	0	0	309	613	387	531	657	487	0	53	90	24	40	31	85	576
TCGA-ET-A4KN-10A-01D-A25A-08_THCA	670	0	0	281	583	366	523	624	299	61	516	0	289	132	0	45	573
TCGA-ET-A4KQ-10A-01D-A25A-08_THCA	656	0	0	285	565	283	514	614	446	0	0	0	0	0	0	94	568
TCGA-EU-5904-10A-01D-1669-08_KIRC	684	247	263	299	596	360	534	658	481	0	0	0	0	0	32	67	577
TCGA-EU-5905-10A-01D-1669-08_KIRC	686	0	0	307	620	384	532	645	474	0	0	0	0	0	0	77	576
TCGA-EU-5906-10A-01D-1669-08_KIRC	761	0	0	307	606	390	533	651	481	0	0	0	0	0	34	78	575
TCGA-EU-5907-10A-01D-1669-08_KIRC	675	244	266	288	617	283	532	646	458	81	640	567	300	138	24	3	577
TCGA-EV-5901-10A-01D-1589-08_KIRP	683	0	0	304	600	387	534	649	482	0	0	0	0	0	33	69	578
TCGA-EV-5902-10A-01D-1589-08_KIRP	754	0	0	302	613	287	530	650	475	0	0	0	0	0	0	113	574
TCGA-EV-5903-10A-01D-1589-08_KIRP	682	0	0	306	607	385	525	652	477	0	0	0	0	0	0	92	573
TCGA-EW-A1IW-10A-01D-A13O-09_BRCA	666	0	0	361	676	370	535	621	453	0	0	0	0	0	19	41	567
TCGA-EW-A1IX-10A-01D-A142-09_BRCA	682	0	0	376	695	466	553	653	469	0	0	0	0	0	28	65	580
TCGA-EW-A1IY-10A-01D-A13O-09_BRCA	683	0	0	376	679	459	556	648	431	99	626	0	345	173	31	0	589
TCGA-EW-A1IZ-10A-01D-A13O-09_BRCA	661	297	321	347	632	362	541	652	447	0	0	0	0	0	28	40	585
TCGA-EW-A1J1-10A-01D-A13O-09_BRCA	693	301	343	354	695	460	554	641	467	0	618	543	0	0	29	55	585

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EW-A1J3-10A-01D-A13O-09_BRCA	595	321	365	0	677	180	557	659	478	0	623	554	0	0	37	80	597
TCGA-EW-A1J5-10A-01D-A13O-09_BRCA	695	298	339	343	658	435	553	652	553	0	0	0	0	0	0	72	592
TCGA-EW-A1J6-10A-01D-A13O-09_BRCA	682	0	0	377	698	465	560	660	572	0	0	0	0	0	40	60	594
TCGA-EW-A1OV-10A-01D-A142-09_BRCA	645	254	292	313	654	345	528	625	425	0	553	497	0	0	0	68	564
TCGA-EW-A1OX-10A-01D-A142-09_BRCA	659	0	0	355	671	440	536	634	453	0	0	0	0	0	0	66	571
TCGA-EW-A1OZ-10A-01D-A142-09_BRCA	638	0	332	337	661	430	545	632	432	0	572	0	368	0	24	30	565
TCGA-EW-A1P0-10A-01D-A142-09_BRCA	692	0	0	373	711	458	560	662	487	0	0	0	0	0	18	40	586
TCGA-EW-A1P1-10A-01D-A14G-09_BRCA	659	274	320	337	677	433	554	659	453	0	564	516	0	0	23	31	573
TCGA-EW-A1P3-10A-01D-A142-09_BRCA	663	0	0	340	687	430	542	641	320	93	608	0	353	172	0	35	564
TCGA-EW-A1P4-10A-01D-A142-09_BRCA	572	316	360	0	652	173	546	636	462	0	609	529	0	0	0	99	587
TCGA-EW-A1P5-10A-01D-A142-09_BRCA	683	284	336	349	622	438	552	620	425	96	575	523	0	164	0	51	574
TCGA-EW-A1P6-10A-01D-A142-09_BRCA	665	275	334	327	647	407	552	639	420	96	594	0	340	160	0	40	561
TCGA-EW-A1P7-10A-01D-A142-09_BRCA	619	265	309	322	523	422	546	629	454	0	0	0	0	0	30	0	563
TCGA-EW-A1P8-10A-01D-A142-09_BRCA	689	316	360	362	680	458	556	653	473	0	0	0	0	0	0	100	587
TCGA-EW-A1PA-10A-01D-A142-09_BRCA	661	0	0	352	650	438	533	610	392	94	520	497	0	155	0	36	560
TCGA-EW-A1PB-10A-01D-A142-09_BRCA	670	0	0	337	667	446	558	638	452	0	0	0	0	0	25	36	585
TCGA-EW-A1PC-10A-01D-A21Q-09_BRCA	663	293	148	309	584	406	502	462	389	0	552	0	351	165	0	35	577
TCGA-EW-A1PD-10A-01D-A142-09_BRCA	534	304	349	0	658	175	551	634	443	97	618	535	0	0	0	83	566
TCGA-EW-A1PE-10A-01D-A142-09_BRCA	670	0	0	362	689	449	542	643	453	0	0	0	0	0	21	43	585
TCGA-EW-A1PG-10A-01D-A142-09_BRCA	666	0	0	365	682	451	543	644	421	97	581	0	333	164	0	35	558
TCGA-EW-A1PH-10A-01D-A14K-09_BRCA	672	304	368	369	713	383	550	645	472	0	638	521	0	0	0	106	586
TCGA-EW-A2FR-10A-01D-A21Q-09_BRCA	689	0	0	361	672	467	552	634	458	0	0	0	0	0	53	6	585
TCGA-EW-A2FS-10A-01D-A17D-09_BRCA	652	0	0	239	645	414	491	586	423	0	0	0	0	0	19	0	576
TCGA-EW-A2FV-10A-01D-A17D-09_BRCA	672	0	0	369	631	442	543	640	434	0	0	0	0	0	17	23	579
TCGA-EW-A2FW-10A-01D-A17D-09_BRCA	673	0	0	356	661	432	529	627	389	90	574	0	341	156	17	0	562
TCGA-EW-A3E8-10A-01D-A243-09_BRCA	674	293	308	290	594	340	505	569	40	85	603	0	447	183	0	9	583
TCGA-EW-A3U0-10A-01D-A22A-09_BRCA	667	275	272	190	667	175	546	590	374	87	596	510	334	162	18	1	577
TCGA-EW-A423-10A-01D-A243-09_BRCA	547	0	0	330	614	437	515	608	333	0	0	0	0	0	18	33	571
TCGA-EX-A1H5-10A-01D-A13W-08_CESC	763	0	0	361	627	390	537	656	493	0	0	0	0	0	42	91	582
TCGA-EX-A1H6-10A-01D-A22X-09_CESC	662	309	338	337	611	353	551	638	545	0	0	0	0	0	40	59	592
TCGA-EX-A3L1-10A-01D-A21Q-09_CESC	591	334	357	0	616	176	554	639	414	99	627	547	0	186	39	2	588
TCGA-EX-A449-10A-01D-A243-09_CESC	685	0	0	349	669	446	553	643	536	0	0	0	0	0	37	35	586
TCGA-EY-A1G7-10A-01D-A13O-09_UCEC	594	322	355	0	607	173	550	624	445	0	544	491	0	0	0	81	584
TCGA-EY-A1G8-10A-01D-A13O-09_UCEC	688	304	319	312	655	444	556	623	324	90	608	545	0	175	0	53	583
TCGA-EY-A1GC-10A-01D-A13O-09_UCEC	695	0	0	370	681	452	547	624	537	0	0	0	0	0	0	84	586
TCGA-EY-A1GD-10A-01D-A13O-09_UCEC	690	0	0	359	678	440	544	610	462	0	0	0	0	0	53	0	580
TCGA-EY-A1GE-10A-01D-A13O-09_UCEC	585	274	331	301	600	333	549	625	529	0	0	0	0	0	30	39	578
TCGA-EY-A1GF-10A-01D-A13O-09_UCEC	696	307	330	209	639	409	555	646	562	0	0	0	0	0	40	64	587
TCGA-EY-A1GH-10A-01D-A13O-09_UCEC	676	295	313	324	602	353	543	626	449	0	0	0	0	0	31	48	585
TCGA-EY-A1GI-10A-01D-A13O-09_UCEC	696	0	0	365	669	455	551	619	446	0	0	0	0	0	51	1	590
TCGA-EY-A1GJ-10A-01D-A142-09_UCEC	701	316	353	346	690	450	554	641	559	0	597	539	0	0	59	0	586
TCGA-EY-A1GK-10A-01D-A13O-09_UCEC	678	0	0	368	666	461	547	641	538	0	0	0	0	0	37	49	584
TCGA-EY-A1GL-10A-01D-A13O-09_UCEC	690	305	331	331	605	358	547	630	443	0	0	0	0	0	31	51	582
TCGA-EY-A1GM-10A-01D-A14G-09_UCEC	697	287	328	336	676	306	556	640	454	0	592	523	0	0	49	0	589
TCGA-EY-A1GO-10A-01D-A14G-09_UCEC	679	305	325	274	609	346	535	501	0	81	621	537	359	179	0	1	583
TCGA-EY-A1GP-10A-01D-A13O-09_UCEC	696	310	341	320	668	357	556	629	538	0	577	0	350	0	37	0	554
TCGA-EY-A1GQ-10A-01D-A13O-09_UCEC	694	0	0	353	656	464	549	627	453	0	0	0	0	0	0	83	588
TCGA-EY-A1GR-10A-01D-A13O-09_UCEC	692	311	341	335	668	447	552	637	433	0	566	0	354	0	0	55	578
TCGA-EY-A1GS-10A-01D-A13O-09_UCEC	674	172	351	212	655	373	549	645	462	0	0	0	0	0	52	50	584
TCGA-EY-A1GT-10A-01D-A13O-09_UCEC	672	285	304	306	605	347	545	613	517	0	0	0	0	0	0	76	585
TCGA-EY-A1GU-10A-01D-A13O-09_UCEC	663	0	0	357	665	429	552	609	537	0	0	0	0	0	46	0	579
TCGA-EY-A1GV-10A-01D-A13O-09_UCEC	593	326	345	0	675	184	546	632	543	0	628	583	0	0	29	54	584
TCGA-EY-A1GW-10A-01D-A13O-09_UCEC	578	321	361	0	652	183	543	632	533	0	595	579	0	0	0	116	585
TCGA-EY-A1GX-10A-01D-A13O-09_UCEC	688	0	0	336	681	376	548	642	540	0	0	0	0	0	31	50	585
TCGA-EY-A1H0-10A-01D-A13O-09_UCEC	583	328	361	0	644	175	554	653	559	0	526	547	0	0	52	57	590
TCGA-EY-A210-10A-01D-A159-09_UCEC	675	0	312	322	673	435	552	631	445	0	517	0	374	0	26	37	584
TCGA-EY-A212-10A-01D-A14K-09_UCEC	670	296	325	348	667	368	547	649	461	0	0	0	0	0	0	80	584
TCGA-EY-A214-10A-01D-A159-09_UCEC	590	319	346	0	606	172	550	611	346	0	558	499	0	0	0	61	585
TCGA-EY-A215-10A-01D-A14K-09_UCEC	700	308	348	336	673	357	550	648	553	0	592	578	0	0	44	57	586
TCGA-EY-A2OM-10A-01D-A18P-09_UCEC	684	294	330	328	623	355	529	499	406	0	576	0	359	179	0	49	584
TCGA-EY-A2ON-10A-01D-A18P-09_UCEC	693	0	0	351	633	454	554	644	552	0	0	0	0	0	58	0	589
TCGA-EY-A2OO-10A-01D-A19Y-09_UCEC	693	303	303	323	655	441	554	619	381	85	613	548	0	172	0	53	583
TCGA-EY-A2OP-10A-01D-A19Y-09_UCEC	579	313	340	0	497	163	547	625	454	0	536	509	0	0	32	36	583
TCGA-EY-A2OQ-10A-01D-A19Y-09_UCEC	696	0	0	370	683	471	550	631	557	0	0	0	0	0	0	115	587
TCGA-EY-A3L3-10A-01D-A22A-09_UCEC	671	300	327	316	681	352	549	627	430	93	616	523	360	177	41	1	584
TCGA-EY-A3QX-10A-01D-A22A-09_UCEC	688	297	306	337	672	440	552	647	408	92	615	525	345	175	0	53	586
TCGA-EY-A4KR-10A-01D-A27P-09_UCEC	694	0	0	369	662	457	554	635	548	0	0	0	0	0	51	2	588
TCGA-EY-A547-10A-01D-A27P-09_UCEC	699	0	0	371	690	466	555	653	554	0	0	0	0	0	50	76	591
TCGA-EY-A548-10A-01D-A27P-09_UCEC	588	323	350	0	0	0	0	0	0	0	621	0	465	183	0	1	592
TCGA-EY-A549-10A-01D-A27P-09_UCEC	701	0	0	364	665	446	547	625	556	0	0	0	0	0	0	116	583
TCGA-EY-A54A-10A-01D-A27P-09_UCEC	690	295	170	206	678	456	550	640	436	92	622	533	351	171	49	0	586
TCGA-EY-A5W2-10A-01D-A31U-09_UCEC	674	0	0	330	640	441	549	622	550	0	0	0	0	0	58	0	587
TCGA-EZ-7264-10A-01D-2024-08_LGG	675	244	253	283	610	372	531	642	57	85	641	558	373	141	0	0	571
TCGA-F1-6177-10A-01D-1800-08_STAD	681	248	264	290	614	376	530	646	461	74	638	565	365	135	31	1	578
TCGA-F1-6874-10A-01D-1882-08_STAD	688	256	262	291	580	379	531	623	455	0	604	0	304	137	0	70	579
TCGA-F1-A448-10A-01D-A24F-08_STAD	680	246	262	275	559	363	529	639	463	0	67	0	88	25	35	0	571
TCGA-F1-A72C-10A-01D-A33W-08_STAD	684	0	0	300	605	387	530	635	471	0	0	0	0	0	39	0	572
TCGA-F2-A44G-10A-01D-A26I-08_PAAD	691	0	0	307	612	386	534	655	0	86	632	0	378	139	0	0	573
TCGA-F2-A44H-10A-01D-A26I-08_PAAD	677	0	0	291	559	389	525	619	387	0	0	0	0	0	28	0	574
TCGA-F4-6459-10A-01D-1771-10_COAD	685	0	0	352	631	416	498	597	344	0	0	0	0	0	0	61	562
TCGA-F4-6460-10B-01D-1771-10_COAD	672	0	0	335	661	368	515	612	328	90	397	0	337	163	25	0	583
TCGA-F4-6461-10A-01D-1806-10_COAD	686	0	0	374	664	442	538	629	456	0	0	0	0	0	18	38	588
TCGA-F4-6463-10A-01D-1719-10_COAD	599	146	123	66	420	325	462	548	323	0	255	231	0	0	5	16	546
TCGA-F4-6569-10A-01D-1771-10_COAD	679	0	0	249	630	429	491	596	340	0	0	0	0	0	0	55	568
TCGA-F4-6570-10A-01D-1771-10_COAD	618	209	196	187	365	0	416	372	287	0	0	0	0	118	0	17	521
TCGA-F4-6703-10A-01D-1835-10_COAD	554	0	0	197	417	300	471	505	217	0	211	0	97	102	0	13	518
TCGA-F4-6805-10A-01D-1835-10_COAD	545	274	296	0	611	177	508	571	293	95	574	536	0	150	0	28	574
TCGA-F4-6806-10A-01D-1835-10_COAD	614	97	61	204	360	243	482	527	255	93	280	0	208	122	8	0	557
TCGA-F4-6807-10A-01D-1835-10_COAD	624	0	0	350	613	409	494	539	332	0	0	0	0	0	0	33	542
TCGA-F4-6808-10A-01D-1835-10_COAD	650	0	0	222	580	162	372	362	0	0	327	0	232	161	0	0	525
TCGA-F4-6809-10A-01D-1835-10_COAD	627	0	0	309	470	287	409	373	268	0	0	0	0	124	0	17	503
TCGA-F4-6854-10A-01D-1924-10_COAD	596	0	0	219	549	302	437	538	0	88	368	0	275	129	0	0	523
TCGA-F4-6855-10A-01D-1924-10_COAD	607	143	96	163	567	328	448	442	265	0	378	327	209	117	0	12	548
TCGA-F4-6856-10A-01D-1924-10_COAD	611	23	84	162	214	320	499	541	256	89	277	0	144	118	0	14	524
TCGA-F5-6464-10A-01D-1733-10_READ	694	0	0	363	628	446	542	611	333	89	412	0	302	161	0	26	563
TCGA-F5-6465-10A-01D-1733-10_READ	677	248	274	341	543	302	515	624	316	90	393	0	307	169	22	0	573

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-F5-6571-10A-01D-1826-10_READ	658	0	0	331	602	350	486	571	320	92	354	0	232	150	15	0	564
TCGA-F5-6702-10A-01D-1826-10_READ	546	283	295	0	542	139	505	583	347	0	371	478	0	0	16	21	571
TCGA-F5-6812-10A-01D-1826-10_READ	604	216	157	278	364	337	488	538	280	0	0	0	0	0	0	41	564
TCGA-F5-6813-10A-01D-1826-10_READ	627	148	189	198	439	279	475	594	427	0	0	0	0	0	11	12	561
TCGA-F5-6814-10A-01D-1924-10_READ	519	243	307	0	595	148	465	575	315	91	484	519	269	146	0	24	544
TCGA-F5-6861-10A-01D-1924-10_READ	629	142	139	226	378	299	512	559	332	0	0	0	0	0	25	0	563
TCGA-F5-6863-10A-01D-1924-10_READ	602	109	175	163	531	330	507	527	331	0	252	373	0	0	0	40	546
TCGA-F5-6864-10A-01D-1924-10_READ	669	0	0	343	659	362	524	616	448	0	0	0	0	0	11	27	582
TCGA-F7-7848-10A-01D-2129-08_HNSC	675	247	0	289	614	137	529	620	14	74	598	0	365	139	0	7	572
TCGA-F7-8298-10A-01D-2394-08_HNSC	686	0	0	298	593	386	530	646	391	73	598	0	296	135	0	70	571
TCGA-F7-8489-10A-01D-2394-08_HNSC	680	242	263	286	608	371	529	643	450	69	636	569	0	134	29	3	573
TCGA-F7-A50G-10A-01D-A25Y-08_HNSC	717	254	273	289	625	141	528	623	472	0	564	574	0	134	0	87	574
TCGA-F7-A624-10A-01D-A30H-08_HNSC	672	267	283	0	595	136	538	654	401	84	639	584	0	139	44	0	582
TCGA-F9-A4JJ-10A-01D-A25F-10_KIRP	690	0	0	371	667	460	553	631	365	0	0	0	0	0	37	69	585
TCGA-FA-8693-10A-01D-2397-10_DLBC	693	0	0	364	679	453	550	623	363	0	0	0	0	0	0	54	576
TCGA-FA-A4BB-10A-01D-A31X-10_DLBC	585	0	0	337	451	361	483	579	331	0	0	0	0	0	0	0	560
TCGA-FA-A6HN-10A-01D-A31X-10_DLBC	524	0	0	233	458	414	475	571	283	0	322	0	245	140	0	0	541
TCGA-FA-A6HO-10A-01D-A31X-10_DLBC	616	0	0	252	502	398	501	578	322	0	0	0	0	0	0	0	552
TCGA-FB-A4P5-10A-01D-A26I-08_PAAD	657	231	237	270	493	257	529	625	460	0	0	0	0	0	29	51	573
TCGA-FB-A4P6-10A-01D-A26I-08_PAAD	675	0	0	295	601	376	529	626	449	0	0	0	0	0	0	85	574
TCGA-FB-A545-10A-01D-A26I-08_PAAD	680	0	0	293	603	376	532	631	378	58	578	0	361	134	0	60	574
TCGA-FB-A5VM-10A-01D-A32N-08_PAAD	676	239	248	269	557	268	531	643	462	0	0	0	0	0	24	57	577
TCGA-FB-A78T-10A-01D-A32N-08_PAAD	685	0	0	301	601	377	526	652	472	0	0	0	0	0	30	62	571
TCGA-FB-A7DR-10A-01D-A33W-08_PAAD	683	0	0	297	589	381	526	631	373	63	520	0	284	131	0	53	570
TCGA-FC-7708-10A-01D-2115-08_PRAD	681	237	254	281	606	132	529	617	215	0	608	563	106	140	0	0	570
TCGA-FC-7961-10A-01D-A29Q-08_PRAD	757	0	0	316	620	399	529	656	488	0	0	0	0	0	47	76	578
TCGA-FC-A4JI-10A-01D-A25A-08_PRAD	684	248	254	278	539	369	533	633	472	0	0	0	0	0	33	60	573
TCGA-FC-A5OB-10A-01D-A29Q-08_PRAD	736	254	267	277	514	282	533	644	0	84	634	0	380	142	0	0	581
TCGA-FC-A66V-10A-01D-A30H-08_PRAD	759	0	0	323	622	404	535	655	489	0	0	0	0	0	37	81	581
TCGA-FC-A6HD-10A-01D-A31J-08_PRAD	684	0	0	305	596	387	534	641	378	75	573	561	0	136	0	68	575
TCGA-FD-A3B3-10A-01D-A202-08_BLCA	682	0	0	295	593	376	529	626	357	58	508	0	286	128	0	48	573
TCGA-FD-A3B4-10A-01D-A202-08_BLCA	671	239	122	269	548	354	511	611	0	72	610	0	373	140	0	0	570
TCGA-FD-A3B5-10A-01D-A20D-08_BLCA	663	0	257	273	601	365	527	645	471	0	584	0	364	0	35	2	573
TCGA-FD-A3B6-10A-01D-A20D-08_BLCA	664	235	246	279	509	265	530	650	477	0	0	0	0	0	26	63	573
TCGA-FD-A3B7-10A-01D-A20D-08_BLCA	750	0	0	296	611	382	527	642	477	0	0	0	0	0	26	61	578
TCGA-FD-A3B8-10A-01D-A20D-08_BLCA	669	239	239	275	605	282	528	643	469	0	612	514	0	0	0	79	577
TCGA-FD-A3N5-10A-01D-A21A-08_BLCA	679	0	0	290	594	385	533	648	472	0	0	0	0	0	30	70	574
TCGA-FD-A3N6-10A-01D-A21A-08_BLCA	680	0	0	259	558	357	533	640	463	0	507	566	0	0	25	56	578
TCGA-FD-A3NA-10A-01D-A21A-08_BLCA	688	242	251	280	569	368	533	658	476	0	0	0	0	0	31	69	578
TCGA-FD-A3SJ-10A-01D-A22Z-08_BLCA	761	0	0	316	621	406	536	655	493	0	0	0	0	0	46	75	582
TCGA-FD-A3SL-10A-01D-A22Z-08_BLCA	674	246	263	291	574	285	536	646	491	0	0	0	0	0	35	70	579
TCGA-FD-A3SM-10A-01D-A22Z-08_BLCA	764	262	0	307	617	384	536	650	0	85	641	0	392	144	0	0	582
TCGA-FD-A3SN-10A-01D-A22Z-08_BLCA	760	0	0	313	610	392	536	653	492	0	0	0	0	0	37	77	579
TCGA-FD-A3SO-10A-01D-A22Z-08_BLCA	674	248	269	292	578	290	534	648	452	71	609	0	377	140	52	0	581
TCGA-FD-A3SP-10A-01D-A22Z-08_BLCA	742	254	279	298	583	289	534	654	483	0	0	0	0	0	43	82	579
TCGA-FD-A3SQ-10A-01D-A22Z-08_BLCA	769	0	0	323	629	404	539	664	387	84	651	571	383	142	0	86	581
TCGA-FD-A3SR-10A-01D-A22Z-08_BLCA	751	247	261	272	610	282	530	650	470	70	640	575	0	140	0	74	579
TCGA-FD-A3SS-10A-01D-A22Z-08_BLCA	689	0	0	319	627	409	538	657	0	89	654	576	394	143	0	0	578
TCGA-FD-A43N-10A-01D-A23U-08_BLCA	681	0	0	292	594	380	529	637	460	0	0	0	0	0	23	54	571
TCGA-FD-A43P-10A-01D-A23U-08_BLCA	669	0	264	95	601	138	530	628	456	0	627	509	303	0	37	3	572
TCGA-FD-A43S-10A-01D-A23U-08_BLCA	674	250	247	270	602	282	528	630	394	0	581	504	0	0	0	68	574
TCGA-FD-A43U-10A-01D-A23U-08_BLCA	739	243	262	269	565	272	528	636	471	0	0	0	0	0	0	127	572
TCGA-FD-A43X-10A-01D-A23U-08_BLCA	761	0	0	300	621	392	538	643	469	81	606	0	378	140	0	76	581
TCGA-FD-A43Y-10A-01D-A26K-08_BLCA	672	0	0	298	580	379	524	614	401	0	0	0	0	0	0	94	575
TCGA-FD-A5BR-10A-01D-A26K-08_BLCA	678	0	0	291	589	372	511	611	361	67	506	0	288	135	24	4	574
TCGA-FD-A5BS-10A-01D-A26K-08_BLCA	671	240	256	165	605	355	525	629	304	0	617	507	287	130	0	51	572
TCGA-FD-A5BT-10A-01D-A26K-08_BLCA	650	239	242	243	489	373	529	624	457	0	0	0	0	0	28	50	572
TCGA-FD-A5BU-10A-01D-A26K-08_BLCA	596	257	266	0	535	132	516	607	372	0	608	504	289	132	35	4	579
TCGA-FD-A5BV-10A-01D-A26K-08_BLCA	593	261	267	0	493	132	506	582	22	71	627	574	353	137	0	0	570
TCGA-FD-A5BX-10A-01D-A26K-08_BLCA	631	236	233	251	566	367	527	640	378	75	619	508	363	135	0	65	576
TCGA-FD-A5BY-10A-01D-A289-08_BLCA	666	245	258	183	547	367	535	632	482	0	0	0	0	0	0	121	578
TCGA-FD-A5BZ-10A-01D-A289-08_BLCA	676	244	266	290	612	379	534	642	476	0	599	566	0	0	0	132	577
TCGA-FD-A5C0-10A-01D-A289-08_BLCA	687	0	0	309	610	395	533	645	481	0	0	0	0	0	0	110	575
TCGA-FD-A5C1-10A-01D-A289-08_BLCA	688	248	273	285	615	387	532	649	486	0	616	566	0	0	0	139	579
TCGA-FD-A62N-10A-01D-A30H-08_BLCA	749	256	272	305	625	397	536	661	475	72	657	586	0	139	0	99	582
TCGA-FD-A62O-10A-01D-A30H-08_BLCA	750	260	275	296	616	386	535	663	473	77	646	584	0	140	43	0	580
TCGA-FD-A62P-10A-01D-A30H-08_BLCA	677	267	283	0	0	0	538	652	493	0	0	0	0	0	41	90	583
TCGA-FD-A62S-10A-01D-A30H-08_BLCA	753	253	273	192	608	319	538	660	488	0	601	0	380	0	0	120	580
TCGA-FD-A6TA-10A-21D-A339-08_BLCA	681	0	0	291	590	377	525	634	466	0	0	0	0	0	0	68	574
TCGA-FD-A6TB-10A-21D-A339-08_BLCA	667	0	0	299	600	374	521	630	473	0	0	0	0	0	23	48	578
TCGA-FD-A6TC-10A-21D-A339-08_BLCA	683	250	263	293	562	375	535	651	484	0	0	0	0	0	0	87	577
TCGA-FD-A6TD-10A-21D-A339-08_BLCA	678	0	0	299	594	379	531	619	460	0	0	0	0	0	0	92	571
TCGA-FD-A6TE-10A-21D-A339-08_BLCA	667	239	259	280	589	277	527	633	466	0	578	563	0	0	0	102	576
TCGA-FD-A6TF-10A-21D-A329-08_BLCA	658	234	245	276	599	353	527	634	477	0	582	497	0	0	0	98	579
TCGA-FD-A6TG-10A-01D-A329-08_BLCA	662	244	251	284	605	366	533	641	390	73	635	565	364	137	26	0	573
TCGA-FD-A6TH-10A-01D-A329-08_BLCA	677	240	250	279	600	367	531	644	454	76	617	569	0	137	20	0	574
TCGA-FD-A6TI-10A-01D-A329-08_BLCA	684	230	254	280	599	372	529	638	472	0	581	502	0	0	20	51	576
TCGA-FD-A6TK-10A-21D-A339-08_BLCA	586	243	269	0	0	0	528	607	458	0	0	0	0	0	0	93	572
TCGA-FE-A22Z-10A-01D-A17V-08_THCA	593	258	272	0	544	134	530	638	479	0	586	558	0	0	27	63	573
TCGA-FE-A230-10A-01D-A14W-08_THCA	668	237	251	269	509	267	526	626	401	0	0	0	0	0	0	81	573
TCGA-FE-A231-10A-01D-A14W-08_THCA	684	0	0	297	609	388	532	628	466	0	0	0	0	0	0	76	576
TCGA-FE-A232-10A-01D-A14W-08_THCA	673	238	254	282	607	373	531	637	384	69	629	502	294	137	22	2	573
TCGA-FE-A233-10A-01D-A14W-08_THCA	669	237	257	271	567	368	500	588	367	0	511	0	287	132	0	41	574
TCGA-FE-A234-10A-01D-A14W-08_THCA	662	233	256	281	541	368	530	633	0	85	621	0	301	139	0	2	574
TCGA-FE-A235-10A-01D-A16O-08_THCA	686	0	0	299	588	277	528	660	486	0	0	0	0	0	31	57	580
TCGA-FE-A236-10A-01D-A16O-08_THCA	754	0	0	309	607	294	525	653	488	0	0	0	0	0	0	129	576
TCGA-FE-A237-10A-01D-A16O-08_THCA	689	0	0	302	614	397	534	649	482	0	0	0	0	0	0	96	575
TCGA-FE-A23A-10A-01D-A17V-08_THCA	672	248	260	181	609	284	530	640	466	0	530	510	0	0	39	0	573
TCGA-FE-A3PA-10A-01D-A21Z-08_THCA	688	0	0	299	615	289	521	629	461	0	0	0	0	0	0	70	573
TCGA-FE-A3PB-10A-01D-A21Z-08_THCA	672	250	254	291	612	279	529	633	477	0	615	562	0	0	0	130	572
TCGA-FE-A3PC-10A-01D-A21Z-08_THCA	687	0	0	303	606	385	531	653	472	0	0	0	0	0	26	70	574
TCGA-FE-A3PD-10A-01D-A21Z-08_THCA	679	0	0	297	602	383	532	643	448	76	613	0	360	134	0	71	576
TCGA-FF-8041-10A-01D-2210-10_DLBC	692	0	0	360	555	453	541	603	328	83	406	485	0	169	0	0	576
TCGA-FF-8042-10A-01D-2210-10_DLBC	683	287	296	244	518	411	519	573	321	0	364	510	0	169	0	0	584
TCGA-FF-8043-10A-01D-2210-10_DLBC	688	0	0	280	668	452	550	619	320	91	370	520	0	169	0	0	587
TCGA-FF-8046-10A-01D-2210-10_DLBC	567	302	347	0	576	173	490	474	333	0	471	503	346	180	0	45	584

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-FG-5962-10A-01D-1893-08_LGG	690	0	0	307	612	391	531	649	481	0	0	0	0	0	0	139	579
TCGA-FG-5963-10A-01D-1705-08_LGG	687	0	0	300	598	388	526	635	351	73	575	0	278	135	0	50	576
TCGA-FG-5964-10A-01D-1705-08_LGG	755	0	0	302	601	389	528	636	385	62	528	0	290	132	0	56	574
TCGA-FG-5965-10A-01D-1893-08_LGG	749	242	263	289	617	290	531	648	0	86	658	575	368	140	0	0	578
TCGA-FG-6688-10A-01D-1893-08_LGG	693	0	0	305	607	386	533	639	475	0	0	0	0	0	39	1	575
TCGA-FG-6689-10A-01D-1893-08_LGG	672	253	271	289	595	279	534	655	471	77	618	0	363	139	0	69	578
TCGA-FG-6690-10A-01D-1893-08_LGG	688	254	267	290	618	286	532	654	462	80	648	567	372	139	36	0	577
TCGA-FG-6691-10A-01D-1893-08_LGG	689	0	0	306	615	395	534	654	479	0	0	0	0	0	0	110	577
TCGA-FG-6692-10A-01D-1893-08_LGG	761	0	0	312	615	389	533	652	480	0	0	0	0	0	0	109	577
TCGA-FG-7634-10A-01D-2086-08_LGG	680	245	247	273	382	0	529	658	469	0	0	0	0	0	22	57	576
TCGA-FG-7636-10A-01D-2086-08_LGG	686	239	244	272	582	365	532	643	471	0	0	0	0	0	25	53	576
TCGA-FG-7637-10A-01D-2086-08_LGG	684	0	0	308	603	384	534	652	383	75	530	520	0	137	0	60	573
TCGA-FG-7638-10A-01D-2086-08_LGG	687	0	0	297	604	383	531	639	439	76	595	0	359	131	0	68	571
TCGA-FG-7641-10A-01D-2253-08_LGG	684	0	0	305	608	377	531	650	451	71	605	0	363	131	23	0	575
TCGA-FG-7643-10A-01D-2086-08_LGG	685	0	0	297	601	372	529	637	452	62	597	0	286	132	0	51	574
TCGA-FG-8181-10A-01D-2253-08_LGG	679	239	255	279	555	358	530	635	475	0	0	0	0	0	0	114	574
TCGA-FG-8182-10A-01D-2253-08_LGG	687	0	0	282	590	289	519	646	483	0	0	0	0	0	29	59	573
TCGA-FG-8185-10A-01D-2253-08_LGG	684	0	0	304	603	294	520	648	480	0	0	0	0	0	0	121	578
TCGA-FG-8186-10A-01D-2253-08_LGG	679	244	247	286	574	366	531	652	462	0	0	0	0	0	32	54	573
TCGA-FG-8187-10A-01D-2253-08_LGG	683	249	267	292	605	379	533	645	0	85	634	0	378	139	0	2	580
TCGA-FG-8188-10A-01D-2253-08_LGG	672	239	250	293	544	373	529	645	455	52	582	0	288	133	31	0	571
TCGA-FG-8189-10A-01D-A289-08_LGG	761	0	0	305	601	396	530	642	477	0	0	0	0	0	0	92	578
TCGA-FG-8191-10A-01D-2253-08_LGG	684	0	0	305	607	384	530	648	381	71	610	0	290	135	0	64	575
TCGA-FG-A4MT-10A-01D-A26K-08_LGG	672	0	0	293	576	370	527	645	466	0	0	0	0	0	24	64	576
TCGA-FG-A4MU-10A-01D-A289-08_LGG	690	0	0	304	609	386	529	641	485	0	0	0	0	0	0	130	575
TCGA-FG-A4MW-10A-01D-A26K-08_LGG	594	238	248	275	570	356	529	640	368	57	519	0	278	128	0	54	574
TCGA-FG-A4MX-10A-01D-A26K-08_LGG	748	0	0	292	594	374	523	630	362	64	510	500	0	129	0	53	575
TCGA-FG-A4MY-10A-01D-A26K-08_LGG	600	251	268	0	477	136	531	629	309	71	616	503	293	133	0	60	573
TCGA-FG-A60J-10A-01D-A289-08_LGG	686	0	0	298	601	380	529	636	467	0	0	0	0	0	0	80	575
TCGA-FG-A60K-10A-01D-A29Q-08_LGG	665	252	268	285	516	388	531	648	454	82	532	0	371	136	40	0	577
TCGA-FG-A60L-10A-01D-A31J-08_LGG	756	0	0	296	602	279	519	641	434	78	590	0	290	135	0	52	575
TCGA-FG-A6IZ-10A-01D-A31J-08_LGG	682	0	0	293	597	283	527	645	465	0	0	0	0	0	27	57	570
TCGA-FG-A6J1-10A-01D-A31J-08_LGG	685	0	0	291	594	384	532	633	469	0	0	0	0	0	35	0	574
TCGA-FG-A6J3-10A-01D-A31J-08_LGG	681	0	0	298	595	374	531	647	446	82	580	0	292	136	0	62	572
TCGA-FG-A713-10A-01D-A329-08_LGG	686	0	0	295	572	373	529	624	0	74	635	0	370	136	0	0	573
TCGA-FI-A2CX-10A-01D-A17D-09_UCEC	691	305	334	328	662	449	553	632	526	0	577	531	0	0	45	57	586
TCGA-FI-A2CY-10A-01D-A17D-09_UCEC	696	0	0	364	679	454	546	641	551	0	0	0	0	0	38	45	580
TCGA-FI-A2D0-10A-01D-A17D-09_UCEC	696	0	0	359	678	463	553	638	542	0	0	0	0	0	0	128	592
TCGA-FI-A2D2-10A-01D-A17D-09_UCEC	674	0	0	380	699	446	541	639	357	0	0	0	0	0	0	83	579
TCGA-FI-A2D4-10A-01D-A17D-09_UCEC	663	0	0	350	671	472	548	628	545	0	0	0	0	0	0	99	581
TCGA-FI-A2D5-10A-01D-A17D-09_UCEC	697	0	0	343	669	459	551	637	411	94	551	0	356	174	37	0	584
TCGA-FI-A2D6-10A-01D-A17D-09_UCEC	687	0	0	367	672	448	549	636	547	0	0	0	0	0	39	67	587
TCGA-FI-A2EU-10A-01D-A17D-09_UCEC	686	295	353	356	669	374	551	650	450	101	620	0	360	176	0	65	593
TCGA-FI-A2EW-10A-01D-A17D-09_UCEC	674	243	283	326	689	416	544	649	454	0	614	497	0	0	37	0	580
TCGA-FI-A2EX-10A-01D-A17D-09_UCEC	670	261	285	333	644	412	553	667	440	106	606	0	327	164	23	0	568
TCGA-FI-A2EY-10A-01D-A18P-09_UCEC	699	313	334	346	702	462	556	644	447	96	632	538	371	178	0	75	588
TCGA-FI-A2F4-10B-01D-A17D-09_UCEC	690	0	0	368	668	459	552	648	552	0	0	0	0	0	46	65	589
TCGA-FI-A2F8-10B-01D-A17D-09_UCEC	560	311	353	0	671	178	552	630	408	103	643	556	343	160	0	38	574
TCGA-FI-A2F9-10B-01D-A17D-09_UCEC	699	314	345	302	624	348	549	639	551	0	0	0	0	0	60	3	590
TCGA-FI-A3PV-10A-01D-A22A-09_UCEC	697	0	0	367	672	446	554	638	556	0	0	0	0	0	36	53	585
TCGA-FI-A3PX-10A-01D-A22A-09_UCEC	693	267	31	328	669	366	545	620	329	81	482	0	335	167	0	49	583
TCGA-FJ-A3Z7-10A-01D-A23K-08_BLCA	753	252	0	294	624	286	533	648	480	0	0	0	0	0	0	174	582
TCGA-FJ-A3Z9-10A-01D-A26K-08_BLCA	687	0	0	293	597	383	530	639	365	75	579	0	293	136	0	53	575
TCGA-FJ-A3ZE-10A-01D-A23K-08_BLCA	688	0	0	295	602	286	523	637	461	0	0	0	0	0	0	84	576
TCGA-FJ-A3ZF-10A-01D-A23K-08_BLCA	688	64	8	302	605	380	529	638	458	74	622	163	363	134	0	53	572
TCGA-FK-A3S3-10A-01D-A22D-08_THCA	688	0	0	305	607	385	531	654	471	0	0	0	0	0	33	68	576
TCGA-FK-A3SB-10A-01D-A22D-08_THCA	685	0	0	301	594	386	533	653	477	79	575	455	0	0	0	124	571
TCGA-FK-A3SD-10A-01D-A22D-08_THCA	635	239	246	287	602	344	530	640	380	75	622	515	350	131	29	0	570
TCGA-FK-A3SE-10A-01D-A22D-08_THCA	687	0	0	296	603	379	535	634	385	69	525	87	351	132	0	63	575
TCGA-FK-A3SG-10A-01D-A22D-08_THCA	685	0	0	302	620	383	535	660	457	85	625	572	359	138	0	63	577
TCGA-FK-A3SH-10A-01D-A22D-08_THCA	677	250	260	281	611	380	532	638	466	0	592	567	0	0	37	2	574
TCGA-FK-A4UB-10A-01D-A25A-08_THCA	679	248	269	284	609	377	529	629	436	72	629	513	0	135	0	53	576
TCGA-FN-7833-10A-01D-2086-08_LGG	675	247	258	268	610	374	532	654	480	0	592	508	0	0	31	62	574
TCGA-FP-7735-10A-01D-2053-08_STAD	673	240	240	288	597	271	527	637	466	0	589	508	0	0	24	33	575
TCGA-FP-7829-10A-01D-2053-08_STAD	685	248	239	272	554	358	532	654	474	0	0	0	0	0	0	111	576
TCGA-FP-7916-10A-01D-2201-08_STAD	739	0	0	308	607	362	532	656	384	71	605	0	288	135	24	0	574
TCGA-FP-7998-10A-01D-2201-08_STAD	729	235	227	276	497	332	535	662	364	66	604	0	275	131	23	1	576
TCGA-FP-8099-10A-01D-2341-08_STAD	759	0	0	313	607	292	525	660	490	0	0	0	0	0	35	73	578
TCGA-FP-8211-10A-01D-2341-08_STAD	692	0	0	312	621	393	532	657	474	0	0	0	0	0	0	94	577
TCGA-FP-8631-10A-01D-2394-08_STAD	598	253	270	0	25	0	529	645	478	0	0	0	0	0	32	76	576
TCGA-FP-A4BF-10A-01D-A24F-08_STAD	680	0	0	297	593	375	532	633	468	0	0	0	0	0	0	94	572
TCGA-FR-A2OS-10B-01D-A21A-08_SKCM	686	0	0	289	606	377	529	640	467	0	0	0	0	0	0	82	576
TCGA-FR-A3R1-10B-01D-A23B-08_SKCM	593	253	273	0	553	134	533	657	469	79	609	514	0	0	40	1	575
TCGA-FR-A3YN-10A-01D-A23B-08_SKCM	683	0	0	307	610	379	535	648	469	0	0	0	0	0	28	55	577
TCGA-FR-A3YO-10A-01D-A23B-08_SKCM	680	246	259	287	613	280	531	651	392	78	643	568	365	137	26	0	576
TCGA-FR-A44A-10A-01D-A24R-08_SKCM	686	0	0	290	609	376	532	657	473	78	0	0	0	0	32	66	573
TCGA-FR-A69P-10A-01D-A30X-08_SKCM	682	0	0	296	591	386	532	626	398	0	0	0	0	0	0	73	574
TCGA-FR-A726-10A-01D-A32N-08_SKCM	683	0	0	300	604	283	523	653	469	0	0	0	0	0	29	63	579
TCGA-FR-A728-10A-01D-A32N-08_SKCM	759	0	0	300	615	383	533	650	464	79	620	0	363	137	0	65	578
TCGA-FS-A1YW-10A-01D-A199-08_SKCM	689	0	0	310	618	366	527	656	480	0	0	0	0	0	0	96	579
TCGA-FS-A1YX-10A-01D-A199-08_SKCM	686	0	0	305	608	390	532	642	385	63	595	508	0	138	0	74	577
TCGA-FS-A1YY-10A-01D-A199-08_SKCM	684	0	0	292	581	356	522	632	373	83	494	0	265	117	0	50	572
TCGA-FS-A1Z0-10A-01D-A199-08_SKCM	685	0	0	295	600	384	527	635	379	63	555	0	355	137	0	62	577
TCGA-FS-A1Z3-10A-01D-A199-08_SKCM	679	0	0	290	600	365	527	645	458	0	0	0	0	0	26	54	577
TCGA-FS-A1Z4-10A-01D-A199-08_SKCM	677	0	0	296	607	380	529	643	472	0	0	0	0	0	33	60	574
TCGA-FS-A1Z7-10A-01D-A199-08_SKCM	687	0	0	292	561	378	530	627	469	0	0	0	0	0	16	48	576
TCGA-FS-A1ZA-10A-01D-A199-08_SKCM	744	243	239	264	602	333	529	643	462	0	564	563	0	0	0	102	577
TCGA-FS-A1ZB-10A-01D-A199-08_SKCM	683	0	0	292	608	385	531	641	377	67	576	0	358	138	19	2	577
TCGA-FS-A1ZC-10A-01D-A199-08_SKCM	675	0	0	292	594	281	495	590	366	0	0	0	0	133	0	44	567
TCGA-FS-A1ZD-10A-01D-A199-08_SKCM	667	235	226	266	483	224	524	640	465	0	0	0	0	0	27	0	578
TCGA-FS-A1ZE-10A-01D-A199-08_SKCM	685	0	0	307	599	376	527	644	478	0	0	0	0	0	0	78	577
TCGA-FS-A1ZF-10A-01D-A199-08_SKCM	673	237	246	274	499	353	533	646	460	0	0	0	0	0	29	0	574
TCGA-FS-A1ZG-10A-01D-A199-08_SKCM	678	240	232	256	494	331	529	635	463	0	0	0	0	0	0	74	577
TCGA-FS-A1ZH-10A-01D-A199-08_SKCM	686	0	0	309	605	388	532	636	0	81	629	0	378	142	0	0	573
TCGA-FS-A1ZJ-10A-01D-A199-08_SKCM	658	247	261	285	547	276	523	648	479	0	0	0	0	0	38	59	576
TCGA-FS-A1ZK-10A-01D-A199-08_SKCM	647	239	262	284	503	274	526	649	475	0	0	0	0	0	24	48	576

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-FS-A1ZM-10A-01D-A199-08_SKCM	748	243	256	279	609	359	533	641	395	63	614	561	0	138	0	60	580
TCGA-FS-A1ZN-10A-01D-A199-08_SKCM	675	246	260	188	596	281	531	635	465	0	570	517	0	0	0	96	580
TCGA-FS-A1ZP-10A-01D-A199-08_SKCM	664	244	262	279	611	377	531	644	441	68	618	577	0	137	0	61	580
TCGA-FS-A1ZQ-10A-01D-A199-08_SKCM	664	234	237	274	608	368	534	635	475	0	514	511	0	0	0	106	580
TCGA-FS-A1ZR-10A-01D-A199-08_SKCM	676	252	273	300	619	278	531	655	386	82	639	566	369	140	0	64	579
TCGA-FS-A1ZS-10A-01D-A199-08_SKCM	678	0	0	269	525	363	509	615	448	0	0	0	0	0	10	27	576
TCGA-FS-A1ZT-10A-01D-A199-08_SKCM	682	0	0	303	597	393	529	644	454	78	583	0	287	135	0	57	579
TCGA-FS-A1ZU-10A-01D-A198-08_SKCM	685	0	0	285	594	282	517	631	469	0	0	107	0	0	0	81	576
TCGA-FS-A1ZW-10A-01D-A199-08_SKCM	658	231	248	257	597	277	525	634	311	60	571	574	0	125	0	46	573
TCGA-FS-A1ZY-10A-01D-A199-08_SKCM	752	253	256	274	551	369	533	646	482	0	0	0	0	0	27	72	578
TCGA-FS-A1ZZ-10A-01D-A199-08_SKCM	686	0	0	301	601	274	519	608	371	0	0	0	0	132	0	56	574
TCGA-FS-A4F0-10A-01D-A24R-08_SKCM	675	235	266	274	508	283	529	648	472	0	0	0	0	0	26	61	577
TCGA-FS-A4F2-10A-01D-A24R-08_SKCM	683	0	0	306	599	377	528	638	471	0	206	128	0	0	0	117	574
TCGA-FS-A4F4-10B-01D-A25O-08_SKCM	666	232	253	262	589	360	518	623	296	61	619	561	0	127	0	49	572
TCGA-FS-A4F5-10B-01D-A25O-08_SKCM	576	232	241	0	531	126	522	618	297	66	495	0	344	129	25	1	572
TCGA-FS-A4F8-10B-01D-A25O-08_SKCM	650	233	255	251	499	269	522	616	463	0	0	0	0	0	24	37	573
TCGA-FS-A4F9-10A-01D-A24R-08_SKCM	588	256	268	0	580	133	530	651	473	0	616	563	11	0	30	62	574
TCGA-FS-A4FB-10B-01D-A25O-08_SKCM	664	0	0	277	539	370	520	610	348	66	483	0	276	129	21	0	567
TCGA-FS-A4FC-10A-01D-A24R-08_SKCM	686	0	0	296	598	283	527	643	470	0	0	0	0	0	27	58	573
TCGA-FS-A4FD-10B-01D-A25O-08_SKCM	662	238	253	187	492	258	501	576	375	0	561	0	279	131	0	66	574
TCGA-FT-A3EE-10A-01D-A202-08_BLCA	587	249	270	0	489	132	516	643	382	61	612	505	358	137	0	49	574
TCGA-FT-A61P-10A-01D-A30H-08_BLCA	758	256	270	294	593	387	537	647	492	0	0	0	0	0	0	166	579
TCGA-FU-A23K-10A-01D-A16O-08_CESC	676	0	0	304	607	401	533	654	476	79	605	0	364	0	0	126	579
TCGA-FU-A23L-10A-01D-A16O-08_CESC	682	0	0	306	612	385	530	647	482	0	0	0	0	0	0	128	577
TCGA-FU-A2QG-10A-01D-A18J-09_CESC	700	0	0	367	684	468	550	624	546	0	0	0	0	0	0	121	581
TCGA-FU-A3HY-10A-01D-A21Q-09_CESC	593	328	360	0	628	174	553	633	545	0	569	539	0	0	0	140	583
TCGA-FU-A3HZ-10A-01D-A20U-09_CESC	582	298	335	340	582	341	552	639	542	0	0	0	0	0	32	50	578
TCGA-FU-A3NI-10A-01D-A21Q-09_CESC	688	291	325	302	663	443	555	638	554	0	578	548	0	0	30	65	586
TCGA-FU-A3TQ-10A-01D-A22X-09_CESC	696	0	0	361	679	453	553	625	449	0	0	0	0	0	0	103	589
TCGA-FU-A3TX-10A-01D-A22X-09_CESC	692	302	326	315	622	425	551	646	434	97	472	548	0	173	0	61	586
TCGA-FU-A3WB-10A-01D-A22X-09_CESC	672	283	324	323	672	441	553	646	453	0	560	539	0	0	37	56	593
TCGA-FU-A3YQ-10A-01D-A22X-09_CESC	687	0	0	342	662	454	554	641	515	97	572	0	356	170	0	67	588
TCGA-FU-A40J-10A-01D-A243-09_CESC	701	297	308	235	624	368	550	640	547	0	0	0	0	0	0	107	595
TCGA-FU-A57G-10A-01D-A26G-09_CESC	691	103	0	360	663	459	552	625	544	0	0	0	0	21	0	77	582
TCGA-FU-A5XV-10A-01D-A28E-09_CESC	683	0	0	334	662	439	532	520	452	0	0	0	0	0	0	91	585
TCGA-FV-A2QQ-10B-01D-A22F-10_LIHC	511	143	194	189	433	277	494	493	322	0	0	0	0	0	0	46	544
TCGA-FV-A3I1-10A-01D-A22F-10_LIHC	535	257	306	0	0	0	516	489	341	0	0	0	0	0	0	45	571
TCGA-FV-A3R3-10A-01D-A22F-10_LIHC	652	0	0	343	584	440	512	573	327	0	0	0	0	0	0	48	557
TCGA-FV-A495-10A-01D-A25V-10_LIHC	681	234	279	339	493	396	522	601	356	0	0	0	0	0	19	53	575
TCGA-FV-A496-10A-01D-A25V-10_LIHC	685	0	0	379	663	395	553	637	0	100	511	476	384	184	0	0	581
TCGA-FV-A4ZQ-10A-01D-A25V-10_LIHC	686	286	305	268	666	443	554	623	446	0	464	513	0	0	44	0	585
TCGA-FW-A3I3-10A-01D-A21A-08_SKCM	681	245	256	295	569	376	532	646	479	0	0	0	0	0	40	2	579
TCGA-FW-A3R5-10A-01D-A23B-08_SKCM	677	251	259	285	611	379	531	658	456	84	641	571	0	135	0	79	576
TCGA-FW-A3TU-10A-01D-A23B-08_SKCM	684	0	0	293	605	289	531	657	472	0	0	0	0	0	39	78	576
TCGA-FW-A3TV-10A-01D-A23B-08_SKCM	655	250	266	283	512	281	514	622	441	0	528	0	374	138	0	65	578
TCGA-FW-A5DX-10A-01D-A27N-08_SKCM	637	237	259	259	549	264	523	634	456	0	0	0	0	0	0	74	575
TCGA-FX-A2QS-10A-01D-A21Q-09_SARC	685	0	0	349	674	449	546	635	453	0	0	0	0	0	0	75	585
TCGA-FX-A3NJ-10A-01D-A21Q-09_SARC	699	0	0	368	674	454	547	631	463	0	0	0	0	0	0	95	587
TCGA-FX-A3NK-10A-01D-A21Q-09_SARC	695	0	0	345	669	369	542	529	544	0	0	0	0	0	0	93	586
TCGA-FX-A3RE-10A-01D-A22A-09_SARC	681	302	322	327	642	440	548	617	543	0	543	515	0	0	0	76	587
TCGA-FX-A3TO-10A-01D-A22A-09_SARC	697	0	0	356	671	454	553	631	337	94	543	0	344	170	0	53	584
TCGA-FX-A48G-10A-01D-A24N-09_SARC	698	295	339	327	625	364	547	652	552	0	0	0	0	0	29	54	584
TCGA-FY-A2QD-10A-01D-A19M-08_THCA	737	241	129	271	599	284	530	644	476	0	592	0	308	0	0	105	577
TCGA-FY-A3BL-10A-01D-A19M-08_THCA	682	0	0	310	613	389	531	643	453	76	607	3	353	135	0	61	578
TCGA-FY-A3I4-10A-01D-A21A-08_THCA	674	0	0	288	563	368	526	634	471	0	0	0	0	0	0	104	576
TCGA-FY-A3I5-10A-01D-A21Z-08_THCA	685	253	0	294	619	376	530	651	458	75	624	0	373	138	0	70	575
TCGA-FY-A3NM-10A-01D-A21A-08_THCA	686	0	0	299	568	371	529	644	471	0	0	0	0	0	32	58	579
TCGA-FY-A3NN-10A-01D-A21A-08_THCA	688	0	0	273	604	375	534	636	384	0	534	0	342	134	25	0	572
TCGA-FY-A3NP-10A-01D-A21A-08_THCA	598	263	270	0	544	136	530	647	481	0	537	562	0	0	30	64	578
TCGA-FY-A3ON-10A-01D-A21Z-08_THCA	685	0	0	299	603	386	534	651	475	0	0	0	0	0	30	58	572
TCGA-FY-A3R6-10A-01D-A21Z-08_THCA	689	0	0	303	603	385	532	647	482	0	0	0	0	0	0	79	575
TCGA-FY-A3R7-10A-01D-A21Z-08_THCA	680	0	0	303	605	378	531	636	475	0	0	0	0	0	0	124	578
TCGA-FY-A3R8-10A-01D-A21Z-08_THCA	762	0	0	305	598	381	529	638	478	0	0	0	0	0	0	82	574
TCGA-FY-A3R9-10A-01D-A21Z-08_THCA	680	249	260	274	609	290	532	650	479	0	606	517	0	0	0	126	579
TCGA-FY-A3RA-10A-01D-A21Z-08_THCA	665	248	252	0	599	136	532	646	361	63	642	575	358	132	0	58	571
TCGA-FY-A3TY-10A-01D-A22Z-08_THCA	671	250	266	292	617	293	533	651	463	77	647	584	0	138	0	66	580
TCGA-FY-A3W9-10A-01D-A22D-08_THCA	689	0	0	290	589	386	529	638	465	0	0	0	0	0	0	79	572
TCGA-FY-A3WA-10A-01D-A22D-08_THCA	678	0	0	289	591	368	532	632	450	0	0	0	0	0	0	73	572
TCGA-FY-A3YR-10A-01D-A22Z-08_THCA	768	257	281	311	616	400	539	668	504	0	0	0	0	0	61	118	582
TCGA-FY-A40K-10A-01D-A23K-08_THCA	676	240	264	289	572	276	528	651	469	0	0	0	0	0	0	80	573
TCGA-FY-A40L-10A-01D-A23K-08_THCA	747	255	273	301	595	288	535	657	486	0	0	0	0	0	0	147	582
TCGA-FY-A40M-10A-01D-A23K-08_THCA	681	247	258	284	605	370	530	643	457	76	635	567	0	132	0	52	571
TCGA-FY-A40N-10A-01D-A23K-08_THCA	682	0	0	300	611	282	532	650	388	69	602	0	368	132	28	2	576
TCGA-FY-A4B0-10A-01D-A23U-08_THCA	688	0	0	297	598	276	527	627	464	0	0	0	0	0	0	89	569
TCGA-FY-A4B3-10A-01D-A23U-08_THCA	680	0	0	294	588	374	528	628	465	0	0	0	0	0	26	54	572
TCGA-FY-A4B4-10A-01D-A23U-08_THCA	752	248	267	294	623	293	537	648	493	0	613	574	0	0	0	147	582
TCGA-G2-A2EC-10A-01D-A17V-08_BLCA	682	230	128	280	575	365	524	615	384	0	584	0	350	134	0	71	580
TCGA-G2-A2EF-10A-01D-A18F-08_BLCA	663	243	257	280	599	365	534	639	377	63	630	569	0	135	0	54	577
TCGA-G2-A2EJ-10A-01D-A17V-08_BLCA	597	263	282	0	589	138	536	666	489	76	548	573	0	0	48	0	581
TCGA-G2-A2EK-10A-01D-A18F-08_BLCA	589	253	268	0	592	139	532	649	469	0	614	568	0	0	35	64	573
TCGA-G2-A2EL-10A-01D-A18F-08_BLCA	664	239	259	282	583	275	528	636	469	0	0	0	0	0	33	59	577
TCGA-G2-A3IB-10A-01D-A20D-08_BLCA	674	0	0	280	591	365	528	633	389	0	0	0	0	0	19	54	578
TCGA-G2-A3IE-10A-01D-A20D-08_BLCA	682	0	0	297	606	373	526	639	469	0	0	0	0	0	0	79	574
TCGA-G2-A3VY-10A-01D-A22Z-08_BLCA	681	255	0	354	621	404	533	655	472	88	644	0	394	143	0	105	581
TCGA-G3-A25S-10A-01D-A16V-10_LIHC	619	0	0	242	550	346	504	574	322	0	0	0	0	0	0	43	564
TCGA-G3-A25T-10A-01D-A16V-10_LIHC	593	0	0	218	467	411	427	533	0	0	410	244	172	154	0	0	523
TCGA-G3-A25U-10A-01D-A16V-10_LIHC	636	0	0	238	574	379	486	553	263	92	263	271	0	112	5	0	537
TCGA-G3-A25V-10A-01D-A16V-10_LIHC	583	119	177	172	490	298	469	537	312	0	303	326	0	0	0	29	541
TCGA-G3-A25Y-10A-01D-A16V-10_LIHC	653	0	0	241	474	397	514	558	0	95	398	397	187	163	0	0	563
TCGA-G3-A25Z-10A-01D-A16V-10_LIHC	599	134	131	209	295	285	480	517	272	0	283	0	192	151	0	28	549
TCGA-G3-A3CG-10A-01D-A20W-10_LIHC	665	261	291	241	646	421	532	591	338	0	475	503	307	175	0	29	570
TCGA-G3-A3CI-10A-01D-A20W-10_LIHC	686	279	334	208	531	364	544	626	357	0	0	0	0	0	21	46	582
TCGA-G3-A3CJ-10A-01D-A20W-10_LIHC	697	0	0	380	693	464	553	639	567	0	0	0	0	0	33	62	587
TCGA-G3-A3CK-10A-01D-A20W-10_LIHC	695	0	0	376	678	448	538	629	363	0	0	0	0	0	27	47	575
TCGA-G3-A5SI-10A-01D-A27I-10_LIHC	679	0	0	280	638	453	546	623	0	98	502	0	369	183	0	2	571
TCGA-G3-A5SJ-10A-01D-A27I-10_LIHC	684	0	0	375	664	381	538	633	341	0	453	516	0	179	0	81	592

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-G3-A5SK-10A-01D-A27I-10_LIHC	674	0	0	284	579	437	537	505	350	0	0	0	0	0	0	73	570
TCGA-G3-A5SL-10A-01D-A27I-10_LIHC	666	259	270	259	442	408	536	615	367	0	0	0	0	0	23	58	584
TCGA-G3-A5SM-10A-01D-A28X-10_LIHC	554	240	187	251	645	362	519	585	342	0	382	482	0	0	0	81	571
TCGA-G4-6293-10A-01D-1719-10_COAD	622	0	0	282	576	348	503	577	325	0	0	0	0	0	0	38	560
TCGA-G4-6294-10A-01D-1771-10_COAD	685	0	0	366	632	367	534	585	319	95	406	0	290	146	0	28	569
TCGA-G4-6295-10A-01D-1719-10_COAD	683	284	292	324	664	416	546	617	337	98	596	529	0	159	0	37	587
TCGA-G4-6297-10A-01D-1719-10_COAD	603	0	0	327	639	354	506	566	300	0	387	0	273	139	0	14	549
TCGA-G4-6298-10A-01D-1719-10_COAD	625	119	141	207	342	311	421	441	243	0	246	0	142	162	5	0	548
TCGA-G4-6299-10A-01D-1771-10_COAD	673	0	0	365	652	432	541	607	440	0	0	0	0	0	12	38	567
TCGA-G4-6302-10A-01D-1719-10_COAD	654	217	314	232	592	334	524	606	428	0	0	0	0	0	15	31	580
TCGA-G4-6303-10A-01D-1771-10_COAD	683	0	0	369	651	443	534	610	359	0	0	0	0	0	17	32	585
TCGA-G4-6304-10A-01D-1924-10_COAD	603	0	0	205	431	299	453	490	245	0	262	0	73	94	0	16	545
TCGA-G4-6306-10A-01D-1771-10_COAD	641	153	183	193	628	389	506	572	296	98	383	491	0	142	0	28	566
TCGA-G4-6307-10A-01D-1720-10_COAD	698	277	328	350	688	442	538	647	469	0	444	526	0	0	28	52	588
TCGA-G4-6309-10A-01D-1835-10_COAD	651	0	222	124	309	302	472	461	174	0	349	0	279	138	0	0	535
TCGA-G4-6310-10A-01D-1720-10_COAD	697	266	307	356	619	438	557	643	462	0	0	0	0	0	24	49	590
TCGA-G4-6314-10A-01D-1720-10_COAD	693	307	334	360	716	455	550	655	469	0	564	532	0	0	0	127	595
TCGA-G4-6315-10A-01D-1720-10_COAD	691	281	333	335	690	366	552	646	368	0	542	516	0	0	30	50	591
TCGA-G4-6317-10A-01D-1720-10_COAD	702	0	0	395	686	475	556	657	482	0	0	0	0	0	0	102	594
TCGA-G4-6320-10A-01D-1720-10_COAD	798	0	0	381	685	465	552	651	352	106	567	0	345	180	0	41	592
TCGA-G4-6321-10A-01D-1720-10_COAD	606	0	0	305	509	408	494	573	292	0	361	0	282	127	0	15	565
TCGA-G4-6323-10A-01D-1720-10_COAD	682	0	0	366	673	441	546	649	457	0	0	0	0	0	17	27	589
TCGA-G4-6586-10A-01D-1771-10_COAD	689	0	0	361	649	441	525	614	322	95	396	0	324	164	0	39	578
TCGA-G4-6588-10A-01D-1771-10_COAD	654	238	280	230	464	407	507	592	436	0	0	0	0	0	29	0	569
TCGA-G4-6626-10A-01D-1771-10_COAD	654	222	292	215	646	333	505	603	298	90	539	550	0	151	15	0	564
TCGA-G4-6628-10A-01D-1835-10_COAD	517	148	255	190	505	255	492	518	313	0	390	446	0	131	0	20	557
TCGA-G5-6233-10A-01D-1733-10_READ	686	272	298	329	687	317	538	608	448	0	535	501	0	0	12	29	589
TCGA-G5-6235-10A-01D-1733-10_READ	680	0	0	353	615	420	510	577	312	91	387	0	287	154	10	1	578
TCGA-G5-6572-10A-01D-1826-10_READ	642	108	230	248	539	310	504	579	335	0	0	0	0	0	0	39	565
TCGA-G5-6641-10A-01D-1826-10_READ	632	223	241	222	374	299	527	578	334	0	0	0	0	0	8	30	548
TCGA-G7-6789-10A-01D-1962-08_KIRP	689	0	0	308	608	398	534	652	483	0	0	0	0	0	28	81	577
TCGA-G7-6790-10A-01D-1962-08_KIRP	678	251	275	291	619	287	535	644	464	73	653	578	0	137	0	73	575
TCGA-G7-6792-10A-01D-1962-08_KIRP	692	0	0	348	632	391	534	655	492	0	0	0	0	0	36	88	575
TCGA-G7-6793-10A-01D-1962-08_KIRP	760	0	0	298	612	388	534	658	468	78	614	0	300	138	0	80	578
TCGA-G7-6795-10A-01D-1962-08_KIRP	755	0	0	308	607	397	534	653	461	76	635	0	366	137	0	77	577
TCGA-G7-6796-10A-01D-1962-08_KIRP	686	252	258	197	519	283	535	652	488	0	0	0	0	0	35	82	574
TCGA-G7-6797-10A-01D-1962-08_KIRP	761	0	0	301	619	295	535	661	473	81	641	571	0	135	0	77	579
TCGA-G7-7501-10A-01D-2201-08_KIRP	688	0	0	301	606	391	531	649	478	0	0	0	0	0	0	136	575
TCGA-G7-7502-10A-01D-2201-08_KIRP	687	0	0	305	596	386	529	642	476	0	0	0	0	0	39	0	571
TCGA-G7-A4TM-10B-01D-A31X-10_KIRP	536	0	0	243	579	419	487	599	342	0	0	0	0	0	0	15	543
TCGA-G9-6329-10A-01D-1961-08_PRAD	756	255	255	285	589	374	533	642	463	74	591	0	293	140	0	76	576
TCGA-G9-6332-10A-01D-1786-08_PRAD	685	253	270	299	597	380	532	651	481	0	0	0	0	0	0	99	580
TCGA-G9-6333-10A-01D-1961-08_PRAD	680	0	0	307	612	292	523	645	491	0	0	0	0	0	0	143	579
TCGA-G9-6336-10A-01D-1786-08_PRAD	642	236	260	282	594	373	531	638	0	79	631	563	369	137	0	2	571
TCGA-G9-6338-10A-01D-1961-08_PRAD	680	253	263	287	617	384	535	652	488	0	597	569	0	0	27	76	581
TCGA-G9-6339-10A-01D-A30X-08_PRAD	683	0	0	293	597	376	530	638	460	0	0	0	0	0	30	62	577
TCGA-G9-6342-10A-01D-1961-08_PRAD	682	247	268	287	573	388	532	651	488	0	0	0	0	0	0	95	577
TCGA-G9-6343-10A-01D-1961-08_PRAD	756	0	0	311	612	294	523	647	470	76	612	0	367	136	36	2	577
TCGA-G9-6347-10A-01D-A31J-08_PRAD	660	0	0	291	588	281	518	633	375	73	522	0	288	131	27	0	572
TCGA-G9-6348-10A-01D-1786-08_PRAD	687	0	0	297	604	388	533	653	383	83	581	0	360	129	0	74	575
TCGA-G9-6351-10A-01D-1961-08_PRAD	692	0	0	300	613	397	533	653	391	76	592	0	376	134	0	78	579
TCGA-G9-6353-10A-01D-1961-08_PRAD	685	0	0	305	610	288	525	658	481	0	0	0	0	0	0	100	579
TCGA-G9-6354-10A-01D-A30X-08_PRAD	748	0	0	293	590	380	529	639	379	74	573	551	0	133	28	0	571
TCGA-G9-6356-10A-01D-1786-08_PRAD	674	249	266	289	611	282	528	649	312	59	634	566	292	134	0	63	575
TCGA-G9-6361-10A-01D-1961-08_PRAD	760	0	0	308	606	386	531	647	474	0	0	0	0	0	0	138	576
TCGA-G9-6362-10A-01D-1786-08_PRAD	598	254	267	0	504	135	532	633	476	0	538	567	0	0	0	119	577
TCGA-G9-6363-10A-01D-1786-08_PRAD	679	241	264	286	508	369	528	648	390	71	608	0	362	134	30	1	574
TCGA-G9-6364-10A-01D-1786-08_PRAD	686	0	0	306	601	383	529	636	473	0	0	0	0	0	0	110	572
TCGA-G9-6365-10A-01D-1786-08_PRAD	633	237	262	277	504	277	529	625	470	0	0	0	0	0	0	111	577
TCGA-G9-6366-10A-01D-2115-08_PRAD	680	0	0	289	587	366	525	635	449	0	0	0	0	0	20	49	570
TCGA-G9-6367-10A-01D-1786-08_PRAD	673	0	0	300	599	376	526	653	469	0	0	0	0	0	23	59	575
TCGA-G9-6369-10A-01D-1961-08_PRAD	759	0	0	313	618	398	535	653	489	0	0	0	0	0	33	75	579
TCGA-G9-6370-10A-01D-1786-08_PRAD	657	243	249	281	612	281	525	640	478	0	596	511	0	0	0	124	575
TCGA-G9-6371-10A-01D-1786-08_PRAD	670	244	256	267	598	360	527	628	363	61	602	565	0	131	0	64	572
TCGA-G9-6373-10A-01D-1786-08_PRAD	687	0	0	305	610	396	531	652	462	77	607	0	299	135	0	74	575
TCGA-G9-6377-10A-01D-1961-08_PRAD	674	250	272	288	605	382	531	645	376	58	629	509	374	137	0	75	575
TCGA-G9-6378-10A-01D-1786-08_PRAD	675	244	254	281	573	374	534	646	214	70	612	515	362	132	0	2	573
TCGA-G9-6379-10A-01D-A31J-08_PRAD	684	0	0	298	600	384	532	634	467	0	0	0	0	0	28	66	577
TCGA-G9-6384-10A-01D-1786-08_PRAD	685	0	0	303	598	384	530	652	474	0	0	0	0	0	31	63	573
TCGA-G9-6385-10A-01D-1786-08_PRAD	594	254	271	0	577	133	531	637	0	86	635	568	0	137	0	0	575
TCGA-G9-6494-10A-01D-1786-08_PRAD	681	247	258	290	606	378	532	654	389	78	621	571	0	135	0	63	576
TCGA-G9-6496-10A-01D-1786-08_PRAD	682	0	0	308	601	380	522	632	403	0	0	0	0	0	0	97	580
TCGA-G9-6498-10A-01D-A30X-08_PRAD	682	0	0	294	573	378	528	619	394	0	0	0	0	0	0	77	571
TCGA-G9-6499-10A-01D-1961-08_PRAD	686	251	264	290	593	383	531	654	0	78	634	0	380	141	0	0	577
TCGA-G9-7510-10A-01D-2260-08_PRAD	681	235	240	268	564	353	530	634	465	0	0	0	0	0	28	54	575
TCGA-G9-7519-10A-01D-2260-08_PRAD	593	255	264	0	0	0	532	641	385	66	578	565	0	135	28	0	573
TCGA-G9-7521-10A-01D-2260-08_PRAD	590	255	265	0	571	139	529	638	463	0	598	567	0	0	0	92	576
TCGA-G9-7522-10A-01D-2260-08_PRAD	685	0	0	293	593	381	533	641	384	72	592	0	353	130	22	0	572
TCGA-G9-7523-10A-01D-2260-08_PRAD	647	244	254	287	600	274	527	639	473	0	533	513	0	0	0	122	579
TCGA-G9-7525-10A-01D-2260-08_PRAD	679	0	0	309	612	386	531	655	478	0	0	0	0	0	33	68	578
TCGA-GC-A3BM-10A-01D-A22Z-08_BLCA	743	248	269	298	532	385	539	645	484	0	0	0	0	0	0	164	577
TCGA-GC-A3I6-10A-01D-A20D-08_BLCA	680	0	0	285	607	376	528	644	461	0	0	0	0	0	0	82	573
TCGA-GC-A3OO-10C-01D-A22Z-08_BLCA	735	247	259	281	616	382	535	648	480	0	609	569	0	0	25	66	581
TCGA-GC-A3RB-10A-01D-A21Z-08_BLCA	689	0	0	303	597	375	529	639	476	0	0	0	0	0	0	116	576
TCGA-GC-A3RC-10B-01D-A22Z-08_BLCA	756	0	0	312	619	406	538	646	383	79	532	0	376	140	0	87	579
TCGA-GC-A3RD-10B-01D-A22Z-08_BLCA	759	262	262	303	572	387	534	655	477	76	580	0	383	138	0	76	580
TCGA-GC-A3WC-10A-01D-A22Z-08_BLCA	747	256	268	282	619	393	532	651	487	0	603	571	0	0	0	142	579
TCGA-GC-A3YS-10A-01D-A23K-08_BLCA	761	0	0	314	624	403	537	666	396	87	635	520	374	140	0	78	581
TCGA-GC-A4ZW-10A-01D-A26K-08_BLCA	677	0	0	301	590	360	529	625	459	0	0	0	0	0	0	80	575
TCGA-GC-A6I1-10A-01D-A31J-08_BLCA	687	0	0	300	604	385	532	643	386	76	610	0	365	138	0	59	579
TCGA-GC-A6I3-10A-01D-A31J-08_BLCA	599	254	276	0	0	0	0	0	0	0	635	0	392	142	0	0	578
TCGA-GD-A2C5-10A-01D-A17V-08_BLCA	759	0	0	348	617	394	535	664	458	78	599	0	306	140	0	85	579
TCGA-GD-A3OP-10A-01D-A21Z-08_BLCA	671	249	261	290	560	380	531	651	470	0	0	0	0	0	28	66	572
TCGA-GD-A3OQ-10A-01D-A21Z-08_BLCA	758	0	0	299	608	384	533	644	455	73	616	0	295	133	0	69	575
TCGA-GD-A3OS-10A-01D-A21Z-08_BLCA	686	0	0	303	613	384	529	641	486	0	0	0	0	0	0	147	571
TCGA-GD-A6C6-10A-01D-A31J-08_BLCA	750	248	265	289	586	287	537	642	447	77	596	0	297	137	29	0	578

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-GD-A76B-10A-01D-A329-08_BLCA	650	229	252	271	608	348	528	639	379	55	635	496	287	139	22	0	572
TCGA-GE-A2C6-10A-01D-A16O-08_THCA	665	238	265	288	604	377	533	645	474	0	594	564	0	0	33	68	575
TCGA-GF-A2C7-10A-01D-A199-08_SKCM	684	0	0	310	610	383	530	632	471	0	0	0	0	0	0	134	579
TCGA-GF-A3OT-10A-01D-A23B-08_SKCM	677	245	262	291	589	374	532	655	478	0	0	0	0	0	31	67	577
TCGA-GF-A4EO-10A-01D-A24R-08_SKCM	679	235	256	286	564	372	531	640	475	0	0	0	0	0	31	64	574
TCGA-GF-A6C8-10A-01D-A30X-08_SKCM	682	0	0	283	593	357	531	635	375	59	560	0	287	136	22	0	573
TCGA-GF-A6C9-10A-01D-A30X-08_SKCM	594	256	269	0	0	0	530	632	475	0	0	0	0	0	0	95	575
TCGA-GF-A769-10A-01D-A32N-08_SKCM	597	259	271	0	0	0	531	637	480	0	0	0	0	0	42	0	576
TCGA-GJ-A6C0-10A-01D-A30V-10_LIHC	605	0	0	256	516	346	482	460	337	0	0	0	0	0	10	30	541
TCGA-GL-6846-10A-01D-1962-08_KIRP	688	254	267	291	619	396	532	650	481	0	610	569	0	0	0	140	578
TCGA-GL-7773-10A-01D-2136-08_KIRP	598	255	270	0	573	134	530	649	467	0	575	513	0	0	0	93	575
TCGA-GL-7966-10A-01D-2201-08_KIRP	684	0	0	298	604	282	529	644	480	0	0	0	0	0	0	121	576
TCGA-GL-8500-10A-01D-2396-08_KIRP	755	244	261	287	606	288	530	634	412	0	611	512	0	0	0	127	572
TCGA-GL-A4EM-10A-01D-A25F-10_KIRP	682	0	0	378	670	450	548	633	366	0	0	0	0	0	0	108	580
TCGA-GL-A59R-10A-01D-A26P-10_KIRP	676	0	0	284	637	377	539	613	311	0	418	0	346	178	0	46	581
TCGA-GL-A59T-10A-01D-A28G-10_KIRP	578	241	284	254	491	427	534	638	356	0	0	0	0	0	23	59	578
TCGA-GM-A2DA-10C-01D-A18P-09_BRCA	687	322	363	0	0	0	554	652	568	0	0	0	0	0	58	0	590
TCGA-GM-A2DB-10C-01D-A18P-09_BRCA	677	303	339	352	650	447	552	639	470	0	0	0	0	0	0	108	591
TCGA-GM-A2DC-10C-01D-A18P-09_BRCA	661	0	0	356	677	447	531	637	449	0	0	0	0	0	26	45	583
TCGA-GM-A2DD-10C-01D-A17W-09_BRCA	695	312	330	225	703	376	557	654	573	0	612	535	0	0	38	63	591
TCGA-GM-A2DF-10C-01D-A17W-09_BRCA	696	0	0	381	713	464	557	661	471	0	0	0	0	0	49	69	589
TCGA-GM-A2DH-10C-01D-A17W-09_BRCA	698	0	0	380	707	386	555	660	465	105	636	0	373	183	0	83	593
TCGA-GM-A2DK-10C-01D-A17W-09_BRCA	688	0	0	380	695	455	553	657	477	0	0	0	0	0	0	111	589
TCGA-GM-A2DL-10C-01D-A18P-09_BRCA	691	0	0	376	703	453	553	646	470	0	0	0	0	0	0	97	584
TCGA-GM-A2DM-10C-01D-A17W-09_BRCA	677	291	359	360	704	454	557	655	440	105	651	538	370	171	31	2	590
TCGA-GM-A2DN-10C-01D-A17W-09_BRCA	695	315	352	367	665	449	558	653	482	0	0	0	0	0	33	60	594
TCGA-GM-A2DO-10D-01D-A18P-09_BRCA	690	0	351	373	704	464	553	658	471	0	617	0	390	0	66	0	590
TCGA-GM-A3NW-10A-01D-A22A-09_BRCA	688	296	335	324	626	445	554	633	553	0	0	0	0	0	32	51	587
TCGA-GM-A3NY-10A-01D-A21Q-09_BRCA	694	0	0	374	680	372	545	639	465	0	0	0	0	0	31	51	591
TCGA-GM-A3XG-10A-01D-A243-09_BRCA	672	0	0	348	661	442	550	620	443	0	0	0	0	0	28	40	578
TCGA-GM-A3XL-10A-01D-A22X-09_BRCA	677	276	305	316	559	431	550	615	449	0	0	0	0	0	48	3	582
TCGA-GM-A3XN-10A-01D-A22X-09_BRCA	692	283	339	324	685	428	548	620	452	0	562	528	0	0	0	80	583
TCGA-GM-A4E0-10A-01D-A25Q-09_BRCA	696	328	370	0	197	88	554	655	356	98	597	0	372	182	0	69	591
TCGA-GM-A5PV-10A-01D-A28E-09_BRCA	692	0	0	332	658	452	550	607	544	0	0	0	0	0	0	68	572
TCGA-GM-A5PX-10A-01D-A28E-09_BRCA	588	319	361	0	678	182	552	642	331	98	651	586	0	177	0	51	590
TCGA-GN-A261-10A-01D-A199-08_SKCM	682	236	256	274	605	363	528	638	475	0	611	505	0	0	0	105	574
TCGA-GN-A262-10A-01D-A198-08_SKCM	596	259	276	0	0	0	530	642	451	70	590	0	359	139	28	0	575
TCGA-GN-A263-10A-01D-A198-08_SKCM	598	236	271	261	537	277	533	646	379	84	582	0	305	137	0	54	572
TCGA-GN-A264-10A-01D-A198-08_SKCM	677	0	0	295	596	271	523	603	369	0	0	0	0	134	0	57	572
TCGA-GN-A265-10A-01D-A199-08_SKCM	689	0	0	300	612	386	534	649	479	0	0	0	0	0	0	114	575
TCGA-GN-A266-10A-01D-A199-08_SKCM	684	251	256	275	609	382	533	651	480	0	593	560	0	0	0	143	579
TCGA-GN-A267-10A-01D-A198-08_SKCM	683	0	0	300	606	380	527	635	476	0	0	0	0	0	0	123	574
TCGA-GN-A268-10A-01D-A198-08_SKCM	662	239	248	262	552	360	528	631	379	0	520	0	281	133	29	0	574
TCGA-GN-A269-10A-01D-A19A-08_SKCM	687	0	0	294	599	383	531	640	476	0	0	0	0	0	0	97	575
TCGA-GN-A26A-10A-01D-A19A-08_SKCM	711	248	259	280	569	281	533	657	410	0	0	0	0	0	22	65	578
TCGA-GN-A26C-10A-01D-A19A-08_SKCM	660	229	263	262	567	340	527	644	471	0	0	0	0	0	16	43	577
TCGA-GN-A26D-10A-01D-A19A-08_SKCM	679	0	0	281	572	279	519	626	475	0	0	0	0	0	0	97	574
TCGA-GN-A4U3-10F-01D-A32N-08_SKCM	685	0	0	308	627	383	531	647	480	0	0	0	0	0	0	91	574
TCGA-GN-A4U4-10B-01D-A32N-08_SKCM	688	0	0	311	617	384	531	657	458	79	615	0	300	138	0	75	573
TCGA-GN-A4U5-10B-01D-A32N-08_SKCM	759	0	0	295	608	288	532	644	482	0	0	0	0	0	0	81	575
TCGA-GN-A4U7-10B-01D-A32N-08_SKCM	596	257	272	0	562	133	530	641	474	0	581	564	0	0	35	0	578
TCGA-GN-A4U8-10B-01D-A32N-08_SKCM	686	0	0	301	606	386	531	649	477	0	0	0	0	0	26	63	572
TCGA-GN-A4U9-10B-01D-A32N-08_SKCM	673	245	264	266	607	285	529	653	382	71	639	516	367	134	0	72	574
TCGA-GR-A4D4-10A-01D-A31X-10_DLBC	534	0	0	265	506	368	496	587	324	0	0	0	0	0	0	1	553
TCGA-GR-A4D5-10A-01D-A31X-10_DLBC	655	0	0	245	484	433	513	555	279	0	407	0	332	138	0	33	563
TCGA-GR-A4D6-10A-01D-A31X-10_DLBC	601	0	0	267	485	412	481	565	314	0	230	0	222	155	0	1	552
TCGA-GR-A4D9-10A-01D-A31X-10_DLBC	510	155	225	232	409	337	503	599	337	0	0	0	0	0	0	52	562
TCGA-GU-A42P-10A-01D-A23U-08_BLCA	671	0	0	277	602	371	528	650	376	74	622	503	293	129	0	60	575
TCGA-GU-A42Q-10A-01D-A23U-08_BLCA	593	248	263	0	9	31	529	628	302	74	553	0	281	132	0	35	572
TCGA-GU-A42R-10A-01D-A23K-08_BLCA	685	0	0	301	608	379	532	650	460	77	607	0	296	136	33	5	575
TCGA-GU-A762-10A-01D-A339-08_BLCA	664	0	0	289	592	376	528	624	361	70	525	0	361	129	0	51	574
TCGA-GU-A763-10A-01D-A329-08_BLCA	655	224	253	254	553	330	529	641	396	0	0	0	0	0	23	45	573
TCGA-GU-A766-10A-01D-A329-08_BLCA	684	0	0	293	606	376	533	634	472	0	0	0	0	0	36	0	572
TCGA-GU-A767-10A-01D-A329-08_BLCA	674	240	252	292	582	351	534	636	473	0	0	0	0	0	0	77	580
TCGA-GV-A3JV-10B-01D-A21Z-08_BLCA	682	0	0	306	603	387	535	646	470	0	0	0	0	0	0	87	575
TCGA-GV-A3JW-10A-01D-A20D-08_BLCA	597	259	270	0	550	134	531	644	391	77	629	572	0	132	0	56	578
TCGA-GV-A3JX-10A-01D-A20D-08_BLCA	675	239	258	276	578	273	533	651	479	0	0	0	0	0	33	71	577
TCGA-GV-A3JZ-10A-01D-A21A-08_BLCA	673	0	0	284	597	280	520	641	470	0	0	0	0	0	0	110	577
TCGA-GV-A3QF-10A-01D-A22Z-08_BLCA	765	0	0	316	619	399	532	656	489	0	0	0	0	0	0	121	582
TCGA-GV-A3QG-10A-01D-A21Z-08_BLCA	686	247	266	287	596	376	533	655	479	0	0	0	0	0	0	100	579
TCGA-GV-A3QH-10A-01D-A21Z-08_BLCA	685	0	0	299	594	387	528	648	470	0	0	0	0	0	33	60	575
TCGA-GV-A3QI-10A-01D-A21Z-08_BLCA	691	0	0	299	603	289	532	646	466	78	611	0	367	133	0	68	578
TCGA-GV-A3QK-10A-01D-A23K-08_BLCA	671	233	264	290	562	378	531	641	471	0	0	0	0	0	37	3	574
TCGA-GV-A40E-10A-01D-A23K-08_BLCA	744	254	274	297	601	294	517	629	390	0	592	0	379	143	0	90	580
TCGA-GV-A40G-10A-01D-A23K-08_BLCA	687	0	0	304	610	387	529	652	482	0	0	0	32	0	0	134	576
TCGA-GV-A6ZA-10A-01D-A339-08_BLCA	654	208	239	248	464	339	516	614	290	0	496	0	272	132	13	0	567
TCGA-H2-A26U-10A-01D-A16O-08_THCA	755	254	267	290	591	379	535	656	484	0	0	0	0	0	36	73	576
TCGA-H2-A2K9-10A-01D-A17V-08_THCA	685	250	277	296	595	284	533	645	485	0	0	0	0	0	0	142	579
TCGA-H2-A3RH-10A-01D-A21Z-08_THCA	685	0	0	300	604	288	519	644	469	0	0	0	0	0	0	82	573
TCGA-H2-A3RI-10A-01D-A21Z-08_THCA	758	248	249	284	564	366	526	613	387	0	608	0	361	135	0	61	580
TCGA-H2-A421-10A-01D-A23K-08_THCA	685	0	0	305	608	393	530	656	474	0	0	0	0	38	32	58	575
TCGA-H2-A422-10A-01D-A23K-08_THCA	761	254	250	307	601	376	539	662	496	0	0	0	0	0	38	76	580
TCGA-H4-A2HO-10A-01D-A17V-08_BLCA	599	260	283	0	43	0	533	657	484	0	0	0	0	0	34	85	577
TCGA-H4-A2HQ-10A-01D-A17V-08_BLCA	680	249	265	291	590	138	533	648	493	0	0	0	0	0	0	147	576
TCGA-H5-A2HR-10A-01D-A17W-09_UCEC	697	298	331	325	669	454	548	632	427	0	579	0	349	0	0	48	558
TCGA-H6-8124-10A-01D-2396-08_PAAD	591	249	265	0	0	0	529	640	379	67	548	0	291	131	0	72	571
TCGA-H6-A45N-10A-01D-A26I-08_PAAD	681	0	0	300	587	383	528	624	463	0	0	0	0	0	0	80	574
TCGA-H7-7774-10A-01D-2078-08_HNSC	660	234	244	258	495	356	529	630	402	0	0	0	0	0	31	0	572
TCGA-H7-8501-10A-01D-2394-08_HNSC	683	241	257	282	608	372	528	634	476	0	523	512	0	0	0	115	576
TCGA-H7-8502-10A-01D-2394-08_HNSC	671	240	249	277	606	366	526	627	471	0	511	511	0	0	0	98	575
TCGA-H7-A6C4-10A-01D-A30H-08_HNSC	674	265	279	0	570	136	536	652	489	0	606	573	0	0	0	134	582
TCGA-H7-A6C5-10A-01D-A30H-08_HNSC	676	271	283	0	607	146	538	659	477	76	662	586	0	143	0	75	581
TCGA-H8-A6C1-10A-01D-A32N-08_PAAD	678	236	246	282	542	360	530	639	473	0	0	0	0	0	0	82	572
TCGA-H9-7775-10A-01D-2115-08_PRAD	671	0	0	294	600	286	520	640	463	0	0	0	0	0	0	103	575
TCGA-H9-A6BX-10A-01D-A30X-08_PRAD	680	0	0	296	595	366	522	628	466	0	0	0	0	0	0	96	575
TCGA-H9-A6BY-10A-01D-A30H-08_PRAD	762	258	277	307	604	397	537	657	495	0	0	0	0	0	46	102	579

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-HB-A2OT-10A-01D-A21Q-09_SARC	701	299	327	198	694	443	551	634	550	0	586	536	0	0	36	57	585
TCGA-HB-A3L4-10A-01D-A21Q-09_SARC	683	0	0	368	655	427	544	614	446	0	0	0	0	0	0	82	585
TCGA-HB-A3YV-10A-01D-A24N-09_SARC	649	287	308	281	671	345	546	611	541	0	465	485	0	0	0	71	580
TCGA-HB-A43Z-10A-01D-A24N-09_SARC	697	0	0	370	683	464	548	633	551	0	0	0	0	0	0	90	584
TCGA-HB-A5W3-10A-01D-A29N-09_SARC	692	0	0	258	668	450	535	620	326	0	545	0	351	166	0	49	580
TCGA-HC-7075-10A-01D-1961-08_PRAD	683	0	0	303	603	287	522	644	477	0	0	0	0	0	31	60	580
TCGA-HC-7077-10A-01D-1961-08_PRAD	600	264	273	0	0	0	530	619	466	0	600	0	371	138	25	1	578
TCGA-HC-7078-10A-01D-2115-08_PRAD	745	235	249	253	493	354	526	628	374	69	526	0	283	129	0	54	575
TCGA-HC-7079-10A-01D-1961-08_PRAD	679	0	0	204	606	293	534	647	476	0	0	0	0	0	0	109	578
TCGA-HC-7080-10A-01D-1961-08_PRAD	692	0	0	313	604	389	535	650	490	0	0	0	0	0	0	134	578
TCGA-HC-7081-10A-01D-1962-08_PRAD	688	0	0	304	599	386	532	646	487	0	0	0	0	0	32	71	581
TCGA-HC-7209-10A-01D-2115-08_PRAD	685	0	0	298	602	285	521	635	470	0	0	0	0	0	0	115	576
TCGA-HC-7210-10A-01D-2115-08_PRAD	690	253	262	289	585	376	530	651	474	0	0	0	0	0	37	82	575
TCGA-HC-7212-10A-01D-2115-08_PRAD	690	0	0	295	597	385	530	652	479	0	0	0	0	0	0	82	579
TCGA-HC-7213-10A-01D-2115-08_PRAD	659	248	254	272	584	274	529	658	478	0	0	0	0	0	25	68	574
TCGA-HC-7230-10A-01D-2115-08_PRAD	676	0	0	281	593	364	530	636	469	0	0	0	0	0	18	50	575
TCGA-HC-7231-10A-01D-2115-08_PRAD	688	0	0	306	601	394	537	647	454	75	615	0	366	133	36	1	579
TCGA-HC-7232-10A-01D-2115-08_PRAD	687	248	256	188	577	276	535	643	392	77	616	0	364	131	28	0	581
TCGA-HC-7233-10A-01D-2115-08_PRAD	689	0	0	303	607	376	529	649	439	81	609	529	0	136	0	67	575
TCGA-HC-7736-10A-01D-2115-08_PRAD	684	252	265	295	635	376	531	654	467	87	636	511	368	134	35	3	577
TCGA-HC-7738-10A-01D-2115-08_PRAD	674	243	247	298	499	273	529	632	471	0	0	0	0	0	0	74	575
TCGA-HC-7740-10A-01D-2115-08_PRAD	667	253	270	0	554	135	523	620	0	80	650	511	372	139	0	0	573
TCGA-HC-7742-10A-01D-2115-08_PRAD	679	241	250	274	611	371	530	637	436	68	629	563	0	131	0	50	576
TCGA-HC-7744-10A-01D-2115-08_PRAD	688	0	0	306	595	388	532	653	386	73	609	0	361	137	0	65	572
TCGA-HC-7745-10A-01D-2115-08_PRAD	681	0	0	303	607	378	528	649	484	0	0	0	0	0	24	62	576
TCGA-HC-7747-10A-01D-2115-08_PRAD	689	0	0	306	609	387	533	646	478	0	0	0	0	0	0	99	576
TCGA-HC-7748-10A-01D-2115-08_PRAD	689	0	0	306	609	386	532	649	479	0	0	0	0	0	0	139	574
TCGA-HC-7749-10A-01D-2115-08_PRAD	688	0	0	298	602	368	528	646	375	73	564	0	352	138	29	0	574
TCGA-HC-7750-10A-01D-2115-08_PRAD	676	0	0	295	603	288	513	644	373	76	525	0	346	132	0	54	572
TCGA-HC-7752-10A-01D-2115-08_PRAD	680	0	0	301	604	294	523	643	477	0	0	0	0	0	28	64	575
TCGA-HC-7817-10A-01D-A29Q-08_PRAD	742	242	272	297	617	284	534	659	481	0	604	572	0	0	38	73	576
TCGA-HC-7818-10A-01D-2115-08_PRAD	684	0	0	298	605	285	524	648	464	78	623	0	367	133	0	71	578
TCGA-HC-7819-10A-01D-2115-08_PRAD	672	242	250	273	550	366	527	646	465	0	0	0	0	0	0	74	573
TCGA-HC-7820-10A-01D-2115-08_PRAD	680	0	0	304	596	284	522	649	478	0	0	0	0	0	0	121	579
TCGA-HC-7821-10A-01D-2115-08_PRAD	685	0	0	302	603	386	530	652	451	67	610	0	364	128	0	72	578
TCGA-HC-8213-10A-01D-A29Q-08_PRAD	760	0	0	310	610	395	532	638	477	0	0	0	0	0	0	135	577
TCGA-HC-8216-10A-01D-A29Q-08_PRAD	760	0	0	309	619	385	532	646	478	0	0	0	0	0	0	114	578
TCGA-HC-8256-10A-01D-2260-08_PRAD	596	257	268	0	546	132	532	643	388	74	626	514	367	131	0	68	577
TCGA-HC-8257-10A-01D-2260-08_PRAD	678	251	260	287	616	285	531	650	483	0	617	568	0	0	0	138	576
TCGA-HC-8258-10A-01D-2260-08_PRAD	665	242	249	270	511	358	533	639	457	0	0	0	0	0	31	67	576
TCGA-HC-8259-10A-01D-2260-08_PRAD	595	249	265	0	594	137	531	637	367	70	630	571	359	132	22	0	575
TCGA-HC-8260-10A-01D-2260-08_PRAD	681	0	0	293	593	383	527	644	450	0	0	0	0	0	29	0	568
TCGA-HC-8261-10A-01D-2260-08_PRAD	679	0	0	294	599	381	533	646	472	76	587	511	0	0	0	100	576
TCGA-HC-8262-10A-01D-2260-08_PRAD	591	254	269	0	599	136	534	651	479	75	633	568	0	0	32	3	573
TCGA-HC-8264-10A-01D-2395-08_PRAD	676	246	261	287	590	282	530	646	477	0	0	0	0	0	36	5	579
TCGA-HC-8265-10A-01D-2260-08_PRAD	594	251	270	0	0	0	0	0	0	0	618	0	372	140	0	0	574
TCGA-HC-8266-10A-01D-2260-08_PRAD	663	256	270	0	512	131	531	648	470	0	577	563	0	0	34	66	573
TCGA-HC-A48F-10A-01D-A25A-08_PRAD	598	260	276	0	555	137	532	648	477	0	605	517	0	0	35	74	573
TCGA-HC-A4ZV-10A-01D-A26K-08_PRAD	689	0	0	307	608	389	533	648	487	0	0	0	0	0	30	70	576
TCGA-HC-A631-10A-01D-A29Q-08_PRAD	762	0	0	309	617	293	533	651	487	0	0	0	0	0	0	141	579
TCGA-HC-A632-10A-01D-A29Q-08_PRAD	671	256	269	300	569	377	532	612	462	0	609	0	374	139	0	82	582
TCGA-HC-A6AL-10A-01D-A30H-08_PRAD	762	0	0	317	619	400	539	657	465	71	597	0	381	142	0	98	581
TCGA-HC-A6AN-10A-01D-A30H-08_PRAD	759	0	0	307	619	407	537	650	486	0	0	0	0	0	41	94	582
TCGA-HC-A6AO-10A-01D-A30H-08_PRAD	766	0	0	323	624	411	537	648	492	0	0	0	0	0	0	194	582
TCGA-HC-A6AP-10A-01D-A30H-08_PRAD	752	249	269	291	642	297	539	648	465	71	644	575	375	137	39	0	581
TCGA-HC-A6AQ-10A-01D-A30H-08_PRAD	752	250	0	303	626	387	536	656	471	75	613	0	382	141	0	87	582
TCGA-HC-A6AS-10A-01D-A30H-08_PRAD	755	0	0	359	614	395	530	653	397	58	603	0	383	139	0	75	582
TCGA-HC-A6HX-10A-01D-A31J-08_PRAD	686	0	0	295	597	382	533	634	464	0	0	0	0	0	0	71	573
TCGA-HC-A6HY-10A-01D-A31J-08_PRAD	666	235	259	278	547	282	528	647	387	76	587	0	297	138	27	1	572
TCGA-HC-A76W-10A-01D-A33W-08_PRAD	687	0	0	296	600	358	525	645	457	0	0	0	0	0	0	62	577
TCGA-HC-A76X-10A-01D-A33W-08_PRAD	682	0	0	293	604	374	535	647	384	72	596	0	367	137	24	0	571
TCGA-HD-7229-10A-01D-2013-08_HNSC	681	260	272	293	602	383	533	655	483	0	0	0	0	0	47	0	580
TCGA-HD-7753-10A-01D-2078-08_HNSC	684	0	0	292	561	377	529	622	470	0	0	0	0	0	0	99	569
TCGA-HD-7754-10A-01D-2078-08_HNSC	677	237	258	281	545	360	525	634	464	0	0	0	0	0	0	72	572
TCGA-HD-7831-10A-01D-2129-08_HNSC	591	259	275	0	581	135	531	647	463	0	601	561	77	0	31	69	572
TCGA-HD-7832-10A-01D-2129-08_HNSC	672	250	261	195	610	282	529	646	470	0	605	566	0	0	30	69	577
TCGA-HD-7917-10A-01D-2229-08_HNSC	689	0	0	308	624	391	529	642	390	72	600	0	289	135	31	0	577
TCGA-HD-8224-10A-01D-2394-08_HNSC	675	243	251	285	561	377	526	645	399	0	0	0	0	0	27	60	573
TCGA-HD-8314-10A-01D-2394-08_HNSC	678	245	264	290	588	271	531	651	474	0	0	0	0	0	27	66	576
TCGA-HD-8634-10A-01D-2394-08_HNSC	672	249	262	291	560	281	530	646	454	77	606	480	0	134	33	5	574
TCGA-HD-8635-10A-01D-2394-08_HNSC	680	239	263	289	554	368	531	641	388	78	613	0	365	133	0	56	577
TCGA-HD-A4C1-10A-02D-A24F-08_HNSC	762	0	0	319	622	392	535	657	484	0	0	0	0	0	0	163	580
TCGA-HD-A6HZ-10A-01D-A31J-08_HNSC	672	225	255	273	494	367	532	626	397	0	0	0	0	0	30	43	570
TCGA-HD-A6I0-10A-01D-A31J-08_HNSC	672	0	0	300	577	364	528	630	465	0	0	0	0	0	0	102	570
TCGA-HE-7128-10A-01D-1962-08_KIRP	760	0	0	309	609	400	536	665	485	76	615	0	308	0	0	117	577
TCGA-HE-7129-10A-01D-1962-08_KIRP	687	0	0	310	611	389	531	654	497	0	0	0	0	0	0	144	578
TCGA-HE-7130-10A-01D-1962-08_KIRP	755	254	0	287	620	287	534	648	467	73	607	0	373	140	0	70	577
TCGA-HE-A5NF-10A-01D-A26P-10_KIRP	654	255	174	256	480	354	539	599	358	0	0	0	0	0	22	55	582
TCGA-HE-A5NH-10A-01D-A26P-10_KIRP	655	0	0	261	618	438	525	604	357	0	0	0	0	0	0	76	554
TCGA-HE-A5NI-10A-01D-A26P-10_KIRP	672	170	286	244	648	443	549	613	340	0	469	492	347	175	0	59	585
TCGA-HE-A5NJ-10A-01D-A26P-10_KIRP	672	0	0	277	642	453	544	591	360	0	0	0	0	0	0	89	578
TCGA-HE-A5NK-10A-01D-A26P-10_KIRP	690	174	240	260	663	444	549	608	343	93	497	513	351	169	0	65	584
TCGA-HE-A5NL-10A-01D-A26P-10_KIRP	681	0	0	273	538	451	538	626	359	0	0	0	0	0	0	109	580
TCGA-HF-7131-10A-01D-2053-08_STAD	595	251	266	0	550	133	531	649	378	77	618	566	350	133	34	0	572
TCGA-HF-7132-10A-01D-2053-08_STAD	657	0	250	269	595	366	533	636	377	0	588	0	369	0	25	55	575
TCGA-HF-7133-10A-01D-2053-08_STAD	681	237	256	277	605	371	530	649	398	0	591	562	0	0	24	61	574
TCGA-HF-7134-10A-01D-2053-08_STAD	663	245	258	288	603	354	528	645	471	0	598	519	0	0	31	57	572
TCGA-HF-7136-10A-01D-2053-08_STAD	680	245	243	278	506	274	532	644	476	0	0	0	0	0	29	51	579
TCGA-HF-A5NB-10A-01D-A31J-08_STAD	676	240	260	281	575	0	527	619	380	0	0	0	0	134	30	0	575
TCGA-HG-A2PA-10B-01D-A20U-09_CESC	674	307	333	336	686	439	549	647	459	0	570	540	0	0	31	43	588
TCGA-HI-7168-10A-01D-2115-08_PRAD	724	241	256	280	609	278	531	641	360	72	620	568	0	134	0	62	572
TCGA-HI-7169-10A-01D-2115-08_PRAD	674	247	256	288	587	377	530	654	478	0	0	0	0	0	0	129	577
TCGA-HI-7170-10A-01D-2115-08_PRAD	662	235	233	253	493	361	528	628	290	69	508	0	282	132	0	51	572
TCGA-HI-7171-10A-01D-2115-08_PRAD	682	0	0	310	595	286	518	651	408	0	0	0	0	0	28	67	575
TCGA-HJ-7597-10A-01D-2201-08_STAD	674	0	0	304	609	369	532	652	368	76	583	0	332	127	30	0	579
TCGA-HL-7533-10A-01D-2229-08_HNSC	681	0	0	301	587	359	528	625	392	0	0	0	0	0	0	93	575

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-HM-A3JJ-10A-01D-A21Q-09_CESC	701	0	0	360	702	456	551	630	549	0	0	0	0	0	37	58	591
TCGA-HM-A3JK-10A-01D-A21Q-09_CESC	690	0	0	365	663	375	540	638	447	0	0	0	0	0	0	85	583
TCGA-HM-A4S6-10A-01D-A26G-09_CESC	682	0	0	353	679	448	555	632	321	91	555	41	356	168	0	57	582
TCGA-HN-A2NL-10A-01D-A18P-09_BRCA	777	301	345	367	710	376	549	655	454	104	653	537	378	176	0	56	593
TCGA-HN-A2OB-10B-01D-A27P-09_BRCA	694	0	0	367	667	450	548	537	438	0	0	0	0	0	0	75	583
TCGA-HP-A5MZ-10A-01D-A27I-10_LIHC	644	240	240	243	517	358	533	612	355	0	343	457	0	0	0	56	587
TCGA-HP-A5N0-10A-01D-A28X-10_LIHC	663	252	297	246	517	435	535	637	347	0	0	0	0	0	0	95	567
TCGA-HQ-A2OE-10A-01D-A202-08_BLCA	672	0	0	288	600	368	526	639	460	0	0	0	0	0	23	46	575
TCGA-HQ-A2OF-10B-01D-A26K-08_BLCA	670	0	0	280	569	377	531	628	445	0	0	0	0	0	0	66	573
TCGA-HQ-A5ND-10A-01D-A26K-08_BLCA	762	0	0	355	622	400	534	653	488	0	0	0	0	0	64	6	581
TCGA-HQ-A5NE-10A-01D-A289-08_BLCA	757	0	0	308	613	288	524	652	487	0	0	0	0	0	37	69	577
TCGA-HR-A2OG-10A-01D-A199-08_SKCM	636	202	226	160	466	252	508	610	438	0	0	0	0	0	21	35	575
TCGA-HR-A2OH-10A-01D-A199-08_SKCM	670	237	242	272	504	356	514	586	376	0	511	0	288	136	0	44	575
TCGA-HR-A5NC-10A-01D-A27N-08_SKCM	669	243	274	279	584	362	530	638	468	0	0	0	0	0	37	1	571
TCGA-HS-A5N7-10A-01D-A26G-09_SARC	647	278	304	208	511	429	548	611	533	0	0	0	0	0	30	40	585
TCGA-HS-A5N8-10A-01D-A26G-09_SARC	696	0	0	360	670	375	550	629	461	0	0	0	0	0	0	94	589
TCGA-HS-A5N9-10A-01D-A26G-09_SARC	694	288	323	330	606	439	548	636	558	0	0	0	0	0	35	43	583
TCGA-HT-7467-10A-01D-2024-08_LGG	668	243	254	277	557	369	530	637	469	0	0	0	0	0	40	6	574
TCGA-HT-7468-10A-01D-2024-08_LGG	671	235	253	271	576	277	524	636	444	0	584	509	0	0	0	80	576
TCGA-HT-7469-10B-01D-2253-08_LGG	666	244	253	281	555	365	530	645	482	0	0	0	0	0	30	63	576
TCGA-HT-7470-10A-01D-2086-08_LGG	679	0	0	299	597	374	526	656	465	0	0	0	0	0	0	78	578
TCGA-HT-7471-10B-01D-2253-08_LGG	648	242	243	277	615	281	531	630	462	0	563	559	0	0	0	87	574
TCGA-HT-7472-10A-01D-2024-08_LGG	591	249	270	0	0	0	532	642	466	0	0	0	0	0	0	82	573
TCGA-HT-7473-10A-01D-2024-08_LGG	683	0	0	300	598	389	532	650	456	80	592	0	292	135	21	0	576
TCGA-HT-7474-10A-01D-2024-08_LGG	592	249	271	0	494	135	530	629	398	0	591	563	0	0	0	71	572
TCGA-HT-7475-10A-01D-2024-08_LGG	687	0	0	306	594	384	530	648	471	0	0	0	0	0	27	55	575
TCGA-HT-7476-10A-01D-2024-08_LGG	679	0	0	297	567	289	522	628	470	0	0	0	0	0	0	78	576
TCGA-HT-7477-10A-01D-A289-08_LGG	590	251	272	0	593	138	532	639	463	0	630	570	0	0	0	74	578
TCGA-HT-7478-10A-01D-2024-08_LGG	685	0	0	302	600	373	529	646	478	0	0	0	0	0	31	57	572
TCGA-HT-7479-10A-01D-2024-08_LGG	680	0	0	300	607	381	531	646	473	0	0	0	0	0	0	114	573
TCGA-HT-7480-10A-01D-2086-08_LGG	672	240	246	277	607	368	529	647	466	0	584	561	0	0	23	59	574
TCGA-HT-7481-10A-01D-2024-08_LGG	679	0	0	300	601	387	531	644	379	72	606	0	292	131	0	70	574
TCGA-HT-7482-10A-01D-2024-08_LGG	657	245	259	281	555	282	529	641	463	0	0	0	0	0	30	54	577
TCGA-HT-7483-10A-01D-2024-08_LGG	761	0	0	304	602	382	528	651	484	0	0	0	0	0	0	129	575
TCGA-HT-7485-10A-01D-2024-08_LGG	661	240	260	296	606	279	531	637	477	0	594	506	0	0	0	116	581
TCGA-HT-7601-10A-01D-2086-08_LGG	683	231	252	181	574	268	531	656	467	0	0	0	0	0	28	62	575
TCGA-HT-7602-10A-01D-2086-08_LGG	688	0	0	299	602	394	532	650	481	0	0	0	0	0	27	62	574
TCGA-HT-7603-10A-01D-2086-08_LGG	682	0	0	306	605	375	531	632	471	0	0	0	0	0	0	129	574
TCGA-HT-7604-10A-01D-2086-08_LGG	676	0	257	283	608	384	535	655	382	80	625	0	392	136	28	1	575
TCGA-HT-7605-10A-01D-2086-08_LGG	684	0	0	303	600	370	528	646	486	0	0	0	0	0	0	120	576
TCGA-HT-7606-10A-01D-2086-08_LGG	674	0	0	289	568	355	527	610	379	0	0	0	0	0	0	67	574
TCGA-HT-7607-10A-01D-2086-08_LGG	684	250	257	279	585	367	531	656	478	0	0	0	0	0	32	71	573
TCGA-HT-7608-10A-01D-2086-08_LGG	678	240	248	275	551	366	532	646	465	0	0	0	0	0	0	123	575
TCGA-HT-7609-10A-01D-2086-08_LGG	599	249	269	0	598	137	532	652	383	86	650	577	280	133	0	57	575
TCGA-HT-7610-10A-01D-2086-08_LGG	680	246	243	260	573	360	530	653	476	0	0	0	0	0	27	60	574
TCGA-HT-7611-10B-01D-2396-08_LGG	595	258	276	0	600	139	529	652	387	76	646	569	299	136	0	63	572
TCGA-HT-7616-10A-01D-2253-08_LGG	686	246	243	287	577	368	532	649	475	0	0	0	0	0	30	73	574
TCGA-HT-7620-10A-01D-2253-08_LGG	675	242	238	269	603	137	528	609	383	0	522	565	0	134	26	2	572
TCGA-HT-7676-10B-01D-2396-08_LGG	687	243	258	283	606	365	531	639	450	76	630	569	0	135	29	4	573
TCGA-HT-7677-10A-01D-2253-08_LGG	689	0	0	297	611	382	532	666	484	69	0	0	0	0	34	65	574
TCGA-HT-7680-10A-01D-2253-08_LGG	674	247	259	293	594	368	533	653	443	77	617	0	357	135	0	61	576
TCGA-HT-7681-10C-01D-2396-08_LGG	684	0	0	304	604	380	528	642	396	0	0	0	0	0	0	78	574
TCGA-HT-7684-10A-01D-2253-08_LGG	682	241	239	273	613	377	535	662	440	82	648	572	346	135	0	62	576
TCGA-HT-7686-10A-01D-2253-08_LGG	691	0	0	304	614	379	531	655	475	0	0	0	0	0	35	78	578
TCGA-HT-7687-10A-01D-2253-08_LGG	672	257	264	0	0	0	529	636	472	0	0	0	0	0	38	1	577
TCGA-HT-7688-10A-01D-2253-08_LGG	685	0	0	299	602	380	530	647	467	0	0	0	0	0	0	87	573
TCGA-HT-7689-10A-01D-2253-08_LGG	660	233	0	273	595	383	532	632	467	0	0	0	0	0	0	81	578
TCGA-HT-7690-10A-01D-2253-08_LGG	683	0	0	283	589	359	522	633	377	83	593	482	0	126	0	50	568
TCGA-HT-7691-10A-01D-2253-08_LGG	684	0	0	305	602	284	521	645	457	70	613	0	298	135	0	53	578
TCGA-HT-7692-10A-01D-2253-08_LGG	666	234	259	289	613	371	532	646	457	79	637	569	0	135	36	0	577
TCGA-HT-7693-10A-01D-2253-08_LGG	669	0	257	292	605	382	533	659	490	0	611	0	387	0	35	70	572
TCGA-HT-7694-10A-01D-2253-08_LGG	680	0	0	300	596	367	528	638	476	0	0	0	0	0	0	107	572
TCGA-HT-7695-10A-01D-2253-08_LGG	685	245	243	281	583	356	531	651	483	0	0	0	0	0	0	120	578
TCGA-HT-7854-10A-01D-2253-08_LGG	685	0	0	341	606	380	532	644	460	0	0	0	0	0	0	90	573
TCGA-HT-7855-10A-01D-2396-08_LGG	762	0	0	296	597	387	532	642	456	79	595	0	364	133	0	64	574
TCGA-HT-7856-10A-01D-2396-08_LGG	685	251	275	289	603	392	537	655	493	0	0	0	0	0	47	94	580
TCGA-HT-7857-10A-01D-2396-08_LGG	682	241	256	272	570	366	530	644	472	0	0	0	0	0	0	96	575
TCGA-HT-7858-10A-01D-2396-08_LGG	593	256	269	0	561	135	530	645	383	73	593	0	296	137	32	6	574
TCGA-HT-7860-10A-01D-2396-08_LGG	689	0	0	305	601	386	529	658	478	0	0	0	0	0	29	72	576
TCGA-HT-7873-10A-01D-2396-08_LGG	685	0	0	303	622	373	527	631	475	0	0	0	0	0	0	122	576
TCGA-HT-7874-10A-01D-2396-08_LGG	682	0	0	295	593	371	528	634	397	0	0	0	0	0	0	74	570
TCGA-HT-7875-10A-01D-2396-08_LGG	682	237	261	291	615	378	532	654	462	85	640	571	295	135	0	66	576
TCGA-HT-7877-10A-01D-2396-08_LGG	595	259	271	0	558	135	529	641	475	0	591	514	0	0	0	78	576
TCGA-HT-7879-10A-01D-2396-08_LGG	600	253	271	0	557	138	531	636	479	0	603	562	0	0	0	122	576
TCGA-HT-7880-10A-01D-2396-08_LGG	687	0	0	301	599	385	530	642	470	0	0	0	0	0	0	87	572
TCGA-HT-7881-10A-01D-2396-08_LGG	686	241	254	191	604	276	534	650	471	0	605	35	316	0	0	100	574
TCGA-HT-7882-10A-01D-2396-08_LGG	683	245	261	294	591	279	529	652	462	83	617	55	362	132	35	0	574
TCGA-HT-7884-10A-01D-2396-08_LGG	681	245	260	288	581	280	530	639	470	0	0	0	0	0	0	128	576
TCGA-HT-7902-10A-01D-2396-08_LGG	672	245	266	282	606	285	528	652	473	0	624	566	107	0	33	70	576
TCGA-HT-8010-10A-01D-2396-08_LGG	680	232	256	287	547	362	528	639	478	0	0	0	0	0	24	50	573
TCGA-HT-8011-10A-01D-2396-08_LGG	679	0	0	298	598	383	528	657	475	0	0	0	0	0	0	110	575
TCGA-HT-8012-10A-01D-2396-08_LGG	590	254	273	0	0	0	532	645	441	73	585	512	0	138	0	65	574
TCGA-HT-8013-10A-01D-2396-08_LGG	670	262	280	0	432	140	537	651	480	0	593	571	0	0	0	109	581
TCGA-HT-8015-10A-01D-A289-08_LGG	679	0	0	296	605	287	532	641	472	0	0	0	0	0	0	127	574
TCGA-HT-8018-10A-01D-2396-08_LGG	759	39	0	295	601	385	532	635	475	0	0	0	0	0	0	117	574
TCGA-HT-8019-10A-01D-2396-08_LGG	676	246	267	283	581	280	528	657	472	0	0	0	0	0	28	63	574
TCGA-HT-8104-10A-01D-2396-08_LGG	686	247	264	280	553	372	535	648	477	0	0	0	0	0	0	82	573
TCGA-HT-8105-10A-01D-2396-08_LGG	594	260	274	0	599	139	531	646	393	79	639	566	363	135	28	3	573
TCGA-HT-8106-10A-01D-2396-08_LGG	761	0	0	311	626	407	536	651	483	0	0	0	0	0	0	135	578
TCGA-HT-8107-10A-01D-2396-08_LGG	687	0	0	304	601	381	529	643	453	77	600	567	0	135	0	56	575
TCGA-HT-8108-10A-01D-2396-08_LGG	685	246	259	285	607	380	530	645	474	0	594	513	0	0	0	117	579
TCGA-HT-8109-10A-01D-2396-08_LGG	682	0	0	297	602	287	528	639	479	0	0	20	0	0	35	0	579
TCGA-HT-8110-10A-01D-2396-08_LGG	653	247	260	292	605	134	526	614	0	73	627	509	293	135	0	3	570
TCGA-HT-8111-10A-01D-2396-08_LGG	684	0	0	303	599	395	531	646	462	78	604	0	362	135	0	66	576
TCGA-HT-8113-10A-01D-2396-08_LGG	758	0	0	354	628	389	538	653	486	0	0	0	0	0	0	132	581
TCGA-HT-8114-10A-01D-2396-08_LGG	685	0	0	299	595	377	525	639	467	0	0	0	0	0	0	83	572

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-HT-8558-10A-01D-2396-08_LGG	679	248	256	286	609	282	531	642	475	0	574	560	0	0	39	2	579
TCGA-HT-8563-10A-01D-2396-08_LGG	665	242	262	291	606	376	530	648	478	0	604	556	0	0	31	57	575
TCGA-HT-8564-10A-01D-2396-08_LGG	742	251	263	292	583	363	531	649	481	0	0	0	15	0	34	56	576
TCGA-HT-A4DS-10A-01D-A26K-08_LGG	681	0	0	283	512	371	531	618	456	0	0	0	0	0	0	78	570
TCGA-HT-A4DV-10A-01D-A26K-08_LGG	585	251	259	0	23	0	528	625	303	67	547	0	281	134	24	3	573
TCGA-HT-A5R5-10A-01D-A289-08_LGG	687	0	0	298	598	388	529	642	468	0	0	0	0	0	0	110	570
TCGA-HT-A5R7-10A-01D-A289-08_LGG	678	248	258	275	608	372	531	633	441	80	627	567	358	137	0	60	573
TCGA-HT-A5R9-10A-01D-A289-08_LGG	690	0	0	297	599	373	531	628	380	64	592	0	286	137	0	52	576
TCGA-HT-A5RA-10A-01D-A289-08_LGG	672	242	264	281	591	363	532	648	470	74	596	563	0	0	28	55	576
TCGA-HT-A5RB-10A-01D-A289-08_LGG	688	240	263	278	554	363	530	638	0	80	627	0	382	137	0	0	580
TCGA-HT-A5RC-10A-01D-A289-08_LGG	651	247	253	272	606	133	515	615	443	0	591	499	0	133	0	55	568
TCGA-HT-A614-10A-01D-A29Q-08_LGG	761	0	0	303	615	400	536	653	479	0	0	0	0	0	0	121	578
TCGA-HT-A615-10A-01D-A29Q-08_LGG	763	239	266	286	621	382	535	642	485	0	615	564	0	0	0	104	580
TCGA-HT-A616-10A-01D-A29Q-08_LGG	677	256	260	280	506	357	534	651	452	76	605	0	368	137	30	0	579
TCGA-HT-A617-10A-01D-A29Q-08_LGG	687	0	0	313	617	399	536	658	482	0	0	0	0	0	0	151	580
TCGA-HT-A618-10A-01D-A29Q-08_LGG	753	242	270	292	571	379	534	654	481	0	0	0	0	0	35	75	579
TCGA-HT-A619-10A-01D-A29Q-08_LGG	681	242	261	295	567	376	534	648	479	0	0	0	0	0	47	0	578
TCGA-HT-A61A-10A-01D-A29Q-08_LGG	693	0	0	318	624	402	536	650	488	0	0	0	0	0	38	81	580
TCGA-HT-A61B-10A-01D-A29Q-08_LGG	756	239	267	292	560	397	534	650	402	75	598	0	370	140	0	80	579
TCGA-HT-A61C-10A-01D-A29Q-08_LGG	671	267	281	0	0	0	535	659	490	0	0	0	0	0	43	82	580
TCGA-HT-A74H-10A-01D-A329-08_LGG	688	0	0	306	605	379	530	652	472	0	0	0	0	0	31	51	570
TCGA-HT-A74J-10A-01D-A329-08_LGG	674	231	247	263	599	354	529	630	377	67	621	510	286	134	0	48	574
TCGA-HT-A74K-10A-01D-A329-08_LGG	684	0	0	290	597	377	528	637	376	70	584	504	0	129	17	0	570
TCGA-HT-A74L-10A-01D-A329-08_LGG	679	0	0	299	563	363	529	627	469	0	0	0	0	0	0	80	579
TCGA-HT-A74O-10A-01D-A329-08_LGG	681	0	0	300	571	368	521	611	388	0	0	0	0	0	0	61	572
TCGA-HU-8238-10A-01D-2341-08_STAD	688	0	0	311	617	388	534	654	486	0	0	0	0	0	36	72	577
TCGA-HU-8243-10A-01D-2341-08_STAD	689	0	0	306	617	396	534	653	466	81	623	0	370	135	33	0	577
TCGA-HU-8244-10A-01D-2341-08_STAD	688	0	0	311	610	390	533	658	469	80	610	0	371	138	33	3	575
TCGA-HU-8245-10A-01D-2341-08_STAD	685	252	264	301	595	386	533	651	471	84	631	0	370	138	39	0	577
TCGA-HU-8249-10A-01D-2341-08_STAD	762	0	0	315	607	387	531	647	478	0	0	0	0	0	46	0	576
TCGA-HU-8602-10A-01D-2394-08_STAD	684	0	0	291	592	382	530	642	380	68	605	0	359	137	27	0	573
TCGA-HU-8604-10A-01D-2394-08_STAD	685	0	0	305	604	377	528	648	467	0	0	0	0	0	40	6	572
TCGA-HU-8608-10A-01D-2394-08_STAD	674	244	129	281	555	370	530	644	474	0	0	0	0	0	29	56	578
TCGA-HU-8610-10A-01D-2394-08_STAD	685	0	0	302	602	383	531	638	472	0	0	0	0	0	40	0	572
TCGA-HU-A4G2-10A-01D-A25E-08_STAD	685	0	0	299	602	379	528	637	470	0	0	0	0	0	37	1	571
TCGA-HU-A4G3-10A-01D-A24F-08_STAD	682	0	0	281	597	377	526	641	379	58	576	9	286	127	30	7	571
TCGA-HU-A4G6-10A-01D-A24F-08_STAD	682	0	0	298	596	381	532	649	462	0	0	0	0	0	33	63	573
TCGA-HU-A4G8-10A-01D-A25E-08_STAD	682	0	0	299	592	383	537	652	477	69	530	502	0	0	0	110	576
TCGA-HU-A4G9-10A-01D-A24F-08_STAD	678	0	0	292	596	376	530	635	465	0	0	0	0	0	26	44	573
TCGA-HU-A4GC-10A-01D-A25E-08_STAD	686	0	0	302	595	385	531	650	471	0	0	0	0	0	33	62	571
TCGA-HU-A4GD-10A-01D-A25E-08_STAD	685	0	0	295	608	386	531	649	479	0	0	0	0	0	30	58	579
TCGA-HU-A4GF-10A-01D-A24F-08_STAD	681	0	0	298	596	375	522	637	467	0	0	0	0	0	27	45	575
TCGA-HU-A4GH-10A-01D-A24F-08_STAD	689	0	0	295	599	383	532	638	383	75	611	0	296	137	0	66	575
TCGA-HU-A4GJ-10A-01D-A25E-08_STAD	754	0	0	297	600	392	530	650	484	0	0	0	0	0	35	71	573
TCGA-HU-A4GN-10A-01D-A25E-08_STAD	690	0	0	305	596	387	532	644	456	81	589	562	0	135	0	66	576
TCGA-HU-A4GP-10A-01D-A25E-08_STAD	685	0	0	301	603	374	531	633	461	0	0	0	0	0	0	80	572
TCGA-HU-A4GQ-10A-01D-A25E-08_STAD	686	0	0	294	603	387	532	649	383	76	609	516	0	138	28	1	575
TCGA-HU-A4GT-10A-01D-A25E-08_STAD	681	0	0	306	604	380	529	646	0	81	627	0	384	137	0	0	574
TCGA-HU-A4GU-10A-01D-A25E-08_STAD	680	253	258	282	587	382	531	640	476	0	0	0	0	0	0	101	578
TCGA-HU-A4GX-10A-01D-A25E-08_STAD	686	0	0	298	568	390	528	642	473	0	0	0	0	0	38	3	578
TCGA-HU-A4GY-10A-01D-A24F-08_STAD	684	0	0	289	570	380	524	642	391	0	0	0	0	0	30	54	574
TCGA-HU-A4H2-10A-01D-A25E-08_STAD	683	0	0	298	605	392	529	623	468	0	0	0	0	0	37	1	574
TCGA-HU-A4H3-10A-01D-A25E-08_STAD	682	0	0	298	598	378	535	640	385	0	0	0	0	0	26	4	578
TCGA-HU-A4H6-10A-01D-A25E-08_STAD	681	0	0	300	598	384	529	625	382	0	0	0	0	0	31	3	577
TCGA-HU-A4H8-10A-01D-A25E-08_STAD	688	241	263	291	604	374	530	647	473	0	597	569	42	0	29	76	574
TCGA-HU-A4HB-10A-01D-A25E-08_STAD	686	0	0	308	617	394	533	663	482	0	0	0	0	0	42	75	578
TCGA-HU-A4HD-10A-01D-A25E-08_STAD	683	0	0	297	594	385	530	630	464	0	0	0	0	0	36	0	575
TCGA-HV-A5A3-10A-01D-A26I-08_PAAD	672	0	0	294	588	374	518	629	304	67	513	55	287	129	0	52	573
TCGA-HV-A5A4-10A-01D-A26I-08_PAAD	674	0	0	284	600	371	524	625	372	70	503	0	285	127	22	5	576
TCGA-HV-A5A5-10A-01D-A26I-08_PAAD	684	0	0	300	567	384	530	639	461	0	0	0	54	9	24	49	577
TCGA-HV-A5A6-10A-01D-A26I-08_PAAD	681	0	0	288	545	382	527	630	348	71	518	495	0	131	0	48	571
TCGA-HV-A7OL-10A-01D-A33W-08_PAAD	683	0	0	293	592	381	528	641	454	0	0	0	0	0	26	48	571
TCGA-HV-A7OP-10A-01D-A33W-08_PAAD	673	0	0	291	594	379	526	633	362	50	568	0	281	128	0	38	575
TCGA-HW-7486-10A-01D-2024-08_LGG	685	0	0	286	600	385	531	629	481	0	0	0	0	0	0	84	576
TCGA-HW-7487-10A-01D-2024-08_LGG	683	0	0	294	595	387	529	633	474	0	0	0	0	0	0	78	573
TCGA-HW-7489-10A-01D-2024-08_LGG	749	250	260	278	575	363	528	649	478	0	0	0	0	0	22	58	574
TCGA-HW-7490-10A-01D-2024-08_LGG	667	245	257	267	510	276	531	650	456	67	601	0	296	134	26	1	576
TCGA-HW-7491-10A-01D-2024-08_LGG	663	245	248	278	551	263	522	644	477	0	0	0	0	0	0	102	580
TCGA-HW-7493-10A-01D-2024-08_LGG	678	0	0	302	596	283	524	641	468	0	0	0	0	0	0	89	574
TCGA-HW-7495-10A-01D-2024-08_LGG	676	0	0	297	592	281	522	634	471	0	0	0	0	0	0	76	572
TCGA-HW-8319-10A-01D-2396-08_LGG	690	0	0	300	605	382	532	644	481	0	0	0	62	6	32	63	573
TCGA-HW-8320-10A-01D-2396-08_LGG	668	237	258	284	559	278	530	642	470	0	0	0	0	0	34	68	574
TCGA-HW-8321-10A-01D-2396-08_LGG	686	0	0	300	596	387	530	636	372	78	589	0	361	135	30	0	571
TCGA-HW-8322-10A-01D-2396-08_LGG	667	248	269	285	587	373	530	650	472	0	0	0	0	0	32	74	576
TCGA-HW-A5KJ-10A-01D-A27N-08_LGG	759	0	0	310	612	388	527	631	472	0	0	0	0	0	0	96	577
TCGA-HW-A5KK-10A-01D-A27N-08_LGG	753	250	264	287	615	386	534	650	388	62	637	575	0	140	33	0	579
TCGA-HW-A5KL-10A-01D-A27N-08_LGG	690	0	0	306	614	395	531	649	487	0	0	0	0	0	0	145	579
TCGA-HW-A5KM-10A-01D-A27N-08_LGG	679	246	264	286	520	376	532	646	0	81	636	0	383	140	0	0	575
TCGA-HZ-7920-10B-01D-2201-08_PAAD	740	251	266	286	605	374	532	644	475	0	615	0	375	0	0	128	575
TCGA-HZ-8001-10A-01D-2201-08_PAAD	677	249	255	279	629	376	529	644	476	0	541	513	0	0	0	104	574
TCGA-HZ-8002-10A-01D-2201-08_PAAD	676	245	265	291	582	389	520	627	0	75	638	0	376	137	0	1	575
TCGA-HZ-8003-10A-01D-2201-08_PAAD	594	254	270	0	0	0	531	647	467	0	0	0	0	0	36	58	576
TCGA-HZ-8005-10A-01D-2201-08_PAAD	683	0	0	290	607	375	523	615	390	0	0	0	0	135	0	64	576
TCGA-HZ-8315-10A-01D-2396-08_PAAD	663	238	258	275	531	357	501	605	380	0	550	0	289	129	0	51	568
TCGA-HZ-8317-10A-01D-2396-08_PAAD	684	0	0	301	583	373	519	622	461	0	0	0	0	0	0	68	571
TCGA-HZ-8519-10A-01D-2396-08_PAAD	671	243	261	273	599	374	531	641	379	72	623	510	295	135	0	65	573
TCGA-HZ-8636-10A-01D-2396-08_PAAD	658	230	251	265	561	265	525	625	388	0	0	0	0	0	0	70	571
TCGA-HZ-8637-10A-01D-2396-08_PAAD	689	0	0	307	604	384	531	650	485	0	0	0	0	0	0	134	577
TCGA-HZ-8638-10A-01D-2396-08_PAAD	591	240	243	263	568	273	522	645	462	0	0	0	0	0	20	45	575
TCGA-HZ-A49G-10A-01D-A26I-08_PAAD	592	231	248	253	569	360	530	638	387	0	504	487	0	0	23	57	577
TCGA-HZ-A49H-10A-01D-A26I-08_PAAD	685	0	0	295	591	384	528	644	401	0	0	0	0	0	0	109	580
TCGA-HZ-A49I-10A-01D-A26I-08_PAAD	768	269	278	315	623	409	539	671	505	0	0	0	0	0	73	136	585
TCGA-HZ-A4BH-10A-01D-A26I-08_PAAD	682	0	0	297	596	385	527	631	376	66	590	0	292	137	0	66	572
TCGA-HZ-A4BK-10A-01D-A26I-08_PAAD	594	249	267	0	20	0	517	608	459	0	0	0	0	0	36	5	573
TCGA-HZ-A77O-10A-01D-A33W-08_PAAD	680	0	0	288	596	287	521	633	356	72	588	0	283	139	0	53	574
TCGA-HZ-A77P-10A-01D-A33W-08_PAAD	655	233	249	263	486	352	528	638	472	0	0	0	0	0	30	51	572

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-IA-A40U-10A-01D-A25F-10_KIRP	567	306	345	0	668	183	553	632	335	93	536	563	349	180	0	64	581
TCGA-IA-A40X-10A-01D-A25F-10_KIRP	668	267	292	244	628	383	534	615	364	0	389	478	0	0	21	37	566
TCGA-IA-A40Y-10A-01D-A25F-10_KIRP	678	279	275	257	597	416	542	619	360	0	0	0	0	0	26	56	586
TCGA-IB-7645-10A-01D-2201-08_PAAD	682	247	257	282	579	363	532	630	470	0	0	0	0	0	43	4	574
TCGA-IB-7890-10A-01D-2201-08_PAAD	665	242	256	283	581	279	530	654	468	0	0	0	0	0	33	71	575
TCGA-IB-7891-10A-01D-2201-08_PAAD	683	0	0	303	601	382	531	639	392	0	0	0	0	0	0	94	574
TCGA-IB-7893-10A-01D-2201-08_PAAD	686	241	258	274	569	371	531	644	473	0	0	0	0	0	0	77	578
TCGA-IB-7897-10A-01D-2201-08_PAAD	686	0	0	298	599	380	529	650	474	0	0	0	0	0	0	117	577
TCGA-IB-8126-10A-01D-2396-08_PAAD	673	0	0	295	597	283	518	632	369	61	593	0	282	132	0	49	574
TCGA-IB-8127-10A-01D-2396-08_PAAD	686	241	251	275	571	361	529	631	405	0	0	0	0	0	0	108	573
TCGA-IB-A5SO-10A-01D-A32N-08_PAAD	665	236	260	272	589	277	525	636	381	68	606	564	0	132	0	46	573
TCGA-IB-A5SP-10A-01D-A32N-08_PAAD	673	242	257	275	503	365	521	610	381	0	561	554	0	128	31	0	577
TCGA-IB-A5SQ-10A-01D-A32N-08_PAAD	644	234	252	274	503	271	525	632	471	0	0	0	0	0	29	47	572
TCGA-IB-A5SS-10A-01D-A32N-08_PAAD	666	238	259	281	557	375	530	649	478	0	0	0	0	0	31	59	575
TCGA-IB-A5ST-10A-01D-A32N-08_PAAD	675	0	0	301	601	286	520	649	382	75	597	0	293	133	0	64	573
TCGA-IB-A6UF-10A-01D-A33W-08_PAAD	596	248	264	0	591	137	531	639	471	0	622	567	0	0	0	110	573
TCGA-IB-A6UG-10A-01D-A33W-08_PAAD	682	0	0	297	593	374	531	641	456	0	0	0	0	0	28	51	574
TCGA-IE-A4EH-10A-01D-A24N-09_SARC	687	0	0	352	663	368	546	643	328	99	566	0	350	169	0	44	591
TCGA-IE-A4EI-10A-01D-A24N-09_SARC	692	0	0	365	671	456	554	649	454	0	0	0	0	0	42	51	585
TCGA-IE-A4EJ-10A-01D-A24N-09_SARC	698	309	354	302	686	441	553	647	537	0	606	551	0	0	35	54	590
TCGA-IE-A4EK-10A-01D-A24N-09_SARC	703	0	0	369	673	456	550	648	556	0	0	0	0	0	0	105	591
TCGA-IE-A6BZ-10A-01D-A307-09_SARC	700	0	0	383	698	475	556	652	573	0	0	0	0	0	74	0	591
TCGA-IH-A3EA-10A-01D-A20D-08_SKCM	685	239	250	286	511	371	531	634	383	72	597	0	368	134	0	64	576
TCGA-IK-7675-10A-01D-2086-08_LGG	687	233	244	290	606	368	530	640	472	0	610	513	0	0	0	107	579
TCGA-IK-8125-10A-01D-2253-08_LGG	598	251	242	0	584	137	530	630	437	73	621	557	347	132	22	0	573
TCGA-IM-A3EB-10A-01D-A202-08_THCA	679	245	264	275	599	380	528	647	477	0	577	565	0	0	0	122	579
TCGA-IM-A3ED-10A-01D-A202-08_THCA	687	0	0	307	610	385	532	657	475	0	0	0	0	0	35	74	577
TCGA-IM-A3U2-10A-01D-A22D-08_THCA	690	0	0	302	608	382	530	638	472	0	0	0	0	0	0	86	574
TCGA-IM-A3U3-10A-01D-A22D-08_THCA	662	234	253	276	598	359	529	637	466	0	527	510	0	0	29	56	574
TCGA-IM-A41Y-10A-01D-A23U-08_THCA	749	0	0	295	595	368	528	633	394	0	0	0	0	0	0	69	572
TCGA-IM-A41Z-10A-01D-A23K-08_THCA	756	242	267	288	607	382	531	653	461	74	641	573	0	137	0	66	574
TCGA-IM-A420-10A-01D-A23K-08_THCA	681	250	266	291	603	380	533	649	485	0	0	0	0	0	0	145	578
TCGA-IM-A4EB-10A-01D-A25A-08_THCA	674	0	0	269	507	369	512	624	445	0	0	0	0	0	26	49	569
TCGA-IN-7806-10A-01D-2053-08_STAD	682	0	0	297	596	383	528	641	476	0	0	0	0	0	0	82	573
TCGA-IN-7808-10A-01D-2201-08_STAD	682	0	0	301	614	377	532	705	429	83	638	566	352	127	0	60	574
TCGA-IN-8462-10A-01D-2341-08_STAD	681	250	264	290	590	280	529	649	484	0	0	0	0	0	33	86	577
TCGA-IN-8663-10A-01D-2394-08_STAD	594	254	268	0	5	0	529	640	473	0	0	0	0	0	0	79	572
TCGA-IN-A6RI-10A-01D-A32N-08_STAD	690	0	0	309	610	385	531	644	466	0	0	0	0	0	0	112	576
TCGA-IN-A6RJ-10A-21D-A33W-08_STAD	685	0	0	301	599	382	532	641	477	0	0	0	0	0	33	54	576
TCGA-IN-A6RL-10A-01D-A32N-08_STAD	688	255	267	195	608	386	532	648	0	80	649	516	382	140	0	0	577
TCGA-IN-A6RN-10A-01D-A33W-08_STAD	681	0	0	299	605	377	531	651	471	0	0	0	0	0	27	64	574
TCGA-IN-A6RO-10A-01D-A33W-08_STAD	679	0	0	300	602	386	532	655	467	75	0	0	0	0	0	93	571
TCGA-IN-A6RP-10A-01D-A33W-08_STAD	690	0	0	309	614	382	531	665	461	76	611	510	0	135	30	0	577
TCGA-IN-A6RR-10A-01D-A32N-08_STAD	673	248	270	289	617	284	527	653	461	72	650	565	296	137	0	76	578
TCGA-IP-7968-10A-01D-2201-08_STAD	737	0	0	297	586	373	532	660	439	0	0	0	0	0	26	55	575
TCGA-IQ-7630-10A-01D-2078-08_HNSC	679	237	250	189	601	277	528	640	382	67	633	562	282	132	0	54	574
TCGA-IQ-7631-10A-01D-2078-08_HNSC	678	0	0	295	590	279	521	640	373	69	523	0	283	134	0	45	574
TCGA-IQ-7632-10A-01D-2078-08_HNSC	655	0	251	275	602	347	534	644	469	0	521	0	307	0	34	0	571
TCGA-IQ-A61E-10A-01D-A30H-08_HNSC	758	0	0	319	630	300	527	656	488	0	0	0	0	0	45	82	581
TCGA-IQ-A61G-10A-01D-A30H-08_HNSC	760	254	0	298	621	389	536	653	395	82	605	0	382	137	42	0	580
TCGA-IQ-A61H-10A-01D-A30H-08_HNSC	763	0	0	318	624	410	538	660	493	0	0	0	0	0	55	110	582
TCGA-IQ-A61I-10A-01D-A30H-08_HNSC	760	0	0	355	623	408	539	656	489	0	0	0	0	0	0	158	581
TCGA-IQ-A61J-10A-01D-A30H-08_HNSC	760	0	0	320	620	411	538	658	391	77	587	0	381	141	0	70	581
TCGA-IQ-A61K-10A-01D-A30H-08_HNSC	762	256	273	301	623	395	534	653	488	0	594	574	0	0	0	158	580
TCGA-IQ-A61L-10A-01D-A30H-08_HNSC	676	265	283	0	598	142	536	639	0	76	660	572	395	143	0	0	582
TCGA-IQ-A61O-10A-01D-A30H-08_HNSC	762	0	0	322	629	403	535	661	489	0	0	0	0	0	48	92	581
TCGA-IR-A3L7-10A-01D-A20U-09_CESC	682	295	318	311	602	432	553	642	517	87	0	0	0	0	0	93	583
TCGA-IR-A3LA-10A-01D-A22X-09_CESC	698	0	0	366	663	458	554	615	411	89	540	0	423	176	37	4	587
TCGA-IR-A3LB-10A-01D-A243-09_CESC	684	0	0	369	670	458	550	636	524	93	601	0	366	178	0	63	582
TCGA-IR-A3LC-10A-01D-A20U-09_CESC	699	291	304	279	575	426	544	628	443	0	0	0	0	0	0	87	584
TCGA-IR-A3LF-10A-01D-A22X-09_CESC	702	0	0	365	693	460	551	634	568	0	0	0	0	0	0	136	591
TCGA-IR-A3LH-10A-01D-A20U-09_CESC	674	284	299	220	661	429	545	609	383	0	574	503	315	165	28	1	581
TCGA-IR-A3LI-10A-01D-A20U-09_CESC	674	0	0	353	662	452	542	625	438	0	0	0	0	0	0	91	589
TCGA-IR-A3LK-10A-01D-A20U-09_CESC	595	316	359	0	0	0	551	648	421	93	490	0	364	176	41	3	586
TCGA-IR-A3LL-10A-01D-A20U-09_CESC	691	0	0	361	670	460	556	637	426	90	574	0	351	170	0	59	592
TCGA-IS-A3K6-10A-01D-A21Q-09_SARC	584	303	322	301	626	348	542	623	451	0	0	0	0	0	0	70	575
TCGA-IS-A3K7-10A-01D-A21Q-09_SARC	685	311	324	194	507	351	553	612	551	0	0	0	0	0	0	86	587
TCGA-IS-A3K8-10A-01D-A21Q-09_SARC	690	0	0	343	678	374	547	636	541	0	0	0	0	0	34	47	584
TCGA-IS-A3KA-10A-01D-A21Q-09_SARC	694	287	316	318	684	454	552	634	312	90	619	580	0	176	30	1	591
TCGA-IW-A3M4-10B-01D-A21Q-09_SARC	682	308	333	345	685	443	546	646	432	95	641	553	361	175	0	60	591
TCGA-IW-A3M5-10A-01D-A21Q-09_SARC	688	0	0	351	658	452	549	621	534	0	0	0	0	0	27	47	585
TCGA-IW-A3M6-10A-01D-A21Q-09_SARC	694	0	0	358	675	462	555	650	419	96	594	0	368	177	0	56	589
TCGA-IZ-8195-10A-01D-2396-08_KIRP	692	0	0	308	611	383	530	642	482	0	0	0	0	0	0	121	574
TCGA-IZ-8196-10A-01D-2396-08_KIRP	682	0	0	288	597	286	532	642	469	0	0	0	0	0	0	134	575
TCGA-IZ-A6M8-10A-01D-A31X-10_KIRP	515	161	233	223	416	310	521	593	334	0	0	0	0	0	28	0	548
TCGA-IZ-A6M9-10A-01D-A31X-10_KIRP	508	0	0	257	528	431	525	481	306	0	333	0	276	140	12	2	552
TCGA-J1-A4AH-10A-01D-A24F-08_LUSC	681	0	0	291	589	376	523	630	368	76	566	0	291	135	0	54	572
TCGA-J2-8192-10A-01D-2238-08_LUAD	668	243	250	296	586	280	529	649	396	69	603	0	290	129	33	0	576
TCGA-J2-8194-10A-01D-2238-08_LUAD	683	0	0	298	604	389	533	634	462	0	0	0	0	0	27	69	577
TCGA-J2-A4AD-10A-01D-A24F-08_LUAD	662	244	258	283	509	274	528	632	457	0	0	0	0	0	37	1	572
TCGA-J2-A4AE-10A-01D-A24F-08_LUAD	677	0	0	292	587	372	530	628	454	0	0	0	0	0	0	69	571
TCGA-J2-A4AG-10A-01D-A24F-08_LUAD	666	247	252	270	604	284	524	637	302	74	617	566	0	132	0	66	570
TCGA-J4-8198-10A-01D-2260-08_PRAD	678	243	262	198	613	282	533	636	448	76	631	570	361	136	0	68	575
TCGA-J4-8200-10A-01D-A29Q-08_PRAD	677	258	268	292	614	395	538	651	462	81	642	575	368	136	0	65	580
TCGA-J4-A67K-10A-01D-A30H-08_PRAD	690	0	0	320	617	406	536	643	486	0	0	0	0	0	42	88	580
TCGA-J4-A67L-10A-01D-A30H-08_PRAD	722	249	274	301	580	287	531	655	491	0	0	0	0	0	0	168	581
TCGA-J4-A67M-10A-01D-A30H-08_PRAD	761	260	274	288	576	385	536	645	488	0	0	0	0	0	0	172	580
TCGA-J4-A67N-10A-01D-A30H-08_PRAD	761	0	0	350	610	390	536	642	386	74	537	0	381	138	0	65	580
TCGA-J4-A67O-10A-01D-A30H-08_PRAD	690	0	0	356	621	387	534	645	478	0	0	0	0	0	0	127	582
TCGA-J4-A67Q-10A-01D-A30H-08_PRAD	745	253	261	188	618	393	534	651	315	75	638	577	0	139	0	74	582
TCGA-J4-A67R-10A-01D-A30H-08_PRAD	756	0	0	320	617	400	535	646	480	0	0	0	0	0	0	124	580
TCGA-J4-A67S-10A-01D-A30H-08_PRAD	748	252	270	302	528	294	533	649	476	0	0	0	0	0	0	131	582
TCGA-J4-A67T-10A-01D-A30X-08_PRAD	651	245	252	276	552	366	530	639	376	54	527	0	293	137	28	0	574
TCGA-J4-A6G1-10A-01D-A30X-08_PRAD	677	0	0	292	586	378	523	630	388	68	559	0	284	132	21	0	575
TCGA-J4-A6G3-10A-01D-A30X-08_PRAD	673	0	0	291	588	367	529	629	475	0	0	0	0	0	0	92	570
TCGA-J4-A6M7-10A-01D-A31J-08_PRAD	679	0	0	291	594	377	527	618	459	0	0	0	0	0	0	80	571

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-J7-6720-10A-01D-2136-08_KIRP	675	247	249	289	557	369	527	646	463	75	601	0	292	138	36	4	576
TCGA-J7-8537-10A-01D-2396-08_KIRP	594	255	270	0	73	0	529	643	458	79	615	484	0	134	0	65	572
TCGA-J8-A3NZ-10A-01D-A21A-08_THCA	715	243	251	277	540	268	529	649	471	0	0	0	0	0	28	67	579
TCGA-J8-A3O0-10A-01D-A21A-08_THCA	673	0	0	297	598	382	527	643	369	68	566	0	283	130	0	65	576
TCGA-J8-A3O1-10A-01D-A21A-08_THCA	758	243	235	258	578	361	532	642	470	0	0	0	0	0	44	0	577
TCGA-J8-A3O2-10A-01D-A23K-08_THCA	757	0	0	354	608	392	539	649	0	89	638	0	391	141	0	0	580
TCGA-J8-A3YD-10A-01D-A22Z-08_THCA	674	0	0	293	565	367	528	627	454	0	0	0	0	0	0	65	571
TCGA-J8-A3YE-10A-01D-A23K-08_THCA	689	0	0	300	596	383	532	651	483	0	0	0	0	0	32	69	573
TCGA-J8-A3YF-10A-01D-A23K-08_THCA	755	257	0	294	624	294	533	653	464	83	588	0	378	140	0	85	580
TCGA-J8-A3YG-10A-01D-A22Z-08_THCA	668	0	0	293	582	359	527	623	452	0	0	0	0	0	0	80	572
TCGA-J8-A3YH-10A-01D-A22Z-08_THCA	676	0	0	290	585	373	523	612	447	0	0	0	0	0	35	0	571
TCGA-J8-A42S-10A-01D-A23K-08_THCA	744	253	270	291	572	281	532	646	459	82	615	159	366	136	0	71	572
TCGA-J8-A4HW-10A-01D-A25A-08_THCA	589	244	261	0	560	135	528	629	0	80	633	574	0	135	0	0	573
TCGA-J8-A4HY-10A-01D-A25A-08_THCA	760	0	0	314	628	391	537	659	396	88	642	511	375	141	0	66	578
TCGA-J9-A52B-10A-01D-A26K-08_PRAD	671	0	0	289	585	383	529	608	310	0	0	0	0	0	0	73	575
TCGA-J9-A52C-10A-01D-A26K-08_PRAD	680	0	0	286	594	386	527	626	307	64	520	0	280	132	0	56	572
TCGA-J9-A52D-10A-01D-A29Q-08_PRAD	687	0	0	298	644	398	529	646	394	77	536	0	365	136	0	75	577
TCGA-J9-A52E-10A-01D-A26K-08_PRAD	663	231	243	265	598	275	532	632	463	0	510	495	0	0	0	86	575
TCGA-JL-A3YW-10B-01D-A23C-09_BRCA	588	318	354	0	673	181	554	649	557	0	611	558	0	0	34	50	586
TCGA-JL-A3YX-10A-01D-A22X-09_BRCA	585	288	338	323	680	449	553	642	432	91	618	524	426	168	26	3	587
TCGA-JV-A5VE-10A-01D-A29N-09_SARC	660	295	320	326	496	354	551	628	440	0	0	0	0	0	0	74	586
TCGA-JV-A5VF-10A-01D-A29N-09_SARC	683	294	338	347	681	448	551	647	549	0	485	529	0	0	0	112	591
TCGA-JW-A5VG-10A-01D-A28E-09_CESC	687	303	323	314	679	447	554	626	523	0	587	568	0	0	60	1	588
TCGA-JW-A5VH-10A-01D-A28E-09_CESC	697	316	342	315	625	431	557	641	558	0	0	0	0	0	0	95	594
TCGA-JW-A5VI-10A-01D-A28E-09_CESC	703	0	0	368	683	473	551	655	561	0	0	0	0	0	82	0	590
TCGA-JW-A5VJ-10A-01D-A28E-09_CESC	701	0	0	367	679	451	548	634	415	85	570	0	374	172	0	60	591
TCGA-JW-A5VK-10A-01D-A28E-09_CESC	698	319	353	356	660	370	556	642	449	0	0	0	0	0	0	124	589
TCGA-JW-A5VL-10A-01D-A28E-09_CESC	700	0	0	367	680	464	553	641	447	0	0	0	0	0	55	1	583
TCGA-JX-A3PZ-10A-01D-A21Q-09_CESC	698	0	0	363	678	458	549	638	559	0	0	0	0	0	42	59	596
TCGA-JX-A3Q0-10A-01D-A21Q-09_CESC	685	0	0	367	673	459	551	642	458	0	0	0	0	0	32	72	588
TCGA-JX-A3Q8-10A-01D-A21Q-09_CESC	700	0	0	372	658	472	553	638	552	0	0	0	0	0	52	0	588
TCGA-JX-A5QV-10A-01D-A28E-09_CESC	691	301	329	324	665	439	551	646	429	89	613	527	341	173	0	59	587
TCGA-K1-A3PN-10A-01D-A22A-09_SARC	660	0	0	345	638	426	543	617	447	0	0	0	0	0	0	64	580
TCGA-K1-A3PO-10A-01D-A21Q-09_SARC	676	0	0	350	665	458	550	630	321	0	433	516	0	172	0	52	582
TCGA-K1-A42W-10A-01D-A24N-09_SARC	690	0	0	313	684	453	550	639	0	105	619	506	439	184	0	0	580
TCGA-K4-A3WS-10A-01D-A22Z-08_BLCA	672	266	283	0	0	0	537	654	473	78	598	0	385	141	0	88	581
TCGA-K4-A3WU-10A-01D-A23K-08_BLCA	680	236	252	285	548	368	530	631	471	0	0	0	0	0	29	62	574
TCGA-K4-A3WV-10A-01D-A22Z-08_BLCA	670	267	278	0	0	0	536	646	486	0	0	0	0	0	0	123	581
TCGA-K4-A4AB-10A-01D-A289-08_BLCA	759	0	0	311	612	392	530	650	479	0	0	0	0	0	0	105	579
TCGA-K4-A4AC-10A-01D-A26K-08_BLCA	676	252	273	266	598	370	535	635	474	0	565	510	0	0	0	94	579
TCGA-K4-A54R-10A-01D-A26K-08_BLCA	656	235	244	288	508	268	528	619	397	0	0	0	0	0	32	61	573
TCGA-K4-A5RH-10A-01D-A30H-08_BLCA	766	0	0	363	628	410	540	667	500	83	0	0	0	0	47	81	581
TCGA-K4-A5RI-10A-01D-A289-08_BLCA	599	263	275	0	558	138	534	645	489	0	597	517	0	0	35	75	580
TCGA-K4-A5RJ-10A-01D-A289-08_BLCA	669	256	273	0	599	141	529	648	393	71	646	577	366	133	0	70	578
TCGA-K4-A6FZ-10A-01D-A31J-08_BLCA	753	0	0	306	604	289	523	649	489	0	0	0	0	0	34	64	578
TCGA-K4-A6MB-10A-01D-A31J-08_BLCA	684	0	0	301	598	379	533	636	472	0	0	0	0	0	0	100	571
TCGA-K6-A3WQ-10A-01D-A22A-09_UCEC	656	253	263	0	476	315	537	612	410	0	0	0	0	0	0	59	567
TCGA-K7-A5RF-10B-01D-A28X-10_LIHC	667	246	276	245	559	422	541	631	344	0	385	492	0	0	26	56	574
TCGA-K7-A5RG-10A-01D-A28X-10_LIHC	647	237	305	116	558	354	537	608	345	0	405	497	0	0	30	57	584
TCGA-K7-A6G5-10A-01D-A30V-10_LIHC	492	134	167	186	320	249	487	465	240	0	273	0	154	129	12	0	512
TCGA-KB-A6F5-10A-01D-A33W-08_STAD	681	251	260	285	611	284	531	650	393	81	634	566	0	134	0	68	574
TCGA-KB-A6F7-10A-01D-A32N-08_STAD	684	0	0	307	607	390	530	654	397	78	613	0	369	134	0	64	571
TCGA-KC-A4BL-10A-01D-A25A-08_PRAD	681	0	271	202	575	282	533	623	464	0	623	0	364	136	0	66	580
TCGA-KC-A4BN-10A-01D-A25A-08_PRAD	682	250	268	287	604	380	535	636	479	0	585	516	0	0	42	1	576
TCGA-KC-A4BO-10A-01D-A25A-08_PRAD	687	0	0	297	605	378	530	637	397	0	0	0	0	0	28	49	575
TCGA-KC-A4BR-10A-01D-A25A-08_PRAD	760	248	273	292	643	388	533	649	486	0	614	573	0	0	0	153	579
TCGA-KC-A4BV-10A-01D-A26K-08_PRAD	737	231	240	254	501	357	520	598	308	0	510	0	280	133	0	50	578
TCGA-KC-A7F3-10A-01D-A33W-08_PRAD	682	0	0	291	601	379	530	641	472	0	0	0	0	0	0	105	575
TCGA-KC-A7F5-10A-01D-A33W-08_PRAD	685	0	0	301	603	380	530	653	483	0	0	0	0	0	27	58	573
TCGA-KC-A7F6-10A-01D-A33W-08_PRAD	599	245	271	77	573	154	530	642	380	72	609	514	91	136	0	57	571
TCGA-KC-A7FA-10A-01D-A33W-08_PRAD	673	0	0	276	580	374	525	625	386	0	0	0	0	0	0	75	570
TCGA-KC-A7FD-10A-01D-A33W-08_PRAD	723	240	256	282	597	278	528	634	471	0	590	505	0	0	0	74	573
TCGA-KC-A7FE-10A-01D-A33W-08_PRAD	681	0	0	290	594	384	531	642	374	69	590	0	292	128	0	58	575
TCGA-KD-A5QS-10A-01D-A27P-09_SARC	671	0	0	349	648	348	511	502	319	0	0	0	0	157	0	47	546
TCGA-KD-A5QT-10A-01D-A27P-09_SARC	697	0	0	349	664	455	552	639	401	91	576	0	347	173	38	1	587
TCGA-KD-A5QU-10A-01D-A27P-09_SARC	684	0	0	366	672	460	553	641	454	0	0	0	0	0	0	99	583
TCGA-KF-A41W-10A-01D-A24N-09_SARC	690	282	319	327	601	351	547	644	547	0	0	0	0	0	0	108	588
TCGA-KJ-A3U4-10A-01D-A22A-09_UCEC	689	308	339	327	618	447	550	645	560	0	0	0	0	0	38	58	586
TCGA-KM-8438-10A-01D-2311-10_KICH	654	155	230	205	417	321	441	388	288	0	248	0	223	166	0	28	565
TCGA-KM-8439-10A-01D-2311-10_KICH	554	283	285	0	454	144	519	527	0	98	477	0	366	181	0	0	568
TCGA-KM-8440-10A-01D-2311-10_KICH	661	0	0	272	633	445	516	598	353	0	0	0	0	0	0	0	564
TCGA-KM-8441-10A-01D-2311-10_KICH	675	0	0	370	621	339	488	545	308	0	0	0	0	166	0	1	535
TCGA-KM-8442-10A-01D-2311-10_KICH	650	0	0	269	595	443	523	580	344	0	0	0	0	0	0	52	563
TCGA-KM-8443-10A-01D-2311-10_KICH	651	0	0	350	581	411	497	597	343	0	0	0	0	0	0	48	563
TCGA-KM-8476-10A-01D-2311-10_KICH	667	0	0	353	511	363	482	561	345	0	0	0	0	0	0	42	554
TCGA-KM-8477-10A-01D-2311-10_KICH	544	246	310	0	0	0	493	490	304	0	303	0	279	162	0	26	567
TCGA-KM-8639-10A-01D-2397-10_KICH	690	0	0	376	680	380	533	629	454	0	0	0	0	0	0	129	587
TCGA-KP-A3VZ-10A-01D-A22A-09_UCEC	582	316	347	0	0	0	549	644	420	101	585	0	358	171	0	65	584
TCGA-KP-A3W0-10A-01D-A22A-09_UCEC	682	0	0	352	659	354	491	584	406	0	0	0	0	176	41	0	555
TCGA-KP-A3W1-10A-01D-A22A-09_UCEC	701	304	339	362	636	368	554	651	551	0	0	0	0	0	37	68	590
TCGA-KP-A3W3-10A-01D-A22A-09_UCEC	692	0	0	347	655	440	547	625	270	99	509	0	324	150	20	0	570
TCGA-KP-A3W4-10A-01D-A22A-09_UCEC	701	177	330	347	640	465	554	646	551	0	0	0	0	0	34	65	589
TCGA-KQ-A41N-10D-01D-A339-08_BLCA	673	0	244	265	590	351	530	620	466	0	562	0	305	0	32	0	572
TCGA-KQ-A41P-10F-01D-A339-08_BLCA	677	0	0	295	605	377	527	627	468	0	0	0	0	0	0	104	570
TCGA-KQ-A41Q-10D-01D-A339-08_BLCA	596	256	268	0	502	128	517	630	457	0	559	498	0	0	0	63	572
TCGA-KQ-A41S-10C-01D-A339-08_BLCA	597	250	270	0	0	0	528	637	383	62	579	523	0	133	35	0	576
TCGA-KT-A74X-10A-01D-A329-08_LGG	683	236	248	272	497	357	531	626	401	0	0	0	0	0	0	71	573
TCGA-KU-A66S-10A-01D-A30H-08_HNSC	760	0	0	320	645	390	535	612	472	0	0	0	0	140	0	102	579
TCGA-KU-A66T-10A-01D-A30H-08_HNSC	761	255	264	294	623	394	539	653	453	73	649	575	307	143	0	74	582
TCGA-KU-A6H7-10A-01D-A31J-08_HNSC	685	0	0	295	598	373	528	628	399	0	0	0	0	0	24	62	576
TCGA-KV-A6GD-10A-01D-A31X-10_KIRP	526	0	0	270	533	417	493	577	336	0	0	0	0	0	12	34	561
TCGA-KV-A6GE-10A-01D-A31X-10_KIRP	611	154	239	209	336	287	511	492	333	0	0	0	0	0	0	52	558
TCGA-L3-A4E7-10A-01D-A25A-08_LUSC	590	259	271	0	549	135	527	634	38	80	648	568	360	139	0	4	573
TCGA-L3-A524-10A-01D-A25L-08_LUSC	686	0	11	340	593	376	528	649	478	0	0	0	0	0	0	87	574
TCGA-L4-A4E5-10A-01D-A24P-08_LUAD	673	238	263	281	537	364	527	631	306	75	565	0	286	133	0	48	570
TCGA-L4-A4E6-10A-01D-A24F-08_LUAD	598	256	278	0	599	138	534	653	478	75	629	578	0	0	0	102	578

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-L6-A4EP-10A-01D-A25A-08_THCA	621	0	0	267	502	351	504	521	369	0	0	0	0	0	0	48	561
TCGA-L6-A4EQ-10A-01D-A25A-08_THCA	759	0	0	322	624	393	536	652	398	75	581	0	383	141	0	59	579
TCGA-L6-A4ET-10A-01D-A25A-08_THCA	672	233	245	265	599	272	524	633	391	0	555	542	0	0	18	55	569
TCGA-L6-A4EU-10A-01D-A25A-08_THCA	680	227	259	256	583	353	521	622	461	0	580	492	0	0	21	41	573
TCGA-L9-A443-10A-01D-A24F-08_LUAD	682	0	0	297	602	387	530	640	481	0	0	0	0	0	27	64	574
TCGA-L9-A444-10A-01D-A24F-08_LUAD	655	241	263	280	612	279	529	637	450	60	620	560	293	134	0	58	574
TCGA-LA-A446-10A-01D-A25A-08_LUSC	682	0	0	295	601	385	523	642	384	64	583	0	286	133	0	56	573
TCGA-LB-A7SX-10A-01D-A33W-08_PAAD	668	0	0	299	575	367	526	631	469	0	0	0	0	0	0	91	574
TCGA-LC-A66R-10A-01D-A30H-08_BLCA	673	268	286	0	605	143	534	643	461	0	646	578	386	142	0	110	582
TCGA-LD-A66U-10A-01D-A31U-09_BRCA	574	294	292	127	669	328	538	624	296	90	620	523	338	170	0	41	581
TCGA-LG-A6GG-10A-01D-A30V-10_LIHC	568	229	184	212	470	322	503	589	322	0	0	0	0	0	19	37	563
TCGA-LI-A67I-10A-01D-A307-09_SARC	699	325	356	359	687	457	558	659	572	0	0	0	0	0	58	82	591
TCGA-LL-A440-10A-01D-A243-09_BRCA	673	0	0	338	649	424	527	597	433	0	0	0	0	0	0	47	560
TCGA-LL-A441-10A-01D-A243-09_BRCA	652	282	325	159	528	426	538	613	271	0	384	499	0	0	25	0	547
TCGA-LL-A50Y-10A-01D-A25Q-09_BRCA	695	0	0	362	675	447	550	647	557	0	0	0	0	0	33	51	586
TCGA-LL-A5YL-10A-01D-A29N-09_BRCA	667	298	327	307	616	349	544	629	417	0	482	0	360	172	42	3	586
TCGA-LL-A5YM-10A-01D-A28E-09_BRCA	661	303	330	338	621	416	551	622	556	0	0	0	0	0	33	47	589
TCGA-LL-A5YN-10A-01D-A28E-09_BRCA	692	0	0	357	674	433	551	631	544	0	0	0	0	0	40	61	581
TCGA-LL-A5YO-10A-01D-A28E-09_BRCA	699	296	319	310	624	424	528	604	331	0	563	0	350	173	0	56	584
TCGA-LL-A5YP-10A-01D-A28E-09_BRCA	685	0	0	343	655	458	546	616	534	0	0	0	0	0	55	0	586
TCGA-LL-A6FP-10A-01D-A31U-09_BRCA	693	0	0	369	673	459	544	618	532	0	0	0	0	0	0	114	592
TCGA-LL-A6FQ-10A-01D-A31U-09_BRCA	670	0	0	362	679	461	549	625	427	0	574	0	352	167	0	51	577
TCGA-LL-A6FR-10B-01D-A31U-09_BRCA	671	0	0	352	651	467	553	629	419	89	425	548	0	169	0	48	583
TCGA-LP-A4AU-10A-01D-A243-09_CESC	682	0	0	360	663	446	542	623	446	0	0	0	0	0	0	82	585
TCGA-LP-A4AV-10A-01D-A243-09_CESC	682	0	0	345	654	458	547	628	534	0	0	0	0	0	35	60	580
TCGA-LP-A4AW-10A-01D-A243-09_CESC	685	0	0	357	671	461	555	632	560	0	0	0	0	0	37	60	587
TCGA-LP-A4AX-10A-01D-A243-09_CESC	684	311	328	337	667	447	556	650	551	97	542	528	0	0	41	46	589
TCGA-LP-A5U2-10A-01D-A28E-09_CESC	681	275	322	221	650	437	553	633	448	0	519	524	0	0	46	0	580
TCGA-LP-A5U3-10A-01D-A28E-09_CESC	697	0	0	361	684	464	554	638	546	0	0	0	0	0	0	83	593
TCGA-LQ-A4E4-10A-01D-A25Q-09_BRCA	582	323	349	0	608	173	553	635	457	0	574	521	0	0	0	67	586
TCGA-LT-A5Z6-10A-01D-A289-08_BLCA	671	244	253	284	564	376	533	646	449	72	599	0	358	135	0	70	577
TCGA-M7-A71Y-10A-01D-A329-08_PRAD	681	0	0	294	593	380	534	633	471	0	0	0	0	0	0	74	575
TCGA-M7-A71Z-10A-01D-A329-08_PRAD	687	0	0	306	601	386	532	655	383	70	608	0	303	140	0	49	575
TCGA-M7-A720-10A-01D-A329-08_PRAD	669	0	0	302	607	378	530	626	381	73	605	0	291	137	0	48	576
TCGA-M7-A721-10A-01D-A329-08_PRAD	690	250	265	291	554	378	527	631	457	0	612	0	368	138	0	71	576
TCGA-M7-A723-10A-01D-A329-08_PRAD	682	251	268	296	614	382	533	655	453	82	641	566	374	137	0	82	577
TCGA-M7-A724-10A-01D-A329-08_PRAD	686	0	0	297	602	282	522	638	374	64	573	0	295	134	0	48	571
TCGA-M7-A725-10A-01D-A329-08_PRAD	687	252	270	296	611	285	531	658	487	0	627	514	0	0	36	74	578
TCGA-M8-A5N4-10A-01D-A26I-08_PAAD	634	234	243	242	522	281	525	615	366	0	482	561	0	0	32	4	567
TCGA-MB-A5Y8-10A-01D-A29N-09_SARC	675	0	0	340	644	438	547	613	440	0	0	0	0	0	0	74	582
TCGA-MB-A5Y9-10A-01D-A29N-09_SARC	633	296	348	305	518	334	550	631	303	99	602	0	364	162	0	33	582
TCGA-MB-A5YA-10A-01D-A29N-09_SARC	659	288	290	280	489	348	538	621	296	0	536	0	332	168	0	38	579
TCGA-MF-A522-10A-01D-A25L-08_LUSC	676	240	262	286	602	378	530	638	470	0	580	536	0	0	0	87	575
TCGA-MH-A55W-10A-01D-A26P-10_KIRP	671	0	0	275	650	458	533	620	359	0	0	0	0	0	40	0	571
TCGA-MH-A55Z-10A-01D-A26P-10_KIRP	642	0	299	0	502	186	550	618	355	0	404	0	353	0	31	69	579
TCGA-MH-A560-10A-01D-A26P-10_KIRP	681	0	0	279	543	456	540	629	359	0	0	0	0	0	0	95	582
TCGA-MH-A561-10A-01D-A26P-10_KIRP	677	0	0	382	523	442	545	607	332	0	414	0	321	178	32	0	591
TCGA-MH-A562-10A-01D-A26P-10_KIRP	663	266	282	258	561	442	546	610	357	0	419	474	0	0	50	3	586
TCGA-MJ-A68H-10A-01D-A307-09_SARC	701	327	353	366	700	189	557	663	567	0	623	586	0	0	0	175	598
TCGA-MJ-A68J-10A-01D-A307-09_SARC	595	329	375	0	712	380	559	667	571	0	649	0	478	0	66	95	594
TCGA-MK-A4N6-10A-01D-A25A-08_THCA	661	0	0	272	548	374	513	630	295	69	508	0	274	129	26	0	571
TCGA-MK-A4N7-10A-01D-A25A-08_THCA	674	0	0	289	588	378	530	630	380	72	517	0	288	131	29	0	571
TCGA-MK-A4N9-10A-01D-A25A-08_THCA	637	233	249	242	495	364	508	626	353	63	498	0	276	126	31	4	568
TCGA-MM-A563-10A-01D-A25V-10_KIRC	697	0	0	379	670	470	545	624	367	0	0	0	0	0	23	64	583
TCGA-MM-A564-10A-01D-A25V-10_KIRC	560	287	318	0	0	0	543	612	325	86	440	0	359	171	0	62	574
TCGA-MN-A4N1-10A-01D-A24P-08_LUAD	686	0	0	296	604	380	530	641	464	0	0	0	0	0	0	82	580
TCGA-MN-A4N4-10A-01D-A24P-08_LUAD	685	0	0	301	597	380	533	641	475	0	0	0	0	0	0	79	575
TCGA-MN-A4N5-10A-01D-A24P-08_LUAD	680	0	0	293	596	382	524	642	484	0	0	0	0	0	31	69	575
TCGA-MO-A47P-10A-01D-A24N-09_SARC	678	303	345	328	517	435	550	642	434	80	585	0	436	178	36	4	587
TCGA-MO-A47R-10A-01D-A24N-09_SARC	669	0	0	355	661	435	544	636	550	0	0	0	0	0	29	45	582
TCGA-MP-A4SV-10A-01D-A24P-08_LUAD	594	248	265	42	61	0	529	631	381	77	601	0	295	130	0	63	573
TCGA-MP-A4SW-10A-01D-A24P-08_LUAD	683	0	0	298	603	373	529	644	365	71	586	0	295	134	0	58	573
TCGA-MP-A4SY-10A-01D-A24P-08_LUAD	673	237	256	277	603	285	528	653	468	0	595	508	0	0	29	54	576
TCGA-MP-A4T2-10A-01D-A24P-08_LUAD	759	0	0	302	608	394	533	658	465	78	602	0	363	135	0	66	579
TCGA-MP-A4T4-10A-01D-A25L-08_LUAD	683	0	0	306	606	285	520	648	475	0	0	0	0	11	0	91	573
TCGA-MP-A4T6-10A-01D-A25L-08_LUAD	597	257	277	0	52	0	528	639	393	65	564	0	368	133	28	9	577
TCGA-MP-A4T7-10A-01D-A24P-08_LUAD	687	0	0	296	594	380	530	633	465	0	0	0	0	0	26	64	576
TCGA-MP-A4T8-10A-01D-A24P-08_LUAD	594	254	268	0	522	131	525	633	365	71	623	505	358	136	29	8	572
TCGA-MP-A4T9-10A-01D-A24P-08_LUAD	673	245	263	290	586	277	532	646	466	0	0	0	0	0	33	60	576
TCGA-MP-A4TA-10A-01D-A24P-08_LUAD	675	0	0	297	600	379	531	640	386	70	528	0	295	136	0	57	572
TCGA-MP-A4TC-10A-01D-A24P-08_LUAD	654	239	260	285	602	279	530	646	382	71	630	563	362	134	0	55	575
TCGA-MP-A4TD-10A-01D-A25L-08_LUAD	758	0	0	301	601	387	533	641	385	82	582	0	288	140	0	60	576
TCGA-MP-A4TE-10A-01D-A25L-08_LUAD	690	249	267	284	579	374	532	639	435	64	559	0	292	130	0	63	576
TCGA-MP-A4TF-10A-01D-A25L-08_LUAD	596	255	275	0	509	134	531	651	386	82	625	559	290	131	0	67	578
TCGA-MP-A4TH-10A-01D-A25L-08_LUAD	681	244	261	288	581	362	533	649	475	0	0	0	0	0	29	71	575
TCGA-MP-A4TI-10A-01D-A24P-08_LUAD	688	11	47	308	606	384	529	648	391	82	616	0	365	138	0	74	575
TCGA-MP-A4TJ-10A-01D-A25L-08_LUAD	594	255	276	0	509	133	534	644	376	69	636	568	0	135	30	6	577
TCGA-MP-A4TK-10A-01D-A24P-08_LUAD	676	239	262	286	553	375	531	656	472	0	0	0	0	0	23	63	576
TCGA-MP-A5C7-10A-01D-A25L-08_LUAD	595	256	272	0	0	0	531	636	384	77	596	0	291	138	31	5	577
TCGA-MR-A520-10A-01D-A25V-10_LIHC	687	0	0	367	649	452	548	622	330	0	423	0	349	172	27	0	592
TCGA-MS-A51U-10A-01D-A25Q-09_BRCA	697	0	0	359	680	377	537	664	560	0	0	0	0	0	32	59	589
TCGA-MT-A51W-10A-01D-A25Y-08_HNSC	680	0	0	302	601	380	530	653	466	0	0	0	0	0	33	59	572
TCGA-MT-A51X-10A-01D-A25Y-08_HNSC	681	244	263	273	566	376	524	616	453	0	597	509	0	137	0	61	574
TCGA-MT-A67A-10A-01D-A30H-08_HNSC	761	252	276	205	523	287	537	652	492	0	0	0	0	0	43	93	579
TCGA-MT-A67D-10A-01D-A30H-08_HNSC	755	256	267	181	605	389	533	624	0	77	639	0	394	145	0	1	581
TCGA-MT-A67F-10A-01D-A30H-08_HNSC	761	0	0	319	631	300	532	653	494	0	0	0	0	0	0	162	581
TCGA-MT-A67G-10A-01D-A30H-08_HNSC	759	0	271	193	622	400	539	656	468	73	644	0	411	142	41	0	580
TCGA-MU-A51Y-10A-01D-A26G-09_CESC	667	0	0	336	666	446	547	638	457	0	0	0	0	0	22	54	582
TCGA-MV-A51V-10A-01D-A26K-08_BLCA	645	233	252	244	594	279	524	625	362	68	595	568	0	128	0	59	573
TCGA-MW-A4EC-10A-01D-A25V-10_KIRC	687	274	293	259	669	373	551	620	355	0	429	492	0	0	0	117	583
TCGA-MX-A5UG-10A-01D-A31J-08_STAD	681	0	0	292	593	389	529	639	379	72	527	0	364	134	30	0	573
TCGA-MX-A5UJ-10A-01D-A31J-08_STAD	675	245	239	275	601	367	531	631	467	0	520	563	0	0	0	100	570
TCGA-MX-A663-10A-01D-A31J-08_STAD	684	0	0	302	592	379	529	636	474	0	0	0	0	0	0	111	573
TCGA-MX-A666-10A-01D-A31J-08_STAD	674	239	250	283	516	366	528	638	377	75	531	0	358	132	29	0	570
TCGA-MY-A5BD-10A-01D-A26G-09_CESC	682	302	296	200	610	408	552	622	541	0	0	0	0	0	45	5	589
TCGA-MY-A5BE-10A-01D-A26G-09_CESC	694	0	0	351	670	449	551	635	422	0	0	0	0	0	0	49	579

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-MY-A5BF-10A-01D-A26G-09_CESC	680	325	361	0	645	305	550	625	81	101	647	553	349	186	0	5	584
TCGA-MZ-A6I9-10A-01D-A31J-08_HNSC	670	240	262	179	598	281	531	651	476	71	575	560	0	0	24	48	575
TCGA-NC-A5HD-10A-01D-A26K-08_LUSC	665	0	0	287	594	377	519	628	464	0	0	0	0	0	0	117	575
TCGA-NC-A5HE-10A-01D-A26K-08_LUSC	684	0	0	292	596	387	532	634	310	0	543	0	359	134	0	70	576
TCGA-NC-A5HF-10A-01D-A26K-08_LUSC	678	0	0	294	596	378	526	627	468	0	0	0	0	0	0	102	571
TCGA-NC-A5HG-10A-01D-A26K-08_LUSC	682	0	0	297	593	388	532	645	461	0	0	0	0	0	28	72	575
TCGA-NC-A5HH-10A-01D-A26K-08_LUSC	683	0	0	298	605	383	531	639	472	0	0	0	0	0	0	125	575
TCGA-NC-A5HI-10A-01D-A26K-08_LUSC	658	237	264	279	502	367	528	642	469	0	0	0	0	0	0	92	574
TCGA-NC-A5HJ-10A-01D-A26K-08_LUSC	681	0	0	296	598	382	529	632	401	0	0	0	0	0	47	0	575
TCGA-NC-A5HK-10A-01D-A26K-08_LUSC	683	0	0	301	600	381	530	655	469	68	0	0	0	0	0	80	577
TCGA-NC-A5HL-10A-01D-A26K-08_LUSC	679	235	260	177	501	271	530	613	476	0	0	0	0	0	42	2	572
TCGA-NC-A5HM-10A-01D-A26K-08_LUSC	684	0	0	296	590	389	534	648	462	0	0	0	0	0	32	55	575
TCGA-NC-A5HN-10A-01D-A26K-08_LUSC	671	234	247	261	592	362	531	631	463	0	526	563	0	0	31	60	577
TCGA-NC-A5HO-10A-01D-A26K-08_LUSC	684	0	0	297	601	379	528	632	403	0	0	0	0	0	32	52	572
TCGA-NC-A5HP-10A-01D-A26K-08_LUSC	683	0	0	301	570	379	526	619	441	0	0	0	0	0	0	89	575
TCGA-NC-A5HQ-10A-01D-A26K-08_LUSC	670	216	239	263	594	356	526	614	371	64	599	499	280	128	0	50	576
TCGA-NC-A5HR-10A-01D-A26K-08_LUSC	667	249	259	262	504	281	504	592	0	81	609	0	370	139	0	5	575
TCGA-NC-A5HT-10A-01D-A26K-08_LUSC	667	244	266	277	505	277	529	635	468	0	0	0	0	0	30	57	576
TCGA-NH-A50T-10A-01D-A28G-10_COAD	690	0	0	282	660	461	546	625	356	0	0	0	0	0	30	57	586
TCGA-NH-A50V-10A-01D-A28G-10_COAD	635	222	273	236	489	404	512	598	307	0	450	0	349	162	28	1	563
TCGA-NI-A4U2-10A-01D-A28X-10_LIHC	672	0	0	261	559	446	544	636	358	0	0	0	0	0	0	113	581
TCGA-NJ-A4YF-10A-01D-A25L-08_LUAD	683	0	0	299	610	385	534	638	463	0	0	0	0	26	0	69	580
TCGA-NJ-A4YG-10A-01D-A25L-08_LUAD	691	0	0	309	605	394	534	657	456	76	525	0	371	138	0	76	577
TCGA-NJ-A4YI-10A-01D-A25L-08_LUAD	757	0	28	301	599	381	527	652	389	61	595	0	299	135	0	73	575
TCGA-NJ-A4YP-10A-01D-A25L-08_LUAD	597	255	271	0	58	0	533	633	388	66	603	0	296	138	0	62	577
TCGA-NJ-A4YQ-10A-01D-A25L-08_LUAD	687	0	0	304	618	393	529	662	468	82	618	562	296	135	0	64	575
TCGA-NJ-A55A-10A-01D-A25L-08_LUAD	682	0	0	310	603	376	528	637	476	0	0	0	0	0	25	65	576
TCGA-NJ-A55O-10A-01D-A25L-08_LUAD	686	0	0	292	602	289	525	636	461	0	0	0	0	0	0	78	579
TCGA-NJ-A55R-10A-01D-A25L-08_LUAD	771	273	289	329	658	414	541	677	494	91	676	587	404	146	0	174	583
TCGA-NK-A5CR-10A-01D-A26K-08_LUSC	745	251	260	271	576	362	531	633	383	54	531	510	0	136	0	59	578
TCGA-NK-A5CT-10A-01D-A26K-08_LUSC	675	248	263	283	551	373	530	634	454	75	538	0	295	134	32	3	575
TCGA-NK-A5CX-10A-01D-A26K-08_LUSC	681	238	261	274	551	361	530	637	382	71	591	0	289	130	31	5	575
TCGA-NK-A5D1-10A-01D-A26K-08_LUSC	676	0	0	293	605	286	522	629	383	66	582	0	296	133	0	60	575
TCGA-O1-A52J-10A-01D-A25L-08_LUAD	676	0	0	302	554	377	521	634	467	0	0	0	0	0	26	60	574
TCGA-O2-A52N-10A-01D-A26K-08_LUSC	675	247	264	290	582	285	531	646	395	72	597	0	370	132	0	55	577
TCGA-O2-A52Q-10A-01D-A26K-08_LUSC	649	240	257	283	573	272	522	635	478	0	519	507	0	0	30	62	575
TCGA-O2-A52S-10A-01D-A25L-08_LUSC	668	241	259	277	553	277	529	639	388	71	593	0	292	139	37	2	576
TCGA-O2-A52V-10A-01D-A25L-08_LUSC	683	0	0	302	602	380	531	635	478	0	0	0	0	0	39	1	575
TCGA-O2-A52W-10A-01D-A26K-08_LUSC	670	240	241	244	437	357	529	624	463	0	0	0	0	0	37	0	572
TCGA-O2-A5IB-10A-01D-A27N-08_LUSC	679	0	0	288	596	284	522	647	465	0	0	0	0	0	28	57	574
TCGA-OD-A75X-10A-01D-A32N-08_SKCM	676	247	264	291	588	282	534	652	458	68	605	0	302	135	0	76	577
TCGA-OE-A75W-10A-01D-A32N-08_PAAD	679	0	0	293	596	283	522	635	462	0	0	0	0	0	25	57	574
TCGA-OK-A5Q2-10A-01D-A27P-09_BRCA	692	0	0	360	649	450	553	613	449	0	0	0	0	0	55	2	583
TCGA-OL-A5D6-10A-01D-A27P-09_BRCA	694	0	0	363	651	465	549	618	452	0	0	0	0	0	0	74	586
TCGA-OL-A5D7-10A-01D-A27P-09_BRCA	668	290	309	302	644	450	540	613	510	0	473	517	0	0	39	0	578
TCGA-OL-A5D8-10A-01D-A27P-09_BRCA	685	0	0	360	659	452	544	633	444	0	0	0	0	0	33	43	584
TCGA-OL-A5DA-10A-01D-A27P-09_BRCA	583	319	349	0	644	181	548	621	406	92	631	584	0	177	0	42	580
TCGA-OL-A5RU-10A-01D-A28E-09_BRCA	698	0	326	313	666	449	549	645	440	0	578	0	377	0	44	48	585
TCGA-OL-A5RV-10A-01D-A28E-09_BRCA	573	0	356	0	645	173	553	635	453	0	586	0	376	0	55	3	587
TCGA-OL-A5RW-10A-01D-A28E-09_BRCA	674	0	0	347	654	457	544	613	320	0	0	0	0	0	24	0	535
TCGA-OL-A5RX-10A-01D-A28E-09_BRCA	571	307	345	0	684	358	551	624	545	0	592	528	359	0	26	42	586
TCGA-OL-A5RY-10A-01D-A28E-09_BRCA	693	282	306	328	590	425	533	496	434	0	463	0	356	175	0	46	586
TCGA-OL-A5RZ-10A-01D-A28E-09_BRCA	691	0	0	361	670	454	552	623	543	0	0	0	0	0	54	0	583
TCGA-OL-A5S0-10A-01D-A28E-09_BRCA	591	321	359	0	0	0	550	619	451	0	0	0	0	0	58	0	587
TCGA-OL-A66H-10A-01D-A29N-09_BRCA	692	290	338	229	660	444	547	614	354	0	577	0	370	0	0	71	582
TCGA-OL-A66I-10A-01D-A29N-09_BRCA	671	292	340	202	674	356	546	618	536	0	452	524	0	0	0	97	588
TCGA-OL-A66J-10A-01D-A29N-09_BRCA	692	313	338	343	655	370	554	652	548	0	0	0	0	0	0	88	592
TCGA-OL-A66K-10A-01D-A29N-09_BRCA	685	309	0	336	667	448	551	626	0	104	600	0	447	181	0	0	585
TCGA-OL-A66L-10A-01D-A31U-09_BRCA	692	0	0	350	657	450	545	627	555	0	0	0	0	0	0	71	587
TCGA-OL-A66N-10A-01D-A31U-09_BRCA	657	297	320	327	615	350	550	633	408	96	470	503	0	175	0	55	584
TCGA-OL-A66O-10A-01D-A31U-09_BRCA	653	300	305	311	611	188	549	636	549	0	0	0	0	0	26	53	588
TCGA-OL-A66P-10A-01D-A31U-09_BRCA	642	300	169	108	671	180	554	638	519	93	569	579	0	0	40	47	590
TCGA-OR-A5J1-10A-01D-A29L-10_ACC	639	0	0	278	575	453	548	610	322	90	457	0	354	172	35	0	580
TCGA-OR-A5J2-10A-01D-A29L-10_ACC	661	0	0	279	563	452	527	612	357	0	0	0	0	0	32	65	575
TCGA-OR-A5J3-10A-01D-A29L-10_ACC	681	259	290	257	570	438	527	605	350	0	448	508	0	0	0	93	573
TCGA-OR-A5J4-10A-01D-A29L-10_ACC	678	0	0	278	563	446	540	611	351	0	0	0	0	0	0	88	578
TCGA-OR-A5J7-10A-01D-A29L-10_ACC	675	267	286	256	657	370	536	637	327	0	512	527	365	165	26	0	573
TCGA-OR-A5J8-10A-01D-A29L-10_ACC	660	251	284	238	542	437	541	607	323	0	478	527	0	171	0	32	566
TCGA-OR-A5J9-10A-01D-A29L-10_ACC	678	0	0	363	588	453	552	662	352	0	464	490	0	0	31	77	579
TCGA-OR-A5JA-10A-01D-A29L-10_ACC	684	0	0	279	564	458	528	609	339	0	0	0	0	0	0	78	570
TCGA-OR-A5JB-10A-01D-A29L-10_ACC	565	175	267	244	562	379	522	595	0	0	517	504	372	180	0	0	572
TCGA-OR-A5JD-10B-01D-A29L-10_ACC	679	269	272	247	471	371	537	601	358	0	0	0	0	0	0	100	578
TCGA-OR-A5JE-10A-01D-A29L-10_ACC	553	237	288	252	538	357	523	614	337	0	417	502	0	0	28	45	575
TCGA-OR-A5JF-10A-01D-A29L-10_ACC	674	0	0	275	564	458	540	596	319	0	479	0	343	158	21	0	586
TCGA-OR-A5JG-10A-01D-A29L-10_ACC	684	239	250	261	475	429	508	625	345	0	0	0	0	0	0	47	584
TCGA-OR-A5JH-10A-01D-A30A-10_ACC	578	247	196	255	508	401	495	472	0	0	469	0	375	176	0	0	584
TCGA-OR-A5JI-10A-01D-A29L-10_ACC	673	223	269	260	655	370	541	613	331	0	494	530	0	181	0	42	581
TCGA-OR-A5JJ-10A-01D-A29L-10_ACC	674	0	0	279	554	434	521	614	339	0	430	0	331	177	0	46	571
TCGA-OR-A5JK-10A-01D-A29L-10_ACC	667	0	0	277	657	440	539	600	349	0	0	0	0	0	27	64	581
TCGA-OR-A5JL-10A-01D-A29L-10_ACC	672	245	237	247	494	415	546	619	319	0	384	0	348	171	0	55	564
TCGA-OR-A5JM-10B-01D-A29L-10_ACC	675	233	271	245	526	438	543	631	343	0	457	0	342	176	0	62	575
TCGA-OR-A5JO-10A-01D-A29L-10_ACC	670	0	0	269	566	442	546	611	360	0	0	0	0	0	0	86	568
TCGA-OR-A5JP-10A-01D-A29L-10_ACC	683	0	0	269	550	451	530	516	349	0	0	0	0	0	29	61	576
TCGA-OR-A5JQ-10A-01D-A29L-10_ACC	568	257	326	245	536	439	524	621	321	0	493	482	339	178	0	39	580
TCGA-OR-A5JR-10A-01D-A29L-10_ACC	590	231	0	245	542	441	527	620	321	0	406	0	331	164	19	1	569
TCGA-OR-A5JS-10A-01D-A29L-10_ACC	667	179	255	237	480	427	526	613	354	0	0	0	0	0	0	90	565
TCGA-OR-A5JT-10A-01D-A29L-10_ACC	570	177	241	247	386	423	537	612	302	0	399	0	312	176	0	47	566
TCGA-OR-A5JU-10A-01D-A30A-10_ACC	583	222	290	248	497	418	520	595	344	0	0	0	0	0	25	48	582
TCGA-OR-A5JV-10A-01D-A29L-10_ACC	560	153	265	220	534	356	530	569	298	0	472	493	0	156	0	34	574
TCGA-OR-A5JW-10A-01D-A29L-10_ACC	662	171	298	257	555	364	525	615	358	0	413	433	0	0	0	100	586
TCGA-OR-A5JX-10B-01D-A29L-10_ACC	671	263	291	244	639	371	544	618	345	90	490	502	343	178	27	1	579
TCGA-OR-A5JY-10A-01D-A29L-10_ACC	584	283	313	254	591	441	518	572	317	0	452	0	356	174	0	72	568
TCGA-OR-A5JZ-10A-01D-A29L-10_ACC	545	261	291	0	459	169	543	601	346	0	390	480	0	0	41	2	561
TCGA-OR-A5K0-10B-01D-A29L-10_ACC	674	0	0	268	655	380	547	606	353	0	0	0	0	0	27	59	587
TCGA-OR-A5K1-10A-01D-A29L-10_ACC	665	174	279	233	502	421	533	606	331	81	422	0	328	166	0	54	581
TCGA-OR-A5K2-10B-01D-A29L-10_ACC	667	0	0	273	554	454	533	596	353	0	0	0	0	0	0	92	573

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-OR-A5K3-10A-01D-A29L-10_ACC	663	0	0	269	672	455	545	621	0	0	508	0	446	183	0	4	565
TCGA-OR-A5K4-10A-01D-A29L-10_ACC	661	0	0	274	553	378	537	617	351	0	0	0	0	0	0	112	581
TCGA-OR-A5K5-10A-01D-A29L-10_ACC	559	238	271	256	467	430	532	606	353	0	0	0	0	0	0	112	577
TCGA-OR-A5K6-10A-01D-A29L-10_ACC	774	273	272	269	534	428	531	612	357	0	0	0	0	0	45	0	583
TCGA-OR-A5K8-10A-01D-A29L-10_ACC	555	0	0	259	554	382	528	578	314	0	391	0	328	160	21	0	572
TCGA-OR-A5KP-10A-01D-A30A-10_ACC	556	216	245	116	484	346	527	589	335	0	0	0	0	0	24	47	561
TCGA-OR-A5KQ-10A-01D-A30A-10_ACC	676	0	0	262	551	434	524	515	351	0	0	0	0	0	0	80	563
TCGA-OR-A5KS-10A-01D-A30A-10_ACC	661	234	294	265	491	365	538	622	323	0	417	0	345	159	0	54	580
TCGA-OR-A5KT-10A-01D-A29L-10_ACC	574	293	327	0	0	0	546	628	356	0	0	0	0	0	0	95	576
TCGA-OR-A5KU-10A-01D-A29L-10_ACC	670	0	0	273	551	456	534	515	361	0	0	0	0	0	0	93	574
TCGA-OR-A5KV-10A-01D-A29L-10_ACC	567	228	0	256	667	359	536	621	332	0	461	0	352	171	0	58	581
TCGA-OR-A5KW-10A-01D-A29L-10_ACC	667	180	263	247	490	409	535	608	363	0	0	0	0	0	19	42	582
TCGA-OR-A5KX-10A-01D-A29L-10_ACC	682	0	0	350	641	375	541	621	361	0	0	0	0	0	0	92	585
TCGA-OR-A5KY-10A-01D-A29L-10_ACC	662	0	0	266	552	460	549	627	305	0	444	0	346	175	0	48	581
TCGA-OR-A5KZ-10A-01D-A29L-10_ACC	676	0	0	283	642	444	536	613	349	0	0	0	0	0	24	41	572
TCGA-OR-A5L1-10A-01D-A30A-10_ACC	653	0	0	272	552	448	539	600	351	0	0	0	0	0	0	98	570
TCGA-OR-A5L2-10A-01D-A30A-10_ACC	680	0	0	250	563	378	541	619	328	0	411	0	338	173	20	1	567
TCGA-OR-A5L3-10A-01D-A29L-10_ACC	633	0	0	259	548	367	525	585	343	0	0	0	0	0	0	54	555
TCGA-OR-A5L4-10A-01D-A29L-10_ACC	691	177	259	273	507	422	540	627	355	0	0	0	0	0	23	61	585
TCGA-OR-A5L6-10C-01D-A29L-10_ACC	658	233	275	254	473	412	550	617	359	0	0	0	0	0	21	39	575
TCGA-OR-A5L8-10A-01D-A29L-10_ACC	577	180	274	255	481	358	544	608	304	0	411	0	341	167	0	42	568
TCGA-OR-A5L9-10B-01D-A29L-10_ACC	671	0	0	283	639	440	546	609	356	0	0	0	0	0	0	101	576
TCGA-OR-A5LA-10A-01D-A29L-10_ACC	657	0	0	274	546	366	513	576	347	0	0	0	0	0	20	42	575
TCGA-OR-A5LB-10A-01D-A29L-10_ACC	553	166	325	247	496	349	550	623	345	0	0	0	0	0	0	88	570
TCGA-OR-A5LC-10A-01D-A29L-10_ACC	565	243	257	246	498	348	516	610	353	0	0	0	0	0	24	58	581
TCGA-OR-A5LD-10A-01D-A29L-10_ACC	670	232	300	119	555	366	545	618	327	90	472	557	0	170	25	1	570
TCGA-OR-A5LE-10A-01D-A29L-10_ACC	565	215	298	248	563	441	537	611	326	0	460	544	0	171	0	51	573
TCGA-OR-A5LF-10A-01D-A30A-10_ACC	558	276	322	0	546	176	525	604	362	0	488	529	0	0	0	99	583
TCGA-OR-A5LG-10A-01D-A29L-10_ACC	655	0	0	271	552	382	539	616	349	0	0	0	0	0	0	83	572
TCGA-OR-A5LH-10A-01D-A29L-10_ACC	670	215	258	254	500	352	535	625	328	0	466	0	323	166	0	55	560
TCGA-OR-A5LI-10A-01D-A30A-10_ACC	550	163	262	116	556	337	540	610	299	0	433	546	0	174	20	2	560
TCGA-OR-A5LJ-10A-01D-A29L-10_ACC	578	280	345	0	511	182	537	627	336	0	501	508	365	168	31	1	578
TCGA-OR-A5LK-10A-01D-A29L-10_ACC	571	0	0	272	567	383	520	636	350	0	0	96	0	0	0	105	572
TCGA-OR-A5LL-10A-01D-A29L-10_ACC	634	225	269	233	557	412	517	596	347	0	380	450	0	0	0	83	573
TCGA-OR-A5LN-10A-01D-A29L-10_ACC	675	233	295	252	568	419	540	620	365	0	422	493	0	0	32	44	577
TCGA-OR-A5LO-10A-01D-A29L-10_ACC	658	232	288	240	652	353	532	603	312	0	472	479	297	166	0	40	563
TCGA-OR-A5LP-10A-01D-A29L-10_ACC	557	298	337	0	503	174	544	619	360	0	468	511	0	0	30	61	569
TCGA-OR-A5LR-10A-01D-A29L-10_ACC	561	290	325	0	481	177	544	633	353	0	426	505	0	0	30	47	580
TCGA-OR-A5LS-10A-01D-A29L-10_ACC	663	0	0	373	642	377	542	604	309	0	452	0	356	158	25	2	581
TCGA-OR-A5LT-10A-01D-A29L-10_ACC	687	0	0	371	546	458	548	621	353	0	0	0	0	0	0	126	574
TCGA-OU-A5PI-10A-01D-A29L-10_ACC	653	170	271	112	572	374	554	642	360	0	403	473	0	0	25	40	572
TCGA-OX-A56R-10A-01D-A33W-08_GBM	684	0	0	295	589	377	525	641	373	59	572	0	282	130	0	59	573
TCGA-P5-A5ET-10A-01D-A27N-08_LGG	746	250	278	284	568	375	536	659	436	87	620	0	387	140	0	71	580
TCGA-P5-A5EU-10A-01D-A27N-08_LGG	593	262	276	0	0	0	532	643	438	77	610	0	300	137	0	63	573
TCGA-P5-A5EV-10A-01D-A27N-08_LGG	758	247	267	278	618	387	531	651	461	69	625	506	296	139	0	67	578
TCGA-P5-A5EW-10A-01D-A27N-08_LGG	753	250	271	280	618	378	533	641	483	0	612	570	0	0	36	63	580
TCGA-P5-A5EX-10A-01D-A289-08_LGG	670	0	0	302	596	365	522	631	470	0	0	0	0	0	0	75	570
TCGA-P5-A5EY-10A-01D-A27N-08_LGG	757	255	257	289	599	290	534	654	485	0	0	0	0	0	39	76	577
TCGA-P5-A5EZ-10A-01D-A27N-08_LGG	758	253	263	309	608	284	531	648	479	0	0	0	0	0	0	104	578
TCGA-P5-A5F0-10A-01D-A289-08_LGG	750	247	255	277	601	368	531	654	474	67	531	512	0	0	30	55	574
TCGA-P5-A5F1-10A-01D-A289-08_LGG	652	238	261	284	606	371	535	644	438	79	636	566	0	134	26	0	575
TCGA-P5-A5F2-10A-01D-A289-08_LGG	687	0	0	305	603	385	527	644	385	74	586	513	0	137	0	65	576
TCGA-P5-A5F4-10A-01D-A289-08_LGG	597	251	273	0	0	0	529	632	381	74	589	0	368	131	0	58	570
TCGA-P5-A5F6-10A-01D-A289-08_LGG	688	0	0	304	593	375	530	630	474	0	0	0	0	0	0	72	574
TCGA-P5-A72U-10A-01D-A329-08_LGG	674	218	228	170	564	265	524	608	304	63	562	0	289	131	0	46	570
TCGA-P5-A72W-10A-01D-A329-08_LGG	680	0	0	302	607	287	523	645	412	0	0	0	0	0	0	76	576
TCGA-P5-A72X-10A-01D-A329-08_LGG	681	228	242	269	597	352	530	640	461	0	506	508	0	0	0	69	574
TCGA-P5-A72Z-10A-01D-A329-08_LGG	674	0	0	297	588	361	518	627	0	78	611	495	289	135	0	0	572
TCGA-P5-A730-10A-01D-A329-08_LGG	679	0	0	295	592	366	518	626	467	0	0	0	0	0	0	100	575
TCGA-P5-A731-10A-01D-A329-08_LGG	674	232	258	254	546	255	528	633	373	75	577	508	0	134	20	0	571
TCGA-P5-A733-10A-01D-A329-08_LGG	682	216	253	286	571	262	526	636	392	0	0	0	0	0	0	59	573
TCGA-P5-A735-10A-01D-A329-08_LGG	678	0	0	287	586	377	529	627	0	77	626	0	372	137	0	0	575
TCGA-P5-A736-10A-01D-A329-08_LGG	591	247	267	0	591	139	531	628	386	68	640	517	291	134	0	0	570
TCGA-P5-A737-10A-01D-A329-08_LGG	682	0	0	289	589	376	526	627	465	0	0	0	0	0	0	69	571
TCGA-P5-A77W-10A-01D-A329-08_LGG	691	0	0	306	602	287	529	634	476	0	0	0	0	0	0	79	573
TCGA-P5-A77X-10A-01D-A329-08_LGG	671	0	0	290	586	353	517	634	371	60	552	457	0	135	0	54	571
TCGA-P5-A780-10A-01D-A329-08_LGG	673	233	245	278	602	350	527	638	377	62	625	560	294	134	0	50	575
TCGA-P5-A781-10A-01D-A329-08_LGG	655	225	233	168	489	266	523	632	463	0	0	0	0	0	0	73	572
TCGA-P6-A5OF-10A-01D-A29L-10_ACC	677	0	0	376	672	462	546	630	332	0	463	0	359	162	25	1	570
TCGA-P6-A5OG-10A-01D-A29L-10_ACC	662	243	302	247	539	427	541	610	309	0	511	504	343	178	0	61	575
TCGA-PA-A5YG-10A-01D-A29L-10_ACC	673	225	257	253	494	421	544	622	320	86	433	0	360	169	0	55	578
TCGA-PC-A5DK-10A-01D-A27P-09_SARC	698	306	349	326	694	459	551	645	410	89	637	584	0	174	49	3	589
TCGA-PC-A5DL-10A-01D-A26G-09_SARC	676	0	0	342	655	432	549	629	459	0	0	0	0	0	25	37	586
TCGA-PC-A5DM-10A-01D-A27P-09_SARC	692	0	0	363	665	467	553	659	530	0	0	0	0	0	38	65	593
TCGA-PC-A5DN-10A-01D-A27P-09_SARC	700	0	0	375	679	471	549	646	555	0	0	0	0	0	0	128	593
TCGA-PC-A5DO-10A-01D-A26G-09_SARC	653	0	0	346	646	441	542	619	443	0	0	0	0	0	27	33	574
TCGA-PC-A5DP-10A-01D-A26G-09_SARC	680	0	0	353	660	449	549	619	548	0	0	0	0	0	0	83	583
TCGA-PD-A5DF-10A-01D-A27I-10_LIHC	671	0	0	270	534	446	532	594	310	0	400	0	330	167	19	3	572
TCGA-PE-A5DC-10A-01D-A27P-09_BRCA	663	0	0	351	653	436	540	625	450	0	0	0	0	0	0	81	581
TCGA-PE-A5DD-10A-01D-A27P-09_BRCA	665	293	344	332	678	453	551	641	451	0	497	539	0	0	0	112	584
TCGA-PE-A5DE-10A-01D-A27P-09_BRCA	583	315	352	0	625	174	550	626	412	86	612	534	354	169	29	0	584
TCGA-PG-A5BC-10A-01D-A27P-09_UCEC	698	0	0	347	661	187	554	637	420	94	593	0	354	179	34	2	586
TCGA-PG-A6IB-10A-01D-A31U-09_UCEC	668	299	314	287	631	406	549	626	557	0	0	0	0	0	30	42	583
TCGA-PJ-A5Z8-10A-01D-A28G-10_KIRP	676	240	322	250	513	416	551	647	327	0	461	0	334	170	0	68	573
TCGA-PJ-A5Z9-10A-01D-A28G-10_KIRP	669	0	0	276	575	448	535	612	363	0	0	0	0	0	0	94	575
TCGA-PK-A5H8-10A-01D-A29L-10_ACC	659	278	278	266	544	361	548	611	362	0	0	0	0	0	42	0	580
TCGA-PK-A5H9-10A-01D-A29L-10_ACC	677	0	0	278	556	439	514	610	319	0	398	0	342	171	0	36	582
TCGA-PK-A5HA-10A-01D-A29L-10_ACC	669	0	0	358	569	446	550	624	326	0	414	0	341	173	0	53	577
TCGA-PQ-A6FI-10A-01D-A31J-08_BLCA	685	0	0	306	606	383	529	639	477	0	0	0	0	0	0	115	579
TCGA-PQ-A6FN-10A-01D-A31J-08_BLCA	685	248	257	180	513	280	531	649	461	78	600	526	0	136	30	0	575
TCGA-PZ-A5RE-10B-01D-A32N-08_PAAD	677	0	0	285	578	375	527	626	453	0	0	0	0	0	0	88	570
TCGA-Q1-A5R1-10A-01D-A28E-09_CESC	691	0	0	361	660	449	547	634	307	83	476	541	0	166	0	45	578
TCGA-Q1-A5R2-10A-01D-A28E-09_CESC	692	304	330	328	628	335	550	635	384	100	568	0	350	182	43	0	589
TCGA-Q1-A5R3-10B-01D-A28E-09_CESC	666	0	0	344	667	371	546	596	462	0	0	0	0	0	0	79	582
TCGA-Q2-A5QZ-10A-01D-A28G-10_KIRP	478	135	224	192	484	341	487	457	306	0	201	387	0	0	9	18	524
TCGA-Q3-A5QY-10A-01D-A32N-08_PAAD	681	0	0	298	605	380	530	644	444	76	586	0	293	136	29	0	576

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-QB-A6FS-10A-01D-A30X-08_SKCM	670	0	0	292	594	285	521	634	451	0	0	0	0	0	0	87	574
TCGA-QF-A5YS-10A-01D-A31U-09_UCEC	676	0	0	356	682	363	545	642	552	0	0	0	0	0	35	51	584
TCGA-QF-A5YT-10A-01D-A31U-09_UCEC	675	0	0	357	657	460	553	616	526	0	0	0	0	0	47	0	577
TCGA-QG-A5YV-10A-01D-A28G-10_COAD	636	270	297	112	573	351	540	576	343	0	443	492	0	0	37	0	546
TCGA-QG-A5YW-10A-01D-A28G-10_COAD	655	0	0	265	546	455	526	601	337	0	0	0	0	0	35	0	565
TCGA-QG-A5YX-10A-01D-A28G-10_COAD	681	0	0	254	568	388	542	593	351	0	459	480	0	0	35	0	579
TCGA-QG-A5Z1-10A-01D-A28G-10_COAD	536	246	318	0	550	178	529	590	301	0	504	438	365	181	12	0	571
TCGA-QG-A5Z2-10A-01D-A28G-10_COAD	672	0	0	281	541	463	528	568	342	0	0	0	0	0	36	0	578
TCGA-QH-A65R-10A-01D-A31J-08_LGG	668	245	252	276	564	275	530	636	472	0	0	0	0	0	0	121	571
TCGA-QH-A65S-10A-01D-A29Q-08_LGG	667	264	280	0	610	140	534	655	489	0	647	579	0	0	0	141	581
TCGA-QH-A65V-10A-01D-A29Q-08_LGG	675	0	0	303	588	290	522	638	372	72	527	563	0	138	0	60	580
TCGA-QH-A65X-10D-01D-A329-08_LGG	678	0	0	295	559	380	528	630	395	0	0	0	0	0	0	69	576
TCGA-QH-A65Z-10A-01D-A29Q-08_LGG	761	0	0	308	618	401	533	652	448	69	594	0	366	141	0	63	579
TCGA-QH-A6CS-10A-01D-A31J-08_LGG	684	0	0	298	597	377	529	640	473	0	0	0	0	0	0	78	571
TCGA-QH-A6CU-10A-01D-A31J-08_LGG	673	246	261	185	606	276	528	634	471	0	577	562	0	0	0	122	573
TCGA-QH-A6CV-10A-01D-A31J-08_LGG	683	0	0	298	602	382	527	641	451	72	528	558	0	133	31	0	573
TCGA-QH-A6CW-10B-01D-A329-08_LGG	680	229	258	276	578	361	528	637	405	0	0	0	0	0	0	76	572
TCGA-QH-A6CX-10A-01D-A329-08_LGG	667	225	240	175	607	275	530	622	363	77	617	507	288	133	0	41	573
TCGA-QH-A6CY-10A-01D-A329-08_LGG	681	0	0	296	606	369	529	643	383	70	584	0	356	135	0	50	574
TCGA-QH-A6CZ-10B-01D-A329-08_LGG	680	239	245	281	607	368	531	640	0	76	647	569	287	138	0	0	569
TCGA-QH-A6X3-10B-01D-A329-08_LGG	671	252	254	276	598	374	521	637	383	76	623	563	0	133	0	63	572
TCGA-QH-A6X4-10B-01D-A329-08_LGG	595	235	242	250	591	271	515	630	408	0	543	496	0	0	0	71	574
TCGA-QH-A6X5-10B-01D-A329-08_LGG	675	0	0	294	583	359	527	635	465	0	0	0	0	0	0	63	577
TCGA-QH-A6X8-10B-01D-A329-08_LGG	677	235	241	264	524	351	518	639	397	0	0	0	0	0	0	71	566
TCGA-QH-A6X9-10B-01D-A329-08_LGG	658	236	242	250	531	348	532	641	401	0	0	0	0	0	12	44	573
TCGA-QH-A6XA-10B-01D-A329-08_LGG	596	233	242	261	586	268	520	629	399	0	537	491	0	0	16	38	572
TCGA-QH-A6XC-10B-01D-A329-08_LGG	758	0	0	299	602	384	528	641	472	0	0	0	0	0	0	82	578
TCGA-QK-A64Z-10A-01D-A30H-08_HNSC	674	268	281	0	576	141	537	657	479	78	657	572	385	141	0	93	579
TCGA-QK-A652-10A-01D-A30H-08_HNSC	758	249	271	296	628	387	538	652	477	80	645	583	0	141	0	91	582
TCGA-QK-A6IF-10A-01D-A31J-08_HNSC	664	247	263	274	559	281	527	643	472	0	0	0	0	0	25	58	573
TCGA-QK-A6IG-10A-01D-A31J-08_HNSC	681	241	254	278	600	361	533	631	475	0	604	563	0	0	0	109	572
TCGA-QK-A6IH-10A-01D-A31J-08_HNSC	664	232	251	270	554	277	526	635	465	0	0	0	0	0	0	107	572
TCGA-QK-A6II-10A-01D-A31J-08_HNSC	660	241	251	272	549	268	526	640	441	61	574	0	287	134	25	0	576
TCGA-QK-A6IJ-10A-01D-A31J-08_HNSC	674	238	256	277	604	136	510	606	0	74	626	546	294	142	0	2	577
TCGA-QS-A5YQ-10A-01D-A31U-09_UCEC	664	0	311	299	661	438	544	613	539	0	483	0	354	0	47	0	578
TCGA-QS-A5YR-10A-01D-A31U-09_UCEC	692	0	0	356	616	457	553	622	410	0	0	0	0	0	33	0	573
TCGA-QU-A6IL-10A-01D-A31J-08_PRAD	676	244	248	281	469	363	526	604	383	0	596	507	0	131	28	0	573
TCGA-QU-A6IM-10A-01D-A31J-08_PRAD	686	0	0	292	592	371	526	644	463	0	0	0	0	0	22	47	572
TCGA-QU-A6IN-10A-01D-A31J-08_PRAD	682	0	0	305	598	385	529	640	0	77	618	0	305	138	0	0	572
TCGA-QU-A6IO-10A-01D-A31J-08_PRAD	682	0	0	288	578	378	529	632	469	0	0	0	0	0	24	59	569
TCGA-QU-A6IP-10A-01D-A31J-08_PRAD	688	0	0	297	604	286	519	642	474	0	0	0	0	0	0	121	576
TCGA-R3-A69X-10A-01D-A30H-08_BLCA	756	0	0	349	614	297	539	645	459	74	586	0	380	142	0	87	580
TCGA-R5-A7O7-10A-01D-A33W-08_STAD	686	0	0	300	597	383	531	646	455	77	613	0	295	136	0	64	576
TCGA-R8-A6MK-10A-01D-A329-08_LGG	666	244	250	285	575	270	529	637	476	0	0	0	0	0	0	104	575
TCGA-R8-A6ML-10A-01D-A329-08_LGG	678	0	0	286	585	379	523	632	463	0	0	0	0	0	18	47	574
TCGA-R8-A6YH-10B-01D-A329-08_LGG	677	0	0	281	574	373	521	635	366	54	501	0	354	128	24	0	572
TCGA-R8-A73M-10C-01D-A329-08_LGG	589	250	266	0	0	0	528	633	295	55	562	0	284	129	0	42	575
TCGA-RB-A7B8-10A-01D-A33W-08_PAAD	589	245	262	0	532	128	527	627	359	61	617	563	0	124	0	46	572
TCGA-RD-A7BS-10A-01D-A32N-08_STAD	686	0	0	300	610	383	532	658	481	0	0	0	0	0	37	77	572
TCGA-RD-A7BT-10A-01D-A33W-08_STAD	656	234	243	274	503	369	529	633	362	65	563	0	295	133	0	47	573
TCGA-RD-A7BW-10A-01D-A32N-08_STAD	759	0	0	308	610	384	533	657	477	0	0	0	0	0	31	74	573
TCGA-RD-A7C1-10A-01D-A32N-08_STAD	595	259	278	0	609	145	533	656	0	90	663	575	379	141	0	0	574
TCGA-RN-A68Q-10A-01D-A307-09_SARC	701	296	335	333	627	435	553	629	556	0	0	0	0	0	55	0	592
TCGA-RP-A690-10A-01D-A30X-08_SKCM	682	0	0	294	588	378	530	629	470	0	0	0	0	0	0	75	573
TCGA-RP-A693-10A-01D-A30X-08_SKCM	682	0	0	292	588	372	529	632	472	0	0	0	0	0	0	82	574
TCGA-RP-A694-10A-01D-A30X-08_SKCM	682	0	0	299	599	377	533	646	407	0	0	0	0	0	32	60	574
TCGA-RP-A695-10A-01D-A30X-08_SKCM	598	254	268	0	533	132	531	630	400	0	518	548	0	0	0	78	574
TCGA-RQ-A68N-10A-01D-A31X-10_DLBC	612	0	0	257	517	417	509	564	320	0	0	0	0	0	0	32	572
TCGA-RQ-A6JB-10A-01D-A31X-10_DLBC	543	154	224	224	329	256	470	500	332	0	0	0	0	0	0	35	555
TCGA-RR-A6KA-10A-01D-A33W-08_GBM	671	233	241	174	558	357	529	618	396	0	499	496	0	0	25	53	570
TCGA-RR-A6KB-10A-01D-A33W-08_GBM	591	251	264	0	571	133	503	591	370	0	619	502	306	138	24	0	576
TCGA-RR-A6KC-10A-01D-A33W-08_GBM	684	0	0	294	598	375	528	639	378	76	634	499	358	132	24	0	575
TCGA-S5-A6DX-10A-01D-A31J-08_BLCA	674	251	262	285	589	282	531	652	483	0	0	0	0	0	33	62	577
TCGA-S9-A6TU-10A-01D-A329-08_LGG	680	235	239	266	538	360	517	640	462	0	0	0	0	0	19	49	569
TCGA-S9-A6TW-10A-01D-A329-08_LGG	681	0	0	293	590	358	521	612	0	83	609	0	371	134	0	0	570
TCGA-S9-A6TX-10A-01D-A329-08_LGG	659	233	247	251	567	347	527	634	467	0	554	487	0	0	19	43	573
TCGA-S9-A6TY-10A-01D-A329-08_LGG	684	0	0	295	596	361	526	643	371	76	589	0	288	126	0	53	573
TCGA-S9-A6TZ-10A-01D-A329-08_LGG	671	0	0	294	557	345	518	625	364	70	504	0	283	134	17	0	571
TCGA-S9-A6U0-10A-01D-A329-08_LGG	679	0	0	297	596	285	522	642	467	0	0	0	0	0	25	55	569
TCGA-S9-A6U9-10A-01D-A329-08_LGG	680	0	0	295	600	379	524	637	469	0	0	0	0	0	28	62	574
TCGA-SL-A6J9-10A-01D-A31U-09_UCEC	693	0	0	346	652	457	542	611	538	0	0	0	0	0	38	46	586
TCGA-SL-A6JA-10A-01D-A31U-09_UCEC	684	0	0	370	666	460	548	629	551	0	0	0	0	0	39	48	587
TCGA-SU-A7E7-10A-01D-A33W-08_PRAD	683	0	0	295	595	386	531	640	475	0	0	0	0	0	36	0	575
TCGA-TM-A7C3-10A-01D-A329-08_LGG	689	0	0	300	601	377	526	641	473	0	0	0	0	0	0	105	575
TCGA-TM-A7C4-10A-01D-A329-08_LGG	654	230	240	265	556	261	529	609	392	0	0	0	0	0	23	42	572
TCGA-TM-A7C5-10A-01D-A329-08_LGG	678	0	0	298	604	367	534	649	480	0	0	0	0	0	22	39	573
TCGA-TM-A7CF-10A-01D-A329-08_LGG	680	0	0	288	590	280	518	630	459	0	0	0	0	0	27	46	570
TCGA-UY-A78K-10A-01D-A339-08_BLCA	682	0	0	307	602	379	520	635	472	0	0	0	0	0	0	117	575
TCGA-UY-A78L-10A-01D-A339-08_BLCA	753	0	0	299	602	284	525	628	386	0	0	0	0	0	0	73	571
TCGA-UY-A78N-10A-01D-A339-08_BLCA	674	0	0	291	590	375	522	613	294	0	506	0	270	133	0	29	575
TCGA-UY-A78O-10A-01D-A339-08_BLCA	597	252	268	0	561	137	532	652	465	72	615	567	0	0	23	58	573

Table A4 KIR genotypes for 2535 samples from the 1000 Genomes Project

sample	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
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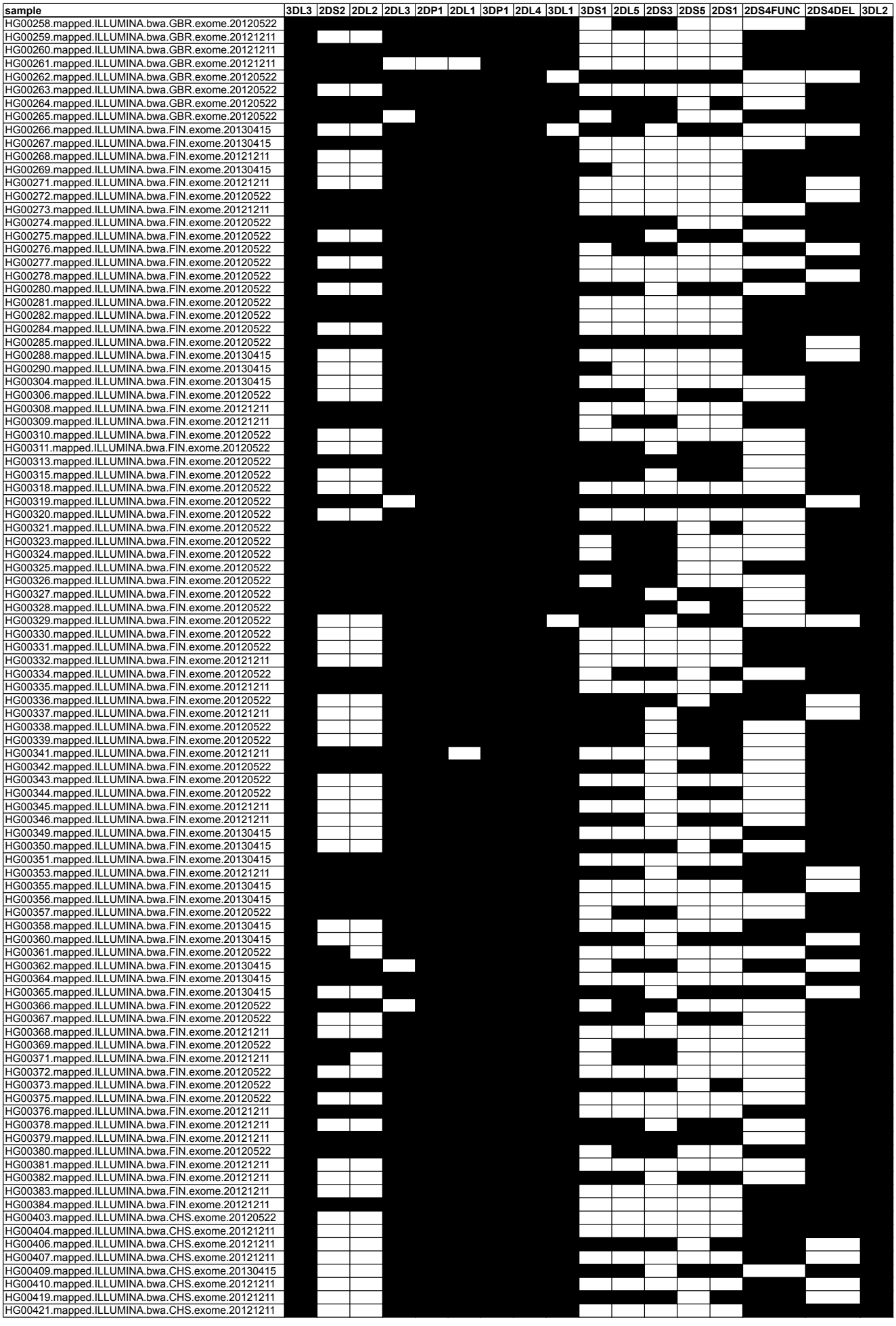
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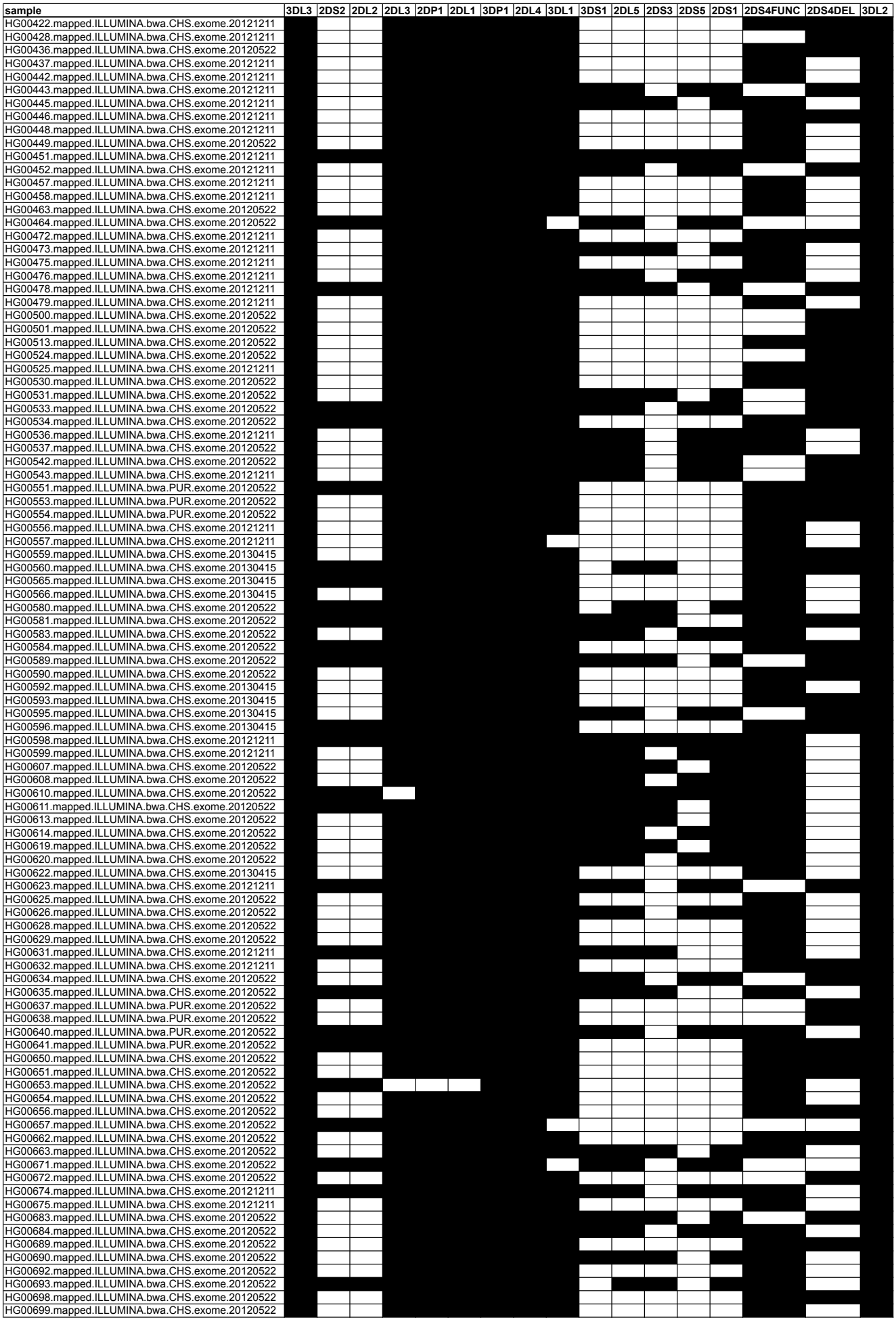
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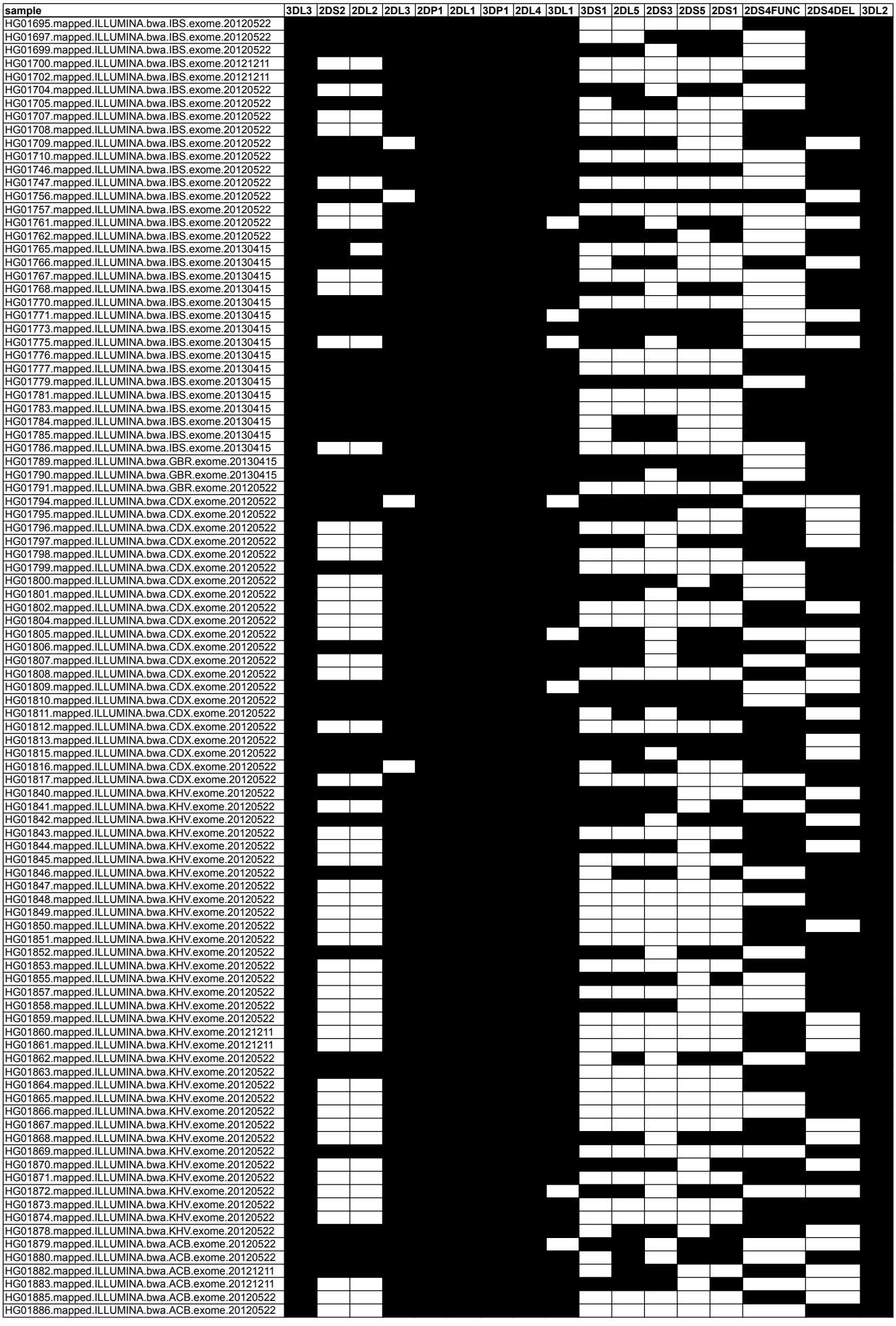
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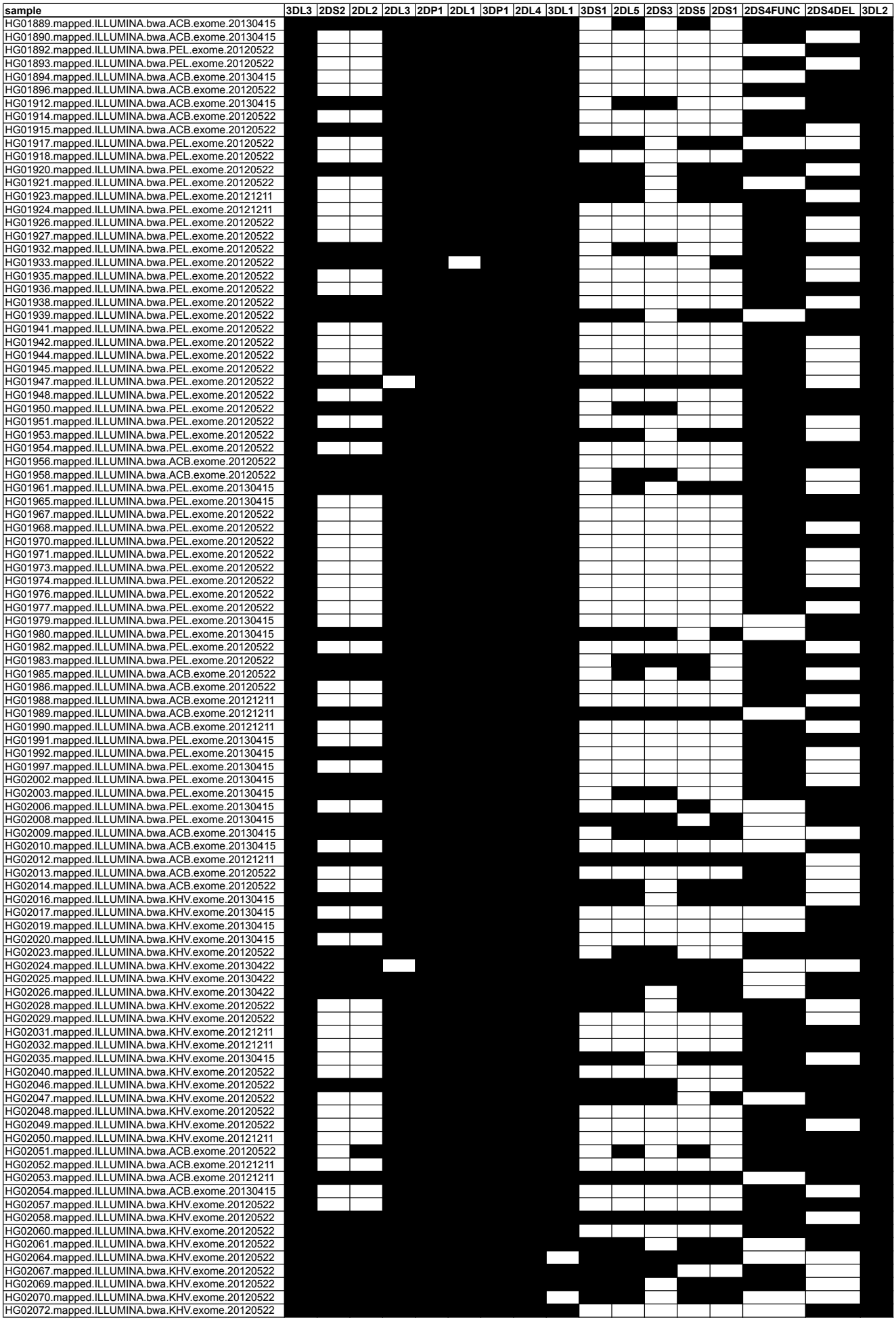
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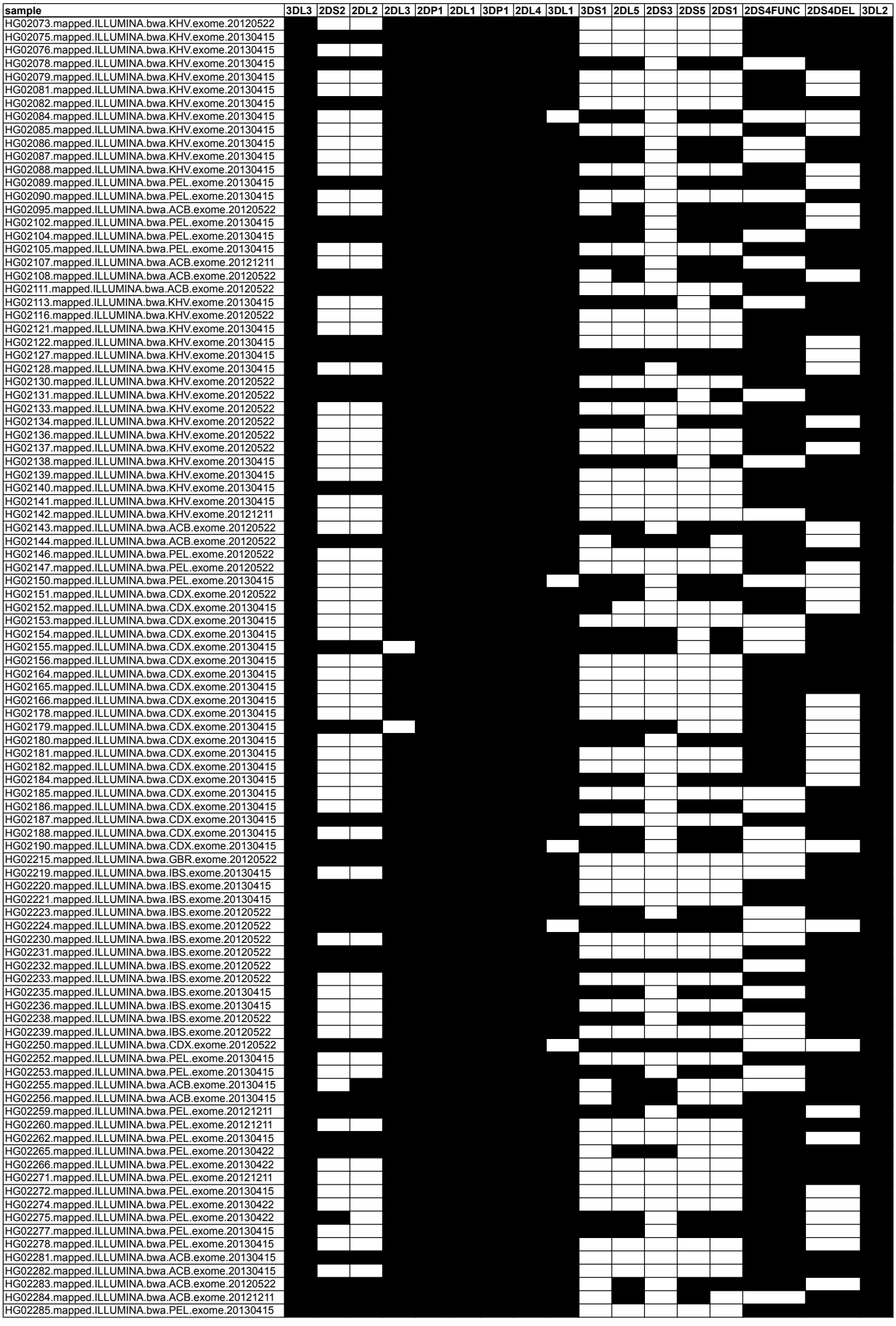
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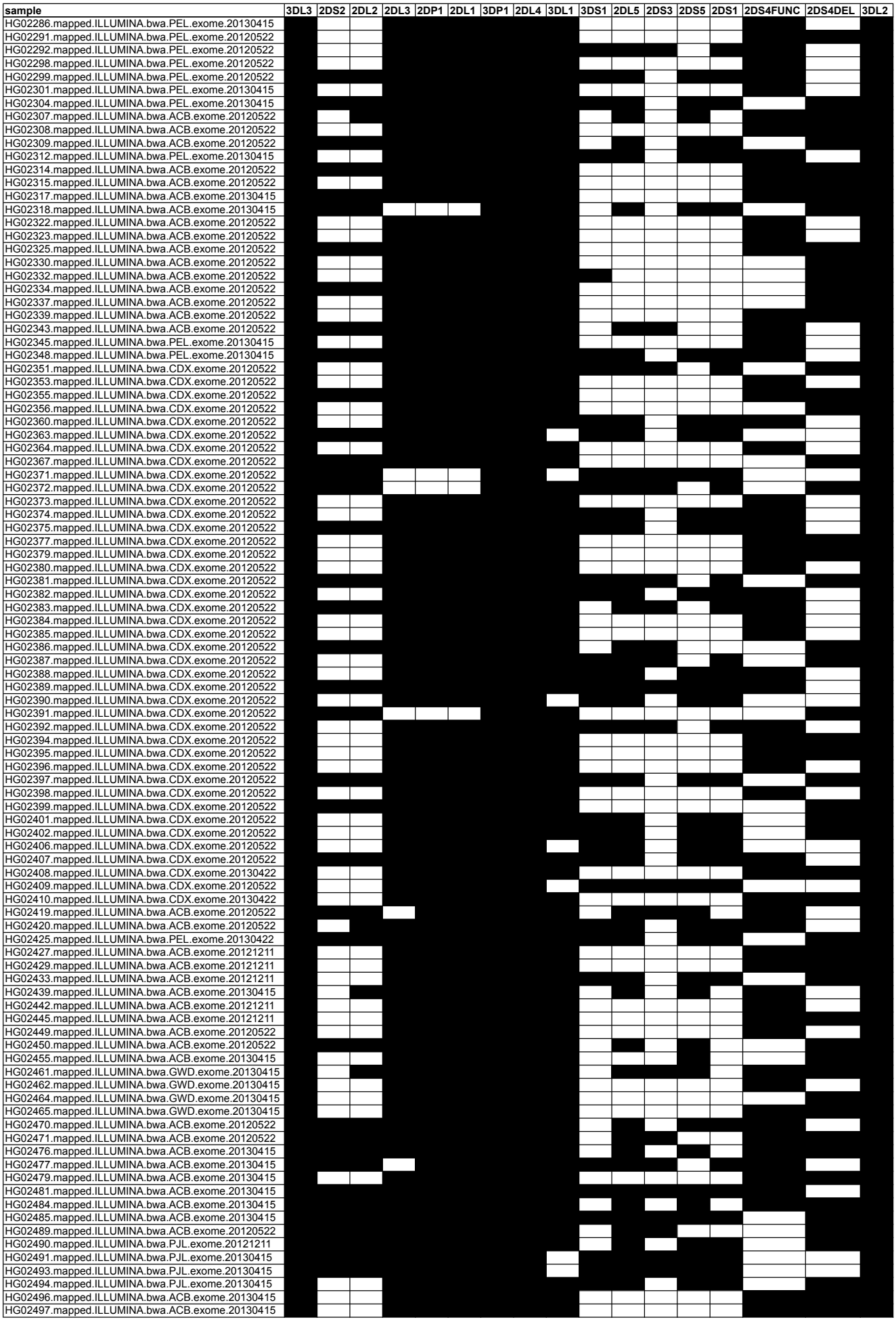
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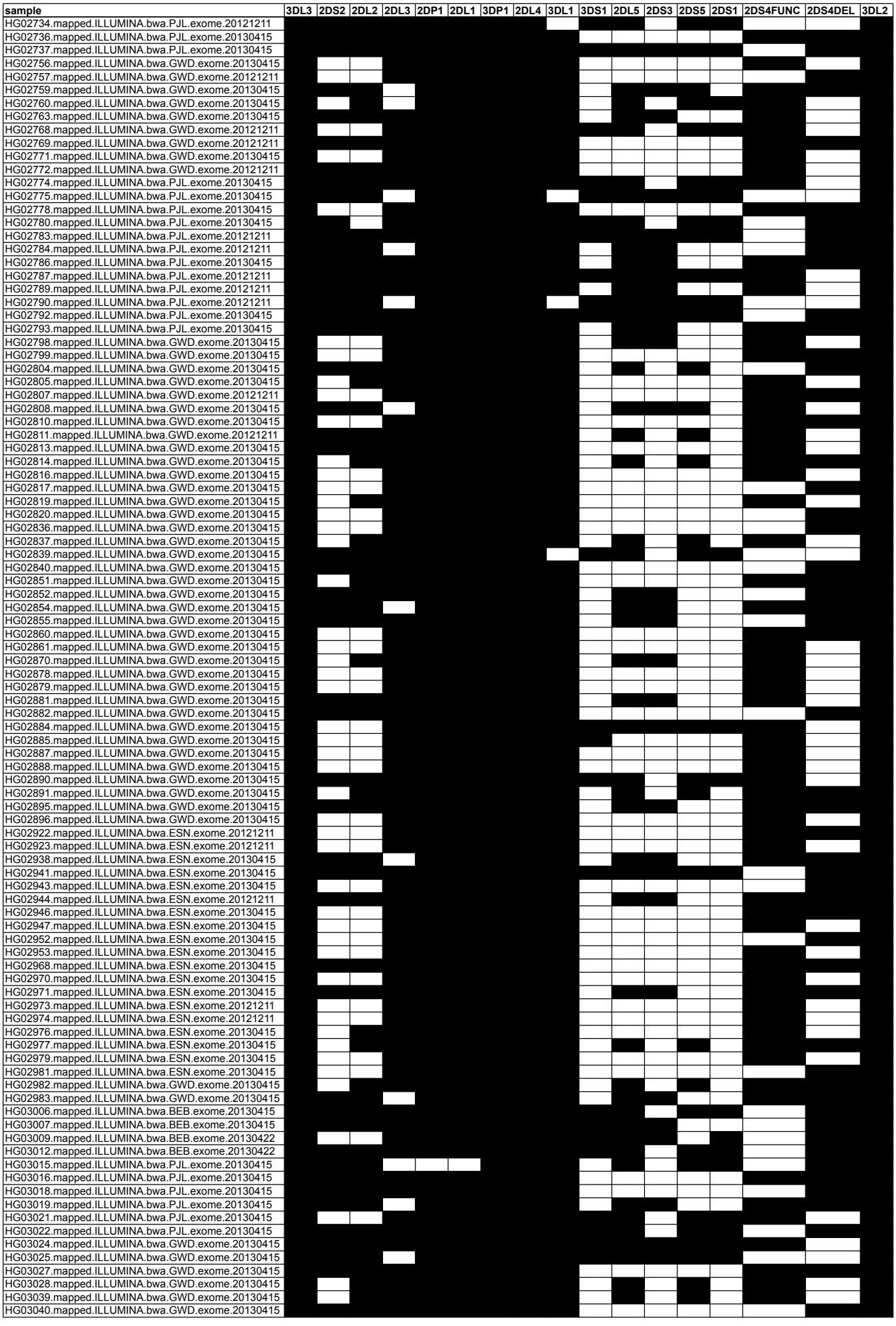
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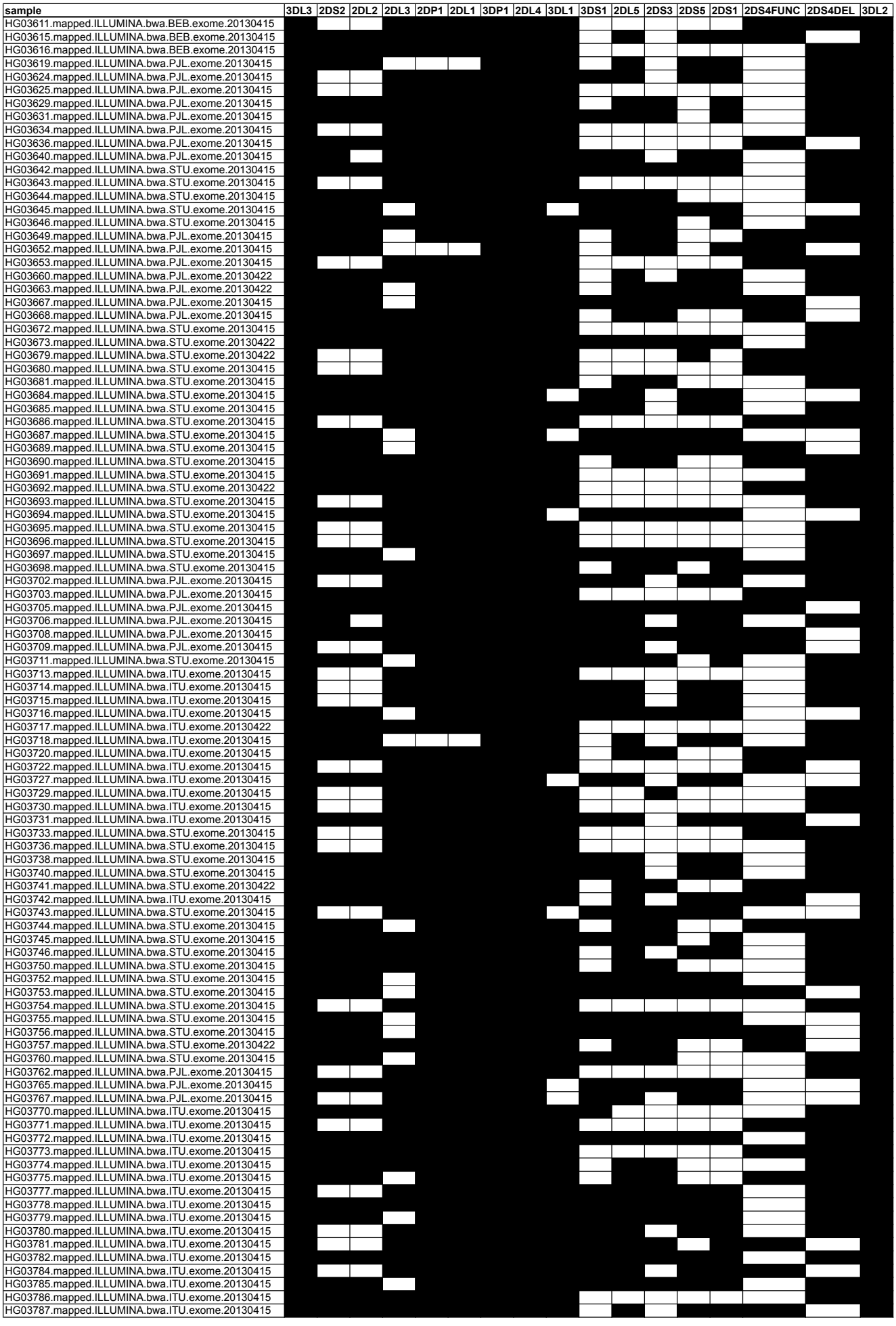
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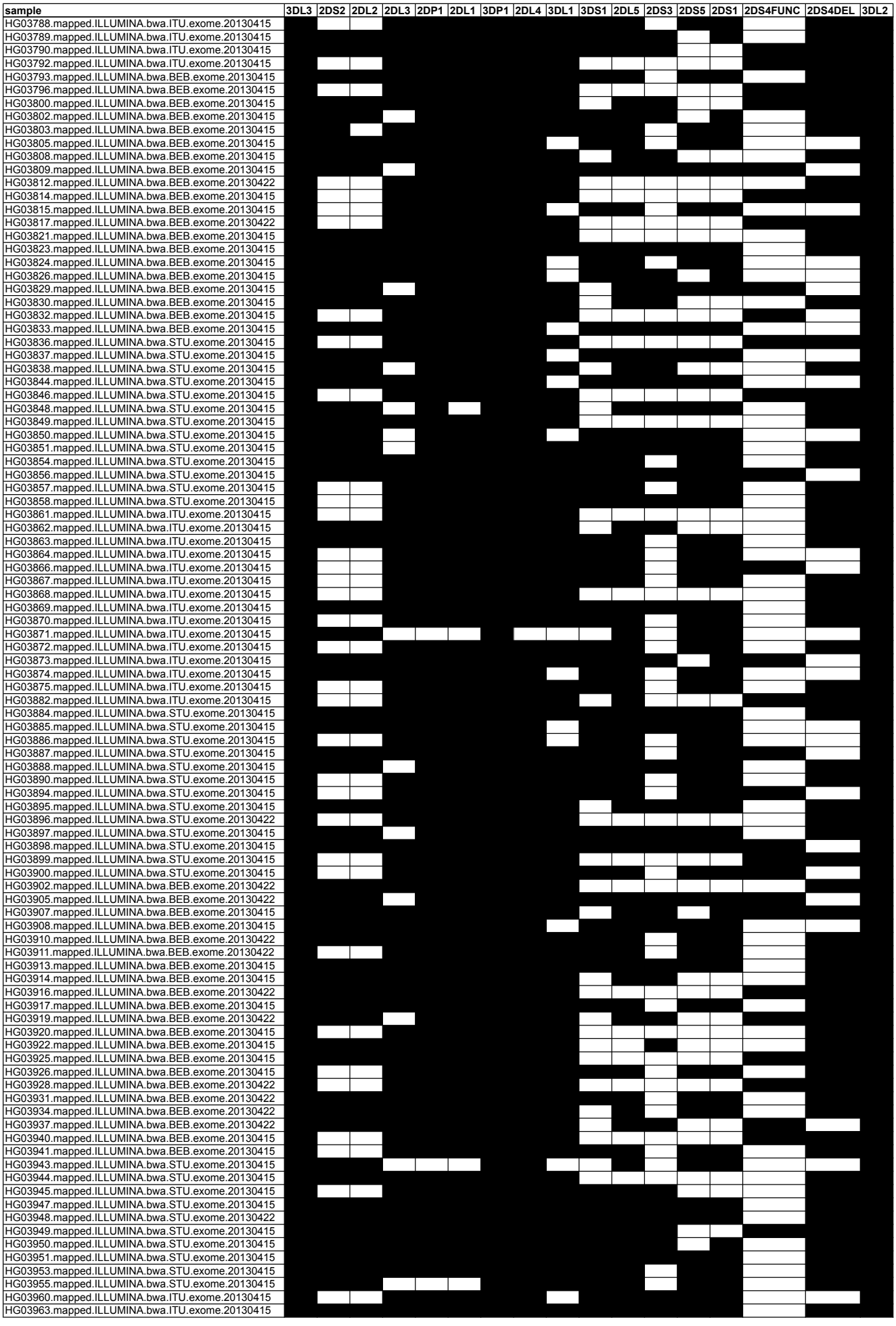
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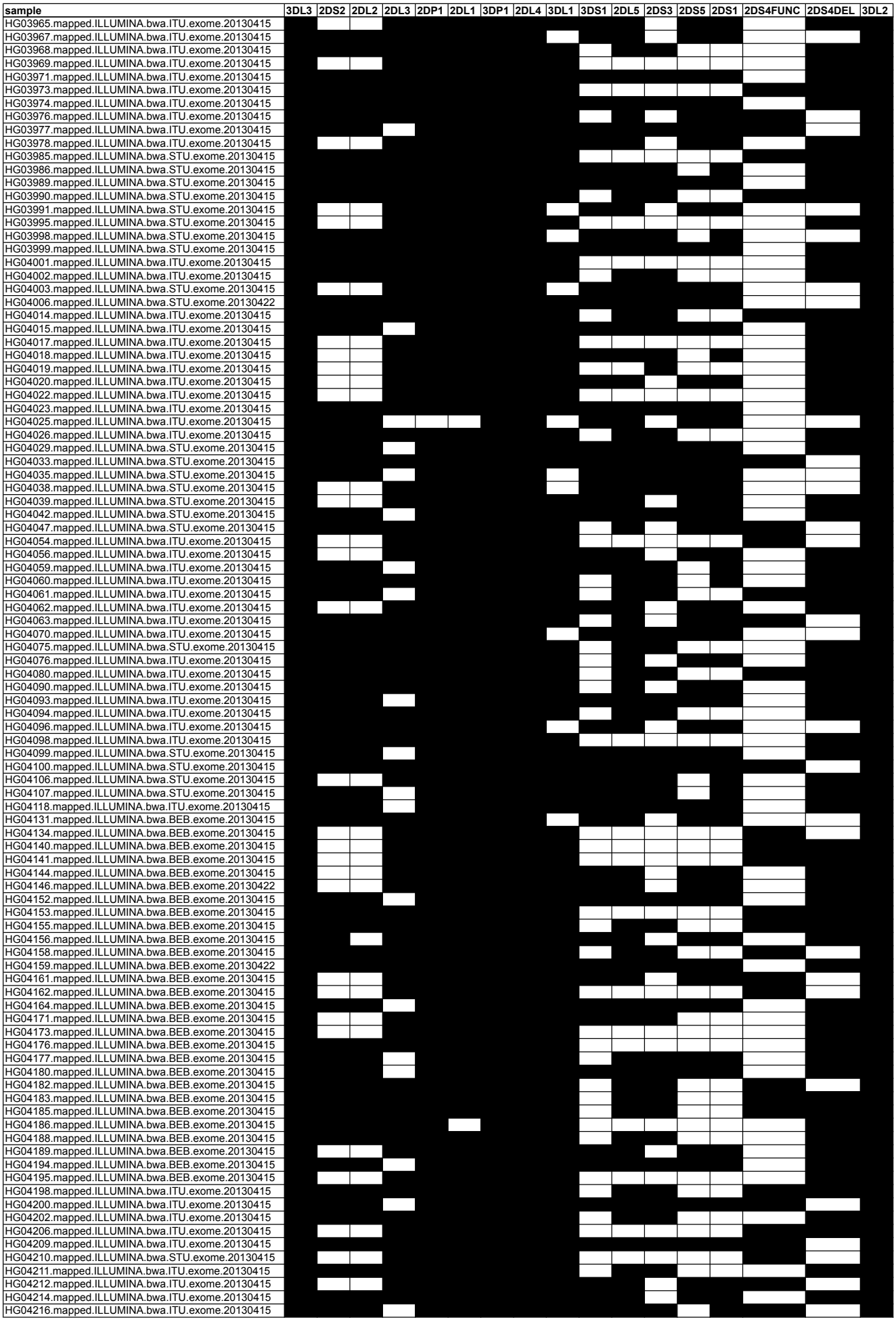
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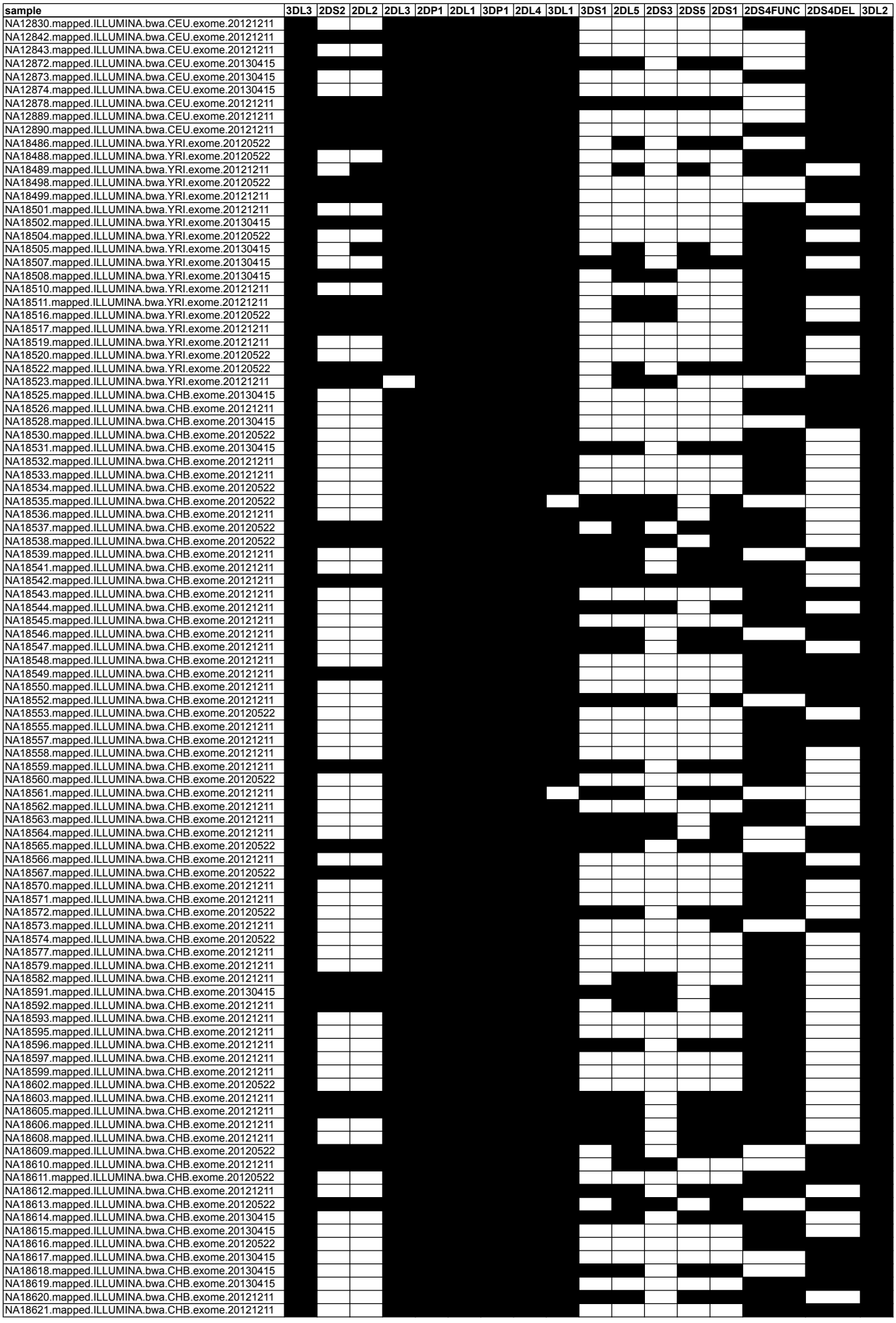
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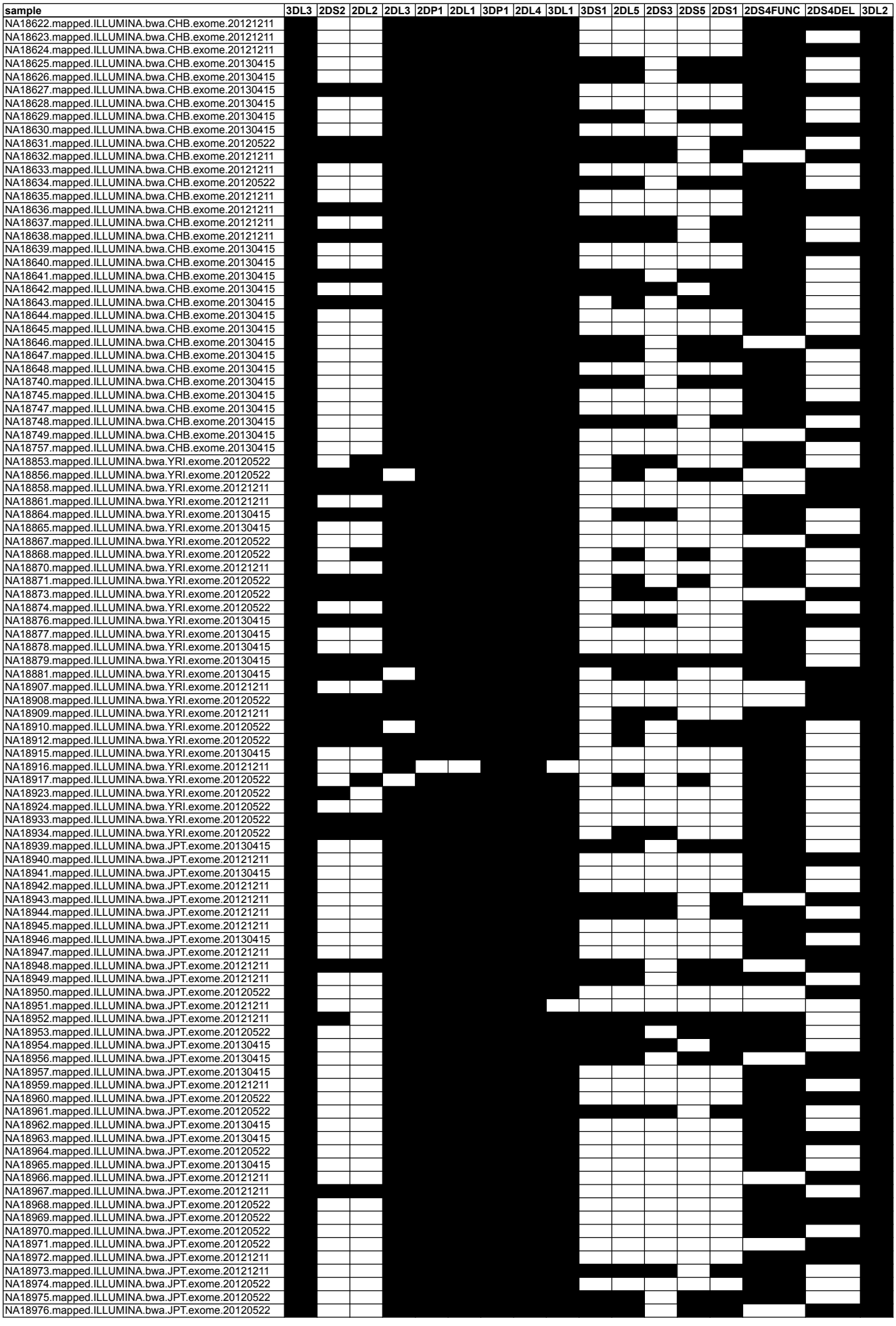
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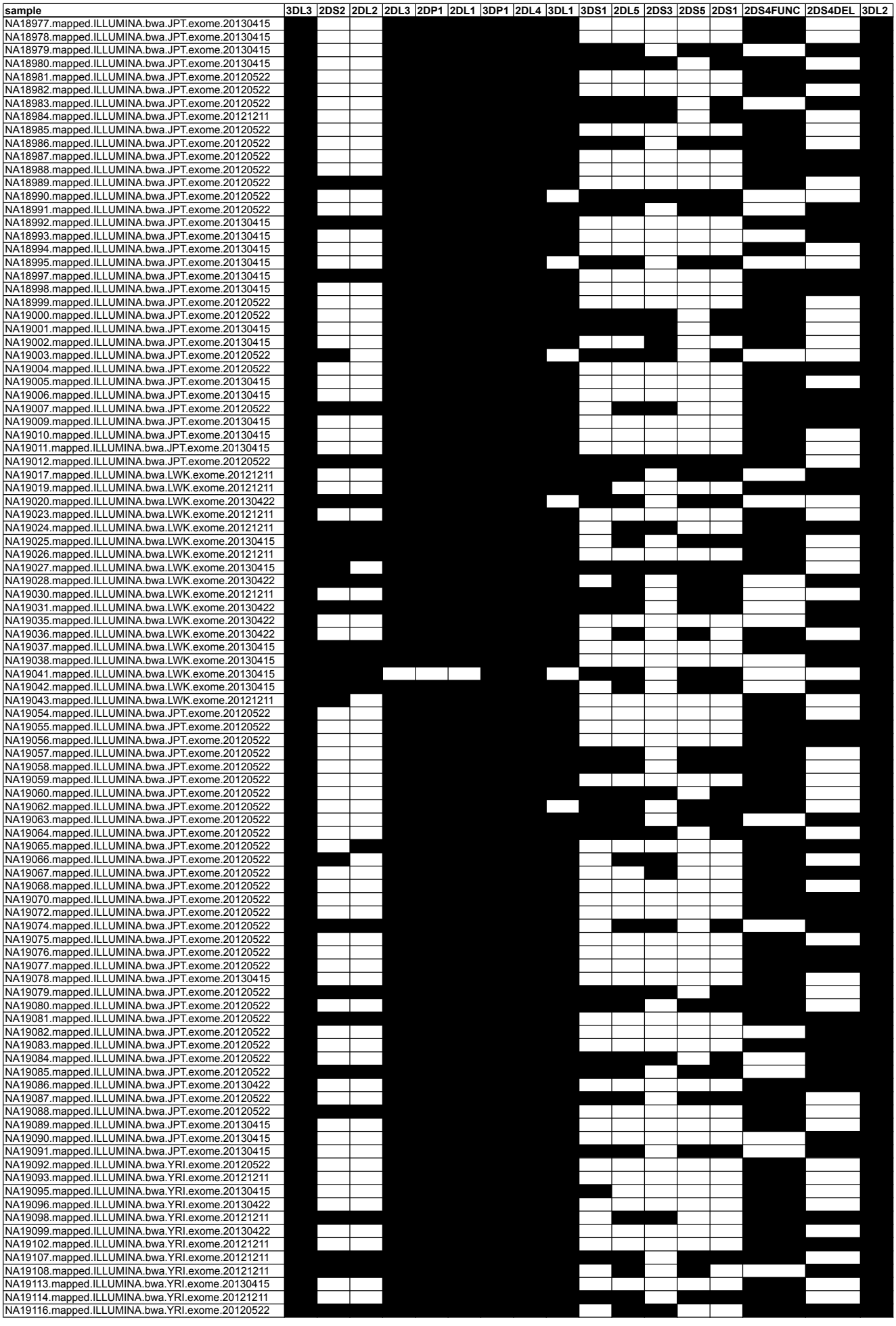
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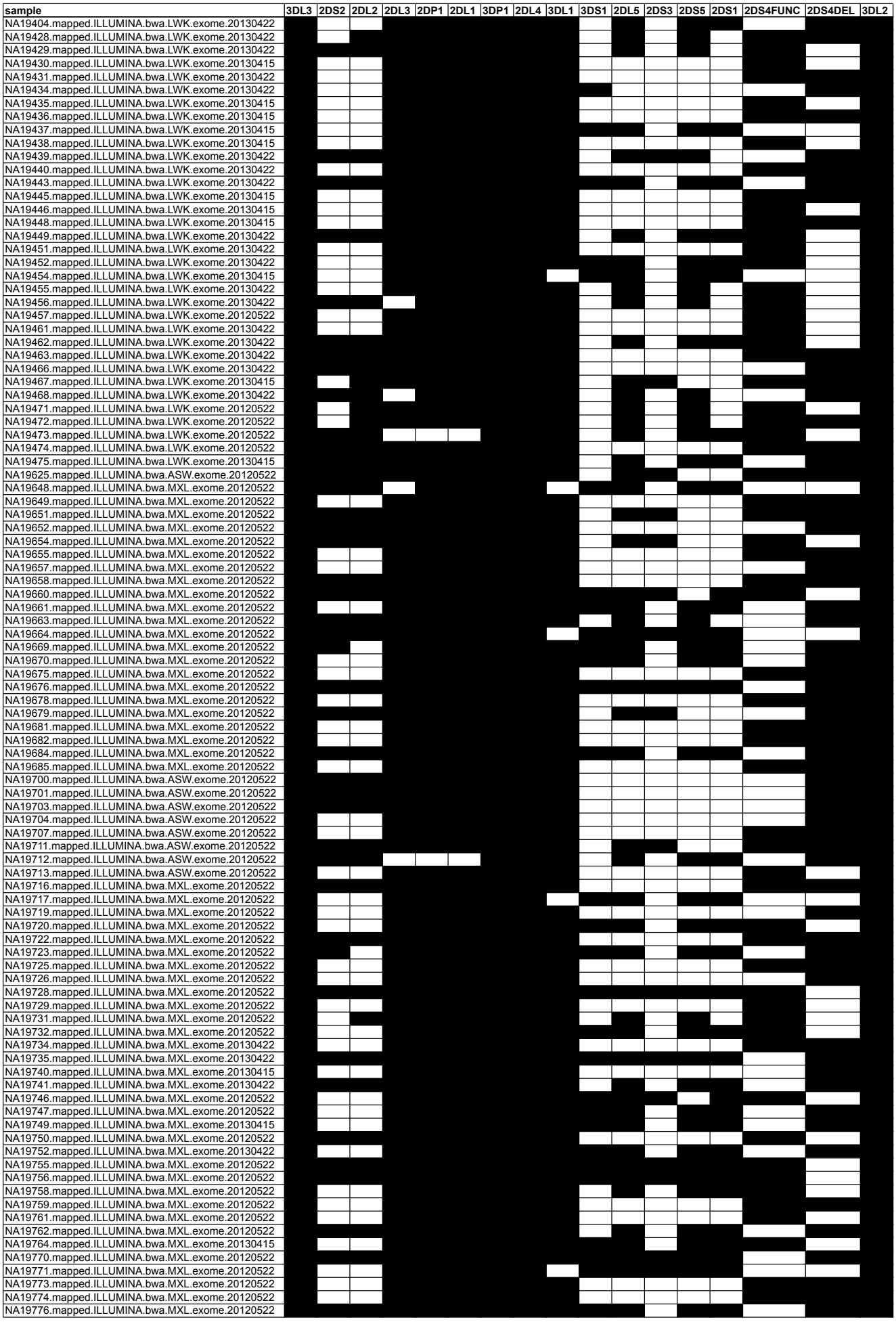
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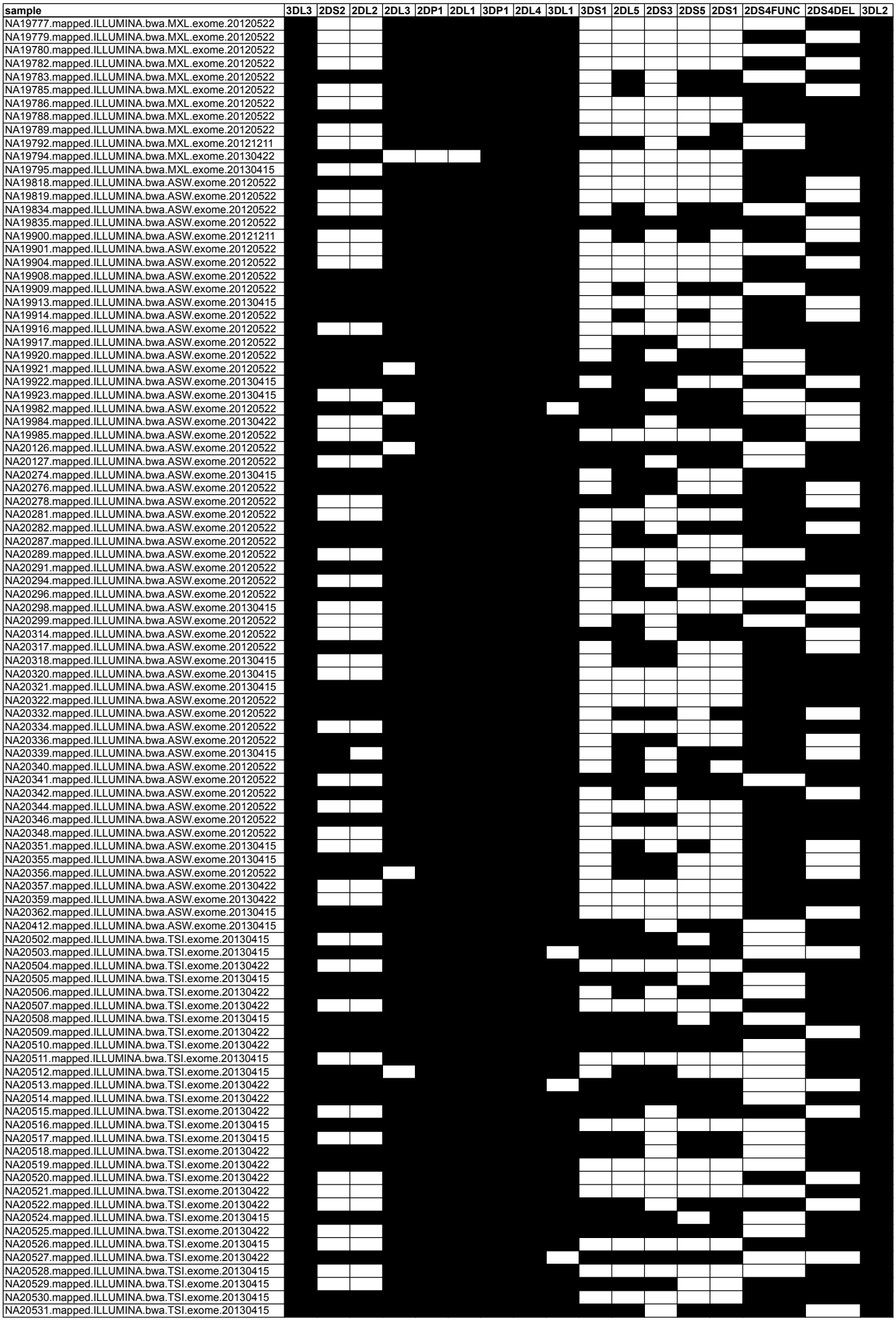
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Table A5 Unique KIR genotypes for the 1000 Genomes cohort

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1	310	0.122																	
2	292	0.115																	
3	237	0.093																	
4	139	0.055																	
5	119	0.047																	
6	104	0.041																	
7	94	0.037																	
8	79	0.031																	
9	73	0.029																	
10	66	0.026																	
11	57	0.022																	
12	45	0.018																	
13	40	0.016																	
14	39	0.015																	
15	39	0.015																	
16	35	0.014																	
17	35	0.014																	
18	34	0.013																	
19	34	0.013																	
20	32	0.013																	
21	32	0.013																	
22	30	0.012																	
23	30	0.012																	
24	24	0.009																	
25	23	0.009																	
26	22	0.009																	
27	22	0.009																	
28	18	0.007																	
29	17	0.007																	
30	16	0.006																	
31	16	0.006																	
32	14	0.006																	
33	12	0.005																	
34	10	0.004																	
35	10	0.004																	
36	9	0.004																	
37	9	0.004																	
38	9	0.004																	
39	9	0.004																	
40	8	0.003																	
41	8	0.003																	
42	8	0.003																	
43	7	0.003																	
44	7	0.003																	
45	7	0.003																	
46	7	0.003																	
47	6	0.002																	
48	6	0.002																	
49	5	0.002																	
50	5	0.002																	
51	5	0.002																	
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67	4	0.002																	
68	3	0.001																	
69	3	0.001																	
70	3	0.001																	
71	3	0.001																	
72	3	0.001																	
73	3	0.001																	
74	3	0.001																	
75	3	0.001																	
76	3	0.001																	
77	2	0.001																	
78	2	0.001																	

kirTypeID	count	freq	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
79	2	0.001																	
80	2	0.001																	
81	2	0.001																	
82	2	0.001																	
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104	2	0.001																	
105	2	0.001																	
106	2	0.001																	
107	1	0.000																	
108	1	0.000																	
109	1	0.000																	
110	1	0.000																	
111	1	0.000																	
112	1	0.000																	
113	1	0.000																	
114	1	0.000																	
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116	1	0.000																	
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143	1	0.000																	
144	1	0.000																	
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146	1	0.000																	
147	1	0.000																	
148	1	0.000																	
149	1	0.000																	
150	1	0.000																	
151	1	0.000																	
152	1	0.000																	
153	1	0.000																	
154	1	0.000																	
155	1	0.000																	
156	1	0.000																	
157	1	0.000																	
158	1	0.000																	

kirTypeID	count	freq	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
159	1	0.000																	
160	1	0.000																	
161	1	0.000																	
162	1	0.000																	
163	1	0.000																	
164	1	0.000																	
165	1	0.000																	
166	1	0.000																	
167	1	0.000																	
168	1	0.000																	
169	1	0.000																	
170	1	0.000																	
171	1	0.000																	
172	1	0.000																	
173	1	0.000																	
174	1	0.000																	
175	1	0.000																	

Table A6 KIR Linkage for the Allele*Frequencies database and the 1000 Genomes cohort

AF

overall

3DL3	48	90	49	54	29	96	96	98	100	93	41	36	42	91	100
	2DS2	39	95	68	72	45	45	47	48	46	56	56	58	46	48
		2DL3	39	48	27	92	91	89	90	85	42	37	42	84	90
			2DL2	68	71	46	46	48	49	47	55	57	57	47	49
				2DL5	72	53	53	53	54	48	81	79	83	48	54
					2DS3	31	30	29	29	30	64	55	62	31	29
						2DL1	97	95	96	90	41	36	42	89	96
							2DP1	96	96	90	41	35	41	89	96
								3DP1	98	91	40	35	41	90	98
									2DL4	93	41	36	42	91	100
										3DL1	35	31	36	96	93
											3DS1	84	91	36	41
												2DS5	87	32	36
													2DS1	37	42
														2DS4	91
															3DL2

both positive

3DL3	48	90	49	54	29	96	96	98	100	93	41	36	42	91	100
	2DS2	38	46	35	24	44	45	47	48	43	23	20	24	43	48
		2DL3	39	46	23	89	89	89	90	84	36	31	37	82	90
			2DL2	36	25	45	46	48	49	44	23	21	24	44	49
				2DL5	28	52	52	53	54	48	39	35	40	47	54
					2DS3	28	28	29	29	26	18	10	17	26	29
						2DL1	95	95	96	89	39	34	40	88	96
							2DP1	96	96	90	39	34	40	89	96
								3DP1	98	91	40	35	41	90	98
									2DL4	93	41	36	42	91	100
										3DL1	35	30	36	90	93
											3DS1	31	37	34	41
												2DS5	33	29	36
													2DS1	35	42
														2DS4	91
															3DL2

both negative

3DL3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	2DS2	1	49	33	47	0	0	0	0	3	33	36	34	4	0
		2DL3	0	2	4	3	2	0	0	1	5	6	5	2	0
			2DL2	32	46	0	0	0	0	3	32	36	33	3	0
				2DL5	44	1	1	0	0	0	43	44	43	1	0
					2DS3	3	2	0	0	4	47	45	45	5	0
						2DL1	2	0	0	1	2	2	2	1	0
							2DP1	0	0	1	1	1	1	1	0
								3DP1	0	0	0	0	0	0	0
									2DL4	0	0	0	0	0	0
										3DL1	0	1	0	6	0
											3DS1	53	53	1	0
												2DS5	54	2	0
													2DS1	1	0
														2DS4	0
															3DL2

OKG

overall

3DL3	47	90	49	54	28	98	98	100	100	94	34	37	38	94	100
	2DS2	38	96	70	73	45	45	47	47	45	57	60	61	45	47
		2DL3	39	46	24	92	92	90	90	87	35	35	37	86	90
			2DL2	72	71	46	47	49	48	47	53	61	59	46	49
				2DL5	74	53	53	53	53	48	79	82	84	47	53
					2DS3	30	30	28	28	29	70	57	66	28	28
						2DL1	100	98	98	93	36	36	38	92	98
							2DP1	98	98	93	36	36	38	92	98
								3DP1	100	94	34	36	38	94	100
									2DL4	94	34	36	38	94	100
										3DL1	30	31	33	99	94
											3DS1	83	91	29	34
												2DS5	89	31	36
													2DS1	32	38
														2DS4	94
															3DL2

both positive

3DL3	47	90	49	54	28	98	98	100	100	94	34	37	38	94	100
	2DS2	38	46	35	24	45	45	47	47	43	19	22	23	43	47
		2DL3	39	45	21	90	90	90	90	86	30	31	33	85	90
			2DL2	37	24	46	47	49	48	45	18	23	23	44	49
				2DL5	28	52	52	53	53	48	33	36	38	47	53
					2DS3	28	28	28	28	26	16	11	16	25	28
						2DL1	98	98	98	92	34	35	37	92	98
							2DP1	98	98	92	34	35	37	92	98
								3DP1	100	94	34	36	38	94	100
									2DL4	94	34	36	38	94	100
										3DL1	29	31	33	93	94
											3DS1	27	32	28	34
												2DS5	32	31	36
													2DS1	32	38
														2DS4	94
															3DL2

both negative

3DL3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	2DS2	0	50	35	49	0	0	0	0	2	38	38	38	2	0
		2DL3	0	1	3	2	2	0	0	1	5	4	4	1	0
			2DL2	35	47	0	0	0	0	2	35	38	36	2	0
				2DL5	46	1	1	0	0	0	46	46	46	0	0
					2DS3	2	2	0	0	3	54	46	50	3	0
						2DL1	2	0	0	1	2	1	1	0	0
							2DP1	0	0	1	2	1	1	0	0
								3DP1	0	0	0	0	0	0	0
									2DL4	0	0	0	0	0	0
										3DL1	1	0	0	6	0
											3DS1	56	59	1	0
												2DS5	57	0	0
													2DS1	0	0
														2DS4	0
															3DL2

Table A7 Chi square significance tests for KIR genotypes within the 1000 Genomes populations

kirTypeID	group1	group2	group1 KirTypeAbsent ObservedCount	group1 KirTypePresent ObservedCount	group2 KirTypeAbsent ObservedCount	group2 KirTypePresent ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2	cohortMinusGroup2	ESN	2174	262	69	30	3.610	2.310	5.650	6.19E-09	9.52E-04	1
2	cohortMinusGroup2	PEL	2183	266	60	26	3.560	2.210	5.740	8.38E-08	1.91E-03	2
2	cohortMinusGroup2	CHB	2169	263	74	29	3.230	2.060	5.060	1.59E-07	2.86E-03	3
1	cohortMinusGroup2	KHV	2153	281	72	29	3.090	1.970	4.840	5.57E-07	3.81E-03	4
3	cohortMinusGroup2	IBS	2213	215	85	22	2.660	1.630	4.340	9.58E-05	4.76E-03	5
3	cohortMinusGroup2	PUR	2214	216	84	21	2.560	1.560	4.210	2.54E-04	5.71E-03	6
2	cohortMinusGroup2	GIH	2137	292	106	0	0.000	0.000	0.000	2.73E-04	6.67E-03	7
4	cohortMinusGroup2	FIN	2311	125	85	14	3.050	1.690	5.520	2.78E-04	7.62E-03	8
2	cohortMinusGroup2	JPT	2163	268	80	24	2.420	1.510	3.890	3.02E-04	8.57E-03	9
2	cohortMinusGroup2	CHS	2159	268	84	24	2.300	1.440	3.680	6.57E-04	9.52E-03	10
2	cohortMinusGroup2	TSI	2136	291	107	1	0.069	0.010	0.493	7.51E-04	1.05E-02	11
2	cohortMinusGroup2	YRI	2158	268	85	24	2.270	1.420	3.630	7.89E-04	1.14E-02	12
4	cohortMinusGroup2	IBS	2303	125	93	14	2.770	1.540	5.000	9.26E-04	1.24E-02	13
1	cohortMinusGroup2	JPT	2145	286	80	24	2.250	1.400	3.610	9.83E-04	1.33E-02	14
2	cohortMinusGroup2	STU	2141	291	102	1	0.072	0.010	0.519	1.09E-03	1.43E-02	15
3	cohortMinusGroup2	GBR	2224	219	74	18	2.470	1.450	4.210	1.17E-03	1.52E-02	16
2	cohortMinusGroup2	CEU	2145	291	98	1	0.075	0.010	0.541	1.47E-03	1.62E-02	17
2	cohortMinusGroup2	IBS	2138	290	105	2	0.140	0.034	0.570	2.37E-03	1.71E-02	18
4	cohortMinusGroup2	ITU	2306	126	90	13	2.640	1.440	4.850	2.46E-03	1.81E-02	19
2	cohortMinusGroup2	ITU	2142	290	101	2	0.146	0.036	0.595	3.17E-03	1.91E-02	20
1	cohortMinusGroup2	PJL	2131	308	94	2	0.147	0.036	0.599	3.34E-03	2.00E-02	21
2	cohortMinusGroup2	PJL	2149	290	94	2	0.158	0.039	0.645	5.28E-03	2.10E-02	22
2	cohortMinusGroup2	GBR	2153	290	90	2	0.165	0.040	0.674	7.07E-03	2.19E-02	23
1	cohortMinusGroup2	GIH	2123	306	102	4	0.272	0.099	0.744	1.04E-02	2.29E-02	24
3	cohortMinusGroup2	CEU	2216	220	82	17	2.090	1.220	3.590	1.07E-02	2.38E-02	25
2	cohortMinusGroup2	FIN	2147	289	96	3	0.232	0.073	0.737	1.11E-02	2.48E-02	26
1	cohortMinusGroup2	ITU	2126	306	99	4	0.281	0.103	0.769	1.29E-02	2.57E-02	27
4	cohortMinusGroup2	GWD	2283	139	113	0	0.000	0.000	0.000	1.60E-02	2.67E-02	28
2	cohortMinusGroup2	PUR	2142	288	101	4	0.295	0.108	0.807	1.77E-02	2.76E-02	29
4	cohortMinusGroup2	YRI	2287	139	109	0	0.000	0.000	0.000	1.85E-02	2.86E-02	30
1	cohortMinusGroup2	PEL	2157	292	68	18	1.960	1.150	3.340	1.94E-02	2.95E-02	31
4	cohortMinusGroup2	ESN	2297	139	99	0	0.000	0.000	0.000	2.64E-02	3.05E-02	32
2	cohortMinusGroup2	BEB	2160	289	83	3	0.270	0.085	0.860	2.77E-02	3.14E-02	33
1	cohortMinusGroup2	CHS	2138	289	87	21	1.790	1.090	2.930	2.86E-02	3.24E-02	34
3	cohortMinusGroup2	CHB	2198	234	100	3	0.282	0.089	0.896	3.42E-02	3.33E-02	35
5	cohortMinusGroup2	IBS	2319	109	97	10	2.190	1.110	4.320	3.65E-02	3.43E-02	36
1	cohortMinusGroup2	MXL	2172	296	53	14	1.940	1.060	3.540	4.49E-02	3.52E-02	37
4	cohortMinusGroup2	TSI	2299	128	97	11	2.040	1.070	3.900	4.80E-02	3.62E-02	38
2	cohortMinusGroup2	GWD	2150	272	93	20	1.700	1.030	2.800	5.06E-02	3.71E-02	39
1	cohortMinusGroup2	CLM	2136	305	89	5	0.393	0.158	0.975	5.44E-02	3.81E-02	40
3	cohortMinusGroup2	YRI	2193	233	105	4	0.359	0.131	0.983	5.56E-02	3.91E-02	41
4	cohortMinusGroup2	CEU	2307	129	89	10	2.010	1.020	3.960	6.67E-02	4.00E-02	42
3	cohortMinusGroup2	TSI	2206	221	92	16	1.740	1.010	3.010	6.80E-02	4.10E-02	43
4	cohortMinusGroup2	LWK	2296	138	100	1	0.166	0.023	1.200	7.17E-02	4.19E-02	44
3	cohortMinusGroup2	PEL	2215	234	83	3	0.342	0.107	1.090	8.71E-02	4.29E-02	45
3	cohortMinusGroup2	CLM	2218	223	80	14	1.740	0.970	3.120	8.89E-02	4.38E-02	46
3	cohortMinusGroup2	MSL	2216	234	82	3	0.346	0.108	1.100	9.19E-02	4.48E-02	47
2	cohortMinusGroup2	CDX	2161	275	82	17	1.630	0.953	2.790	1.02E-01	4.57E-02	48
1	cohortMinusGroup2	STU	2129	303	96	7	0.512	0.235	1.110	1.18E-01	4.67E-02	49
3	cohortMinusGroup2	GIH	2207	222	91	15	1.640	0.934	2.880	1.18E-01	4.76E-02	50
1	cohortMinusGroup2	CHB	2140	292	85	18	1.550	0.919	2.620	1.32E-01	4.86E-02	51
4	cohortMinusGroup2	CDX	2306	130	90	9	1.770	0.872	3.590	1.67E-01	4.95E-02	52
3	cohortMinusGroup2	LWK	2202	232	96	5	0.494	0.199	1.230	1.69E-01	5.05E-02	53
4	cohortMinusGroup2	KHV	2297	137	99	2	0.339	0.083	1.390	1.75E-01	5.14E-02	54
3	cohortMinusGroup2	BEB	2216	233	82	4	0.464	0.169	1.280	1.82E-01	5.24E-02	55
3	cohortMinusGroup2	CDX	2204	232	94	5	0.505	0.203	1.250	1.86E-01	5.33E-02	56
2	cohortMinusGroup2	MSL	2172	278	71	14	1.540	0.857	2.770	2.00E-01	5.43E-02	57
2	cohortMinusGroup2	MXL	2180	288	63	4	0.481	0.174	1.330	2.12E-01	5.52E-02	58
2	cohortMinusGroup2	KHV	2158	276	85	16	1.470	0.849	2.540	2.19E-01	5.62E-02	59
3	cohortMinusGroup2	CHS	2196	231	102	6	0.559	0.243	1.290	2.24E-01	5.71E-02	60
5	cohortMinusGroup2	GIH	2312	117	104	2	0.380	0.093	1.560	2.45E-01	5.81E-02	61
3	cohortMinusGroup2	ASW	2235	234	63	3	0.455	0.142	1.460	2.53E-01	5.91E-02	62
3	cohortMinusGroup2	FIN	2212	224	86	13	1.490	0.818	2.710	2.53E-01	6.00E-02	63
3	cohortMinusGroup2	JPT	2200	231	98	6	0.583	0.253	1.340	2.68E-01	6.10E-02	64
3	cohortMinusGroup2	KHV	2203	231	95	6	0.602	0.261	1.390	3.05E-01	6.19E-02	65
1	cohortMinusGroup2	PUR	2129	301	96	9	0.663	0.331	1.330	3.10E-01	6.29E-02	66
1	cohortMinusGroup2	GWD	2122	300	103	10	0.687	0.355	1.330	3.30E-01	6.38E-02	67
4	cohortMinusGroup2	STU	2296	136	100	3	0.506	0.158	1.620	3.43E-01	6.48E-02	68
2	cohortMinusGroup2	LWK	2157	277	86	15	1.360	0.775	2.390	3.62E-01	6.57E-02	69
3	cohortMinusGroup2	ACB	2208	231	90	6	0.637	0.276	1.470	3.76E-01	6.67E-02	70
1	cohortMinusGroup2	LWK	2133	301	92	9	0.693	0.346	1.390	3.77E-01	6.76E-02	71
1	cohortMinusGroup2	ACB	2144	295	81	15	1.350	0.768	2.370	3.81E-01	6.86E-02	72
2	cohortMinusGroup2	ASW	2182	287	61	5	0.623	0.248	1.560	4.11E-01	6.95E-02	73
1	cohortMinusGroup2	ESN	2135	301	90	9	0.709	0.354	1.420	4.15E-01	7.05E-02	74
1	cohortMinusGroup2	CEU	2135	301	90	9	0.709	0.354	1.420	4.15E-01	7.05E-02	74
4	cohortMinusGroup2	ACB	2303	136	93	3	0.546	0.171	1.750	4.20E-01	7.14E-02	75
2	cohortMinusGroup2	ACB	2161	278	82	14	1.330	0.744	2.380	4.26E-01	7.24E-02	76
3	cohortMinusGroup2	ITU	2202	230	96	7	0.698	0.320	1.520	4.62E-01	7.33E-02	77
1	cohortMinusGroup2	MSL	2153	297	72	13	1.310	0.717	2.390	4.78E-01	7.43E-02	78
3	cohortMinusGroup2	GWD	2193	229	105	8	0.730	0.351	1.520	4.95E-01	7.52E-02	79
1	cohortMinusGroup2	BEB	2147	302	78	8	0.729	0.349	1.520	4.99E-01	7.62E-02	80
4	cohortMinusGroup2	CHB	2297	135	99	4	0.687	0.249	1.890	6.12E-01	7.71E-02	81
1	cohortMinusGroup2	IBS	2129	299	96	11	0.816	0.432	1.540	6.33E-01	7.81E-02	82
2	cohortMinusGroup2	CLM	2158	283	85	9	0.807	0.401	1.620	6.62E-01	7.91E-02	83
1	cohortMinusGroup2	GBR	2146	297	79	13	1.190	0.654	2.170	6.85E-01	8.00E-02	84
3	cohortMinusGroup2	STU	2203	229	95	8	0.810	0.389	1.690	6.96E-01	8.10E-02	85
5	cohortMinusGroup2	CHS	2312	115	104	4	0.773	0.280	2.140	7.91E-01	8.19E-02	86
5	cohortMinusGroup2	TSI	2312	115	104	4	0.773	0.280	2.140	7.91E-01	8.19E-02	86
4	cohortMinusGroup2	CHS	2295	132	101	7	1.200	0.547	2.630	8.03E-01	8.29E-02	87
1	cohortMinusGroup2	TSI	2129	298	96	12	0.893	0.484	1.650	8.32E-01	8.38E-02	88
1	cohortMinusGroup2	ASW	2168	301	57	9	1.140	0.559	2.330	8.70E-01	8.48E-02	89
4	cohortMinusGroup2	GIH	2295	134	101	5	0.848	0.340	2.120	8.92E-01	8.57E-02	90
4	cohortMinusGroup2	PUR	2296	134	100	5	0.857	0.343	2.140	9.10E-01	8.67E-02	91
4	cohortMinusGroup2	PJL	2306	133	90	6	1.160	0.498	2.700	9.14E-01	8.76E-02	92
5	cohortMinusGroup2	GWD	2308	114	108	5	0.937	0.375	2.340	1.00E+00	8.86E-02	93
4	cohortMinusGroup2	GBR	2309	134	87	5	0.990	0.395	2.480	1.00E+00	8.95E-02	94
1	cohortMinusGroup2	FIN	2138	298	87	12	0.990	0.535	1.830	1.00E+00	8.95E-02	94
1	cohortMinusGroup2	CDX	2138	298	87	12	0.990	0.535	1.830	1.00E+00	8.95E-02	94
4	cohortMinusGroup2	JPT	2298	133	98	6	1.060	0.456	2.460	1.00E+00	9.05E-02	95
3	cohortMinusGroup2	PJL	2211	228	87	9	1.000	0.497	2.010	1.00E+00	9.14E-02	96
5	cohortMinusGroup2	YRI	2312	114	104	5	0.975	0.390	2.440	1.00E+00	9.14E-02	96
3	cohortMinusGroup2	ESN	2208	228	90	9	0.968	0.481	1.950	1.00E+00	9.24E-02	97
1	cohortMinusGroup2	YRI	2129	297	96	13	0.971	0.537	1.750	1.00E+00	9.24E-02	97
4	cohortMinusGroup2	CLM	2307	134	89	5	0.967	0.386	2.420	1.00E+00	9.33E-02	98
3	cohortMinusGroup2	MXL	2237	231	61	6	0.953	0.408	2.230	1.00E+00	9.43E-02	99

Table A8a Chi square significance tests for KIR variants within the 1000 Genomes populations, reference homozygous versus heterozygous

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	969	cohortMinusGroup2	PEL	C/C	C/T	1628	358	10	42	19.100	9.490	38.400	1.78E-28	8.56E-05	1
3DL3	969	cohortMinusGroup2	CHS	C/C	C/T	1599	342	39	58	6.950	4.560	10.600	7.12E-24	1.71E-04	2
3DL3	969	cohortMinusGroup2	JPT	C/C	C/T	1599	348	39	52	6.130	3.980	9.430	1.05E-19	2.57E-04	3
3DL3	969	cohortMinusGroup2	CDX	C/C	C/T	1605	354	33	46	6.320	3.980	10.000	4.47E-18	3.43E-04	4
3DL2	474	cohortMinusGroup2	CHB	G/G	G/T	1531	692	15	52	7.670	4.290	13.700	3.49E-15	4.28E-04	5
2DL4	1023	cohortMinusGroup2	CHS	G/G	G/A	1528	615	27	59	5.430	3.410	8.640	7.20E-15	5.14E-04	6
2DL4	1023	cohortMinusGroup2	CHB	G/G	G/A	1536	623	19	51	6.620	3.880	11.300	8.74E-15	5.99E-04	7
3DL2	474	cohortMinusGroup2	CHS	G/G	G/T	1527	690	19	54	6.290	3.700	10.700	3.89E-14	6.85E-04	8
2DL4	1023	cohortMinusGroup2	JPT	G/G	G/A	1530	619	25	55	5.440	3.360	8.810	5.72E-14	7.71E-04	9
3DL2	474	cohortMinusGroup2	PEL	G/G	G/T	1532	701	14	43	6.710	3.650	12.300	6.50E-12	8.56E-04	10
3DL3	804	cohortMinusGroup2	JPT	G/G	G/A	1401	702	103	1	0.019	0.003	0.139	9.16E-12	9.42E-04	11
2DL4	1023	cohortMinusGroup2	PEL	G/G	G/A	1540	634	15	40	6.480	3.550	11.800	1.06E-11	1.03E-03	12
3DP1	479	cohortMinusGroup2	FIN	A/A	A/C	1884	489	49	49	3.850	2.560	5.790	1.17E-11	1.11E-03	13
3DL3	969	cohortMinusGroup2	CHB	C/C	C/T	1595	359	43	41	4.240	2.720	6.600	1.62E-11	1.20E-03	14
2DL4	1023	cohortMinusGroup2	YRI	G/G	G/A	1448	673	107	1	0.020	0.003	0.144	2.20E-11	1.28E-03	15
2DL4	1023	cohortMinusGroup2	GWD	G/G	G/A	1444	672	111	2	0.039	0.010	0.157	2.79E-11	1.37E-03	16
3DL2	474	cohortMinusGroup2	JPT	G/G	G/T	1522	694	24	50	4.570	2.790	7.500	1.33E-10	1.46E-03	17
2DL4	1023	cohortMinusGroup2	LWK	G/G	G/A	1456	673	99	1	0.022	0.003	0.157	1.53E-10	1.54E-03	18
3DP1	479	cohortMinusGroup2	GBR	A/A	A/C	1890	495	43	43	3.820	2.470	5.900	2.56E-10	1.63E-03	19
3DL2	474	cohortMinusGroup2	CDX	G/G	G/T	1524	698	22	46	4.570	2.730	7.660	7.60E-10	1.71E-03	20
3DL3	408	cohortMinusGroup2	JPT	G/G	G/A	1587	651	103	1	0.024	0.003	0.170	8.04E-10	1.80E-03	21
3DL3	804	cohortMinusGroup2	CHS	G/G	G/A	1401	698	103	5	0.097	0.040	0.240	9.31E-10	1.88E-03	22
3DL3	969	cohortMinusGroup2	MXL	C/C	C/T	1617	374	21	26	5.350	2.980	9.610	1.47E-09	1.97E-03	23
2DL4	762	cohortMinusGroup2	GBR	C/C	C/T	1122	913	13	58	5.480	2.980	10.100	2.00E-09	2.06E-03	24
3DL1	607	cohortMinusGroup2	IBS	C/C	C/T	1539	466	29	37	4.210	2.560	6.920	2.35E-09	2.14E-03	25
2DL5	517	cohortMinusGroup2	STU	A/A	A/G	604	218	19	35	5.100	2.860	9.110	4.64E-09	2.23E-03	26
3DL2	474	cohortMinusGroup2	LWK	G/G	G/T	1452	739	94	5	0.105	0.043	0.259	4.92E-09	2.31E-03	27
3DL3	804	cohortMinusGroup2	KHV	G/G	G/A	1408	698	96	5	0.105	0.043	0.259	5.50E-09	2.40E-03	28
2DL4	1023	cohortMinusGroup2	MSL	G/G	G/A	1471	673	84	1	0.026	0.004	0.187	5.62E-09	2.48E-03	29
3DL3	738	cohortMinusGroup2	YRI	C/C	C/T	850	159	67	42	3.350	2.200	5.110	8.88E-09	2.57E-03	30
3DL3	408	cohortMinusGroup2	CDX	G/G	G/A	1593	650	97	2	0.051	0.012	0.205	9.34E-09	2.65E-03	31
3DL3	777	cohortMinusGroup2	JPT	A/A	A/G	1580	569	103	1	0.027	0.004	0.194	1.00E-08	2.74E-03	32
3DL2	474	cohortMinusGroup2	KHV	G/G	G/T	1519	697	27	47	3.790	2.340	6.140	1.46E-08	2.83E-03	33
3DP1	479	cohortMinusGroup2	TSI	A/A	A/C	1880	494	53	44	3.160	2.090	4.770	1.94E-08	2.91E-03	34
3DP1	939	cohortMinusGroup2	GWD	T/T	T/G	553	87	68	38	3.550	2.250	5.610	2.99E-08	3.00E-03	35
2DL5	583	cohortMinusGroup2	STU	G/G	G/A	531	216	19	36	4.660	2.610	8.310	4.17E-08	3.08E-03	36
2DP1	471	cohortMinusGroup2	GWD	A/A	A/G	1724	409	54	40	3.120	2.040	4.760	6.75E-08	3.17E-03	37
3DL3	906	cohortMinusGroup2	IBS	C/C	C/T	1672	474	49	43	3.100	2.030	4.730	8.00E-08	3.25E-03	38
3DL3	692	cohortMinusGroup2	YRI	G/G	G/A	751	155	66	42	3.080	2.020	4.710	1.30E-07	3.34E-03	39
2DL4	762	cohortMinusGroup2	IBS	C/C	C/T	1117	913	18	58	3.940	2.310	6.730	1.41E-07	3.43E-03	40
2DL4	1023	cohortMinusGroup2	KHV	G/G	G/A	1518	626	37	48	3.150	2.030	4.890	1.53E-07	3.51E-03	41
3DL3	906	cohortMinusGroup2	JPT	C/C	C/T	1622	516	99	1	0.032	0.004	0.229	1.58E-07	3.60E-03	42
3DL3	408	cohortMinusGroup2	CHS	G/G	G/A	1588	646	102	6	0.145	0.063	0.332	2.22E-07	3.68E-03	43
3DL3	961	cohortMinusGroup2	FIN	C/C	C/A	970	331	29	36	3.640	2.200	6.030	2.32E-07	3.77E-03	44
3DL3	408	cohortMinusGroup2	KHV	G/G	G/A	1594	647	96	5	0.128	0.052	0.316	2.85E-07	3.85E-03	45
2DP1	1313	cohortMinusGroup2	CHB	A/A	A/C	1335	555	94	5	0.128	0.052	0.316	2.91E-07	3.94E-03	46
2DL4	1023	cohortMinusGroup2	ACB	G/G	G/A	1465	668	90	6	0.146	0.064	0.335	3.09E-07	4.02E-03	47
2DP1	1313	cohortMinusGroup2	JPT	A/A	A/C	1337	555	92	5	0.131	0.053	0.324	4.45E-07	4.11E-03	48
2DP1	522	cohortMinusGroup2	GWD	T/T	T/C	1661	493	52	44	2.850	1.880	4.310	4.70E-07	4.20E-03	49
3DL3	906	cohortMinusGroup2	TSI	C/C	C/T	1668	474	53	43	2.860	1.890	4.330	4.90E-07	4.28E-03	50
3DP1	939	cohortMinusGroup2	MSL	T/T	T/G	575	97	46	28	3.610	2.150	6.050	7.34E-07	4.37E-03	51
3DL3	777	cohortMinusGroup2	CHS	A/A	A/G	1580	565	103	5	0.136	0.055	0.335	7.40E-07	4.45E-03	52
3DL3	692	cohortMinusGroup2	TSI	G/G	G/A	713	196	104	1	0.035	0.005	0.252	8.50E-07	4.54E-03	53
3DL3	502	cohortMinusGroup2	GWD	G/G	G/A	586	1101	61	42	0.366	0.244	0.549	8.82E-07	4.62E-03	54
3DL3	777	cohortMinusGroup2	IBS	A/A	A/G	1632	525	51	45	2.740	1.810	4.140	1.24E-06	4.71E-03	55
2DP1	471	cohortMinusGroup2	MSL	A/A	A/G	1740	419	38	30	3.280	2.010	5.360	1.25E-06	4.80E-03	56
3DP1	479	cohortMinusGroup2	YRI	A/A	A/C	1827	535	106	3	0.097	0.031	0.306	1.57E-06	4.88E-03	57
2DL4	762	cohortMinusGroup2	CHB	C/C	C/T	1060	950	75	21	0.312	0.191	0.510	1.84E-06	4.97E-03	58
3DL2	474	cohortMinusGroup2	ESN	G/G	G/T	1457	734	89	10	0.223	0.115	0.431	2.00E-06	5.05E-03	59
3DL3	969	cohortMinusGroup2	GWD	C/C	C/T	1537	399	101	1	0.038	0.005	0.274	2.17E-06	5.14E-03	60
3DL3	738	cohortMinusGroup2	TSI	C/C	C/T	810	200	107	1	0.038	0.005	0.273	2.32E-06	5.22E-03	61
3DL3	906	cohortMinusGroup2	PUR	C/C	C/T	1664	474	57	43	2.650	1.760	3.990	2.49E-06	5.31E-03	62
3DL3	777	cohortMinusGroup2	KHV	A/A	A/G	1587	565	96	5	0.146	0.059	0.361	2.65E-06	5.39E-03	63
3DP1	479	cohortMinusGroup2	CEU	A/A	A/C	1877	498	56	40	2.690	1.770	4.080	2.71E-06	5.48E-03	64
2DP1	1313	cohortMinusGroup2	CHS	A/A	A/C	1333	552	96	8	0.201	0.097	0.416	3.25E-06	5.57E-03	65
3DL3	969	cohortMinusGroup2	YRI	C/C	C/T	1541	399	97	1	0.040	0.006	0.286	3.78E-06	5.65E-03	66
2DP1	766	cohortMinusGroup2	STU	G/G	G/C	1327	307	40	29	3.130	1.910	5.130	4.28E-06	5.74E-03	67
3DP1	774	cohortMinusGroup2	ACB	G/G	G/C	1584	703	39	47	2.720	1.760	4.200	5.01E-06	5.82E-03	68
3DL3	906	cohortMinusGroup2	CHS	C/C	C/T	1618	512	103	5	0.153	0.062	0.377	5.33E-06	5.91E-03	69
2DP1	522	cohortMinusGroup2	JPT	T/T	T/C	1614	532	99	5	0.153	0.062	0.378	5.34E-06	5.99E-03	70
3DP1	479	cohortMinusGroup2	LWK	A/A	A/C	1836	535	97	3	0.106	0.034	0.336	6.18E-06	6.08E-03	71
2DP1	522	cohortMinusGroup2	CHB	T/T	T/C	1615	532	98	5	0.155	0.063	0.383	6.31E-06	6.16E-03	72
3DL1	607	cohortMinusGroup2	GBR	C/C	C/T	1534	471	34	32	3.070	1.870	5.030	6.39E-06	6.25E-03	73
2DL4	480	cohortMinusGroup2	KHV	G/G	G/A	1597	367	100	1	0.044	0.006	0.313	1.09E-05	6.34E-03	74
3DL2	474	cohortMinusGroup2	YRI	G/G	G/T	1454	731	92	13	0.281	0.156	0.506	1.10E-05	6.42E-03	75
3DL3	408	cohortMinusGroup2	YRI	G/G	G/A	1635	603	55	49	2.420	1.630	3.600	1.22E-05	6.51E-03	76
3DL1	1303	cohortMinusGroup2	GWD	A/A	A/G	1098	90	86	22	3.120	1.860	5.220	1.35E-05	6.59E-03	77
3DL3	969	cohortMinusGroup2	KHV	C/C	C/T	1585	367	53	33	2.690	1.720	4.220	1.47E-05	6.68E-03	78
3DL3	692	cohortMinusGroup2	CLM	G/G	G/A	725	195	92	2	0.081	0.020	0.331	1.60E-05	6.76E-03	79
3DL3	1042	cohortMinusGroup2	MSL	G/G	G/C	986	131	31	16	3.880	2.070	7.290	1.81E-05	6.85E-03	80
3DL3	777	cohortMinusGroup2	PUR	A/A	A/G	1627	526	56	44	2.430	1.620	3.650	1.85E-05	6.94E-03	81
3DL3	906	cohortMinusGroup2	KHV	C/C	C/T	1626	512	95	5	0.167	0.068	0.413	1.93E-05	7.02E-03	82
2DL4	480	cohortMinusGroup2	IBS	G/G	G/A	1629	333	68	35	2.520	1.650	3.850	2.00E-05	7.11E-03	83
2DL4	395	cohortMinusGroup2	KHV	C/C	C/T	2075	205	77	22	2.890	1.760	4.740	2.53E-05	7.19E-03	84
3DL3	969	cohortMinusGroup2	ESN	C/C	C/T	1548	398	90	2	0.086	0.021	0.352	2.93E-05	7.28E-03	85
3DL2	474	cohortMinusGroup2	ACB	G/G	G/T	1462	732	84	12	0.285	0.155	0.525	3.17E-05	7.36E-03	86
3DL3	969	cohortMinusGroup2	ACB	C/C	C/T	1549	398	89	2	0.088	0.022	0.357	3.36E-05	7.45E-03	87
3DL3	969	cohortMinusGroup2	GBR	C/C	C/T	1557	399	81	1	0.048	0.007	0.347	3.44E-05	7.53E-03	88
2DP1	471	cohortMinusGroup2	CHB	A/A	A/G	1679	445	99	4	0.152	0.056	0.415	4.30E-05	7.62E-03	89
3DL3	738	cohortMinusGroup2	PEL	C/C	C/T	832	200	85	1	0.049	0.007	0.353	4.49E-05	7.71E-03	90
2DL4	625	cohortMinusGroup2	GIH	C/C	C/G	811	903	60	25	0.374	0.232	0.602	4.51E-05	7.79E-03	91
2DL4	412	cohortMinusGroup2	CHB	G/G	G/A	966	974	17	53	3.090	1.780	5.370	4.65E-05	7.88E-03	92
3DL3	777	cohortMinusGroup2	TSI	A/A	A/G	1628	528	55	42	2.350	1.550	3.550	5.14E-05	7.96E-03	93
3DL3	738	cohortMinusGroup2	CLM	C/C	C/T	825	199	92	2	0.090	0.022	0.369	5.32E-05	8.05E-03	94
2DL4	762	cohortMinusGroup2	CEU	C/C	C/T	1116	924	19	47	2.990	1.740	5.130	5.53E-05	8.13E-03	95
3DL3	408	cohortMinusGroup2	PEL	G/G	G/A	1611	645	79	7	0.221	0.101	0.481	5.57E-05	8.22E-03	96
3DL3	502	cohortMinusGroup2	ESN	G/G	G/A	597	1105	50	38	0.411	0.266	0.634	5.68E-05	8.31E-03	97
2DP1	1313	cohortMinusGroup2	CDX	A/A	A/C	1352	553	77	7	0.222	0.102	0.484	6.24E-05	8.39E-03	98
3DL1	1303	cohortMinusGroup2	ACB	A/A	A/G	1116	94	68	18	3.140	1.790	5.500	6.37E-05	8.48E-03	99
3DP1	479	cohortMinusGroup2	ESN	A/A	A/C	1839	533	94	5	0.184	0.075	0.455	6.59E-05	8.56E-03	100
3DL3	804	cohortMinusGroup2	PEL	G/G	G/A	1428	693	76	10	0.271	0.139	0.527	6.65E-05	8.65E-03	101
3DP1	796	cohortMinusGroup2	YRI	T/T	T/C	1583	707	42	45	2.400	1.560	3.690	6.68E-05	8.73E-03	102
3DP1	479	cohortMinusGroup2	MSL	A/A	A/C	1852	535	81	3	0.128	0.040	0.407	6.95E-05	8.82E-03	103
3DL3	408	cohortMinusGroup2	ACB	G/G	G/A	1644	611	46	41	2.400	1.560	3.690	7.23E-05	8.90E-03	104
3DL1	1180	cohortMinusGroup2	GWD	G/G	G/C	1460	374	66	39	2.310	1.530	3.490	7.67E-05	8.99E-03	105
2DL4	480	cohortMinusGroup2	BEB	G/G	G/A	1613	367	84	1	0.052	0.007	0.377	7.80E-05	9.08E-03	106
3DP1	796	cohortMinusGroup2	ACB	T/T	T/C	1584	708	41	44	2.400	1.550	3.710	7.98E-05	9.16E-03	107

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL1	607	cohortMinusGroup2	FIN	C/C	C/T	1530	472	38	31	2.640	1.620	4.290	8.72E-05	9.25E-03	108
2DL4	1019	cohortMinusGroup2	GWD	C/C	C/T	860	42	96	16	3.410	1.850	6.300	8.74E-05	9.33E-03	109
2DP1	522	cohortMinusGroup2	CHS	T/T	T/C	1615	529	98	8	0.249	0.120	0.515	8.81E-05	9.42E-03	110
3DL3	969	cohortMinusGroup2	MSL	C/C	C/T	1564	399	74	1	0.053	0.007	0.382	8.99E-05	9.50E-03	111
2DL4	412	cohortMinusGroup2	CEU	G/G	G/A	918	998	65	29	0.410	0.262	0.641	9.01E-05	9.59E-03	112
2DL4	625	cohortMinusGroup2	PEL	C/C	C/G	863	892	8	36	4.350	2.010	9.410	9.22E-05	9.68E-03	113
3DL3	971	cohortMinusGroup2	JPT	T/T	T/C	1625	344	98	2	0.096	0.024	0.393	9.35E-05	9.76E-03	114
2DL4	625	cohortMinusGroup2	TSI	C/C	C/G	813	903	58	25	0.388	0.240	0.626	9.86E-05	9.85E-03	115
3DL3	692	cohortMinusGroup2	PUR	G/G	G/A	717	192	100	5	0.187	0.075	0.466	1.04E-04	9.93E-03	116
3DL3	971	cohortMinusGroup2	CHB	T/T	T/C	1626	344	97	2	0.098	0.024	0.397	1.05E-04	1.00E-02	117
3DL3	1042	cohortMinusGroup2	LWK	G/G	G/C	970	128	47	19	3.060	1.740	5.380	1.05E-04	1.01E-02	118
3DL1	1026	cohortMinusGroup2	GWD	G/G	G/C	1147	164	78	28	2.510	1.580	3.980	1.06E-04	1.02E-02	119
2DP1	471	cohortMinusGroup2	JPT	A/A	A/G	1679	444	99	5	0.191	0.077	0.472	1.08E-04	1.03E-02	120
2DL4	480	cohortMinusGroup2	TSI	G/G	G/A	1626	334	71	34	2.330	1.520	3.570	1.08E-04	1.04E-02	121
3DL2	394	cohortMinusGroup2	KHV	C/C	C/A	2203	217	79	21	2.700	1.640	4.460	1.14E-04	1.05E-02	122
3DL3	969	cohortMinusGroup2	TSI	C/C	C/T	1551	397	87	3	0.135	0.043	0.429	1.21E-04	1.05E-02	123
3DL3	869	cohortMinusGroup2	YRI	A/A	A/C	1877	504	65	39	2.230	1.480	3.360	1.31E-04	1.06E-02	124
3DP1	796	cohortMinusGroup2	CHB	T/T	T/C	1538	738	87	14	0.335	0.189	0.593	1.36E-04	1.07E-02	125
3DL3	502	cohortMinusGroup2	YRI	G/G	G/A	593	1098	54	45	0.450	0.299	0.677	1.37E-04	1.08E-02	126
3DP1	774	cohortMinusGroup2	CHB	G/G	G/C	1536	736	87	14	0.336	0.190	0.595	1.39E-04	1.09E-02	127
2DL4	762	cohortMinusGroup2	ESN	C/C	C/T	1069	948	66	23	0.393	0.243	0.637	1.39E-04	1.10E-02	128
2DL4	412	cohortMinusGroup2	TSI	G/G	G/A	914	994	69	33	0.440	0.288	0.673	1.54E-04	1.10E-02	129
2DP1	448	cohortMinusGroup2	CHS	G/G	G/C	635	823	3	30	7.720	2.350	25.400	1.58E-04	1.11E-02	130
3DL1	496	cohortMinusGroup2	LWK	C/C	C/A	1729	115	80	16	3.010	1.700	5.320	1.69E-04	1.12E-02	131
3DL3	971	cohortMinusGroup2	BEB	T/T	T/C	1682	324	41	22	2.790	1.640	4.750	1.70E-04	1.13E-02	132
3DL3	971	cohortMinusGroup2	PJL	T/T	T/C	1682	324	41	22	2.790	1.640	4.750	1.70E-04	1.13E-02	132
3DL3	502	cohortMinusGroup2	JPT	G/G	G/A	642	1098	5	45	5.260	2.080	13.300	1.74E-04	1.14E-02	133
2DP1	1313	cohortMinusGroup2	KHV	A/A	A/C	1345	550	84	10	0.291	0.150	0.565	1.76E-04	1.15E-02	134
3DP1	939	cohortMinusGroup2	PUR	T/T	T/G	543	124	78	1	0.056	0.008	0.407	1.84E-04	1.16E-02	135
3DL3	621	cohortMinusGroup2	KHV	G/G	G/A	1714	203	76	23	2.560	1.570	4.170	1.95E-04	1.16E-02	136
3DL3	971	cohortMinusGroup2	ITU	T/T	T/C	1666	319	57	27	2.470	1.540	3.970	2.02E-04	1.17E-02	137
2DP1	766	cohortMinusGroup2	BEB	G/G	G/C	1327	311	40	25	2.670	1.600	4.470	2.07E-04	1.18E-02	138
3DL2	497	cohortMinusGroup2	IBS	G/G	G/A	1754	166	85	21	2.610	1.580	4.320	2.21E-04	1.19E-02	139
3DL2	474	cohortMinusGroup2	MSL	G/G	G/T	1474	733	72	11	0.307	0.162	0.583	2.22E-04	1.20E-02	140
3DL2	497	cohortMinusGroup2	GBR	G/G	G/A	1766	168	73	19	2.740	1.610	4.650	2.25E-04	1.21E-02	141
2DP1	1313	cohortMinusGroup2	GWD	A/A	A/C	1377	517	52	43	2.200	1.450	3.340	2.31E-04	1.22E-02	142
3DL3	738	cohortMinusGroup2	ACB	C/C	C/T	855	171	62	30	2.420	1.520	3.860	2.40E-04	1.22E-02	143
2DL4	625	cohortMinusGroup2	CHB	C/C	C/G	856	882	15	46	2.980	1.650	5.380	2.54E-04	1.23E-02	144
2DL4	412	cohortMinusGroup2	CHS	G/G	G/A	960	969	23	58	2.500	1.530	4.090	2.56E-04	1.24E-02	145
2DP1	471	cohortMinusGroup2	CHS	A/A	A/G	1679	443	99	6	0.230	0.100	0.528	2.57E-04	1.25E-02	146
3DL1	1091	cohortMinusGroup2	GWD	G/G	G/A	1096	173	74	28	2.400	1.510	3.820	2.62E-04	1.26E-02	147
3DP1	479	cohortMinusGroup2	IBS	A/A	A/C	1870	501	63	37	2.190	1.440	3.330	2.69E-04	1.27E-02	148
2DL4	625	cohortMinusGroup2	CHS	C/C	C/G	849	871	22	57	2.530	1.530	4.180	2.88E-04	1.28E-02	149
3DL3	869	cohortMinusGroup2	LWK	A/A	A/C	1879	506	63	37	2.180	1.440	3.310	2.96E-04	1.28E-02	150
3DP1	796	cohortMinusGroup2	GWD	T/T	T/C	1573	703	52	49	2.110	1.410	3.150	2.97E-04	1.29E-02	151
2DP1	522	cohortMinusGroup2	CDX	T/T	T/C	1628	530	85	7	0.253	0.116	0.550	3.06E-04	1.30E-02	152
3DL3	692	cohortMinusGroup2	MXL	G/G	G/A	753	196	64	1	0.060	0.008	0.435	3.11E-04	1.31E-02	153
3DP1	774	cohortMinusGroup2	GWD	G/G	G/C	1569	700	54	50	2.080	1.400	3.090	3.35E-04	1.32E-02	154
3DL1	732	cohortMinusGroup2	CHB	T/T	T/C	392	253	1	12	18.600	2.400	144.000	3.46E-04	1.33E-02	155
3DL3	738	cohortMinusGroup2	PUR	C/C	C/T	817	196	100	5	0.208	0.084	0.518	3.55E-04	1.34E-02	156
3DL3	969	cohortMinusGroup2	IBS	C/C	C/T	1546	395	92	5	0.213	0.086	0.527	3.91E-04	1.34E-02	157
3DL3	971	cohortMinusGroup2	LWK	T/T	T/C	1670	321	53	25	2.450	1.500	4.000	3.95E-04	1.35E-02	158
2DP1	471	cohortMinusGroup2	BEB	A/A	A/G	1730	421	48	28	2.400	1.490	3.870	3.96E-04	1.36E-02	159
2DL4	412	cohortMinusGroup2	JPT	G/G	G/A	961	972	22	55	2.470	1.490	4.080	4.26E-04	1.37E-02	160
2DP1	522	cohortMinusGroup2	ACB	T/T	T/C	1663	503	50	34	2.250	1.440	3.520	4.49E-04	1.38E-02	161
3DL3	906	cohortMinusGroup2	GWD	C/C	C/T	1620	507	101	10	0.316	0.164	0.610	4.69E-04	1.39E-02	162
3DL2	474	cohortMinusGroup2	GWD	G/G	G/T	1453	725	93	19	0.409	0.248	0.675	4.76E-04	1.40E-02	163
2DP1	448	cohortMinusGroup2	JPT	G/G	G/C	635	826	3	27	6.920	2.090	22.900	5.00E-04	1.40E-02	164
2DL4	412	cohortMinusGroup2	IBS	G/G	G/A	915	992	68	35	0.475	0.313	0.721	5.28E-04	1.41E-02	165
3DL3	738	cohortMinusGroup2	MXL	C/C	C/T	851	200	66	1	0.065	0.009	0.468	5.40E-04	1.42E-02	166
2DL4	412	cohortMinusGroup2	GWD	G/G	G/A	965	979	18	48	2.630	1.520	4.550	5.61E-04	1.43E-02	167
2DL4	625	cohortMinusGroup2	IBS	C/C	C/G	819	904	52	24	0.418	0.255	0.684	5.63E-04	1.44E-02	168
2DP1	522	cohortMinusGroup2	MSL	T/T	T/C	1675	509	38	28	2.420	1.470	3.980	5.75E-04	1.45E-02	169
2DL4	412	cohortMinusGroup2	PEL	G/G	G/A	971	989	12	38	3.110	1.620	5.990	6.16E-04	1.46E-02	170
3DL3	906	cohortMinusGroup2	CEU	C/C	C/T	1665	482	56	35	2.160	1.400	3.330	6.20E-04	1.46E-02	171
2DL4	480	cohortMinusGroup2	GIH	G/G	G/A	1599	363	98	5	0.225	0.091	0.557	6.84E-04	1.47E-02	172
3DL3	502	cohortMinusGroup2	CHB	G/G	G/A	643	1106	4	37	5.380	1.910	15.200	6.89E-04	1.48E-02	173
3DP1	774	cohortMinusGroup2	YRI	G/G	G/C	1579	708	44	42	2.130	1.380	3.280	7.17E-04	1.49E-02	174
3DL1	1180	cohortMinusGroup2	CDX	G/G	G/C	1453	409	73	4	0.195	0.071	0.537	7.24E-04	1.50E-02	175
2DL4	625	cohortMinusGroup2	GWD	C/C	C/G	853	880	18	48	2.580	1.490	4.470	7.34E-04	1.51E-02	176
3DP1	796	cohortMinusGroup2	ESN	T/T	T/C	1587	714	38	38	2.220	1.400	3.510	7.42E-04	1.52E-02	177
3DL3	906	cohortMinusGroup2	FIN	C/C	C/T	1662	481	59	36	2.110	1.380	3.230	7.47E-04	1.52E-02	178
3DL3	961	cohortMinusGroup2	ACB	C/C	C/A	923	358	76	9	0.305	0.151	0.615	7.52E-04	1.53E-02	179
2DL4	480	cohortMinusGroup2	GBR	G/G	G/A	1637	340	60	28	2.250	1.420	3.580	7.67E-04	1.54E-02	180
2DL4	1023	cohortMinusGroup2	CDX	G/G	G/A	1512	635	43	39	2.160	1.390	3.360	7.86E-04	1.55E-02	181
3DL1	607	cohortMinusGroup2	CEU	C/C	C/T	1534	477	34	26	2.460	1.460	4.140	8.42E-04	1.56E-02	182
2DP1	1313	cohortMinusGroup2	STU	A/A	A/C	1389	526	40	34	2.240	1.400	3.580	8.49E-04	1.57E-02	183
2DL4	762	cohortMinusGroup2	JPT	C/C	C/T	1070	945	65	26	0.453	0.285	0.720	8.90E-04	1.58E-02	184
2DL4	625	cohortMinusGroup2	JPT	C/C	C/G	852	879	19	49	2.500	1.460	4.280	8.99E-04	1.58E-02	185
2DP1	471	cohortMinusGroup2	ESN	A/A	A/G	1719	418	59	31	2.160	1.380	3.380	9.21E-04	1.59E-02	186
2DL4	480	cohortMinusGroup2	FIN	G/G	G/A	1633	339	64	29	2.180	1.380	3.430	9.43E-04	1.60E-02	187
3DL3	804	cohortMinusGroup2	PUR	G/G	G/A	1452	656	52	47	2.000	1.330	3.000	9.56E-04	1.61E-02	188
2DL4	412	cohortMinusGroup2	GIH	G/G	G/A	917	992	66	35	0.490	0.322	0.745	1.00E-03	1.62E-02	189
3DP1	796	cohortMinusGroup2	PJL	T/T	T/C	1545	737	80	15	0.393	0.225	0.687	1.05E-03	1.63E-02	190
3DL3	447	cohortMinusGroup2	KHV	G/G	G/T	2136	284	76	23	2.280	1.410	3.690	1.07E-03	1.64E-02	191
3DL3	804	cohortMinusGroup2	YRI	G/G	G/A	1450	655	54	48	1.970	1.320	2.940	1.09E-03	1.64E-02	192
2DP1	766	cohortMinusGroup2	CHS	G/G	G/C	1284	331	83	5	0.234	0.094	0.582	1.10E-03	1.65E-02	193
3DL3	969	cohortMinusGroup2	PJL	C/C	C/T	1568	397	70	3	0.169	0.053	0.540	1.16E-03	1.66E-02	194
3DL3	804	cohortMinusGroup2	ACB	G/G	G/A	1459	661	45	42	2.060	1.340	3.170	1.21E-03	1.67E-02	195
3DL3	906	cohortMinusGroup2	LWK	C/C	C/T	1632	508	89	9	0.325	0.163	0.650	1.28E-03	1.68E-02	196
3DL3	961	cohortMinusGroup2	PEL	C/C	C/A	926	358	73	9	0.319	0.158	0.644	1.28E-03	1.69E-02	197
2DP1	522	cohortMinusGroup2	KHV	T/T	T/C	1623	527	90	10	0.342	0.177	0.662	1.34E-03	1.70E-02	198
2DP1	766	cohortMinusGroup2	JPT	G/G	G/C	1286	331	81	5	0.240	0.097	0.597	1.43E-03	1.70E-02	199
2DL3	953	cohortMinusGroup2	FIN	G/G	G/A	1338	476	41	32	2.190	1.360	3.520	1.43E-03	1.71E-02	200
3DL3	869	cohortMinusGroup2	CHB	A/A	A/C	1848	534	94	9	0.331	0.166	0.660	1.54E-03	1.72E-02	201
3DL1	1026	cohortMinusGroup2	IBS	G/G	G/C	1189	177	36	15	2.800	1.500	5.220	1.56E-03	1.73E-02	202
3DL3	699	cohortMinusGroup2	GWD	G/G	G/A	753	62	92	19	2.510	1.440	4.380	1.64E-03	1.74E-02	203
3DL3	971	cohortMinusGroup2	CHS	T/T	T/C	1626	341	97	5	0.246	0.099	0.609	1.66E-03	1.75E-02	204
3DL3	738	cohortMinusGroup2	LWK	C/C	C/T	847	171	70	30	2.120	1.340	3.350	1.67E-03	1.76E-02	205
2DL5	517	cohortMinusGroup2	LWK	A/A	A/G	582	250	41	3	0.170	0.052	0.554	1.67E-03	1.76E-02	206
3DL1	1091	cohortMinusGroup2	BEB	G/G	G/A	1098	200	72	1	0.076	0.011	0.551	1.75E-03	1.77E-02	207
2DP1	522	cohortMinusGroup2	ASW	T/T	T/C	1678	512	35	25	2.340	1.390	3.950	1.78E-03	1.78E-02	208
3DL3	804	cohortMinusGroup2	IBS	G/G	G/A	1453	658	51	45	1.950	1.290	2.940	1.82E-03	1.79E-02	209
2DL4	395	cohortMinusGroup2	JPT	C/C	C/T	2071	208	81	19	2.340	1.390	3.930	1.84E-03	1.80E-02	210
3DL3	777	cohortMinusGroup2	PEL	A/A	A/G	1606	561	77	9	0.335	0.167	0.673	1.93E-03	1.81E-02	211
3DL3	961	cohortMinusGroup2	GBR	C/C	C/A	975	345	24	22	2.590	1.430	4.680	1.98E-03	1.82E-02	212
3DL3	502	cohortMinusGroup2	STU	G/G	G/A	636	1090	11	53	2.810	1.460	5.420	2.05E-03	1.82E-02	213
3DL3	692	cohortMinusGroup2	ACB	G/G	G/A	756	168	61	29	2.140	1.330	3.430	2.11E-03	1.83E-02	214
2DP1	1313	cohortMinusGroup2	MSL	A/A	A/C	1395	531	34	29	2.240	1.350	3.710	2.19E-03	1.84E-02	215

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DP1	774	cohortMinusGroup2	PJL	G/G	G/C	1544	734	79	16	0.426	0.247	0.734	2.32E-03	1.85E-02	216
3DL3	408	cohortMinusGroup2	TSI	G/G	G/A	1631	610	59	42	1.900	1.270	2.850	2.39E-03	1.86E-02	217
2DP1	448	cohortMinusGroup2	KHV	G/G	G/C	632	823	6	30	3.840	1.590	9.280	2.39E-03	1.87E-02	218
3DL1	1021	cohortMinusGroup2	ESN	A/A	A/G	1210	125	67	17	2.460	1.400	4.320	2.41E-03	1.88E-02	219
3DL3	502	cohortMinusGroup2	ACB	G/G	G/A	604	1104	43	39	0.496	0.318	0.774	2.47E-03	1.88E-02	220
3DL2	893	cohortMinusGroup2	PEL	G/G	G/A	2122	307	85	1	0.081	0.011	0.586	2.50E-03	1.89E-02	221
3DL2	456	cohortMinusGroup2	PEL	C/C	C/T	2125	306	85	1	0.082	0.011	0.589	2.58E-03	1.90E-02	222
2DL4	625	cohortMinusGroup2	CEU	C/C	C/G	822	903	49	25	0.464	0.284	0.758	2.61E-03	1.91E-02	223
3DP1	939	cohortMinusGroup2	IBS	T/T	T/G	564	124	57	1	0.080	0.011	0.582	2.62E-03	1.92E-02	224
3DL1	1194	cohortMinusGroup2	KHV	C/C	C/T	1871	175	70	16	2.440	1.390	4.290	2.66E-03	1.93E-02	225
2DP1	766	cohortMinusGroup2	CHB	G/G	G/C	1291	331	76	5	0.257	0.103	0.640	2.71E-03	1.94E-02	226
3DP1	796	cohortMinusGroup2	LWK	T/T	T/C	1580	712	45	40	1.970	1.280	3.040	2.75E-03	1.94E-02	227
3DL1	1026	cohortMinusGroup2	BEB	G/G	G/C	1152	191	73	1	0.083	0.011	0.598	2.93E-03	1.95E-02	228
3DL3	408	cohortMinusGroup2	GWD	G/G	G/A	1632	611	58	41	1.890	1.250	2.850	3.03E-03	1.96E-02	229
3DL1	1303	cohortMinusGroup2	JPT	A/A	A/G	1087	112	97	0	0.000	0.000	NaN	3.06E-03	1.97E-02	230
3DL3	408	cohortMinusGroup2	MSL	G/G	G/A	1647	619	43	33	2.040	1.280	3.240	3.17E-03	1.98E-02	231
3DP1	796	cohortMinusGroup2	PEL	T/T	T/C	1554	738	71	14	0.415	0.232	0.741	3.25E-03	1.99E-02	232
3DL1	1303	cohortMinusGroup2	IBS	A/A	A/G	1088	112	96	0	0.000	0.000	NaN	3.25E-03	2.00E-02	233
2DP1	522	cohortMinusGroup2	STU	T/T	T/C	1665	507	48	30	2.050	1.290	3.270	3.26E-03	2.00E-02	234
2DL4	762	cohortMinusGroup2	FIN	C/C	C/T	1108	924	27	47	2.090	1.290	3.380	3.29E-03	2.01E-02	235
3DL3	969	cohortMinusGroup2	ASW	C/C	C/T	1583	398	55	2	0.145	0.035	0.597	3.30E-03	2.02E-02	236
3DP1	774	cohortMinusGroup2	PEL	G/G	G/C	1552	736	71	14	0.416	0.233	0.743	3.31E-03	2.03E-02	237
2DP1	471	cohortMinusGroup2	CDX	A/A	A/G	1693	442	85	7	0.315	0.145	0.686	3.36E-03	2.04E-02	238
2DL4	480	cohortMinusGroup2	GWD	G/G	G/A	1617	336	80	32	1.920	1.250	2.940	3.39E-03	2.05E-02	239
3DL1	496	cohortMinusGroup2	ESN	C/C	C/A	1727	117	82	14	2.520	1.390	4.580	3.42E-03	2.06E-02	240
2DP1	766	cohortMinusGroup2	GIH	G/G	G/C	1326	314	41	22	2.270	1.330	3.870	3.43E-03	2.06E-02	241
3DL1	1026	cohortMinusGroup2	KHV	G/G	G/C	1154	191	71	1	0.085	0.012	0.616	3.52E-03	2.07E-02	242
3DP1	939	cohortMinusGroup2	CLM	T/T	T/G	558	123	63	2	0.144	0.035	0.596	3.54E-03	2.08E-02	243
3DP1	796	cohortMinusGroup2	MSL	T/T	T/C	1587	717	38	35	2.040	1.280	3.260	3.55E-03	2.09E-02	244
3DL3	447	cohortMinusGroup2	CHS	G/G	G/T	2129	284	83	23	2.080	1.290	3.360	3.65E-03	2.10E-02	245
2DL4	762	cohortMinusGroup2	TSI	C/C	C/T	1105	921	30	50	2.000	1.260	3.170	3.92E-03	2.11E-02	246
2DP1	471	cohortMinusGroup2	STU	A/A	A/G	1727	423	51	26	2.080	1.280	3.380	3.93E-03	2.12E-02	247
2DL3	953	cohortMinusGroup2	CHB	G/G	G/A	1293	494	86	14	0.426	0.240	0.757	4.01E-03	2.12E-02	248
3DL3	961	cohortMinusGroup2	LWK	C/C	C/T	313	75	53	28	2.200	1.300	3.710	4.16E-03	2.13E-02	249
2DP1	448	cohortMinusGroup2	GWD	G/G	G/C	584	813	54	40	0.532	0.349	0.812	4.24E-03	2.14E-02	250
3DL3	502	cohortMinusGroup2	LWK	G/G	G/A	603	1101	44	42	0.523	0.339	0.807	4.29E-03	2.15E-02	251
3DL2	497	cohortMinusGroup2	GIH	G/G	G/A	1734	186	105	1	0.089	0.012	0.640	4.30E-03	2.16E-02	252
3DL3	961	cohortMinusGroup2	CHB	C/C	C/A	914	353	85	14	0.426	0.239	0.760	4.40E-03	2.17E-02	253
3DL1	732	cohortMinusGroup2	YRI	T/T	T/C	358	257	35	8	0.318	0.145	0.697	4.57E-03	2.18E-02	254
3DL1	607	cohortMinusGroup2	CHB	C/C	C/T	1484	492	84	11	0.395	0.209	0.747	4.59E-03	2.18E-02	255
3DL1	1091	cohortMinusGroup2	IBS	G/G	G/A	1134	186	36	15	2.540	1.360	4.730	4.60E-03	2.19E-02	256
3DL1	732	cohortMinusGroup2	PEL	T/T	T/C	389	252	4	13	5.020	1.620	15.600	4.62E-03	2.20E-02	257
3DL3	906	cohortMinusGroup2	YRI	C/C	C/T	1627	505	94	12	0.411	0.224	0.756	4.65E-03	2.21E-02	258
2DL4	480	cohortMinusGroup2	PJL	G/G	G/A	1609	362	88	6	0.303	0.131	0.698	4.68E-03	2.22E-02	259
3DL3	777	cohortMinusGroup2	LWK	A/A	A/G	1595	557	88	13	0.423	0.234	0.763	4.76E-03	2.23E-02	260
2DP1	448	cohortMinusGroup2	PEL	G/G	G/C	635	832	3	21	5.340	1.590	18.000	4.87E-03	2.24E-02	261
2DP1	766	cohortMinusGroup2	ITU	G/G	G/C	1316	311	51	25	2.070	1.260	3.390	5.06E-03	2.24E-02	262
2DL4	480	cohortMinusGroup2	STU	G/G	G/A	1603	361	94	7	0.331	0.152	0.719	5.12E-03	2.25E-02	263
2DL3	953	cohortMinusGroup2	PEL	G/G	G/A	1306	497	73	11	0.396	0.208	0.753	5.16E-03	2.26E-02	264
2DP1	816	cohortMinusGroup2	GWD	G/G	G/A	660	45	95	16	2.470	1.340	4.540	5.17E-03	2.27E-02	265
2DL4	762	cohortMinusGroup2	CHS	C/C	C/T	1064	937	71	34	0.544	0.358	0.826	5.20E-03	2.28E-02	266
3DL2	394	cohortMinusGroup2	CHS	C/C	C/A	2193	219	89	19	2.140	1.280	3.580	5.25E-03	2.29E-02	267
3DL2	394	cohortMinusGroup2	LWK	C/C	C/A	2183	237	99	1	0.093	0.013	0.670	5.57E-03	2.30E-02	268
2DL3	953	cohortMinusGroup2	CEU	G/G	G/A	1345	482	34	26	2.130	1.260	3.590	5.69E-03	2.30E-02	269
3DL3	777	cohortMinusGroup2	FIN	A/A	A/G	1624	534	59	36	1.860	1.210	2.850	5.70E-03	2.31E-02	270
3DL3	502	cohortMinusGroup2	MSL	G/G	G/A	609	1108	38	35	0.506	0.316	0.809	5.70E-03	2.32E-02	271
3DL2	497	cohortMinusGroup2	KHV	G/G	G/A	1739	186	100	1	0.094	0.013	0.674	5.80E-03	2.33E-02	272
2DP1	522	cohortMinusGroup2	PEL	T/T	T/C	1638	528	75	9	0.372	0.185	0.748	5.93E-03	2.34E-02	273
3DL3	777	cohortMinusGroup2	CEU	A/A	A/G	1626	535	57	35	1.870	1.210	2.880	5.99E-03	2.35E-02	274
3DL3	455	cohortMinusGroup2	TSI	G/G	G/A	1365	75	95	13	2.490	1.330	4.650	6.13E-03	2.35E-02	275
3DL1	607	cohortMinusGroup2	GIH	C/C	C/T	1495	494	73	9	0.373	0.185	0.751	6.20E-03	2.36E-02	276
3DL3	869	cohortMinusGroup2	PEL	A/A	A/C	1864	535	78	8	0.357	0.171	0.744	6.27E-03	2.37E-02	277
3DL3	692	cohortMinusGroup2	LWK	G/G	G/A	754	169	63	28	1.980	1.230	3.190	6.39E-03	2.38E-02	278
3DL3	502	cohortMinusGroup2	CHS	G/G	G/A	638	1100	9	43	2.770	1.340	5.720	6.47E-03	2.39E-02	279
3DP1	939	cohortMinusGroup2	PEL	T/T	T/G	563	123	58	2	0.158	0.038	0.656	6.47E-03	2.40E-02	280
3DL1	1303	cohortMinusGroup2	ESN	A/A	A/G	1104	96	80	16	2.300	1.290	4.090	6.54E-03	2.41E-02	281
2DL4	762	cohortMinusGroup2	CLM	C/C	C/T	1108	926	27	45	1.990	1.230	3.230	6.54E-03	2.41E-02	282
3DP1	479	cohortMinusGroup2	PEL	A/A	A/C	1855	530	78	8	0.359	0.172	0.748	6.54E-03	2.42E-02	283
3DL2	394	cohortMinusGroup2	JPT	C/C	C/A	2198	220	84	18	2.140	1.260	3.630	6.55E-03	2.43E-02	284
3DP1	774	cohortMinusGroup2	JPT	G/G	G/C	1541	731	82	19	0.488	0.294	0.810	6.59E-03	2.44E-02	285
2DL5	517	cohortMinusGroup2	CHB	A/A	A/G	597	252	26	1	0.091	0.012	0.675	6.60E-03	2.45E-02	286
3DL1	1026	cohortMinusGroup2	FIN	G/G	G/C	1175	175	50	17	2.280	1.290	4.040	6.64E-03	2.46E-02	287
3DL1	1303	cohortMinusGroup2	GIH	A/A	A/G	1100	112	84	0	0.000	0.000	NaN	6.64E-03	2.47E-02	288
3DL1	1303	cohortMinusGroup2	STU	A/A	A/G	1100	112	84	0	0.000	0.000	NaN	6.64E-03	2.47E-02	288
3DL2	393	cohortMinusGroup2	ESN	G/G	G/T	607	26	88	11	2.920	1.390	6.120	6.70E-03	2.47E-02	289
2DP1	766	cohortMinusGroup2	PEL	G/G	G/C	1305	332	62	4	0.254	0.092	0.703	7.18E-03	2.48E-02	290
3DL3	969	cohortMinusGroup2	GIH	C/C	C/T	1563	394	75	6	0.317	0.137	0.733	7.30E-03	2.49E-02	291
3DL1	1180	cohortMinusGroup2	IBS	G/G	G/C	1484	390	42	23	2.080	1.240	3.500	7.65E-03	2.50E-02	292
3DL1	1180	cohortMinusGroup2	TSI	G/G	G/C	1484	390	42	23	2.080	1.240	3.500	7.65E-03	2.50E-02	292
2DL4	395	cohortMinusGroup2	LWK	C/C	C/T	2060	226	92	1	0.099	0.014	0.714	7.93E-03	2.51E-02	293
3DL1	1091	cohortMinusGroup2	FIN	G/G	G/A	1120	183	50	18	2.200	1.260	3.860	8.09E-03	2.52E-02	294
3DP1	774	cohortMinusGroup2	CLM	G/G	G/C	1548	733	75	17	0.479	0.281	0.817	8.10E-03	2.53E-02	295
3DL3	869	cohortMinusGroup2	GWD	A/A	A/C	1867	507	75	36	1.770	1.180	2.670	8.23E-03	2.53E-02	296
2DL4	762	cohortMinusGroup2	YRI	C/C	C/T	1075	943	60	28	0.532	0.337	0.840	8.35E-03	2.54E-02	297
3DL2	497	cohortMinusGroup2	TSI	G/G	G/A	1750	169	89	18	2.090	1.230	3.550	8.89E-03	2.55E-02	298
2DP1	471	cohortMinusGroup2	PEL	A/A	A/G	1701	442	77	7	0.350	0.160	0.764	8.90E-03	2.56E-02	299
3DL1	1021	cohortMinusGroup2	JPT	A/A	A/G	1232	130	45	12	2.530	1.310	4.900	9.02E-03	2.57E-02	300
2DL5	583	cohortMinusGroup2	CHB	G/G	G/A	528	251	22	1	0.096	0.013	0.713	9.05E-03	2.58E-02	301
2DL5	583	cohortMinusGroup2	PUR	G/G	G/A	524	250	26	2	0.161	0.038	0.684	9.06E-03	2.59E-02	302
3DP1	796	cohortMinusGroup2	STU	T/T	T/C	1545	733	80	19	0.501	0.301	0.833	9.07E-03	2.59E-02	303
3DL1	1180	cohortMinusGroup2	FIN	G/G	G/C	1478	388	48	25	1.980	1.210	3.250	9.10E-03	2.60E-02	304
2DP1	1313	cohortMinusGroup2	TSI	A/A	A/C	1379	525	50	35	1.840	1.180	2.870	9.19E-03	2.61E-02	305
3DP1	774	cohortMinusGroup2	STU	G/G	G/C	1543	731	80	19	0.501	0.301	0.833	9.23E-03	2.62E-02	306
3DL3	502	cohortMinusGroup2	PEL	G/G	G/A	637	1099	10	44	2.550	1.270	5.100	9.49E-03	2.63E-02	307
3DP1	479	cohortMinusGroup2	GWD	A/A	A/C	1833	525	100	13	0.454	0.253	0.816	9.58E-03	2.64E-02	308
3DL1	496	cohortMinusGroup2	MSL	C/C	C/A	1737	119	72	12	2.430	1.280	4.600	9.58E-03	2.65E-02	309
2DP1	1313	cohortMinusGroup2	PEL	A/A	A/C	1371	551	58	9	0.386	0.190	0.784	9.67E-03	2.65E-02	310
3DL3	804	cohortMinusGroup2	TSI	G/G	G/A	1450	660	54	43	1.750	1.160	2.640	9.71E-03	2.66E-02	311
3DL3	804	cohortMinusGroup2	MSL	G/G	G/A	1463	668	41	35	1.870	1.180	2.960	9.92E-03	2.67E-02	312
2DL4	1023	cohortMinusGroup2	ASW	G/G	G/A	1499	664	56	10	0.403	0.204	0.795	1.01E-02	2.68E-02	313
3DL1	1026	cohortMinusGroup2	TSI	G/G	G/C	1190	179	35	13	2.470	1.280	4.760	1.01E-02	2.69E-02	314
3DP1	774	cohortMinusGroup2	ESN	G/G	G/C	1583	716	40	34	1.880	1.180	2.990	1.02E-02	2.70E-02	315
2DP1	448	cohortMinusGroup2	CHB	G/G	G/C	635	834	3	19	4.820	1.420	16.400	1.02E-02	2.71E-02	316
2DP1	766	cohortMinusGroup2	TSI	G/G	G/C	1333	318	34	18	2.220	1.240	3.980	1.04E-02	2.71E-02	317
3DL3	969	cohortMinusGroup2	CEU	C/C	C/T	1560	393	78	7	0.356	0.163	0.778	1.04E-02	2.72E-02	318
2DL4	762	cohortMinusGroup2	BEB	C/C	C/T	1105	924	30	47	1.870	1.170	2.980	1.04E-02	2.73E-02	319
2DL4	480	cohortMinusGroup2	PUR	G/G	G/A	1624	340	73	28	1.830	1.170	2.870	1.13E-02	2.74E-02	320
3DL1	607	cohortMinusGroup2	TSI	C/C	C/T	1523	476	45	27	1.920	1.180	3.130	1.17E-02	2.75E-02	321
3DL2	893	cohortMinusGroup2	ITU	G/G	G/A	2127	287	80	21	1.950	1.190	3.200	1.18E-02	2.76E-02	322

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	408	cohortMinusGroup2	PUR	G/G	G/A	1628	612	62	40	1.720	1.140	2.590	1.21E-02	2.77E-02	323
3DL1	1303	cohortMinusGroup2	PUR	A/A	A/G	1092	111	92	1	0.107	0.015	0.775	1.23E-02	2.77E-02	324
2DP1	1219	cohortMinusGroup2	LWK	A/A	A/G	619	30	85	11	2.670	1.290	5.520	1.24E-02	2.78E-02	325
3DL3	961	cohortMinusGroup2	IBS	C/C	C/A	956	338	43	29	1.910	1.170	3.110	1.24E-02	2.79E-02	326
3DL1	732	cohortMinusGroup2	CHS	T/T	T/C	386	250	7	15	3.310	1.330	8.230	1.26E-02	2.80E-02	327
3DL2	893	cohortMinusGroup2	CHB	G/G	G/A	2108	304	99	4	0.280	0.102	0.766	1.28E-02	2.81E-02	328
3DL3	447	cohortMinusGroup2	CDX	G/G	G/T	2136	287	76	20	1.960	1.180	3.260	1.31E-02	2.82E-02	329
3DL2	456	cohortMinusGroup2	CHB	C/C	C/T	2111	303	99	4	0.281	0.103	0.769	1.32E-02	2.83E-02	330
3DL2	474	cohortMinusGroup2	GIH	G/G	G/T	1463	722	83	22	0.537	0.333	0.866	1.32E-02	2.83E-02	331
3DL3	961	cohortMinusGroup2	GWD	C/C	C/T	280	91	86	12	0.429	0.224	0.821	1.33E-02	2.84E-02	332
3DL3	906	cohortMinusGroup2	PEL	C/C	C/T	1649	508	72	9	0.406	0.202	0.818	1.34E-02	2.85E-02	333
2DL4	625	cohortMinusGroup2	KHV	C/C	C/G	846	879	25	49	1.890	1.160	3.090	1.42E-02	2.86E-02	334
3DL3	699	cohortMinusGroup2	PUR	G/G	G/A	742	79	103	2	0.182	0.044	0.752	1.42E-02	2.87E-02	335
3DL1	732	cohortMinusGroup2	FIN	T/T	T/C	383	247	10	18	2.790	1.270	6.140	1.43E-02	2.88E-02	336
3DL1	1180	cohortMinusGroup2	GBR	G/G	G/C	1484	391	42	22	1.990	1.170	3.370	1.46E-02	2.89E-02	337
3DP1	774	cohortMinusGroup2	GBR	G/G	G/C	1575	712	48	38	1.750	1.130	2.700	1.48E-02	2.89E-02	338
3DP1	774	cohortMinusGroup2	LWK	G/G	G/C	1575	712	48	38	1.750	1.130	2.700	1.48E-02	2.89E-02	338
3DL3	502	cohortMinusGroup2	KHV	G/G	G/A	635	1096	12	47	2.270	1.200	4.310	1.50E-02	2.90E-02	339
3DL1	1180	cohortMinusGroup2	CHB	G/G	G/C	1453	405	73	8	0.393	0.188	0.822	1.52E-02	2.91E-02	340
2DP1	816	cohortMinusGroup2	TSI	G/G	G/A	656	60	99	1	0.110	0.015	0.803	1.53E-02	2.92E-02	341
3DP1	796	cohortMinusGroup2	CLM	T/T	T/C	1551	734	74	18	0.514	0.305	0.867	1.53E-02	2.93E-02	342
3DL1	1021	cohortMinusGroup2	KHV	A/A	A/G	1223	129	54	13	2.280	1.210	4.290	1.56E-02	2.94E-02	343
3DL3	777	cohortMinusGroup2	YRI	A/A	A/G	1592	554	91	16	0.505	0.294	0.867	1.60E-02	2.95E-02	344
3DL3	961	cohortMinusGroup2	TSI	C/C	C/A	969	345	30	22	2.060	1.170	3.620	1.63E-02	2.95E-02	345
3DP1	774	cohortMinusGroup2	ASW	G/G	G/C	1591	722	32	28	1.930	1.150	3.230	1.64E-02	2.96E-02	346
3DL1	732	cohortMinusGroup2	ESN	T/T	T/C	358	255	35	10	0.401	0.195	0.825	1.64E-02	2.97E-02	347
2DP1	1313	cohortMinusGroup2	ACB	A/A	A/C	1390	532	39	28	1.880	1.150	3.090	1.70E-02	2.98E-02	348
2DL5	583	cohortMinusGroup2	YRI	G/G	G/A	523	249	27	3	0.233	0.070	0.775	1.75E-02	2.99E-02	349
3DL3	971	cohortMinusGroup2	MXL	T/T	T/C	1672	344	51	2	0.191	0.046	0.788	1.77E-02	3.00E-02	350
2DL5	517	cohortMinusGroup2	PUR	A/A	A/G	597	251	26	2	0.183	0.043	0.777	1.79E-02	3.01E-02	351
3DL3	621	cohortMinusGroup2	CHS	G/G	G/A	1703	206	87	20	1.900	1.140	3.150	1.81E-02	3.01E-02	352
3DL2	497	cohortMinusGroup2	ESN	G/G	G/A	1742	185	97	2	0.194	0.047	0.793	1.81E-02	3.02E-02	353
2DL5	517	cohortMinusGroup2	PJL	A/A	A/G	594	230	29	23	2.050	1.160	3.620	1.83E-02	3.03E-02	354
3DL1	607	cohortMinusGroup2	LWK	C/C	C/T	1490	491	78	12	0.467	0.252	0.865	1.87E-02	3.04E-02	355
3DL3	971	cohortMinusGroup2	TSI	T/T	T/C	1663	324	60	22	1.880	1.140	3.110	1.87E-02	3.05E-02	356
2DL4	412	cohortMinusGroup2	MSL	G/G	G/A	966	991	17	36	2.060	1.150	3.690	1.90E-02	3.06E-02	357
3DL3	738	cohortMinusGroup2	GWD	C/C	C/T	837	172	80	29	1.760	1.120	2.780	1.94E-02	3.07E-02	358
2DL5	583	cohortMinusGroup2	GBR	G/G	G/A	541	240	9	12	3.010	1.250	7.240	1.95E-02	3.07E-02	359
3DL2	497	cohortMinusGroup2	CEU	G/G	G/A	1757	171	82	16	2.000	1.140	3.500	2.09E-02	3.08E-02	360
3DL1	496	cohortMinusGroup2	PEL	C/C	C/A	1725	131	84	0	0.000	0.000	NaN	2.15E-02	3.09E-02	361
3DL3	969	cohortMinusGroup2	FIN	C/C	C/T	1555	391	83	9	0.431	0.215	0.865	2.15E-02	3.10E-02	362
3DL1	1180	cohortMinusGroup2	PJL	G/G	G/C	1461	406	65	7	0.388	0.177	0.853	2.15E-02	3.11E-02	363
3DP1	774	cohortMinusGroup2	CHS	G/G	G/C	1540	728	83	22	0.561	0.348	0.905	2.18E-02	3.12E-02	364
2DP1	1313	cohortMinusGroup2	GIH	A/A	A/C	1389	532	40	28	1.830	1.120	3.000	2.19E-02	3.13E-02	365
3DL1	607	cohortMinusGroup2	PJL	C/C	C/T	1504	494	64	9	0.428	0.211	0.866	2.22E-02	3.13E-02	366
3DL3	906	cohortMinusGroup2	ESN	C/C	C/T	1635	504	86	13	0.490	0.271	0.885	2.23E-02	3.14E-02	367
2DL4	625	cohortMinusGroup2	MSL	C/C	C/G	854	892	17	36	2.030	1.130	3.640	2.28E-02	3.15E-02	368
2DL3	953	cohortMinusGroup2	TSI	G/G	G/A	1342	483	37	25	1.880	1.120	3.160	2.30E-02	3.16E-02	369
3DL1	1303	cohortMinusGroup2	PEL	A/A	A/G	1103	111	81	1	0.123	0.017	0.892	2.33E-02	3.17E-02	370
2DL4	480	cohortMinusGroup2	ITU	G/G	G/A	1605	359	92	9	0.437	0.218	0.875	2.35E-02	3.18E-02	371
3DL3	906	cohortMinusGroup2	PJL	C/C	C/T	1659	486	62	31	1.710	1.100	2.660	2.35E-02	3.19E-02	372
2DP1	766	cohortMinusGroup2	CDX	G/G	G/C	1297	329	70	7	0.394	0.179	0.865	2.42E-02	3.19E-02	373
2DP1	471	cohortMinusGroup2	KHV	A/A	A/G	1688	438	90	11	0.471	0.250	0.889	2.45E-02	3.20E-02	374
2DP1	1000	cohortMinusGroup2	GWD	A/A	A/G	286	21	50	10	2.720	1.210	6.120	2.45E-02	3.21E-02	375
3DL1	1194	cohortMinusGroup2	ESN	C/C	C/T	1862	176	79	15	2.010	1.130	3.570	2.47E-02	3.22E-02	376
3DL2	474	cohortMinusGroup2	ASW	G/G	G/T	1494	732	52	12	0.471	0.250	0.888	2.48E-02	3.23E-02	377
3DL3	699	cohortMinusGroup2	ESN	G/G	G/A	762	66	83	15	2.090	1.140	3.830	2.50E-02	3.24E-02	378
3DL3	621	cohortMinusGroup2	CDX	G/G	G/A	1712	208	78	18	1.900	1.120	3.240	2.55E-02	3.25E-02	379
3DL2	456	cohortMinusGroup2	ITU	C/C	C/T	2129	287	81	20	1.830	1.100	3.030	2.58E-02	3.25E-02	380
2DP1	766	cohortMinusGroup2	KHV	G/G	G/C	1292	328	75	8	0.420	0.201	0.879	2.59E-02	3.26E-02	381
3DL3	869	cohortMinusGroup2	GBR	A/A	A/C	1880	514	62	29	1.710	1.090	2.690	2.60E-02	3.27E-02	382
3DP1	796	cohortMinusGroup2	ASW	T/T	T/C	1593	725	32	27	1.850	1.100	3.110	2.64E-02	3.28E-02	383
2DL4	625	cohortMinusGroup2	STU	C/C	C/G	814	890	57	38	0.610	0.400	0.930	2.67E-02	3.29E-02	384
2DL4	412	cohortMinusGroup2	STU	G/G	G/A	925	989	58	38	0.613	0.403	0.932	2.73E-02	3.30E-02	385
3DP1	796	cohortMinusGroup2	CHS	T/T	T/C	1541	729	84	23	0.579	0.362	0.926	2.77E-02	3.31E-02	386
2DL5	583	cohortMinusGroup2	LWK	G/G	G/A	525	249	25	3	0.253	0.076	0.846	2.81E-02	3.31E-02	387
2DL4	762	cohortMinusGroup2	LWK	C/C	C/T	1083	945	52	26	0.573	0.355	0.925	2.85E-02	3.32E-02	388
3DP1	796	cohortMinusGroup2	JPT	T/T	T/C	1544	730	81	22	0.574	0.355	0.927	2.89E-02	3.33E-02	389
2DL4	625	cohortMinusGroup2	PJL	C/C	C/G	819	894	52	34	0.599	0.385	0.932	2.92E-02	3.34E-02	390
3DL3	906	cohortMinusGroup2	GBR	C/C	C/T	1663	488	58	29	1.700	1.080	2.680	2.93E-02	3.35E-02	391
2DP1	1269	cohortMinusGroup2	GIH	A/A	A/G	1378	68	88	10	2.300	1.140	4.620	3.01E-02	3.36E-02	392
3DP1	796	cohortMinusGroup2	GIH	T/T	T/C	1547	731	78	21	0.570	0.349	0.930	3.02E-02	3.37E-02	393
3DL3	1042	cohortMinusGroup2	ITU	G/G	G/C	966	146	51	1	0.130	0.018	0.948	3.04E-02	3.37E-02	394
3DP1	774	cohortMinusGroup2	KHV	G/G	G/C	1545	729	78	21	0.571	0.350	0.932	3.06E-02	3.38E-02	395
2DL4	395	cohortMinusGroup2	CHS	C/C	C/T	2063	210	89	17	1.880	1.100	3.220	3.08E-02	3.39E-02	396
3DL3	621	cohortMinusGroup2	PEL	G/G	G/A	1707	223	83	3	0.277	0.087	0.884	3.19E-02	3.40E-02	397
3DL1	607	cohortMinusGroup2	CLM	C/C	C/T	1523	478	45	25	1.770	1.070	2.920	3.35E-02	3.41E-02	398
2DL4	412	cohortMinusGroup2	ACB	G/G	G/A	958	982	25	45	1.760	1.070	2.890	3.35E-02	3.42E-02	399
2DL4	1023	cohortMinusGroup2	GIH	G/G	G/A	1473	653	82	21	0.578	0.355	0.942	3.41E-02	3.43E-02	400
2DL5	517	cohortMinusGroup2	YRI	A/A	A/G	596	250	27	3	0.265	0.080	0.882	3.43E-02	3.43E-02	401
3DL1	607	cohortMinusGroup2	BEB	C/C	C/T	1503	493	65	10	0.469	0.239	0.920	3.43E-02	3.44E-02	402
3DL1	1180	cohortMinusGroup2	GIH	G/G	G/C	1465	406	61	7	0.414	0.188	0.912	3.52E-02	3.45E-02	403
3DL1	1026	cohortMinusGroup2	GBR	G/G	G/C	1184	179	41	13	2.100	1.100	4.000	3.56E-02	3.46E-02	404
2DL5	583	cohortMinusGroup2	PJL	G/G	G/A	521	228	29	24	1.890	1.080	3.320	3.60E-02	3.47E-02	405
2DL4	762	cohortMinusGroup2	GIH	C/C	C/T	1103	926	32	45	1.680	1.060	2.670	3.61E-02	3.48E-02	406
3DL3	961	cohortMinusGroup2	CEU	C/C	C/A	964	344	35	23	1.840	1.070	3.160	3.63E-02	3.49E-02	407
2DL5	517	cohortMinusGroup2	GBR	A/A	A/G	611	241	12	12	2.540	1.130	5.730	3.69E-02	3.49E-02	408
2DL4	412	cohortMinusGroup2	PJL	G/G	G/A	931	993	52	34	0.613	0.394	0.953	3.74E-02	3.50E-02	409
3DL3	408	cohortMinusGroup2	ASW	G/G	G/A	1653	627	37	25	1.780	1.060	2.980	3.76E-02	3.51E-02	410
3DL3	971	cohortMinusGroup2	CLM	T/T	T/C	1670	327	53	19	1.830	1.070	3.130	3.79E-02	3.52E-02	411
3DL3	621	cohortMinusGroup2	ACB	G/G	G/A	1698	222	92	4	0.333	0.121	0.915	3.79E-02	3.53E-02	412
3DP1	479	cohortMinusGroup2	PJL	A/A	A/C	1850	526	83	12	0.508	0.275	0.938	3.80E-02	3.54E-02	413
2DL4	886	cohortMinusGroup2	TSI	C/C	C/G	678	51	97	1	0.137	0.019	1.000	3.88E-02	3.55E-02	414
2DP1	1062	cohortMinusGroup2	FIN	C/C	C/T	1000	54	82	10	2.260	1.110	4.600	3.89E-02	3.55E-02	415
3DL3	971	cohortMinusGroup2	FIN	T/T	T/C	1650	340	73	6	0.399	0.172	0.925	3.91E-02	3.56E-02	416
3DL1	607	cohortMinusGroup2	STU	C/C	C/T	1504	493	64	10	0.477	0.243	0.936	3.91E-02	3.57E-02	417
3DL3	804	cohortMinusGroup2	GWD	G/G	G/A	1447	662	57	41	1.570	1.040	2.370	3.95E-02	3.58E-02	418
3DL1	1303	cohortMinusGroup2	LWK	A/A	A/G	1112	99	72	13	2.030	1.090	3.790	3.96E-02	3.59E-02	419
2DP1	522	cohortMinusGroup2	BEB	T/T	T/C	1666	512	47	25	1.730	1.050	2.840	3.98E-02	3.60E-02	420
3DP1	796	cohortMinusGroup2	GBR	T/T	T/C	1576	716	49	36	1.620	1.040	2.510	4.09E-02	3.60E-02	421
2DL4	412	cohortMinusGroup2	KHV	G/G	G/A	952	975	31	52	1.640	1.040	2.580	4.15E-02	3.61E-02	422
2DL4	762	cohortMinusGroup2	CDX	C/C	C/T	1076	939	59	32	0.622	0.401	0.965	4.20E-02	3.62E-02	423
2DL4	625	cohortMinusGroup2	ITU	C/C	C/G	817	891	54	37	0.628	0.409	0.964	4.21E-02	3.63E-02	424
2DL5	517	cohortMinusGroup2	PEL	A/A	A/G	601	251	22	2	0.218	0.051	0.934	4.30E-02	3.64E-02	425
2DP1	448	cohortMinusGroup2	MXL	G/G	G/C	629	826	9	27	2.280	1.060	4.880	4.41E-02	3.65E-02	426
2DL4	1023	cohortMinusGroup2	FIN	G/G	G/A	1500	637	55	37	1.580	1.030	2.420	4.42E-02	3.66E-02	427
2DL5	583	cohortMinusGroup2	CHS	G/G	G/A	527	249	23	3	0.276	0.082	0.928	4.49E-02	3.66E-02	428
3DL3	961	cohortMinusGroup2	YRI	C/C	C/T	289	91	77	12	0.495	0.258	0.950	4.50E-02	3.67E-02	429
3DP1	774	cohortMinusGroup2	GIH	G/G	G/C	1545	728	78	22	0.599	0.370	0.969	4.54E-02	3.68E-02	430

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DP1	448	cohortMinusGroup2	CDX	G/G	G/C	630	828	8	25	2.380	1.070	5.310	4.55E-02	3.69E-02	431
3DL2	497	cohortMinusGroup2	MSL	G/G	G/A	1758	185	81	2	0.235	0.057	0.964	4.57E-02	3.70E-02	432
2DP1	491	cohortMinusGroup2	LWK	T/T	T/C	618	31	87	10	2.290	1.080	4.830	4.64E-02	3.71E-02	433
3DL2	394	cohortMinusGroup2	CHB	C/C	C/A	2195	222	87	16	1.820	1.050	3.160	4.71E-02	3.72E-02	434
2DL4	1019	cohortMinusGroup2	PUR	C/C	C/T	853	57	103	1	0.145	0.020	1.060	4.74E-02	3.72E-02	435
3DL3	455	cohortMinusGroup2	GBR	G/G	G/A	1378	78	82	10	2.150	1.070	4.310	4.74E-02	3.73E-02	436
3DL1	732	cohortMinusGroup2	MSL	T/T	T/C	364	256	29	9	0.441	0.205	0.947	4.80E-02	3.74E-02	437
2DL4	762	cohortMinusGroup2	PUR	C/C	C/T	1102	926	33	45	1.620	1.030	2.560	4.81E-02	3.75E-02	438
3DL1	1303	cohortMinusGroup2	ASW	A/A	A/G	1133	102	51	10	2.180	1.070	4.420	4.84E-02	3.76E-02	439
3DL3	621	cohortMinusGroup2	MXL	G/G	G/A	1725	224	65	2	0.237	0.058	0.975	4.84E-02	3.77E-02	440
2DP1	471	cohortMinusGroup2	ITU	A/A	A/G	1714	423	64	26	1.650	1.030	2.630	4.86E-02	3.78E-02	441
2DP1	448	cohortMinusGroup2	GBR	G/G	G/C	602	824	36	29	0.589	0.357	0.971	4.88E-02	3.78E-02	442
3DL3	869	cohortMinusGroup2	ESN	A/A	A/C	1879	515	63	28	1.620	1.030	2.560	4.90E-02	3.79E-02	443
3DL3	906	cohortMinusGroup2	CLM	C/C	C/T	1660	488	61	29	1.620	1.030	2.550	4.91E-02	3.80E-02	444
3DL2	456	cohortMinusGroup2	STU	C/C	C/T	2129	288	81	19	1.730	1.030	2.890	4.94E-02	3.81E-02	445
2DL3	953	cohortMinusGroup2	GBR	G/G	G/A	1347	487	32	21	1.820	1.040	3.190	5.03E-02	3.82E-02	446
2DL5	583	cohortMinusGroup2	PEL	G/G	G/A	531	250	19	2	0.224	0.052	0.969	5.09E-02	3.83E-02	447
3DL2	497	cohortMinusGroup2	FIN	G/G	G/A	1756	172	83	15	1.850	1.040	3.280	5.10E-02	3.84E-02	448
3DL3	869	cohortMinusGroup2	JPT	A/A	A/C	1853	529	89	14	0.551	0.311	0.976	5.12E-02	3.84E-02	449
3DP1	796	cohortMinusGroup2	KHV	T/T	T/C	1548	730	77	22	0.606	0.374	0.981	5.15E-02	3.85E-02	450
3DL2	893	cohortMinusGroup2	STU	G/G	G/A	2126	289	81	19	1.730	1.030	2.890	5.16E-02	3.86E-02	451
3DL1	1194	cohortMinusGroup2	YRI	C/C	C/T	1855	176	86	15	1.840	1.040	3.250	5.16E-02	3.87E-02	452
2DL3	953	cohortMinusGroup2	IBS	G/G	G/A	1332	480	47	28	1.650	1.020	2.660	5.22E-02	3.88E-02	453
2DL4	1023	cohortMinusGroup2	GBR	G/G	G/A	1501	638	54	36	1.570	1.020	2.420	5.22E-02	3.89E-02	454
3DL3	621	cohortMinusGroup2	CHB	G/G	G/A	1692	221	98	5	0.391	0.157	0.971	5.25E-02	3.90E-02	455
3DL1	1180	cohortMinusGroup2	ESN	G/G	G/C	1463	386	63	27	1.620	1.020	2.580	5.33E-02	3.90E-02	456
3DL3	699	cohortMinusGroup2	ASW	G/G	G/A	780	80	65	1	0.150	0.021	1.100	5.34E-02	3.91E-02	457
2DP1	1313	cohortMinusGroup2	ASW	A/A	A/C	1397	538	32	22	1.790	1.030	3.110	5.34E-02	3.92E-02	458
3DL1	1091	cohortMinusGroup2	PJL	G/G	G/A	1106	197	64	4	0.351	0.126	0.975	5.44E-02	3.93E-02	459
2DP1	448	cohortMinusGroup2	CLM	G/G	G/C	609	831	29	22	0.556	0.316	0.977	5.45E-02	3.94E-02	460
2DL4	762	cohortMinusGroup2	PEL	C/C	C/T	1083	943	52	28	0.618	0.387	0.986	5.52E-02	3.95E-02	461
3DL3	971	cohortMinusGroup2	YRI	T/T	T/C	1647	339	76	7	0.447	0.204	0.978	5.54E-02	3.96E-02	462
3DL1	496	cohortMinusGroup2	GWD	C/C	C/A	1710	118	99	13	1.900	1.030	3.490	5.55E-02	3.96E-02	463
3DL3	971	cohortMinusGroup2	ASW	T/T	T/C	1675	343	48	3	0.305	0.095	0.985	5.61E-02	3.97E-02	464
3DL3	699	cohortMinusGroup2	MXL	G/G	G/A	781	80	64	1	0.153	0.021	1.120	5.67E-02	3.98E-02	465
3DL3	738	cohortMinusGroup2	MSL	C/C	C/T	855	179	62	22	1.690	1.010	2.820	5.87E-02	3.99E-02	466
2DP1	522	cohortMinusGroup2	YRI	T/T	T/C	1651	507	62	30	1.580	1.010	2.470	5.96E-02	4.00E-02	467
3DL3	408	cohortMinusGroup2	ESN	G/G	G/A	1630	617	60	35	1.540	1.000	2.360	5.99E-02	4.01E-02	468
3DL1	607	cohortMinusGroup2	GWD	C/C	C/T	1492	467	76	36	1.510	1.000	2.280	6.01E-02	4.02E-02	469
3DL3	1042	cohortMinusGroup2	STU	G/G	G/C	974	146	43	1	0.155	0.021	1.130	6.05E-02	4.02E-02	470
3DL3	692	cohortMinusGroup2	GWD	G/G	G/A	737	168	80	29	1.590	1.010	2.510	6.06E-02	4.03E-02	471
3DP1	774	cohortMinusGroup2	MSL	G/G	G/C	1579	718	44	32	1.600	1.010	2.540	6.07E-02	4.04E-02	472
3DP1	479	cohortMinusGroup2	ACB	A/A	A/C	1850	525	83	13	0.552	0.305	0.998	6.19E-02	4.05E-02	473
3DL1	1180	cohortMinusGroup2	BEB	G/G	G/C	1460	404	66	9	0.493	0.244	0.998	6.25E-02	4.06E-02	474
3DP1	796	cohortMinusGroup2	TSI	T/T	T/C	1563	710	62	42	1.490	0.997	2.230	6.38E-02	4.07E-02	475
3DL3	869	cohortMinusGroup2	MXL	A/A	A/C	1883	535	59	8	0.477	0.227	1.000	6.57E-02	4.08E-02	476
2DL4	412	cohortMinusGroup2	YRI	G/G	G/A	959	986	24	41	1.660	0.995	2.770	6.60E-02	4.08E-02	477
3DL1	732	cohortMinusGroup2	JPT	T/T	T/C	385	252	8	13	2.480	1.010	6.070	6.75E-02	4.09E-02	478
2DP1	448	cohortMinusGroup2	PJL	G/G	G/C	604	825	34	28	0.603	0.362	1.010	6.76E-02	4.10E-02	479
3DL3	699	cohortMinusGroup2	CLM	G/G	G/A	754	78	91	3	0.319	0.099	1.030	6.89E-02	4.11E-02	480
3DL3	502	cohortMinusGroup2	CDX	G/G	G/A	634	1101	13	42	1.860	0.991	3.490	6.89E-02	4.12E-02	481
3DL3	408	cohortMinusGroup2	LWK	G/G	G/A	1629	617	61	35	1.510	0.986	2.310	7.07E-02	4.13E-02	482
3DL1	1091	cohortMinusGroup2	GIH	G/G	G/A	1109	197	61	4	0.369	0.133	1.030	7.08E-02	4.14E-02	483
3DL1	1091	cohortMinusGroup2	GBR	G/G	G/A	1129	188	41	13	1.900	0.999	3.610	7.20E-02	4.14E-02	484
3DL3	869	cohortMinusGroup2	BEB	A/A	A/C	1870	532	72	11	0.537	0.283	1.020	7.30E-02	4.15E-02	485
3DL1	607	cohortMinusGroup2	ITU	C/C	C/T	1501	491	67	12	0.548	0.294	1.020	7.36E-02	4.16E-02	486
3DL1	1026	cohortMinusGroup2	PJL	G/G	G/C	1159	188	66	4	0.374	0.135	1.040	7.42E-02	4.17E-02	487
2DL5	517	cohortMinusGroup2	BEB	A/A	A/G	602	237	21	16	1.940	0.995	3.780	7.44E-02	4.18E-02	488
2DP1	899	cohortMinusGroup2	ACB	C/C	C/A	326	34	38	9	2.270	1.010	5.090	7.45E-02	4.19E-02	489
3DL3	777	cohortMinusGroup2	MSL	A/A	A/G	1627	541	56	29	1.560	0.986	2.470	7.52E-02	4.20E-02	490
3DL1	1091	cohortMinusGroup2	TSI	G/G	G/A	1133	189	37	12	1.940	0.994	3.790	7.59E-02	4.20E-02	491
3DL3	969	cohortMinusGroup2	PUR	C/C	C/T	1562	390	76	10	0.527	0.270	1.030	7.68E-02	4.21E-02	492
3DL3	447	cohortMinusGroup2	MXL	G/G	G/T	2148	304	64	3	0.331	0.103	1.060	7.74E-02	4.22E-02	493
2DL4	395	cohortMinusGroup2	ESN	C/C	C/T	2068	212	84	15	1.740	0.987	3.070	7.74E-02	4.23E-02	494
2DP1	766	cohortMinusGroup2	ASW	G/G	G/C	1345	325	22	11	2.070	0.994	4.310	7.81E-02	4.24E-02	495
2DL5	517	cohortMinusGroup2	CHS	A/A	A/G	600	250	23	3	0.313	0.093	1.050	7.82E-02	4.25E-02	496
3DL2	497	cohortMinusGroup2	CLM	G/G	G/A	1759	173	80	14	1.780	0.988	3.210	7.84E-02	4.26E-02	497
3DL1	496	cohortMinusGroup2	CHB	C/C	C/A	1710	129	99	2	0.268	0.065	1.100	7.85E-02	4.26E-02	498
3DL2	893	cohortMinusGroup2	CDX	G/G	G/A	2114	302	93	6	0.452	0.196	1.040	7.85E-02	4.27E-02	499
2DL3	953	cohortMinusGroup2	ESN	G/G	G/A	1332	481	47	27	1.590	0.979	2.580	7.86E-02	4.28E-02	500
3DL1	1091	cohortMinusGroup2	LWK	G/G	G/A	1136	200	34	1	0.167	0.023	1.230	7.88E-02	4.29E-02	501
3DL1	607	cohortMinusGroup2	ESN	C/C	C/T	1490	488	78	15	0.587	0.335	1.030	7.95E-02	4.30E-02	502
3DL2	497	cohortMinusGroup2	STU	G/G	G/A	1740	183	99	4	0.384	0.140	1.060	8.02E-02	4.31E-02	503
3DL3	971	cohortMinusGroup2	GWD	T/T	T/C	1632	336	91	10	0.534	0.275	1.040	8.06E-02	4.32E-02	504
3DL2	456	cohortMinusGroup2	CDX	C/C	C/T	2117	301	93	6	0.454	0.197	1.050	8.07E-02	4.32E-02	505
3DL3	447	cohortMinusGroup2	ESN	G/G	G/T	2119	301	93	6	0.454	0.197	1.050	8.11E-02	4.33E-02	506
2DP1	1219	cohortMinusGroup2	CLM	A/A	A/G	613	40	91	1	0.168	0.023	1.240	8.19E-02	4.34E-02	507
2DL3	953	cohortMinusGroup2	PJL	G/G	G/A	1328	498	51	10	0.523	0.263	1.040	8.23E-02	4.35E-02	508
2DP1	491	cohortMinusGroup2	CLM	T/T	T/C	614	40	91	1	0.169	0.023	1.240	8.23E-02	4.36E-02	509
3DL1	1194	cohortMinusGroup2	LWK	C/C	C/T	1868	189	73	2	0.271	0.066	1.110	8.24E-02	4.37E-02	510
3DL2	394	cohortMinusGroup2	PEL	C/C	C/A	2199	235	83	3	0.338	0.106	1.080	8.29E-02	4.38E-02	511
2DP1	522	cohortMinusGroup2	ESN	T/T	T/C	1654	509	59	28	1.540	0.972	2.440	8.40E-02	4.38E-02	512
2DL4	886	cohortMinusGroup2	LWK	C/C	C/G	705	43	70	9	2.110	0.987	4.510	8.51E-02	4.39E-02	513
3DP1	479	cohortMinusGroup2	ASW	A/A	A/C	1876	530	57	8	0.497	0.236	1.050	8.52E-02	4.40E-02	514
3DL1	496	cohortMinusGroup2	TSI	C/C	C/A	1712	129	97	2	0.274	0.067	1.120	8.53E-02	4.41E-02	515
3DL3	869	cohortMinusGroup2	MSL	A/A	A/C	1884	518	58	25	1.570	0.973	2.530	8.56E-02	4.42E-02	516
3DL1	1194	cohortMinusGroup2	JPT	C/C	C/T	1865	178	76	13	1.790	0.975	3.290	8.61E-02	4.43E-02	517
2DL4	412	cohortMinusGroup2	ITU	G/G	G/A	930	989	53	38	0.674	0.440	1.030	8.61E-02	4.44E-02	518
3DL1	1194	cohortMinusGroup2	CHS	C/C	C/T	1857	177	84	14	1.750	0.974	3.150	8.74E-02	4.44E-02	519
2DL4	886	cohortMinusGroup2	PUR	C/C	C/G	675	50	100	2	0.270	0.065	1.130	8.82E-02	4.45E-02	520
3DL3	447	cohortMinusGroup2	ASW	G/G	G/T	2159	294	53	13	1.800	0.970	3.340	8.93E-02	4.46E-02	521
3DL3	1042	cohortMinusGroup2	BEB	G/G	G/C	968	145	49	2	0.272	0.065	1.130	8.93E-02	4.47E-02	522
3DL3	777	cohortMinusGroup2	PJL	A/A	A/G	1621	539	62	31	1.500	0.964	2.330	8.95E-02	4.48E-02	523
2DP1	1313	cohortMinusGroup2	ESN	A/A	A/C	1376	529	53	31	1.520	0.965	2.390	8.95E-02	4.49E-02	524
2DL4	625	cohortMinusGroup2	BEB	C/C	C/G	827	897	44	31	0.650	0.407	1.040	8.98E-02	4.50E-02	525
3DL1	1026	cohortMinusGroup2	PUR	G/G	G/C	1163	176	62	16	1.710	0.965	3.030	9.33E-02	4.50E-02	526
3DL3	869	cohortMinusGroup2	CEU	A/A	A/C	1859	529	83	14	0.593	0.334	1.050	9.33E-02	4.51E-02	527
2DL4	762	cohortMinusGroup2	GWD	C/C	C/T	1069	931	66	40	0.696	0.465	1.040	9.41E-02	4.52E-02	528
2DP1	899	cohortMinusGroup2	PJL	C/C	C/A	308	41	56	2	0.268	0.063	1.140	9.42E-02	4.53E-02	529
3DL3	906	cohortMinusGroup2	GIH	C/C	C/T	1650	486	71	31	1.480	0.959	2.280	9.53E-02	4.54E-02	530
3DL1	732	cohortMinusGroup2	KHV	T/T	T/C	381	249	12	16	2.040	0.949	4.390	9.63E-02	4.55E-02	531
3DL3	869	cohortMinusGroup2	PUR	A/A	A/C	1855	528	87	15	0.606	0.347	1.060	9.67E-02	4.56E-02	532
3DL1	1180	cohortMinusGroup2	PEL	G/G	G/C	1464	404	62	9	0.526	0.259	1.070	9.68E-02	4.56E-02	533
3DL1	1303	cohortMinusGroup2	MSL	A/A	A/G	1119	101	65	11	1.870	0.956	3.660	9.80E-02	4.57E-02	534
3DL3	447	cohortMinusGroup2	ACB	G/G	G/T	2122	301	90	6	0.470	0.204	1.080	9.81E-02	4.58E-02	535
3DL3	447	cohortMinusGroup2	PJL	G/G	G/T	2122	301	90	6	0.470	0.204	1.080	9.81E-02	4.58E-02	535
3DL3	969	cohortMinusGroup2	BEB	C/C	C/T	1575	392	63	8	0.510	0.242	1.070	9.83E-02	4.59E-02	536
2DP1	1313	cohortMinusGroup2	BEB	A/A	A/C	1388	535	41	25	1.580	0.951	2.620	9.95E-02	4.60E-02	537
3DL3	961	cohortMinusGroup2	ITU	C/C	C/A	968	348	31	19	1.700	0.948	3.050	9.96E-02	4.61E-02	538

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DP1	1269	cohortMinusGroup2	LWK	A/A	A/G	1369	77	97	1	0.183	0.025	1.330	1.00E-01	4.62E-02	539
2DL4	480	cohortMinusGroup2	CEU	G/G	G/A	1627	345	70	23	1.550	0.954	2.520	1.00E-01	4.62E-02	540
2DL4	625	cohortMinusGroup2	ACB	C/C	C/G	850	892	21	36	1.630	0.944	2.810	1.01E-01	4.63E-02	541
2DL5	583	cohortMinusGroup2	TSI	G/G	G/A	534	238	16	14	1.960	0.941	4.080	1.02E-01	4.64E-02	542
2DL4	810	cohortMinusGroup2	BEB	A/A	A/AGT	47	44	3	10	3.560	0.919	13.800	1.03E-01	4.65E-02	543
3DL3	971	cohortMinusGroup2	IBS	T/T	T/C	1655	325	68	21	1.570	0.949	2.600	1.03E-01	4.66E-02	544
3DL3	1042	cohortMinusGroup2	ACB	G/G	G/C	970	135	47	12	1.830	0.947	3.540	1.03E-01	4.67E-02	545
3DL3	1042	cohortMinusGroup2	PUR	G/G	G/C	960	144	57	3	0.351	0.108	1.140	1.04E-01	4.68E-02	546
3DL1	1180	cohortMinusGroup2	STU	G/G	G/C	1460	403	66	10	0.549	0.280	1.080	1.04E-01	4.68E-02	547
2DL5	517	cohortMinusGroup2	ITU	A/A	A/G	591	232	32	21	1.670	0.943	2.960	1.04E-01	4.69E-02	548
3DL3	804	cohortMinusGroup2	STU	G/G	G/A	1428	679	76	24	0.664	0.416	1.060	1.06E-01	4.70E-02	549
2DL4	1023	cohortMinusGroup2	MXL	G/G	G/A	1518	649	37	25	1.580	0.943	2.650	1.07E-01	4.71E-02	550
2DP1	522	cohortMinusGroup2	TSI	T/T	T/C	1647	507	66	30	1.480	0.950	2.300	1.07E-01	4.72E-02	551
2DL4	412	cohortMinusGroup2	BEB	G/G	G/A	939	996	44	31	0.664	0.416	1.060	1.08E-01	4.73E-02	552
3DL3	408	cohortMinusGroup2	IBS	G/G	G/A	1624	616	66	36	1.440	0.949	2.180	1.09E-01	4.74E-02	553
3DP1	479	cohortMinusGroup2	PUR	A/A	A/C	1861	509	72	29	1.470	0.945	2.290	1.09E-01	4.74E-02	554
3DL1	1026	cohortMinusGroup2	GIH	G/G	G/C	1164	188	61	4	0.406	0.146	1.130	1.10E-01	4.75E-02	555
3DP1	479	cohortMinusGroup2	CHB	A/A	A/C	1847	523	86	15	0.616	0.353	1.080	1.10E-01	4.76E-02	556
2DP1	471	cohortMinusGroup2	ACB	A/A	A/G	1721	427	57	22	1.560	0.943	2.580	1.12E-01	4.77E-02	557
3DL3	906	cohortMinusGroup2	ASW	C/C	C/T	1666	508	55	9	0.537	0.264	1.090	1.12E-01	4.78E-02	558
3DL3	1042	cohortMinusGroup2	YRI	G/G	G/C	964	134	53	13	1.760	0.935	3.310	1.12E-01	4.79E-02	559
3DP1	774	cohortMinusGroup2	TSI	G/G	G/C	1561	710	62	40	1.420	0.945	2.130	1.14E-01	4.80E-02	560
2DL4	625	cohortMinusGroup2	YRI	C/C	C/G	848	890	23	38	1.570	0.928	2.660	1.16E-01	4.80E-02	561
3DL1	1180	cohortMinusGroup2	CHS	G/G	G/C	1443	399	83	14	0.610	0.343	1.090	1.17E-01	4.81E-02	562
3DL3	502	cohortMinusGroup2	FIN	G/G	G/A	629	1093	18	50	1.600	0.925	2.770	1.18E-01	4.82E-02	563
3DL2	456	cohortMinusGroup2	PUR	C/C	C/T	2126	289	84	18	1.580	0.936	2.670	1.18E-01	4.83E-02	564
3DL1	1091	cohortMinusGroup2	ESN	G/G	G/A	1085	193	85	8	0.529	0.252	1.110	1.19E-01	4.84E-02	565
3DL3	502	cohortMinusGroup2	BEB	G/G	G/A	634	1104	13	39	1.720	0.911	3.250	1.21E-01	4.85E-02	566
2DP1	471	cohortMinusGroup2	CLM	A/A	A/G	1709	439	69	10	0.564	0.288	1.100	1.21E-01	4.85E-02	567
3DL2	893	cohortMinusGroup2	PUR	G/G	G/A	2123	290	84	18	1.570	0.930	2.650	1.22E-01	4.86E-02	568
3DL1	1021	cohortMinusGroup2	CHS	A/A	A/G	1206	129	71	13	1.710	0.921	3.170	1.25E-01	4.87E-02	569
3DL1	732	cohortMinusGroup2	GIH	T/T	T/C	380	262	13	3	0.335	0.095	1.190	1.29E-01	4.88E-02	570
3DL1	496	cohortMinusGroup2	GBR	C/C	C/A	1722	129	87	2	0.307	0.075	1.260	1.29E-01	4.89E-02	571
3DL1	1194	cohortMinusGroup2	GBR	C/C	C/T	1862	188	79	3	0.376	0.118	1.200	1.29E-01	4.90E-02	572
3DP1	774	cohortMinusGroup2	MXL	G/G	G/C	1584	723	39	27	1.520	0.923	2.500	1.30E-01	4.91E-02	573
3DL1	1091	cohortMinusGroup2	ITU	G/G	G/A	1101	195	69	6	0.491	0.210	1.150	1.31E-01	4.91E-02	574
3DL1	1091	cohortMinusGroup2	STU	G/G	G/A	1101	195	69	6	0.491	0.210	1.150	1.31E-01	4.91E-02	574
3DP1	796	cohortMinusGroup2	MXL	T/T	T/C	1586	725	39	27	1.510	0.917	2.490	1.31E-01	4.92E-02	575
2DP1	1269	cohortMinusGroup2	IBS	A/A	A/G	1371	69	95	9	1.880	0.910	3.880	1.32E-01	4.93E-02	576
2DP1	448	cohortMinusGroup2	TSI	G/G	G/C	594	811	44	42	0.699	0.452	1.080	1.32E-01	4.94E-02	577
2DP1	448	cohortMinusGroup2	STU	G/G	G/C	601	819	37	34	0.674	0.418	1.090	1.33E-01	4.95E-02	578
3DL2	474	cohortMinusGroup2	FIN	G/G	G/T	1491	707	55	37	1.420	0.927	2.170	1.33E-01	4.96E-02	579
3DL3	692	cohortMinusGroup2	MSL	G/G	G/A	755	175	62	22	1.530	0.916	2.560	1.36E-01	4.97E-02	580
2DP1	448	cohortMinusGroup2	GIH	G/G	G/C	602	820	36	33	0.673	0.415	1.090	1.37E-01	4.97E-02	581
2DL3	953	cohortMinusGroup2	STU	G/G	G/A	1325	496	54	12	0.594	0.315	1.120	1.37E-01	4.98E-02	582
3DL1	651	cohortMinusGroup2	STU	CA/CA	CA/C	29	17	6	10	2.840	0.876	9.200	1.38E-01	4.99E-02	583
3DL1	732	cohortMinusGroup2	GBR	T/T	T/C	380	249	13	16	1.880	0.889	3.980	1.39E-01	5.00E-02	584
3DL3	455	cohortMinusGroup2	IBS	G/G	G/A	1363	78	97	10	1.800	0.903	3.590	1.39E-01	5.01E-02	585
3DL1	496	cohortMinusGroup2	CLM	C/C	C/A	1724	129	85	2	0.314	0.076	1.290	1.40E-01	5.02E-02	586
2DP1	816	cohortMinusGroup2	PUR	G/G	G/A	664	58	91	3	0.377	0.116	1.230	1.41E-01	5.03E-02	587
2DP1	471	cohortMinusGroup2	CEU	A/A	A/G	1701	437	77	12	0.607	0.327	1.130	1.42E-01	5.03E-02	588
2DL4	625	cohortMinusGroup2	LWK	C/C	C/G	858	904	13	24	1.750	0.885	3.460	1.42E-01	5.04E-02	589
3DL3	502	cohortMinusGroup2	PJL	G/G	G/A	627	1090	20	53	1.520	0.900	2.570	1.43E-01	5.05E-02	590
3DL3	621	cohortMinusGroup2	GIH	G/G	G/A	1701	209	89	17	1.550	0.905	2.660	1.44E-01	5.06E-02	591
3DL2	394	cohortMinusGroup2	ESN	C/C	C/A	2197	224	85	14	1.620	0.905	2.900	1.46E-01	5.07E-02	592
3DL3	777	cohortMinusGroup2	GBR	A/A	A/G	1625	542	58	28	1.450	0.914	2.300	1.46E-01	5.08E-02	593
2DP1	816	cohortMinusGroup2	YRI	G/G	G/A	662	49	93	12	1.740	0.893	3.390	1.47E-01	5.09E-02	594
2DL4	762	cohortMinusGroup2	KHV	C/C	C/T	1077	935	58	36	0.715	0.467	1.090	1.48E-01	5.09E-02	595
2DL5	583	cohortMinusGroup2	GIH	G/G	G/A	524	233	26	19	1.640	0.890	3.020	1.50E-01	5.10E-02	596
3DL2	474	cohortMinusGroup2	GBR	G/G	G/T	1492	708	54	36	1.400	0.910	2.150	1.51E-01	5.11E-02	597
2DL4	395	cohortMinusGroup2	IBS	C/C	C/T	2056	222	96	5	0.482	0.194	1.200	1.52E-01	5.12E-02	598
3DL2	456	cohortMinusGroup2	LWK	C/C	C/T	2129	290	81	17	1.540	0.900	2.630	1.52E-01	5.13E-02	599
2DL5	583	cohortMinusGroup2	CEU	G/G	G/A	536	240	14	12	1.910	0.870	4.190	1.53E-01	5.14E-02	600
3DL3	408	cohortMinusGroup2	MXL	G/G	G/A	1648	628	42	24	1.500	0.901	2.500	1.53E-01	5.15E-02	601
3DL2	893	cohortMinusGroup2	CHS	G/G	G/A	2107	300	100	8	0.562	0.271	1.170	1.56E-01	5.15E-02	602
3DL2	893	cohortMinusGroup2	LWK	G/G	G/A	2126	291	81	17	1.530	0.894	2.620	1.57E-01	5.16E-02	603
2DL5	517	cohortMinusGroup2	GIH	A/A	A/G	591	233	32	20	1.590	0.891	2.840	1.57E-01	5.17E-02	604
2DL5	517	cohortMinusGroup2	TSI	A/A	A/G	601	238	22	15	1.720	0.877	3.370	1.57E-01	5.18E-02	605
3DL3	804	cohortMinusGroup2	ASW	G/G	G/A	1468	678	36	25	1.500	0.893	2.520	1.58E-01	5.19E-02	606
3DL3	621	cohortMinusGroup2	PJL	G/G	G/A	1700	220	90	6	0.515	0.223	1.190	1.58E-01	5.20E-02	607
2DL5	583	cohortMinusGroup2	BEB	G/G	G/A	529	236	21	16	1.710	0.877	3.340	1.60E-01	5.21E-02	608
3DL2	456	cohortMinusGroup2	CHS	C/C	C/T	2110	299	100	8	0.565	0.272	1.170	1.60E-01	5.21E-02	609
3DL3	455	cohortMinusGroup2	FIN	G/G	G/A	1363	86	97	2	0.327	0.079	1.350	1.61E-01	5.22E-02	610
3DL1	1021	cohortMinusGroup2	CDX	A/A	A/G	1211	139	66	3	0.396	0.123	1.280	1.61E-01	5.23E-02	611
3DL2	497	cohortMinusGroup2	ITU	G/G	G/A	1741	182	98	5	0.488	0.196	1.210	1.61E-01	5.24E-02	612
3DL1	496	cohortMinusGroup2	ACB	C/C	C/A	1727	121	82	10	1.740	0.880	3.440	1.62E-01	5.25E-02	613
3DL3	969	cohortMinusGroup2	ITU	C/C	C/T	1565	389	73	11	0.606	0.318	1.150	1.62E-01	5.26E-02	614
2DP1	471	cohortMinusGroup2	PJL	A/A	A/G	1728	430	50	19	1.530	0.893	2.620	1.62E-01	5.27E-02	615
2DL4	412	cohortMinusGroup2	ASW	G/G	G/A	967	1000	16	27	1.630	0.873	3.040	1.62E-01	5.27E-02	616
3DL3	804	cohortMinusGroup2	ITU	G/G	G/A	1429	678	75	25	0.703	0.443	1.120	1.63E-01	5.28E-02	617
2DL4	480	cohortMinusGroup2	PEL	G/G	G/A	1621	358	76	10	0.596	0.305	1.160	1.65E-01	5.29E-02	618
3DL3	408	cohortMinusGroup2	FIN	G/G	G/A	1612	631	78	21	0.688	0.421	1.120	1.65E-01	5.30E-02	619
3DL1	1091	cohortMinusGroup2	CLM	G/G	G/A	1123	188	47	13	1.650	0.876	3.110	1.67E-01	5.31E-02	620
2DL4	886	cohortMinusGroup2	ACB	C/C	C/G	696	43	79	9	1.840	0.865	3.920	1.68E-01	5.32E-02	621
3DL1	1021	cohortMinusGroup2	YRI	A/A	A/G	1217	131	60	11	1.700	0.872	3.310	1.68E-01	5.33E-02	622
2DP1	816	cohortMinusGroup2	ESN	G/G	G/A	670	50	85	11	1.730	0.867	3.450	1.70E-01	5.33E-02	623
3DP1	774	cohortMinusGroup2	ITU	G/G	G/C	1550	726	73	24	0.702	0.439	1.120	1.70E-01	5.34E-02	624
3DL1	1180	cohortMinusGroup2	JPT	G/G	G/C	1456	401	70	12	0.622	0.334	1.160	1.71E-01	5.35E-02	625
3DL1	607	cohortMinusGroup2	MSL	C/C	C/T	1501	489	67	14	0.641	0.357	1.150	1.72E-01	5.36E-02	626
2DL5	583	cohortMinusGroup2	FIN	G/G	G/A	527	247	23	5	0.464	0.174	1.230	1.72E-01	5.37E-02	627
2DL5	517	cohortMinusGroup2	JPT	A/A	A/G	604	250	19	3	0.381	0.112	1.300	1.74E-01	5.38E-02	628
2DP1	1313	cohortMinusGroup2	YRI	A/A	A/C	1376	531	53	29	1.420	0.893	2.260	1.75E-01	5.39E-02	629
2DL3	953	cohortMinusGroup2	YRI	G/G	G/A	1327	481	52	27	1.430	0.888	2.300	1.75E-01	5.39E-02	630
3DL1	607	cohortMinusGroup2	YRI	C/C	C/T	1483	484	85	19	0.685	0.412	1.140	1.77E-01	5.40E-02	631
3DL2	394	cohortMinusGroup2	CEU	C/C	C/A	2188	233	94	5	0.499	0.201	1.240	1.77E-01	5.41E-02	632
2DL3	738	cohortMinusGroup2	ESN	C/C	C/T	842	178	75	23	1.450	0.884	2.380	1.79E-01	5.42E-02	633
3DL1	1194	cohortMinusGroup2	IBS	C/C	C/T	1855	187	86	4	0.461	0.167	1.270	1.79E-01	5.43E-02	634
2DP1	766	cohortMinusGroup2	MSL	G/G	G/C	1318	318	49	18	1.520	0.874	2.640	1.80E-01	5.44E-02	635
3DL3	777	cohortMinusGroup2	MXL	A/A	A/G	1641	549	42	21	1.490	0.875	2.540	1.80E-01	5.45E-02	636
3DL3	447	cohortMinusGroup2	PEL	G/G	G/T	2132	301	80	6	0.531	0.230	1.230	1.82E-01	5.45E-02	637
3DL2	474	cohortMinusGroup2	CEU	G/G	G/T	1474	719	72	25	0.712	0.448	1.130	1.83E-01	5.46E-02	638
3DL3	961	cohortMinusGroup2	KHV	C/C	C/A	925	348	74	19	0.682	0.406	1.150	1.84E-01	5.47E-02	639
2DP1	1062	cohortMinusGroup2	STU	C/C	C/T	988	62	94	2	0.339	0.082	1.410	1.84E-01	5.48E-02	640
3DL1	1194	cohortMinusGroup2	GIH	C/C	C/T	1869	188	72	3	0.414	0.129	1.330	1.85E-01	5.49E-02	641
3DL1	1026	cohortMinusGroup2	ESN	G/G	G/C	1139	184	86	8	0.576	0.275	1.210	1.86E-01	5.50E-02	642
2DL4	1019	cohortMinusGroup2	CLM	C/C	C/T	865	56	91	2	0.339	0.081	1.410	1.86E-01	5.51E-02	643
2DP1	448	cohortMinusGroup2	LWK	G/G	G/C	605	822	33	31	0.691	0.419	1.140	1.87E-01	5.51E-02	644
3DL2	497	cohortMinusGroup2	PUR	G/G	G/A	1748	173	91	14	1.550	0.864	2.780	1.87E-01	5.52E-02	645
3DL2	497	cohortMinusGroup2	GWD	G/G	G/A	1732	181	107	6	0.537	0.233	1.240	1.89E-01	5.53E-02	646

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DP1	1062	cohortMinusGroup2	ITU	C/C	C/T	989	62	93	2	0.343	0.083	1.420	1.91E-01	5.54E-02	647
3DL3	1042	cohortMinusGroup2	GBR	G/G	G/C	959	143	58	4	0.463	0.166	1.290	1.91E-01	5.55E-02	648
3DL1	1026	cohortMinusGroup2	ITU	G/G	G/C	1155	186	70	6	0.532	0.228	1.240	1.91E-01	5.56E-02	649
3DL1	1026	cohortMinusGroup2	STU	G/G	G/C	1155	186	70	6	0.532	0.228	1.240	1.91E-01	5.56E-02	649
2DL4	480	cohortMinusGroup2	LWK	G/G	G/A	1612	356	85	12	0.639	0.345	1.180	1.93E-01	5.57E-02	650
2DL4	762	cohortMinusGroup2	MSL	C/C	C/T	1088	942	47	29	0.713	0.445	1.140	1.94E-01	5.57E-02	651
2DL4	395	cohortMinusGroup2	CEU	C/C	C/T	2061	222	91	5	0.510	0.205	1.270	1.94E-01	5.58E-02	652
2DL4	395	cohortMinusGroup2	PJL	C/C	C/T	2061	222	91	5	0.510	0.205	1.270	1.94E-01	5.58E-02	652
2DL5	517	cohortMinusGroup2	FIN	A/A	A/G	598	248	25	5	0.482	0.182	1.270	1.95E-01	5.59E-02	653
3DL3	961	cohortMinusGroup2	STU	C/C	C/A	969	350	30	17	1.570	0.855	2.880	1.95E-01	5.60E-02	654
2DL4	412	cohortMinusGroup2	FIN	G/G	G/A	933	988	50	39	0.737	0.480	1.130	1.95E-01	5.61E-02	655
2DP1	522	cohortMinusGroup2	IBS	T/T	T/C	1631	519	82	18	0.690	0.410	1.160	1.98E-01	5.62E-02	656
3DL3	502	cohortMinusGroup2	IBS	G/G	G/A	623	1084	24	59	1.410	0.868	2.290	1.98E-01	5.63E-02	657
3DL3	906	cohortMinusGroup2	MXL	C/C	C/T	1678	498	43	19	1.490	0.860	2.580	2.02E-01	5.63E-02	658
2DP1	1313	cohortMinusGroup2	CLM	A/A	A/C	1372	545	57	15	0.662	0.372	1.180	2.03E-01	5.64E-02	659
3DL2	394	cohortMinusGroup2	PJL	C/C	C/A	2191	233	91	5	0.517	0.208	1.280	2.04E-01	5.65E-02	660
3DL3	1042	cohortMinusGroup2	PJL	G/G	G/C	969	144	48	3	0.421	0.129	1.370	2.05E-01	5.66E-02	661
2DP1	766	cohortMinusGroup2	MXL	G/G	G/C	1338	333	29	3	0.416	0.126	1.370	2.07E-01	5.67E-02	662
2DL3	953	cohortMinusGroup2	CHS	G/G	G/A	1297	486	82	22	0.716	0.442	1.160	2.11E-01	5.68E-02	663
3DL3	502	cohortMinusGroup2	MXL	G/G	G/A	632	1103	15	40	1.530	0.838	2.790	2.12E-01	5.69E-02	664
3DL3	777	cohortMinusGroup2	CLM	A/A	A/G	1622	542	61	28	1.370	0.867	2.170	2.15E-01	5.69E-02	665
2DL5	583	cohortMinusGroup2	JPT	G/G	G/A	534	249	16	3	0.402	0.116	1.390	2.17E-01	5.70E-02	666
2DP1	522	cohortMinusGroup2	PJL	T/T	T/C	1666	516	47	21	1.440	0.853	2.430	2.17E-01	5.71E-02	667
3DP1	774	cohortMinusGroup2	FIN	G/G	G/C	1562	713	61	37	1.330	0.876	2.020	2.20E-01	5.72E-02	668
2DL4	395	cohortMinusGroup2	YRI	C/C	C/T	2062	213	90	14	1.510	0.845	2.700	2.22E-01	5.73E-02	669
2DL3	953	cohortMinusGroup2	CLM	G/G	G/A	1329	496	50	12	0.643	0.340	1.220	2.22E-01	5.74E-02	670
3DL2	394	cohortMinusGroup2	IBS	C/C	C/A	2181	232	101	6	0.558	0.242	1.290	2.23E-01	5.75E-02	671
3DL1	1091	cohortMinusGroup2	YRI	G/G	G/A	1094	193	76	8	0.597	0.284	1.260	2.25E-01	5.75E-02	672
3DL2	497	cohortMinusGroup2	PJL	G/G	G/A	1748	182	91	5	0.528	0.212	1.320	2.25E-01	5.76E-02	673
3DL1	1026	cohortMinusGroup2	CEU	G/G	G/C	1191	183	34	9	1.720	0.812	3.640	2.26E-01	5.77E-02	674
2DL3	959	cohortMinusGroup2	GWD	C/C	C/T	540	26	91	8	1.830	0.804	4.170	2.28E-01	5.78E-02	675
2DL3	953	cohortMinusGroup2	KHV	G/G	G/A	1304	488	75	20	0.713	0.431	1.180	2.28E-01	5.79E-02	676
2DP1	522	cohortMinusGroup2	CEU	T/T	T/C	1640	521	73	16	0.690	0.398	1.200	2.29E-01	5.80E-02	677
3DL1	1021	cohortMinusGroup2	IBS	A/A	A/G	1229	140	48	2	0.366	0.088	1.520	2.30E-01	5.81E-02	678
3DL2	474	cohortMinusGroup2	MXL	G/G	G/T	1509	719	37	25	1.420	0.848	2.380	2.31E-01	5.81E-02	679
3DL2	394	cohortMinusGroup2	MXL	C/C	C/A	2218	235	64	3	0.442	0.138	1.420	2.31E-01	5.82E-02	680
3DL3	961	cohortMinusGroup2	CHS	C/C	C/A	918	345	81	22	0.723	0.444	1.180	2.32E-01	5.83E-02	681
3DL1	732	cohortMinusGroup2	CEU	T/T	T/C	376	259	17	6	0.512	0.199	1.320	2.32E-01	5.84E-02	682
3DL2	893	cohortMinusGroup2	PJL	G/G	G/A	2127	292	80	16	1.460	0.842	2.530	2.35E-01	5.85E-02	683
3DL3	804	cohortMinusGroup2	CEU	G/G	G/A	1447	668	57	35	1.330	0.865	2.050	2.35E-01	5.86E-02	684
2DP1	1062	cohortMinusGroup2	PUR	C/C	C/T	995	62	87	2	0.369	0.089	1.530	2.35E-01	5.87E-02	685
3DL3	1042	cohortMinusGroup2	CEU	G/G	G/C	962	143	55	4	0.489	0.175	1.370	2.35E-01	5.87E-02	686
2DL4	395	cohortMinusGroup2	CLM	C/C	C/T	2065	222	87	5	0.535	0.215	1.330	2.35E-01	5.88E-02	687
2DP1	1269	cohortMinusGroup2	STU	A/A	A/G	1369	76	97	2	0.371	0.090	1.530	2.35E-01	5.89E-02	688
3DL3	447	cohortMinusGroup2	LWK	G/G	G/T	2119	299	93	8	0.610	0.293	1.270	2.37E-01	5.90E-02	689
2DP1	471	cohortMinusGroup2	LWK	A/A	A/G	1707	437	71	12	0.660	0.355	1.230	2.38E-01	5.91E-02	690
3DL3	804	cohortMinusGroup2	FIN	G/G	G/A	1445	667	59	36	1.320	0.863	2.020	2.38E-01	5.92E-02	691
2DL5	583	cohortMinusGroup2	ITU	G/G	G/A	518	231	32	21	1.470	0.830	2.600	2.39E-01	5.93E-02	692
2DP1	471	cohortMinusGroup2	GIH	A/A	A/G	1718	428	60	21	1.400	0.842	2.330	2.40E-01	5.93E-02	693
3DL1	607	cohortMinusGroup2	CHS	C/C	C/T	1490	485	78	18	0.709	0.420	1.200	2.40E-01	5.94E-02	694
3DL3	971	cohortMinusGroup2	STU	T/T	T/C	1668	330	55	16	1.470	0.832	2.600	2.41E-01	5.95E-02	695
2DL4	395	cohortMinusGroup2	PUR	C/C	C/T	2054	221	98	6	0.569	0.247	1.310	2.43E-01	5.96E-02	696
2DP1	1269	cohortMinusGroup2	ITU	A/A	A/G	1370	76	96	2	0.376	0.091	1.550	2.43E-01	5.97E-02	697
2DP1	766	cohortMinusGroup2	GWD	G/G	G/C	1312	317	55	19	1.430	0.837	2.440	2.44E-01	5.98E-02	698
3DL2	394	cohortMinusGroup2	GBR	C/C	C/A	2195	233	87	5	0.541	0.217	1.350	2.47E-01	5.99E-02	699
3DL3	961	cohortMinusGroup2	CDX	C/C	C/A	931	349	68	18	0.706	0.414	1.200	2.47E-01	5.99E-02	700
3DP1	796	cohortMinusGroup2	FIN	T/T	T/C	1553	727	72	25	0.742	0.467	1.180	2.48E-01	6.00E-02	701
3DL3	869	cohortMinusGroup2	ASW	A/A	A/C	1897	525	45	18	1.450	0.832	2.530	2.49E-01	6.01E-02	702
3DL3	621	cohortMinusGroup2	ASW	G/G	G/A	1728	222	62	4	0.502	0.181	1.390	2.50E-01	6.02E-02	703
3DL3	906	cohortMinusGroup2	BEB	C/C	C/T	1662	493	59	24	1.370	0.843	2.230	2.51E-01	6.03E-02	704
2DL3	953	cohortMinusGroup2	GWD	G/G	G/A	1329	483	50	25	1.380	0.844	2.260	2.52E-01	6.04E-02	705
2DP1	471	cohortMinusGroup2	IBS	A/A	A/G	1694	434	84	15	0.697	0.398	1.220	2.53E-01	6.05E-02	706
3DL1	1303	cohortMinusGroup2	CLM	A/A	A/G	1103	108	81	4	0.504	0.181	1.400	2.56E-01	6.05E-02	707
3DL2	474	cohortMinusGroup2	IBS	G/G	G/T	1470	716	76	28	0.756	0.486	1.180	2.57E-01	6.06E-02	708
2DL4	762	cohortMinusGroup2	MXL	C/C	C/T	1113	944	22	27	1.450	0.820	2.560	2.57E-01	6.07E-02	709
2DP1	766	cohortMinusGroup2	ESN	G/G	G/C	1300	325	67	11	0.657	0.343	1.260	2.57E-01	6.08E-02	710
3DL1	1194	cohortMinusGroup2	CEU	C/C	C/T	1863	187	78	4	0.511	0.185	1.410	2.62E-01	6.09E-02	711
3DL3	621	cohortMinusGroup2	GBR	G/G	G/A	1713	212	77	14	1.470	0.817	2.640	2.62E-01	6.10E-02	712
3DL2	394	cohortMinusGroup2	TSI	C/C	C/A	2188	224	94	14	1.450	0.813	2.580	2.67E-01	6.10E-02	713
3DL3	804	cohortMinusGroup2	ESN	G/G	G/A	1446	668	58	35	1.310	0.853	2.010	2.67E-01	6.11E-02	714
3DL1	1180	cohortMinusGroup2	ITU	G/G	G/C	1461	401	65	12	0.673	0.360	1.260	2.68E-01	6.12E-02	715
3DL3	906	cohortMinusGroup2	ACB	C/C	C/T	1643	500	78	17	0.716	0.420	1.220	2.69E-01	6.13E-02	716
3DL3	621	cohortMinusGroup2	TSI	G/G	G/A	1699	210	91	16	1.420	0.819	2.460	2.70E-01	6.14E-02	717
3DL1	1021	cohortMinusGroup2	PJL	A/A	A/G	1220	139	57	3	0.462	0.143	1.490	2.71E-01	6.15E-02	718
3DL3	455	cohortMinusGroup2	GIH	G/G	G/A	1357	85	103	3	0.465	0.145	1.500	2.72E-01	6.16E-02	719
2DL4	625	cohortMinusGroup2	ASW	C/C	C/G	856	904	15	24	1.520	0.792	2.920	2.73E-01	6.16E-02	720
3DL3	777	cohortMinusGroup2	GIH	A/A	A/G	1612	539	71	31	1.310	0.850	2.020	2.74E-01	6.17E-02	721
2DP1	1313	cohortMinusGroup2	PJL	A/A	A/C	1397	542	32	18	1.450	0.807	2.610	2.76E-01	6.18E-02	722
3DL3	447	cohortMinusGroup2	GIH	G/G	G/T	2123	290	89	17	1.400	0.822	2.390	2.77E-01	6.19E-02	723
3DL3	447	cohortMinusGroup2	CEU	G/G	G/T	2122	299	90	8	0.631	0.303	1.310	2.78E-01	6.20E-02	724
3DL2	456	cohortMinusGroup2	GIH	C/C	C/T	2121	290	89	17	1.400	0.822	2.390	2.79E-01	6.21E-02	725
3DL3	1042	cohortMinusGroup2	PEL	G/G	G/C	956	142	61	5	0.552	0.218	1.400	2.79E-01	6.22E-02	726
3DL1	1091	cohortMinusGroup2	MXL	G/G	G/A	1133	198	37	3	0.464	0.142	1.520	2.83E-01	6.22E-02	727
2DL4	395	cohortMinusGroup2	GBR	C/C	C/T	2069	222	83	5	0.561	0.225	1.400	2.84E-01	6.23E-02	728
3DL2	893	cohortMinusGroup2	GIH	G/G	G/A	2118	291	89	17	1.390	0.816	2.370	2.87E-01	6.24E-02	729
2DL5	583	cohortMinusGroup2	GWD	G/G	G/A	527	246	23	6	0.559	0.225	1.390	2.87E-01	6.25E-02	730
3DL1	1194	cohortMinusGroup2	CLM	C/C	C/T	1865	187	76	4	0.525	0.190	1.450	2.87E-01	6.26E-02	731
3DL1	1194	cohortMinusGroup2	PJL	C/C	C/T	1865	187	76	4	0.525	0.190	1.450	2.87E-01	6.26E-02	731
2DL4	395	cohortMinusGroup2	GIH	C/C	C/T	2058	221	94	6	0.594	0.257	1.370	2.90E-01	6.27E-02	732
3DL2	474	cohortMinusGroup2	TSI	G/G	G/T	1469	715	77	29	0.774	0.500	1.200	2.94E-01	6.28E-02	733
3DL1	1180	cohortMinusGroup2	PUR	G/G	G/C	1465	391	61	22	1.350	0.819	2.230	2.95E-01	6.28E-02	734
3DL3	447	cohortMinusGroup2	TSI	G/G	G/T	2122	290	90	17	1.380	0.810	2.350	2.96E-01	6.29E-02	735
3DP1	796	cohortMinusGroup2	PUR	T/T	T/C	1550	725	75	27	0.770	0.492	1.210	2.99E-01	6.30E-02	736
2DL4	886	cohortMinusGroup2	ESN	C/C	C/G	686	43	89	9	1.610	0.759	3.410	3.00E-01	6.31E-02	737
2DL4	395	cohortMinusGroup2	ASW	C/C	C/T	2097	218	55	9	1.570	0.765	3.220	3.02E-01	6.32E-02	738
2DL3	953	cohortMinusGroup2	CDX	G/G	G/A	1310	489	69	19	0.738	0.439	1.240	3.02E-01	6.33E-02	739
2DL5	583	cohortMinusGroup2	ESN	G/G	G/A	530	247	20	5	0.536	0.199	1.440	3.03E-01	6.34E-02	740
3DL3	961	cohortMinusGroup2	MXL	C/C	C/A	958	357	41	10	0.655	0.325	1.320	3.03E-01	6.34E-02	741
3DL1	1021	cohortMinusGroup2	ACB	A/A	A/G	1222	139	55	3	0.480	0.148	1.550	3.03E-01	6.35E-02	742
3DL1	1091	cohortMinusGroup2	CEU	G/G	G/A	1132	191	38	10	1.560	0.764	3.180	3.06E-01	6.36E-02	743
3DL3	777	cohortMinusGroup2	ESN	A/A	A/G	1605	550	78	20	0.748	0.453	1.230	3.08E-01	6.37E-02	744
3DL3	969	cohortMinusGroup2	CLM	C/C	C/T	1584	382	54	18	1.380	0.800	2.380	3.09E-01	6.38E-02	745
3DL3	621	cohortMinusGroup2	CLM	G/G	G/A	1703	219	87	7	0.626	0.286	1.370	3.09E-01	6.39E-02	746
3DL3	971	cohortMinusGroup2	GIH	T/T	T/C	1661	329	62	17	1.380	0.797	2.390	3.12E-01	6.40E-02	747
2DL3	953	cohortMinusGroup2	ACB	G/G	G/A	1332	485	47	23	1.340	0.805	2.230	3.15E-01	6.40E-02	748
2DP1	448	cohortMinusGroup2	FIN	G/G	G/C	611	806	27	47	1.320	0.813	2.140	3.16E-01	6.41E-02	749
3DL2	474	cohortMinusGroup2	ITU	G/G	G/T	1472	716	74	28	0.778	0.499	1.210	3.16E-01	6.42E-02	750
2DL5	583	cohortMinusGroup2	IBS	G/G	G/A	535	241	15	11	1.630	0.738	3.600	3.17E-01	6.43E-02	751
3DL1	1180	cohortMinusGroup2	CLM	G/G	G/C	1474	394	52	19	1.370	0.801	2.340	3.19E-01	6.44E-02	752

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	455	cohortMinusGroup2	LWK	G/G	G/A	1362	85	98	3	0.491	0.152	1.580	3.19E-01	6.45E-02	753
3DL3	408	cohortMinusGroup2	CLM	G/G	G/A	1629	622	61	30	1.290	0.825	2.020	3.20E-01	6.46E-02	754
3DL3	408	cohortMinusGroup2	ITU	G/G	G/A	1613	629	77	23	0.766	0.476	1.230	3.22E-01	6.46E-02	755
3DL1	1303	cohortMinusGroup2	YRI	A/A	A/G	1094	100	90	12	1.460	0.773	2.760	3.24E-01	6.47E-02	756
2DL4	625	cohortMinusGroup2	FIN	C/C	C/G	827	891	44	37	0.781	0.499	1.220	3.30E-01	6.48E-02	757
3DL1	1194	cohortMinusGroup2	ASW	C/C	C/T	1889	183	52	8	1.590	0.744	3.400	3.30E-01	6.49E-02	758
3DL3	961	cohortMinusGroup2	ESN	C/C	C/T	302	80	64	23	1.360	0.795	2.330	3.30E-01	6.50E-02	759
2DP1	522	cohortMinusGroup2	GIH	T/T	T/C	1654	513	59	24	1.310	0.807	2.130	3.33E-01	6.51E-02	760
3DL2	893	cohortMinusGroup2	CLM	G/G	G/A	2121	300	86	8	0.658	0.316	1.370	3.34E-01	6.52E-02	761
2DP1	471	cohortMinusGroup2	YRI	A/A	A/G	1711	427	67	22	1.320	0.806	2.160	3.38E-01	6.52E-02	762
3DL1	607	cohortMinusGroup2	PUR	C/C	C/T	1513	480	55	23	1.320	0.803	2.170	3.39E-01	6.53E-02	763
2DL4	625	cohortMinusGroup2	ESN	C/C	C/G	847	894	24	34	1.340	0.788	2.280	3.39E-01	6.54E-02	764
3DL1	1021	cohortMinusGroup2	GIH	A/A	A/G	1224	139	53	3	0.498	0.154	1.610	3.39E-01	6.55E-02	765
3DL2	456	cohortMinusGroup2	CLM	C/C	C/T	2124	299	86	8	0.661	0.317	1.380	3.41E-01	6.56E-02	766
3DL1	1026	cohortMinusGroup2	CLM	G/G	G/C	1182	182	43	10	1.510	0.746	3.060	3.43E-01	6.57E-02	767
2DL4	395	cohortMinusGroup2	CDX	C/C	C/T	2062	221	90	6	0.622	0.269	1.440	3.45E-01	6.58E-02	768
3DL1	1180	cohortMinusGroup2	YRI	G/G	G/C	1460	390	66	23	1.300	0.798	2.120	3.48E-01	6.58E-02	769
3DL3	447	cohortMinusGroup2	CHB	G/G	G/T	2118	298	94	9	0.680	0.340	1.360	3.48E-01	6.59E-02	770
3DL3	447	cohortMinusGroup2	PUR	G/G	G/T	2118	298	94	9	0.680	0.340	1.360	3.48E-01	6.59E-02	770
3DL2	474	cohortMinusGroup2	STU	G/G	G/T	1473	716	73	28	0.789	0.506	1.230	3.49E-01	6.60E-02	771
3DL2	456	cohortMinusGroup2	ASW	C/C	C/T	2155	296	55	11	1.460	0.756	2.820	3.50E-01	6.61E-02	772
3DL3	455	cohortMinusGroup2	PJL	G/G	G/A	1372	80	88	8	1.560	0.731	3.330	3.53E-01	6.62E-02	773
3DL3	692	cohortMinusGroup2	ESN	G/G	G/A	742	174	75	23	1.310	0.798	2.150	3.53E-01	6.63E-02	774
3DL2	474	cohortMinusGroup2	PJL	G/G	G/T	1480	719	66	25	0.780	0.488	1.250	3.53E-01	6.64E-02	775
2DP1	899	cohortMinusGroup2	ESN	C/C	C/A	312	34	52	9	1.590	0.721	3.510	3.53E-01	6.64E-02	776
2DL4	1019	cohortMinusGroup2	ACB	C/C	C/T	868	50	88	8	1.580	0.726	3.440	3.53E-01	6.65E-02	777
3DL3	971	cohortMinusGroup2	CDX	T/T	T/C	1652	336	71	10	0.692	0.353	1.360	3.55E-01	6.66E-02	778
3DL1	732	cohortMinusGroup2	CDX	T/T	T/C	383	254	10	11	1.660	0.695	3.970	3.56E-01	6.67E-02	779
2DL4	480	cohortMinusGroup2	CLM	G/G	G/A	1626	348	71	20	1.320	0.793	2.200	3.58E-01	6.68E-02	780
3DL2	893	cohortMinusGroup2	ASW	G/G	G/A	2152	297	55	11	1.450	0.750	2.800	3.58E-01	6.69E-02	781
2DL4	480	cohortMinusGroup2	MSL	G/G	G/A	1626	357	71	11	0.706	0.370	1.350	3.59E-01	6.70E-02	782
2DP1	1313	cohortMinusGroup2	GBR	A/A	A/C	1377	534	52	26	1.290	0.797	2.090	3.63E-01	6.70E-02	783
3DL1	1026	cohortMinusGroup2	YRI	G/G	G/C	1150	184	75	8	0.667	0.317	1.410	3.64E-01	6.71E-02	784
3DP1	479	cohortMinusGroup2	ITU	A/A	A/C	1862	513	71	25	1.280	0.803	2.040	3.64E-01	6.72E-02	785
2DL4	412	cohortMinusGroup2	ESN	G/G	G/A	959	994	24	33	1.330	0.780	2.270	3.64E-01	6.73E-02	786
3DL1	1091	cohortMinusGroup2	PUR	G/G	G/A	1105	186	65	15	1.370	0.765	2.450	3.67E-01	6.74E-02	787
2DP1	448	cohortMinusGroup2	ESN	G/G	G/C	613	810	25	43	1.300	0.785	2.150	3.67E-01	6.75E-02	788
3DP1	939	cohortMinusGroup2	ASW	T/T	T/G	580	120	41	5	0.589	0.228	1.520	3.68E-01	6.76E-02	789
2DP1	448	cohortMinusGroup2	ACB	G/G	G/C	615	813	23	40	1.320	0.782	2.230	3.68E-01	6.76E-02	790
3DL3	961	cohortMinusGroup2	ASW	C/C	C/T	333	90	33	13	1.460	0.738	2.890	3.69E-01	6.77E-02	791
3DL1	496	cohortMinusGroup2	IBS	C/C	C/A	1714	127	95	4	0.568	0.206	1.570	3.69E-01	6.78E-02	792
3DP1	939	cohortMinusGroup2	ESN	T/T	T/G	552	107	69	18	1.350	0.772	2.360	3.72E-01	6.79E-02	793
2DP1	522	cohortMinusGroup2	ITU	T/T	T/C	1650	512	63	25	1.280	0.797	2.060	3.72E-01	6.80E-02	794
3DL3	455	cohortMinusGroup2	ACB	G/G	G/A	1367	85	93	3	0.519	0.161	1.670	3.73E-01	6.81E-02	795
3DL2	456	cohortMinusGroup2	PJL	C/C	C/T	2129	292	81	15	1.350	0.768	2.370	3.75E-01	6.82E-02	796
3DL1	732	cohortMinusGroup2	TSI	T/T	T/C	378	259	15	6	0.584	0.224	1.530	3.76E-01	6.82E-02	797
3DL3	804	cohortMinusGroup2	LWK	G/G	G/A	1443	668	61	35	1.240	0.810	1.900	3.80E-01	6.83E-02	798
2DP1	448	cohortMinusGroup2	PUR	G/G	G/C	609	823	29	30	0.765	0.454	1.290	3.82E-01	6.84E-02	799
3DL3	502	cohortMinusGroup2	TSI	G/G	G/A	612	1093	35	50	0.800	0.514	1.250	3.82E-01	6.85E-02	800
3DL1	1180	cohortMinusGroup2	CEU	G/G	G/C	1482	397	44	16	1.360	0.759	2.440	3.84E-01	6.86E-02	801
3DL3	738	cohortMinusGroup2	ASW	C/C	C/T	866	186	51	15	1.370	0.754	2.490	3.84E-01	6.87E-02	802
2DL4	1023	cohortMinusGroup2	CEU	G/G	G/A	1483	649	72	25	0.793	0.498	1.260	3.87E-01	6.88E-02	803
3DL2	394	cohortMinusGroup2	MSL	C/C	C/A	2205	233	77	5	0.615	0.246	1.530	3.89E-01	6.88E-02	804
3DL1	1194	cohortMinusGroup2	MXL	C/C	C/T	1884	188	57	3	0.527	0.163	1.700	3.90E-01	6.89E-02	805
3DL2	394	cohortMinusGroup2	CLM	C/C	C/A	2194	232	88	6	0.645	0.279	1.490	3.93E-01	6.90E-02	806
3DL2	497	cohortMinusGroup2	ACB	G/G	G/A	1749	181	90	6	0.644	0.278	1.490	3.94E-01	6.91E-02	807
3DL3	777	cohortMinusGroup2	ACB	A/A	A/G	1608	550	75	20	0.780	0.472	1.290	3.94E-01	6.92E-02	808
3DL3	408	cohortMinusGroup2	PJL	G/G	G/A	1627	622	63	30	1.250	0.801	1.950	3.94E-01	6.93E-02	809
2DL3	953	cohortMinusGroup2	ITU	G/G	G/A	1325	493	54	15	0.747	0.418	1.340	3.95E-01	6.94E-02	810
3DP1	796	cohortMinusGroup2	IBS	T/T	T/C	1559	715	66	37	1.220	0.808	1.840	3.96E-01	6.94E-02	811
2DL4	412	cohortMinusGroup2	LWK	G/G	G/A	956	991	27	36	1.290	0.777	2.140	3.97E-01	6.95E-02	812
3DL1	496	cohortMinusGroup2	FIN	C/C	C/A	1717	127	92	4	0.588	0.213	1.630	4.08E-01	6.96E-02	813
3DL3	961	cohortMinusGroup2	BEB	C/C	C/A	969	352	30	15	1.380	0.734	2.600	4.10E-01	6.97E-02	814
3DL2	394	cohortMinusGroup2	GIH	C/C	C/A	2184	231	98	7	0.675	0.310	1.470	4.10E-01	6.98E-02	815
3DL3	906	cohortMinusGroup2	MSL	C/C	C/T	1652	501	69	16	0.765	0.440	1.330	4.11E-01	6.99E-02	816
2DP1	1313	cohortMinusGroup2	IBS	A/A	A/C	1370	542	59	18	0.771	0.451	1.320	4.11E-01	7.00E-02	817
3DL3	621	cohortMinusGroup2	CEU	G/G	G/A	1700	218	90	8	0.693	0.332	1.450	4.14E-01	7.00E-02	818
2DP1	766	cohortMinusGroup2	LWK	G/G	G/C	1339	332	28	4	0.576	0.201	1.650	4.16E-01	7.01E-02	819
2DP1	1313	cohortMinusGroup2	LWK	A/A	A/C	1385	538	44	22	1.290	0.766	2.170	4.17E-01	7.02E-02	820
3DL2	456	cohortMinusGroup2	MSL	C/C	C/T	2140	294	70	13	1.350	0.738	2.470	4.18E-01	7.03E-02	821
2DP1	522	cohortMinusGroup2	CLM	T/T	T/C	1647	521	66	16	0.766	0.440	1.330	4.18E-01	7.04E-02	822
2DL4	762	cohortMinusGroup2	ASW	C/C	C/T	1107	953	28	18	0.747	0.411	1.360	4.18E-01	7.05E-02	823
2DP1	1219	cohortMinusGroup2	ACB	A/A	A/G	613	38	91	3	0.532	0.161	1.760	4.18E-01	7.06E-02	824
3DL1	1091	cohortMinusGroup2	PEL	G/G	G/A	1117	195	53	6	0.648	0.275	1.530	4.19E-01	7.06E-02	825
2DP1	1313	cohortMinusGroup2	FIN	A/A	A/C	1371	532	58	28	1.240	0.781	1.970	4.20E-01	7.07E-02	826
2DP1	448	cohortMinusGroup2	CEU	G/G	G/C	607	820	31	33	0.788	0.477	1.300	4.21E-01	7.08E-02	827
3DL1	1194	cohortMinusGroup2	PUR	C/C	C/T	1850	185	91	6	0.659	0.285	1.530	4.25E-01	7.09E-02	828
3DL3	1042	cohortMinusGroup2	IBS	G/G	G/C	939	139	78	8	0.693	0.328	1.470	4.26E-01	7.10E-02	829
2DP1	1000	cohortMinusGroup2	MSL	A/A	A/G	279	28	57	3	0.524	0.154	1.780	4.26E-01	7.11E-02	830
3DL2	893	cohortMinusGroup2	MSL	G/G	G/A	2137	295	70	13	1.350	0.738	2.470	4.27E-01	7.12E-02	831
2DP1	448	cohortMinusGroup2	BEB	G/G	G/C	615	814	23	39	1.280	0.757	2.170	4.27E-01	7.12E-02	832
2DL4	395	cohortMinusGroup2	CHB	C/C	C/T	2067	215	85	12	1.360	0.731	2.530	4.28E-01	7.13E-02	833
2DL4	480	cohortMinusGroup2	MXL	G/G	G/A	1639	359	58	9	0.708	0.348	1.440	4.28E-01	7.14E-02	834
3DL3	447	cohortMinusGroup2	GBR	G/G	G/T	2135	293	77	14	1.320	0.737	2.360	4.32E-01	7.15E-02	835
2DL5	517	cohortMinusGroup2	GWD	A/A	A/G	600	247	23	6	0.634	0.255	1.580	4.34E-01	7.16E-02	836
2DP1	816	cohortMinusGroup2	MSL	G/G	G/A	675	57	80	4	0.592	0.209	1.670	4.36E-01	7.17E-02	837
2DL5	517	cohortMinusGroup2	ESN	A/A	A/G	603	248	20	5	0.608	0.226	1.640	4.41E-01	7.18E-02	838
2DL4	1023	cohortMinusGroup2	STU	G/G	G/A	1482	648	73	26	0.815	0.516	1.290	4.42E-01	7.18E-02	839
3DL2	393	cohortMinusGroup2	LWK	G/G	G/T	598	34	97	3	0.544	0.164	1.810	4.45E-01	7.19E-02	840
3DL1	732	cohortMinusGroup2	ACB	T/T	T/C	377	258	16	7	0.639	0.259	1.580	4.45E-01	7.20E-02	841
3DL1	732	cohortMinusGroup2	GWD	T/T	T/C	377	258	16	7	0.639	0.259	1.580	4.45E-01	7.20E-02	841
3DL3	408	cohortMinusGroup2	STU	G/G	G/A	1614	628	76	24	0.812	0.508	1.300	4.46E-01	7.21E-02	842
2DL4	625	cohortMinusGroup2	GBR	C/C	C/G	832	894	39	34	0.811	0.507	1.300	4.50E-01	7.22E-02	843
2DL4	762	cohortMinusGroup2	ITU	C/C	C/T	1091	926	44	45	1.200	0.785	1.830	4.51E-01	7.23E-02	844
3DL3	699	cohortMinusGroup2	YRI	G/G	G/A	749	69	96	12	1.360	0.711	2.600	4.57E-01	7.24E-02	845
2DL4	625	cohortMinusGroup2	PUR	C/C	C/G	824	886	47	42	0.831	0.542	1.270	4.58E-01	7.24E-02	846
3DL1	1180	cohortMinusGroup2	LWK	G/G	G/C	1480	404	46	9	0.717	0.348	1.480	4.59E-01	7.25E-02	847
3DL1	1021	cohortMinusGroup2	STU	A/A	A/G	1219	138	58	4	0.609	0.218	1.700	4.61E-01	7.26E-02	848
2DL4	1023	cohortMinusGroup2	PJL	G/G	G/A	1490	651	65	23	0.810	0.499	1.310	4.62E-01	7.27E-02	849
3DL3	971	cohortMinusGroup2	MSL	T/T	T/C	1665	331	58	15	1.300	0.728	2.320	4.64E-01	7.28E-02	850
2DL4	395	cohortMinusGroup2	MXL	C/C	C/T	2091	223	61	4	0.615	0.222	1.710	4.66E-01	7.29E-02	851
3DP1	774	cohortMinusGroup2	BEB	G/G	G/C	1562	727	61	23	0.810	0.497	1.320	4.66E-01	7.30E-02	852
3DL3	869	cohortMinusGroup2	FIN	A/A	A/C	1862	525	80	18	0.798	0.474	1.340	4.67E-01	7.30E-02	853
3DL2	456	cohortMinusGroup2	BEB	C/C	C/T	2138	294	72	13	1.310	0.717	2.390	4.72E-01	7.31E-02	854
3DL3	777	cohortMinusGroup2	ASW	A/A	A/G	1633	557	50	13	0.762	0.411	1.410	4.73E-01	7.32E-02	855
3DP1	774	cohortMinusGroup2	IBS	G/G	G/C	1557	714	66	36	1.190	0.785	1.800	4.78E-01	7.33E-02	856
3DL3	502	cohortMinusGroup2	ASW	G/G	G/A	623	1109	24	34	0.796	0.468	1.350	4.81E-01	7.34E-02	857
3DL2	893	cohortMinusGroup2	BEB	G/G	G/A	2135	295	72	13	1.310	0.717	2.390	4.82E-01	7.35E-02	858
3DL1	732	cohortMinusGroup2	ASW	T/T	T/C	374	256	19	9	0.692	0.308	1.550	4.84E-01	7.35E-02	859

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL2	456	cohortMinusGroup2	TSI	C/C	C/T	2118	291	92	16	1.270	0.737	2.190	4.84E-01	7.36E-02	860
3DL3	502	cohortMinusGroup2	PUR	G/G	G/A	612	1091	35	52	0.833	0.537	1.290	4.85E-01	7.37E-02	861
3DL1	607	cohortMinusGroup2	CDX	C/C	C/T	1509	488	59	15	0.786	0.442	1.400	4.95E-01	7.38E-02	862
3DL2	893	cohortMinusGroup2	TSI	G/G	G/A	2115	292	92	16	1.260	0.731	2.170	4.95E-01	7.39E-02	863
3DL3	869	cohortMinusGroup2	STU	A/A	A/C	1859	524	83	19	0.812	0.489	1.350	4.95E-01	7.40E-02	864
3DL1	732	cohortMinusGroup2	LWK	T/T	T/C	381	260	12	5	0.611	0.213	1.750	5.00E-01	7.41E-02	865
3DL1	1180	cohortMinusGroup2	ASW	G/G	G/C	1486	399	40	14	1.300	0.700	2.410	5.01E-01	7.41E-02	866
3DL1	1194	cohortMinusGroup2	STU	C/C	C/T	1866	186	75	5	0.669	0.267	1.670	5.06E-01	7.42E-02	867
2DL5	583	cohortMinusGroup2	MSL	G/G	G/A	528	245	22	7	0.686	0.289	1.630	5.11E-01	7.43E-02	868
3DL2	893	cohortMinusGroup2	GWD	G/G	G/A	2106	297	101	11	0.772	0.410	1.460	5.13E-01	7.44E-02	869
2DL5	517	cohortMinusGroup2	CEU	A/A	A/G	601	241	22	12	1.360	0.663	2.790	5.17E-01	7.45E-02	870
3DL2	394	cohortMinusGroup2	ITU	C/C	C/A	2192	226	90	12	1.290	0.696	2.390	5.19E-01	7.46E-02	871
2DL4	412	cohortMinusGroup2	PUR	G/G	G/A	936	985	47	42	0.849	0.555	1.300	5.19E-01	7.47E-02	872
3DL3	971	cohortMinusGroup2	GBR	T/T	T/C	1658	336	65	10	0.759	0.386	1.490	5.20E-01	7.47E-02	873
3DL3	777	cohortMinusGroup2	BEB	A/A	A/G	1624	546	59	24	1.210	0.745	1.960	5.20E-01	7.48E-02	874
3DP1	796	cohortMinusGroup2	ITU	T/T	T/C	1556	725	69	27	0.840	0.534	1.320	5.20E-01	7.49E-02	875
3DL1	607	cohortMinusGroup2	JPT	C/C	C/T	1493	483	75	20	0.824	0.498	1.360	5.28E-01	7.50E-02	876
3DL3	621	cohortMinusGroup2	JPT	G/G	G/A	1701	212	89	14	1.260	0.705	2.250	5.31E-01	7.51E-02	877
3DL3	869	cohortMinusGroup2	PJL	A/A	A/C	1864	525	78	18	0.819	0.486	1.380	5.33E-01	7.52E-02	878
2DL5	583	cohortMinusGroup2	CDX	G/G	G/A	521	242	29	10	0.742	0.356	1.550	5.35E-01	7.53E-02	879
2DL3	953	cohortMinusGroup2	JPT	G/G	G/A	1302	484	77	24	0.838	0.524	1.340	5.35E-01	7.53E-02	880
3DL3	692	cohortMinusGroup2	ASW	G/G	G/A	767	182	50	15	1.260	0.692	2.290	5.44E-01	7.54E-02	881
2DL4	395	cohortMinusGroup2	MSL	C/C	C/T	2073	221	79	6	0.712	0.307	1.650	5.45E-01	7.55E-02	882
2DL5	583	cohortMinusGroup2	CLM	G/G	G/A	526	244	24	8	0.719	0.318	1.620	5.46E-01	7.56E-02	883
3DL3	969	cohortMinusGroup2	STU	C/C	C/T	1576	388	62	12	0.786	0.419	1.470	5.46E-01	7.57E-02	884
2DP1	766	cohortMinusGroup2	PJL	G/G	G/C	1318	321	49	15	1.260	0.698	2.280	5.49E-01	7.58E-02	885
3DL3	455	cohortMinusGroup2	ITU	G/G	G/A	1361	84	99	4	0.655	0.235	1.820	5.51E-01	7.59E-02	886
3DL3	455	cohortMinusGroup2	STU	G/G	G/A	1361	84	99	4	0.655	0.235	1.820	5.51E-01	7.59E-02	886
3DL3	447	cohortMinusGroup2	STU	G/G	G/T	2120	297	92	10	0.776	0.400	1.510	5.51E-01	7.59E-02	887
3DP1	479	cohortMinusGroup2	BEB	A/A	A/C	1870	517	63	21	1.210	0.731	2.000	5.52E-01	7.60E-02	888
2DP1	522	cohortMinusGroup2	FIN	T/T	T/C	1637	517	76	20	0.833	0.504	1.380	5.55E-01	7.61E-02	889
3DL3	502	cohortMinusGroup2	ITU	G/G	G/A	629	1104	18	39	1.230	0.698	2.170	5.56E-01	7.62E-02	890
3DL1	1026	cohortMinusGroup2	PEL	G/G	G/C	1172	186	53	6	0.713	0.302	1.680	5.61E-01	7.63E-02	891
3DL2	893	cohortMinusGroup2	KHV	G/G	G/A	2116	298	91	10	0.780	0.401	1.520	5.63E-01	7.64E-02	892
3DL1	1021	cohortMinusGroup2	PUR	A/A	A/G	1213	137	64	5	0.692	0.274	1.750	5.63E-01	7.65E-02	893
2DP1	1269	cohortMinusGroup2	TSI	A/A	A/G	1369	71	97	7	1.390	0.623	3.100	5.63E-01	7.65E-02	894
2DL4	1023	cohortMinusGroup2	ITU	G/G	G/A	1485	648	70	26	0.851	0.537	1.350	5.66E-01	7.66E-02	895
2DP1	766	cohortMinusGroup2	YRI	G/G	G/C	1310	319	57	17	1.220	0.700	2.130	5.70E-01	7.67E-02	896
3DL2	456	cohortMinusGroup2	KHV	C/C	C/T	2119	297	91	10	0.784	0.404	1.520	5.72E-01	7.68E-02	897
3DL1	1194	cohortMinusGroup2	GWD	C/C	C/T	1843	179	98	12	1.260	0.679	2.340	5.73E-01	7.69E-02	898
2DL4	886	cohortMinusGroup2	YRI	C/C	C/G	684	44	91	8	1.370	0.625	3.000	5.74E-01	7.70E-02	899
2DP1	491	cohortMinusGroup2	ESN	T/T	T/C	615	34	90	7	1.410	0.607	3.280	5.77E-01	7.71E-02	900
3DL2	394	cohortMinusGroup2	ACB	C/C	C/A	2193	231	89	7	0.747	0.342	1.630	5.77E-01	7.71E-02	901
3DL3	869	cohortMinusGroup2	ACB	A/A	A/C	1872	520	70	23	1.180	0.729	1.910	5.77E-01	7.72E-02	902
3DL3	961	cohortMinusGroup2	JPT	C/C	C/A	923	343	76	24	0.850	0.528	1.370	5.79E-01	7.73E-02	903
2DP1	1219	cohortMinusGroup2	ESN	A/A	A/G	614	34	90	7	1.400	0.603	3.250	5.79E-01	7.74E-02	904
3DL3	408	cohortMinusGroup2	GBR	G/G	G/A	1623	630	67	22	0.846	0.518	1.380	5.83E-01	7.75E-02	905
3DL2	497	cohortMinusGroup2	PEL	G/G	G/A	1759	181	80	6	0.729	0.314	1.690	5.84E-01	7.76E-02	906
3DL1	1180	cohortMinusGroup2	MXL	G/G	G/C	1479	403	47	10	0.781	0.391	1.560	5.90E-01	7.77E-02	907
2DL4	412	cohortMinusGroup2	GBR	G/G	G/A	938	986	45	41	0.867	0.563	1.340	5.90E-01	7.77E-02	908
3DL3	502	cohortMinusGroup2	CLM	G/G	G/A	625	1097	22	46	1.190	0.709	2.000	5.93E-01	7.78E-02	909
2DL4	480	cohortMinusGroup2	ACB	G/G	G/A	1623	349	74	19	1.190	0.709	2.000	5.93E-01	7.79E-02	910
2DL3	953	cohortMinusGroup2	PUR	G/G	G/A	1331	487	48	21	1.200	0.711	2.020	5.95E-01	7.80E-02	911
2DL5	583	cohortMinusGroup2	ASW	G/G	G/A	534	247	16	5	0.676	0.245	1.870	6.01E-01	7.81E-02	912
3DL2	893	cohortMinusGroup2	YRI	G/G	G/A	2110	297	97	11	0.806	0.427	1.520	6.04E-01	7.82E-02	913
2DP1	816	cohortMinusGroup2	LWK	G/G	G/A	684	57	71	4	0.676	0.238	1.920	6.10E-01	7.83E-02	914
3DP1	479	cohortMinusGroup2	JPT	A/A	A/C	1855	513	78	25	1.160	0.732	1.840	6.13E-01	7.83E-02	915
3DL2	394	cohortMinusGroup2	YRI	C/C	C/A	2188	226	94	12	1.240	0.670	2.300	6.13E-01	7.84E-02	916
3DL2	456	cohortMinusGroup2	YRI	C/C	C/T	2113	296	97	11	0.810	0.429	1.530	6.15E-01	7.85E-02	917
2DP1	1000	cohortMinusGroup2	ESN	A/A	A/G	278	24	58	7	1.400	0.576	3.400	6.20E-01	7.86E-02	918
2DP1	448	cohortMinusGroup2	MSL	G/G	G/C	610	821	28	32	0.849	0.506	1.430	6.27E-01	7.87E-02	919
3DL2	394	cohortMinusGroup2	PUR	C/C	C/A	2185	230	97	8	0.784	0.376	1.630	6.29E-01	7.88E-02	920
3DP1	774	cohortMinusGroup2	CDX	G/G	G/C	1554	722	69	28	0.873	0.558	1.370	6.30E-01	7.89E-02	921
3DL3	971	cohortMinusGroup2	PEL	T/T	T/C	1656	335	67	11	0.812	0.425	1.550	6.33E-01	7.89E-02	922
2DL4	762	cohortMinusGroup2	ACB	C/C	C/T	1086	934	49	37	0.878	0.568	1.360	6.35E-01	7.90E-02	923
2DP1	1313	cohortMinusGroup2	ITU	A/A	A/C	1376	536	53	24	1.160	0.709	1.900	6.38E-01	7.91E-02	924
3DL3	804	cohortMinusGroup2	BEB	G/G	G/A	1445	679	59	24	0.866	0.534	1.400	6.42E-01	7.92E-02	925
3DL3	869	cohortMinusGroup2	KHV	A/A	A/C	1867	519	75	24	1.150	0.719	1.840	6.43E-01	7.93E-02	926
2DL4	395	cohortMinusGroup2	ACB	C/C	C/T	2067	220	85	7	0.774	0.354	1.690	6.44E-01	7.94E-02	927
3DL1	496	cohortMinusGroup2	PUR	C/C	C/A	1716	126	93	5	0.732	0.292	1.830	6.44E-01	7.95E-02	928
3DL3	971	cohortMinusGroup2	CEU	T/T	T/C	1660	331	63	15	1.190	0.669	2.120	6.52E-01	7.95E-02	929
3DL1	732	cohortMinusGroup2	CLM	T/T	T/C	375	250	18	15	1.250	0.618	2.530	6.60E-01	7.96E-02	930
2DL5	517	cohortMinusGroup2	CLM	A/A	A/G	595	244	28	9	0.784	0.365	1.690	6.60E-01	7.97E-02	931
3DL3	699	cohortMinusGroup2	MSL	G/G	G/A	769	72	76	9	1.260	0.606	2.620	6.68E-01	7.98E-02	932
2DL4	412	cohortMinusGroup2	CLM	G/G	G/A	940	987	43	40	0.886	0.571	1.380	6.69E-01	7.99E-02	933
2DL4	1023	cohortMinusGroup2	IBS	G/G	G/A	1480	645	75	29	0.887	0.572	1.380	6.70E-01	8.00E-02	934
2DP1	766	cohortMinusGroup2	GBR	G/G	G/C	1323	323	44	13	1.210	0.644	2.270	6.71E-01	8.01E-02	935
3DL3	961	cohortMinusGroup2	CLM	C/C	C/A	951	352	48	15	0.844	0.467	1.530	6.78E-01	8.01E-02	936
3DL1	1021	cohortMinusGroup2	GWD	A/A	A/G	1203	132	74	10	1.230	0.620	2.440	6.82E-01	8.02E-02	937
2DL5	517	cohortMinusGroup2	ASW	A/A	A/G	606	248	17	5	0.719	0.262	1.970	6.84E-01	8.03E-02	938
2DL4	1023	cohortMinusGroup2	TSI	G/G	G/A	1478	644	77	30	0.894	0.580	1.380	6.89E-01	8.04E-02	939
3DL3	869	cohortMinusGroup2	IBS	A/A	A/C	1857	522	85	21	0.879	0.540	1.430	6.90E-01	8.05E-02	940
2DL4	395	cohortMinusGroup2	STU	C/C	C/T	2059	219	93	8	0.809	0.388	1.690	6.94E-01	8.06E-02	941
3DL3	804	cohortMinusGroup2	MXL	G/G	G/A	1463	681	41	22	1.150	0.680	1.950	6.94E-01	8.07E-02	942
3DL3	971	cohortMinusGroup2	KHV	T/T	T/C	1642	332	81	14	0.855	0.479	1.530	6.96E-01	8.07E-02	943
3DL1	1091	cohortMinusGroup2	ASW	G/G	G/A	1133	193	37	8	1.270	0.583	2.770	6.99E-01	8.08E-02	944
3DL2	394	cohortMinusGroup2	GWD	C/C	C/A	2178	229	104	9	0.823	0.411	1.650	7.00E-01	8.09E-02	945
2DP1	1313	cohortMinusGroup2	MXL	A/A	A/C	1387	541	42	19	1.160	0.669	2.010	7.02E-01	8.10E-02	946
2DP1	522	cohortMinusGroup2	LWK	T/T	T/C	1648	514	65	23	1.130	0.695	1.840	7.02E-01	8.11E-02	947
2DL5	517	cohortMinusGroup2	IBS	A/A	A/G	601	242	22	11	1.240	0.592	2.600	7.04E-01	8.12E-02	948
3DL2	893	cohortMinusGroup2	JPT	G/G	G/A	2114	297	93	11	0.842	0.445	1.590	7.06E-01	8.13E-02	949
3DL2	456	cohortMinusGroup2	GWD	C/C	C/T	2109	295	101	12	0.849	0.461	1.560	7.06E-01	8.13E-02	950
2DL5	517	cohortMinusGroup2	CDX	A/A	A/G	593	243	30	10	0.813	0.391	1.690	7.07E-01	8.14E-02	951
3DL3	447	cohortMinusGroup2	GWD	G/G	G/T	2111	295	101	12	0.850	0.462	1.570	7.08E-01	8.15E-02	952
2DL5	517	cohortMinusGroup2	MSL	A/A	A/G	601	246	22	7	0.777	0.328	1.840	7.15E-01	8.16E-02	953
3DL2	456	cohortMinusGroup2	JPT	C/C	C/T	2117	296	93	11	0.846	0.448	1.600	7.17E-01	8.17E-02	954
3DL1	1303	cohortMinusGroup2	MXL	A/A	A/G	1127	108	57	4	0.732	0.261	2.060	7.19E-01	8.18E-02	955
2DP1	448	cohortMinusGroup2	IBS	G/G	G/C	607	816	31	37	0.888	0.545	1.450	7.25E-01	8.19E-02	956
3DL3	699	cohortMinusGroup2	LWK	G/G	G/A	757	71	88	10	1.210	0.602	2.430	7.26E-01	8.19E-02	957
2DL3	953	cohortMinusGroup2	MSL	G/G	G/A	1332	493	47	15	0.862	0.478	1.560	7.29E-01	8.20E-02	958
3DL1	1021	cohortMinusGroup2	MSL	A/A	A/G	1219	137	58	5	0.767	0.302	1.940	7.30E-01	8.21E-02	959
3DL3	971	cohortMinusGroup2	ESN	T/T	T/C	1658	331	65	15	1.160	0.654	2.060	7.32E-01	8.22E-02	960
3DP1	479	cohortMinusGroup2	MXL	A/A	A/C	1883	522	50	16	1.150	0.650	2.040	7.33E-01	8.23E-02	961
3DL3	502	cohortMinusGroup2	GIH	G/G	G/A	626	1101	21	42	1.140	0.669	1.940	7.34E-01	8.24E-02	962
3DL3	621	cohortMinusGroup2	STU	G/G	G/A	1697	216	93	10	0.845	0.433	1.650	7.37E-01	8.25E-02	963
3DP1	796	cohortMinusGroup2	CDX	T/T	T/C	1556	723	69	29	0.905	0.581	1.410	7.39E-01	8.25E-02	964
2DP1	1219	cohortMinusGroup2	YRI	A/A	A/G	606	34	98	7	1.270	0.548	2.940	7.39E-01	8.26E-02	965
3DP1	774	cohortMinusGroup2	CEU	G/G	G/C	1560	718	63	32	1.100	0.712	1.700	7.40E-01	8.27E-02	966
3DL1	732	cohortMinusGroup2	PJL	T/T	T/C	378	257	15	8	0.784	0.328	1.880	7.41E-01	8.28E-02	967

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DP1	1313	cohortMinusGroup2	CEU	A/A	A/C	1379	538	50	22	1.130	0.678	1.880	7.43E-01	8.29E-02	968
2DP1	491	cohortMinusGroup2	ACB	T/T	T/C	615	37	90	4	0.739	0.257	2.120	7.47E-01	8.30E-02	969
3DL3	1042	cohortMinusGroup2	GIH	G/G	G/C	978	140	39	7	1.250	0.548	2.850	7.54E-01	8.31E-02	970
3DL1	1194	cohortMinusGroup2	CDX	C/C	C/T	1866	185	75	6	0.807	0.347	1.880	7.64E-01	8.31E-02	971
2DL4	395	cohortMinusGroup2	ITU	C/C	C/T	2062	216	90	11	1.170	0.616	2.220	7.65E-01	8.32E-02	972
2DP1	522	cohortMinusGroup2	MXL	T/T	T/C	1665	520	48	17	1.130	0.644	1.980	7.71E-01	8.33E-02	973
3DL3	447	cohortMinusGroup2	JPT	G/G	G/T	2123	293	89	14	1.140	0.640	2.030	7.71E-01	8.34E-02	974
3DL1	607	cohortMinusGroup2	MXL	C/C	C/T	1530	489	38	14	1.150	0.618	2.140	7.76E-01	8.35E-02	975
3DL1	1194	cohortMinusGroup2	FIN	C/C	C/T	1856	184	85	7	0.831	0.379	1.820	7.82E-01	8.36E-02	976
3DL3	1042	cohortMinusGroup2	FIN	G/G	G/C	951	136	66	11	1.170	0.603	2.270	7.83E-01	8.37E-02	977
2DL4	1019	cohortMinusGroup2	YRI	C/C	C/T	854	53	102	5	0.790	0.309	2.020	7.85E-01	8.37E-02	978
2DL3	953	cohortMinusGroup2	BEB	G/G	G/A	1333	493	46	15	0.882	0.488	1.590	7.87E-01	8.38E-02	979
3DL2	400	cohortMinusGroup2	GWD	C/C	C/G	524	23	107	6	1.280	0.509	3.220	7.87E-01	8.39E-02	980
3DL1	1026	cohortMinusGroup2	MSL	G/G	G/C	1158	180	67	12	1.150	0.610	2.170	7.88E-01	8.40E-02	981
3DL3	804	cohortMinusGroup2	CLM	G/G	G/A	1445	673	59	30	1.090	0.696	1.710	7.89E-01	8.41E-02	982
3DL2	893	cohortMinusGroup2	MXL	G/G	G/A	2147	301	60	7	0.832	0.377	1.840	7.90E-01	8.42E-02	983
2DP1	522	cohortMinusGroup2	PUR	T/T	T/C	1646	518	67	19	0.901	0.536	1.510	7.91E-01	8.43E-02	984
2DL4	625	cohortMinusGroup2	CDX	C/C	C/G	837	895	34	33	0.908	0.557	1.480	7.91E-01	8.43E-02	985
3DP1	796	cohortMinusGroup2	BEB	T/T	T/C	1566	727	59	25	0.913	0.567	1.470	7.97E-01	8.44E-02	986
2DL3	953	cohortMinusGroup2	MXL	G/G	G/A	1336	494	43	14	0.881	0.478	1.620	7.98E-01	8.45E-02	987
3DL1	1180	cohortMinusGroup2	KHV	G/G	G/C	1464	398	62	15	0.890	0.501	1.580	7.98E-01	8.46E-02	988
3DL2	456	cohortMinusGroup2	MXL	C/C	C/T	2150	300	60	7	0.836	0.379	1.850	7.99E-01	8.47E-02	989
3DL3	777	cohortMinusGroup2	GWD	A/A	A/G	1600	544	83	26	0.921	0.587	1.450	8.08E-01	8.48E-02	990
3DL2	394	cohortMinusGroup2	CDX	C/C	C/A	2193	230	89	8	0.857	0.410	1.790	8.15E-01	8.49E-02	991
2DP1	448	cohortMinusGroup2	YRI	G/G	G/C	604	804	34	49	1.080	0.689	1.690	8.17E-01	8.49E-02	992
3DL1	1194	cohortMinusGroup2	MSL	C/C	C/T	1868	185	73	6	0.830	0.356	1.930	8.17E-01	8.50E-02	993
2DL4	412	cohortMinusGroup2	MXL	G/G	G/A	956	996	27	31	1.100	0.652	1.860	8.18E-01	8.51E-02	994
3DL1	732	cohortMinusGroup2	IBS	T/T	T/C	374	254	19	11	0.852	0.399	1.820	8.24E-01	8.52E-02	995
2DL5	583	cohortMinusGroup2	ACB	G/G	G/A	527	243	23	9	0.849	0.387	1.860	8.29E-01	8.53E-02	996
3DL3	804	cohortMinusGroup2	GIH	G/G	G/A	1433	672	71	31	0.931	0.605	1.430	8.29E-01	8.54E-02	997
3DL2	456	cohortMinusGroup2	ESN	C/C	C/T	2126	294	84	13	1.120	0.617	2.030	8.32E-01	8.55E-02	998
2DL4	1023	cohortMinusGroup2	CLM	G/G	G/A	1495	646	60	28	1.080	0.683	1.710	8.33E-01	8.55E-02	999
3DL2	893	cohortMinusGroup2	GBR	G/G	G/A	2126	298	81	10	0.881	0.452	1.720	8.34E-01	8.56E-02	1000
3DL1	1194	cohortMinusGroup2	BEB	C/C	C/T	1871	183	70	8	1.170	0.554	2.470	8.36E-01	8.57E-02	1001
2DP1	766	cohortMinusGroup2	CLM	G/G	G/C	1325	327	42	9	0.868	0.418	1.800	8.41E-01	8.58E-02	1002
3DL3	804	cohortMinusGroup2	PJL	G/G	G/A	1442	672	62	31	1.070	0.689	1.660	8.42E-01	8.59E-02	1003
2DL4	412	cohortMinusGroup2	CDX	G/G	G/A	943	988	40	39	0.931	0.594	1.460	8.43E-01	8.60E-02	1004
3DL2	893	cohortMinusGroup2	ESN	G/G	G/A	2123	295	84	13	1.110	0.611	2.020	8.45E-01	8.60E-02	1005
3DL2	456	cohortMinusGroup2	GBR	C/C	C/T	2129	297	81	10	0.885	0.454	1.730	8.45E-01	8.61E-02	1006
3DL2	893	cohortMinusGroup2	FIN	G/G	G/A	2119	297	88	11	0.892	0.471	1.690	8.45E-01	8.62E-02	1007
3DL3	869	cohortMinusGroup2	ITU	A/A	A/C	1861	522	81	21	0.924	0.566	1.510	8.47E-01	8.63E-02	1008
3DL1	496	cohortMinusGroup2	CDX	C/C	C/A	1726	126	83	5	0.825	0.329	2.070	8.48E-01	8.64E-02	1009
3DL3	777	cohortMinusGroup2	ITU	A/A	A/G	1607	546	76	24	0.929	0.581	1.490	8.51E-01	8.65E-02	1010
3DL3	777	cohortMinusGroup2	STU	A/A	A/G	1607	546	76	24	0.929	0.581	1.490	8.51E-01	8.65E-02	1010
3DL3	502	cohortMinusGroup2	CEU	G/G	G/A	624	1099	23	44	1.090	0.652	1.820	8.53E-01	8.66E-02	1011
3DL2	456	cohortMinusGroup2	FIN	C/C	C/T	2122	296	88	11	0.896	0.473	1.700	8.57E-01	8.66E-02	1012
2DL3	953	cohortMinusGroup2	LWK	G/G	G/A	1329	488	50	20	1.090	0.642	1.850	8.57E-01	8.67E-02	1013
2DL4	625	cohortMinusGroup2	MXL	C/C	C/G	846	899	25	29	1.090	0.633	1.880	8.59E-01	8.68E-02	1014
3DL3	1042	cohortMinusGroup2	TSI	G/G	G/C	961	140	56	7	0.858	0.383	1.920	8.59E-01	8.69E-02	1015
3DL3	447	cohortMinusGroup2	FIN	G/G	G/T	2124	296	88	11	0.897	0.474	1.700	8.59E-01	8.70E-02	1016
2DP1	1313	cohortMinusGroup2	PUR	A/A	A/C	1382	540	47	20	1.090	0.640	1.860	8.60E-01	8.71E-02	1017
2DP1	899	cohortMinusGroup2	YRI	C/C	C/A	313	36	51	7	1.190	0.503	2.820	8.64E-01	8.72E-02	1018
3DL2	456	cohortMinusGroup2	IBS	C/C	C/T	2115	295	95	12	0.906	0.491	1.670	8.68E-01	8.72E-02	1019
3DL1	1194	cohortMinusGroup2	ITU	C/C	C/T	1860	182	81	9	1.140	0.563	2.310	8.69E-01	8.73E-02	1020
2DL4	395	cohortMinusGroup2	TSI	C/C	C/T	2058	216	94	11	1.110	0.585	2.110	8.70E-01	8.74E-02	1021
2DL4	480	cohortMinusGroup2	YRI	G/G	G/A	1611	348	86	20	1.080	0.655	1.780	8.74E-01	8.75E-02	1022
2DP1	491	cohortMinusGroup2	GWD	T/T	T/C	600	34	105	7	1.180	0.510	2.730	8.77E-01	8.76E-02	1023
2DL3	953	cohortMinusGroup2	GIH	G/G	G/A	1329	491	50	17	0.920	0.526	1.610	8.80E-01	8.77E-02	1024
3DL2	497	cohortMinusGroup2	YRI	G/G	G/A	1741	176	98	11	1.110	0.584	2.110	8.81E-01	8.78E-02	1025
2DP1	766	cohortMinusGroup2	PUR	G/G	G/C	1305	322	62	14	0.915	0.506	1.660	8.84E-01	8.78E-02	1026
3DL2	893	cohortMinusGroup2	IBS	G/G	G/A	2113	296	94	12	0.911	0.494	1.680	8.84E-01	8.79E-02	1027
3DL3	971	cohortMinusGroup2	ACB	T/T	T/C	1659	332	64	14	1.090	0.604	1.970	8.88E-01	8.80E-02	1028
3DP1	479	cohortMinusGroup2	CHS	A/A	A/C	1849	516	84	22	0.938	0.581	1.520	8.89E-01	8.81E-02	1029
3DP1	479	cohortMinusGroup2	CLM	A/A	A/C	1860	519	73	19	0.933	0.558	1.560	8.91E-01	8.82E-02	1030
2DL4	810	cohortMinusGroup2	GWD	A/A	A/AGT	44	49	6	5	0.748	0.213	2.620	8.93E-01	8.83E-02	1031
2DL4	810	cohortMinusGroup2	STU	A/A	A/AGT	44	46	6	8	1.280	0.411	3.990	8.94E-01	8.84E-02	1032
3DL1	1180	cohortMinusGroup2	ACB	G/G	G/C	1464	395	62	18	1.080	0.632	1.850	8.98E-01	8.84E-02	1033
3DL1	1021	cohortMinusGroup2	CHB	A/A	A/G	1215	136	62	6	0.865	0.367	2.040	9.00E-01	8.85E-02	1034
2DL5	517	cohortMinusGroup2	ACB	A/A	A/G	598	244	25	9	0.882	0.406	1.920	9.02E-01	8.86E-02	1035
3DP1	479	cohortMinusGroup2	GIH	A/A	A/C	1853	517	80	21	0.941	0.576	1.540	9.04E-01	8.87E-02	1036
3DL3	869	cohortMinusGroup2	CDX	A/A	A/C	1866	523	76	20	0.939	0.568	1.550	9.04E-01	8.88E-02	1037
2DP1	471	cohortMinusGroup2	FIN	A/A	A/G	1702	431	76	18	0.935	0.553	1.580	9.05E-01	8.89E-02	1038
3DL3	408	cohortMinusGroup2	CEU	G/G	G/A	1621	624	69	28	1.050	0.670	1.640	9.09E-01	8.90E-02	1039
3DL2	394	cohortMinusGroup2	ASW	C/C	C/A	2223	231	59	7	1.140	0.515	2.520	9.09E-01	8.90E-02	1040
3DL1	1194	cohortMinusGroup2	ACB	C/C	C/T	1861	184	80	7	0.885	0.403	1.940	9.10E-01	8.91E-02	1041
2DL4	395	cohortMinusGroup2	BEB	C/C	C/T	2075	218	77	9	1.110	0.549	2.250	9.12E-01	8.92E-02	1042
2DP1	766	cohortMinusGroup2	IBS	G/G	G/C	1314	324	53	12	0.918	0.485	1.740	9.18E-01	8.93E-02	1043
2DL4	1019	cohortMinusGroup2	LWK	C/C	C/T	861	53	95	5	0.855	0.334	2.190	9.21E-01	8.94E-02	1044
3DL1	607	cohortMinusGroup2	ACB	C/C	C/T	1500	480	68	23	1.060	0.653	1.720	9.21E-01	8.95E-02	1045
3DL3	408	cohortMinusGroup2	BEB	G/G	G/A	1631	628	59	24	1.060	0.654	1.720	9.22E-01	8.96E-02	1046
3DL3	906	cohortMinusGroup2	ITU	C/C	C/T	1645	493	76	24	1.050	0.656	1.680	9.23E-01	8.96E-02	1047
3DL3	906	cohortMinusGroup2	STU	C/C	C/T	1645	493	76	24	1.050	0.656	1.680	9.23E-01	8.96E-02	1047
2DL4	395	cohortMinusGroup2	GWD	C/C	C/T	2049	217	103	10	0.917	0.472	1.780	9.26E-01	8.97E-02	1048
2DP1	766	cohortMinusGroup2	ACB	G/G	G/C	1306	322	61	14	0.931	0.514	1.690	9.30E-01	8.98E-02	1049
3DL3	621	cohortMinusGroup2	PUR	G/G	G/A	1696	215	94	11	0.923	0.486	1.750	9.31E-01	8.99E-02	1050
3DL3	961	cohortMinusGroup2	GIH	C/C	C/A	958	353	41	14	0.927	0.499	1.720	9.32E-01	9.00E-02	1051
2DL5	583	cohortMinusGroup2	KHV	G/G	G/A	539	246	11	6	1.200	0.439	3.280	9.33E-01	9.01E-02	1052
2DP1	471	cohortMinusGroup2	ASW	A/A	A/G	1734	437	44	12	1.080	0.566	2.060	9.44E-01	9.02E-02	1053
3DL1	1091	cohortMinusGroup2	MSL	G/G	G/A	1105	189	65	12	1.080	0.572	2.040	9.44E-01	9.02E-02	1054
3DP1	479	cohortMinusGroup2	STU	A/A	A/C	1854	517	79	21	0.953	0.583	1.560	9.46E-01	9.03E-02	1055
2DP1	816	cohortMinusGroup2	ACB	G/G	G/A	672	55	83	6	0.883	0.369	2.110	9.48E-01	9.04E-02	1056
3DL3	447	cohortMinusGroup2	YRI	G/G	G/T	2117	293	95	14	1.060	0.597	1.880	9.49E-01	9.05E-02	1057
3DL1	1194	cohortMinusGroup2	CHB	C/C	C/T	1857	182	84	9	1.090	0.539	2.200	9.50E-01	9.06E-02	1058
2DL4	1023	cohortMinusGroup2	PUR	G/G	G/A	1486	643	69	31	1.040	0.674	1.600	9.53E-01	9.07E-02	1059
2DL4	1023	cohortMinusGroup2	BEB	G/G	G/A	1502	650	53	24	1.050	0.643	1.720	9.56E-01	9.08E-02	1060
3DL3	869	cohortMinusGroup2	GIH	A/A	A/C	1860	521	82	22	0.958	0.592	1.550	9.56E-01	9.08E-02	1061
3DL3	447	cohortMinusGroup2	MSL	G/G	G/T	2138	296	74	11	1.070	0.561	2.040	9.62E-01	9.09E-02	1062
3DL1	1021	cohortMinusGroup2	FIN	A/A	A/G	1226	137	51	5	0.877	0.344	2.230	9.62E-01	9.10E-02	1063
3DP1	939	cohortMinusGroup2	ACB	T/T	T/G	570	114	51	11	1.080	0.546	2.140	9.68E-01	9.11E-02	1064
3DL3	699	cohortMinusGroup2	ACB	G/G	G/A	758	72	87	9	1.090	0.527	2.260	9.69E-01	9.12E-02	1065
2DL4	625	cohortMinusGroup2	CLM	C/C	C/G	835	891	36	37	0.963	0.603	1.540	9.70E-01	9.13E-02	1066
3DL1	496	cohortMinusGroup2	KHV	C/C	C/A	1721	124	88	7	1.100	0.499	2.430	9.72E-01	9.14E-02	1067
3DP1	774	cohortMinusGroup2	PUR	G/G	G/C	1556	720	67	30	0.968	0.624	1.500	9.72E-01	9.14E-02	1068
3DL1	607	cohortMinusGroup2	KHV	C/C	C/T	1502	481	66	22	1.040	0.635	1.700	9.74E-01	9.15E-02	1069
2DP1	766	cohortMinusGroup2	FIN	G/G	G/C	1307	322	60	14	0.947	0.523	1.720	9.76E-01	9.16E-02	1070
3DP1	796	cohortMinusGroup2	CEU	T/T	T/C	1560	721	65	31	1.030	0.665	1.590	9.77E-01	9.17E-02	1071
2DL4	480	cohortMinusGroup2	ASW	G/G	G/A	1643	357	54	11	0.937	0.485	1.810	9.78E-01	9.18E-02	1072
3DL3	804	cohortMinusGroup2	GBR	G/G	G/A	1446	675	58	28	1.030	0.650	1.630	9.80E-01	9.19E-02	1073
3DL2	474	cohortMinusGroup2	CLM	G/G	G/T	1486	716	60	28	0.969	0.613	1.530	9.83E-01	9.20E-02	1074

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	1042	cohortMinusGroup2	ESN	G/G	G/C	966	139	51	8	1.090	0.507	2.350	9.84E-01	9.20E-02	1075
3DL2	393	cohortMinusGroup2	YRI	G/G	G/T	593	31	102	6	1.130	0.460	2.780	9.84E-01	9.21E-02	1076
3DL1	732	cohortMinusGroup2	ITU	T/T	T/C	381	256	12	9	1.120	0.465	2.700	9.85E-01	9.22E-02	1077
2DL4	762	cohortMinusGroup2	STU	C/C	C/T	1086	928	49	43	1.030	0.678	1.570	9.86E-01	9.23E-02	1078
2DP1	471	cohortMinusGroup2	TSI	A/A	A/G	1704	431	74	18	0.962	0.569	1.630	9.90E-01	9.24E-02	1079
3DL3	961	cohortMinusGroup2	PUR	C/C	C/A	948	349	51	18	0.959	0.553	1.660	9.92E-01	9.25E-02	1080
3DL3	869	cohortMinusGroup2	CLM	A/A	A/C	1868	523	74	20	0.965	0.583	1.600	9.92E-01	9.26E-02	1081
2DL4	480	cohortMinusGroup2	ESN	G/G	G/A	1617	350	80	18	1.040	0.616	1.760	9.92E-01	9.26E-02	1082
2DP1	471	cohortMinusGroup2	GBR	A/A	A/G	1712	433	66	16	0.958	0.549	1.670	9.93E-01	9.27E-02	1083
3DL3	447	cohortMinusGroup2	BEB	G/G	G/T	2138	297	74	10	0.973	0.497	1.900	1.00E+00	9.28E-02	1084
3DL3	447	cohortMinusGroup2	IBS	G/G	G/T	2118	294	94	13	0.996	0.551	1.800	1.00E+00	9.28E-02	1084
3DL3	455	cohortMinusGroup2	CEU	G/G	G/A	1367	82	93	6	1.080	0.459	2.540	1.00E+00	9.29E-02	1085
3DL3	455	cohortMinusGroup2	CLM	G/G	G/A	1371	83	89	5	0.928	0.367	2.350	1.00E+00	9.30E-02	1086
3DL1	496	cohortMinusGroup2	JPT	C/C	C/A	1717	124	92	7	1.050	0.477	2.310	1.00E+00	9.31E-02	1087
3DL2	394	cohortMinusGroup2	FIN	C/C	C/A	2192	229	90	9	0.957	0.476	1.920	1.00E+00	9.32E-02	1088
3DL2	497	cohortMinusGroup2	LWK	G/G	G/A	1750	178	89	9	0.994	0.492	2.010	1.00E+00	9.32E-02	1089
2DP1	471	cohortMinusGroup2	PUR	A/A	A/G	1709	431	69	18	1.030	0.607	1.750	1.00E+00	9.33E-02	1090
2DL3	953	cohortMinusGroup2	ASW	G/G	G/A	1342	495	37	13	0.953	0.502	1.810	1.00E+00	9.34E-02	1091
3DL1	1026	cohortMinusGroup2	ACB	G/G	G/C	1164	182	61	10	1.050	0.528	2.090	1.00E+00	9.35E-02	1092
2DL5	583	cohortMinusGroup2	MXL	G/G	G/A	530	243	20	9	0.981	0.440	2.190	1.00E+00	9.36E-02	1093
3DL3	621	cohortMinusGroup2	IBS	G/G	G/A	1695	214	95	12	1.000	0.540	1.850	1.00E+00	9.36E-02	1093
3DL3	621	cohortMinusGroup2	FIN	G/G	G/A	1702	215	88	11	0.990	0.521	1.880	1.00E+00	9.37E-02	1094
3DP1	939	cohortMinusGroup2	LWK	T/T	T/G	593	119	28	6	1.070	0.434	2.640	1.00E+00	9.38E-02	1095
2DL5	517	cohortMinusGroup2	KHV	A/A	A/G	607	247	16	6	0.922	0.357	2.380	1.00E+00	9.38E-02	1096
2DP1	471	cohortMinusGroup2	MXL	A/A	A/G	1727	436	51	13	1.010	0.544	1.870	1.00E+00	9.39E-02	1097
2DL4	1019	cohortMinusGroup2	ESN	C/C	C/T	863	52	93	6	1.070	0.448	2.560	1.00E+00	9.40E-02	1098
2DP1	1219	cohortMinusGroup2	GWD	A/A	A/G	598	35	106	6	0.967	0.397	2.360	1.00E+00	9.40E-02	1098
3DL3	447	cohortMinusGroup2	CLM	G/G	G/T	2129	296	83	11	0.953	0.502	1.810	1.00E+00	9.40E-02	1098
2DP1	491	cohortMinusGroup2	YRI	T/T	T/C	606	35	99	6	1.050	0.430	2.560	1.00E+00	9.41E-02	1099
3DL3	869	cohortMinusGroup2	TSI	A/A	A/C	1860	520	82	23	1.000	0.623	1.600	1.00E+00	9.41E-02	1099
3DL3	502	cohortMinusGroup2	GBR	G/G	G/A	622	1100	25	43	0.973	0.589	1.610	1.00E+00	9.42E-02	1100
3DL3	971	cohortMinusGroup2	PUR	T/T	T/C	1655	332	68	14	1.030	0.573	1.850	1.00E+00	9.42E-02	1100
3DP1	479	cohortMinusGroup2	CDX	A/A	A/C	1856	517	77	21	0.979	0.598	1.600	1.00E+00	9.42E-02	1100
3DL3	961	cohortMinusGroup2	MSL	C/C	C/T	313	88	53	15	1.010	0.543	1.880	1.00E+00	9.43E-02	1101
2DP1	522	cohortMinusGroup2	GBR	T/T	T/C	1648	517	65	20	0.981	0.589	1.630	1.00E+00	9.44E-02	1102
3DL1	607	cohortMinusGroup2	ASW	C/C	C/T	1523	489	45	14	0.969	0.527	1.780	1.00E+00	9.44E-02	1102
3DL1	732	cohortMinusGroup2	STU	T/T	T/C	376	254	17	11	0.958	0.441	2.080	1.00E+00	9.44E-02	1102
3DL1	607	cohortMinusGroup2	PEL	C/C	C/T	1510	484	58	19	1.020	0.602	1.730	1.00E+00	9.44E-02	1103
3DL1	732	cohortMinusGroup2	MXL	T/T	T/C	384	259	9	6	0.988	0.347	2.810	1.00E+00	9.44E-02	1103
3DL2	497	cohortMinusGroup2	ASW	G/G	G/A	1779	181	60	6	0.983	0.419	2.310	1.00E+00	9.44E-02	1103
3DL1	1021	cohortMinusGroup2	ITU	A/A	A/G	1222	136	55	6	0.980	0.414	2.320	1.00E+00	9.45E-02	1104
3DL1	1091	cohortMinusGroup2	ACB	G/G	G/A	1110	191	60	10	0.969	0.488	1.930	1.00E+00	9.45E-02	1104
3DL2	394	cohortMinusGroup2	STU	C/C	C/A	2190	228	92	10	1.040	0.534	2.030	1.00E+00	9.45E-02	1104
3DL3	447	cohortMinusGroup2	ITU	G/G	G/T	2122	294	90	13	1.040	0.574	1.880	1.00E+00	9.45E-02	1104
3DL3	621	cohortMinusGroup2	BEB	G/G	G/A	1715	217	75	9	0.948	0.468	1.920	1.00E+00	9.45E-02	1104
2DL4	762	cohortMinusGroup2	PJL	C/C	C/T	1092	935	43	36	0.978	0.623	1.540	1.00E+00	9.46E-02	1105
2DP1	766	cohortMinusGroup2	CEU	G/G	G/C	1331	327	36	9	1.020	0.486	2.140	1.00E+00	9.46E-02	1105
3DL1	496	cohortMinusGroup2	CEU	C/C	C/A	1723	125	86	6	0.962	0.412	2.240	1.00E+00	9.46E-02	1105
3DL1	496	cohortMinusGroup2	CHS	C/C	C/A	1715	124	94	7	1.030	0.468	2.270	1.00E+00	9.46E-02	1105
3DL1	496	cohortMinusGroup2	YRI	C/C	C/A	1710	124	99	7	0.975	0.443	2.140	1.00E+00	9.46E-02	1105
3DL1	732	cohortMinusGroup2	BEB	T/T	T/C	376	253	17	12	1.050	0.493	2.240	1.00E+00	9.46E-02	1105
3DL1	732	cohortMinusGroup2	PUR	T/T	T/C	379	256	14	9	0.952	0.406	2.230	1.00E+00	9.46E-02	1105
3DL1	1180	cohortMinusGroup2	MSL	G/G	G/C	1467	397	59	16	1.000	0.569	1.760	1.00E+00	9.46E-02	1105
3DL1	1194	cohortMinusGroup2	TSI	C/C	C/T	1856	183	85	8	0.955	0.455	2.000	1.00E+00	9.46E-02	1105
3DL2	456	cohortMinusGroup2	CEU	C/C	C/T	2123	295	87	12	0.993	0.536	1.840	1.00E+00	9.46E-02	1105
3DL2	497	cohortMinusGroup2	MXL	G/G	G/A	1778	181	61	6	0.966	0.412	2.270	1.00E+00	9.46E-02	1105
3DL2	893	cohortMinusGroup2	ACB	G/G	G/A	2123	296	84	12	1.020	0.550	1.890	1.00E+00	9.46E-02	1105
3DL2	893	cohortMinusGroup2	CEU	G/G	G/A	2120	296	87	12	0.988	0.534	1.830	1.00E+00	9.46E-02	1105
3DL3	408	cohortMinusGroup2	GIH	G/G	G/A	1616	624	74	28	0.980	0.628	1.530	1.00E+00	9.46E-02	1105
3DL3	455	cohortMinusGroup2	PUR	G/G	G/A	1361	82	99	6	1.010	0.430	2.370	1.00E+00	9.46E-02	1105
3DL3	869	cohortMinusGroup2	CHS	A/A	A/C	1859	520	83	23	0.991	0.618	1.590	1.00E+00	9.46E-02	1105
3DP1	479	cohortMinusGroup2	KHV	A/A	A/C	1856	516	77	22	1.030	0.635	1.670	1.00E+00	9.46E-02	1105
2DL4	395	cohortMinusGroup2	FIN	C/C	C/T	2065	218	87	9	0.980	0.486	1.970	1.00E+00	9.47E-02	1106
2DL4	886	cohortMinusGroup2	GWD	C/C	C/G	669	45	106	7	0.982	0.432	2.230	1.00E+00	9.47E-02	1106
2DL4	886	cohortMinusGroup2	MSL	C/C	C/G	695	47	80	5	0.924	0.357	2.390	1.00E+00	9.47E-02	1106
2DP1	448	cohortMinusGroup2	ASW	G/G	G/C	618	826	20	27	1.010	0.561	1.820	1.00E+00	9.47E-02	1106
2DP1	448	cohortMinusGroup2	ITU	G/G	G/C	609	815	29	38	0.979	0.597	1.610	1.00E+00	9.47E-02	1106
2DP1	899	cohortMinusGroup2	MSL	C/C	C/A	318	38	46	5	0.910	0.341	2.430	1.00E+00	9.47E-02	1106
3DL1	1021	cohortMinusGroup2	BEB	A/A	A/G	1221	136	56	6	0.962	0.407	2.270	1.00E+00	9.47E-02	1106
3DL2	394	cohortMinusGroup2	BEB	C/C	C/A	2204	230	78	8	0.983	0.469	2.060	1.00E+00	9.47E-02	1106
3DL2	456	cohortMinusGroup2	ACB	C/C	C/T	2126	295	84	12	1.030	0.556	1.910	1.00E+00	9.47E-02	1106
3DL2	474	cohortMinusGroup2	BEB	G/G	G/T	1492	718	54	26	1.000	0.621	1.610	1.00E+00	9.47E-02	1106
3DL2	474	cohortMinusGroup2	PUR	G/G	G/T	1478	711	68	33	1.010	0.660	1.550	1.00E+00	9.47E-02	1106
3DL3	621	cohortMinusGroup2	ITU	G/G	G/A	1699	214	91	12	1.050	0.566	1.950	1.00E+00	9.47E-02	1106
3DL3	961	cohortMinusGroup2	PJL	C/C	C/A	966	355	33	12	0.990	0.506	1.940	1.00E+00	9.47E-02	1106
3DP1	939	cohortMinusGroup2	YRI	T/T	T/G	559	112	62	13	1.050	0.558	1.970	1.00E+00	9.47E-02	1106
2DL4	810	cohortMinusGroup2	PJL	A/A	A/AGT	44	47	6	7	1.090	0.340	3.500	1.00E+00	9.48E-02	1107
2DL5	517	cohortMinusGroup2	MXL	A/A	A/G	601	244	22	9	1.010	0.459	2.220	1.00E+00	9.48E-02	1107
3DL2	393	cohortMinusGroup2	GWD	G/G	G/T	588	31	107	6	1.060	0.432	2.600	1.00E+00	9.48E-02	1107
3DL3	1042	cohortMinusGroup2	CLM	G/G	G/C	963	139	54	8	1.030	0.480	2.210	1.00E+00	9.48E-02	1107

Table A8b Chi square significance tests for KIR variants within the 1000 Genomes populations, heterozygous versus alternate homozygous

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DP1	448	cohortMinusGroup2	CHB	G/C	C/C	834	857	19	81	4.150	2.500	6.900	6.80E-09	2.33E-04	1
3DP1	774	cohortMinusGroup2	ESN	G/C	C/C	716	122	34	23	3.970	2.260	6.970	8.30E-07	4.66E-04	2
3DL3	502	cohortMinusGroup2	CHB	G/A	A/A	1106	683	37	62	2.710	1.780	4.120	2.15E-06	6.99E-04	3
3DL1	607	cohortMinusGroup2	GWD	C/T	T/T	467	274	36	0	0.000	0.000	NaN	1.32E-05	9.32E-04	4
2DL4	412	cohortMinusGroup2	ESN	G/A	A/A	994	463	33	42	2.730	1.710	4.360	2.38E-05	1.17E-03	5
2DP1	448	cohortMinusGroup2	JPT	G/C	C/C	826	864	27	74	2.620	1.670	4.110	2.38E-05	1.40E-03	6
3DP1	796	cohortMinusGroup2	ESN	T/C	C/C	714	125	38	22	3.310	1.890	5.790	2.40E-05	1.63E-03	7
3DL3	969	cohortMinusGroup2	PEL	C/T	T/T	358	77	42	28	3.100	1.810	5.310	3.99E-05	1.87E-03	8
2DL4	1023	cohortMinusGroup2	PEL	G/A	A/A	634	168	40	30	2.830	1.710	4.680	5.18E-05	2.10E-03	9
2DP1	448	cohortMinusGroup2	TSI	G/C	C/C	811	924	42	14	0.293	0.159	0.540	5.55E-05	2.33E-03	10
3DP1	774	cohortMinusGroup2	YRI	G/C	C/C	708	123	42	22	3.020	1.740	5.240	8.89E-05	2.56E-03	11
2DP1	448	cohortMinusGroup2	PEL	G/C	C/C	832	878	21	60	2.710	1.630	4.490	1.01E-04	2.80E-03	12
2DL4	625	cohortMinusGroup2	ESN	C/G	G/G	894	400	34	39	2.560	1.590	4.120	1.05E-04	3.03E-03	13
2DP1	448	cohortMinusGroup2	CHS	G/C	C/C	823	865	30	73	2.320	1.500	3.590	1.63E-04	3.26E-03	14
2DL4	1023	cohortMinusGroup2	CHB	G/A	A/A	623	165	51	33	2.440	1.520	3.910	2.35E-04	3.50E-03	15
2DP1	1313	cohortMinusGroup2	PJL	A/C	C/C	542	187	18	21	3.380	1.760	6.480	2.38E-04	3.73E-03	16
3DL2	474	cohortMinusGroup2	CHB	G/T	T/T	692	204	52	36	2.350	1.490	3.700	2.61E-04	3.96E-03	17
3DP1	796	cohortMinusGroup2	YRI	T/C	C/C	707	125	45	22	2.770	1.610	4.770	2.94E-04	4.20E-03	18
2DL5	517	cohortMinusGroup2	STU	A/G	G/G	218	409	35	24	0.365	0.212	0.629	3.23E-04	4.43E-03	19
2DL5	583	cohortMinusGroup2	STU	G/A	A/A	216	386	36	24	0.373	0.217	0.642	4.16E-04	4.66E-03	20
2DL4	625	cohortMinusGroup2	GWD	C/G	G/G	880	393	48	46	2.150	1.410	3.280	4.56E-04	4.90E-03	21
3DL3	502	cohortMinusGroup2	CHS	G/A	A/A	1100	689	43	56	2.080	1.380	3.130	5.17E-04	5.13E-03	22
2DL4	412	cohortMinusGroup2	GIH	G/A	A/A	992	503	35	2	0.113	0.027	0.472	5.97E-04	5.36E-03	23
2DL4	412	cohortMinusGroup2	GWD	G/A	A/A	979	458	48	47	2.090	1.380	3.170	6.22E-04	5.59E-03	24
2DP1	448	cohortMinusGroup2	CDX	G/C	C/C	828	877	25	61	2.300	1.430	3.700	6.24E-04	5.83E-03	25
2DL5	583	cohortMinusGroup2	PUR	G/A	A/A	250	383	2	27	8.810	2.080	37.400	8.39E-04	6.06E-03	26
2DP1	448	cohortMinusGroup2	GWD	G/C	C/C	813	921	40	17	0.375	0.211	0.667	8.70E-04	6.29E-03	27
2DL5	517	cohortMinusGroup2	PUR	A/G	G/G	251	405	2	28	8.680	2.050	36.800	9.20E-04	6.53E-03	28
3DL2	474	cohortMinusGroup2	CHS	G/T	T/T	690	205	54	35	2.180	1.390	3.430	9.30E-04	6.76E-03	29
3DL3	961	cohortMinusGroup2	CHS	C/A	A/A	345	239	22	1	0.066	0.009	0.490	9.61E-04	6.99E-03	30
2DP1	448	cohortMinusGroup2	YRI	G/C	C/C	804	914	49	24	0.431	0.262	0.709	1.02E-03	7.23E-03	31
3DL2	474	cohortMinusGroup2	CDX	G/T	T/T	698	209	46	31	2.250	1.390	3.640	1.20E-03	7.46E-03	32
2DL4	625	cohortMinusGroup2	YRI	C/G	G/G	890	402	38	37	2.160	1.350	3.450	1.59E-03	7.69E-03	33
3DL3	502	cohortMinusGroup2	YRI	G/A	A/A	1098	735	45	10	0.332	0.166	0.663	1.71E-03	7.93E-03	34
2DL3	953	cohortMinusGroup2	CHS	G/A	A/A	486	358	22	2	0.123	0.029	0.526	1.74E-03	8.16E-03	35
2DP1	522	cohortMinusGroup2	PJL	T/C	C/C	516	198	21	22	2.730	1.470	5.070	1.85E-03	8.39E-03	36
2DL4	412	cohortMinusGroup2	YRI	G/A	A/A	986	465	41	40	2.070	1.320	3.240	1.88E-03	8.63E-03	37
2DL4	412	cohortMinusGroup2	GBR	G/A	A/A	986	500	41	5	0.240	0.094	0.611	2.09E-03	8.86E-03	38
3DL3	408	cohortMinusGroup2	GWD	G/A	A/A	611	73	41	14	2.860	1.490	5.500	2.25E-03	9.09E-03	39
2DL3	953	cohortMinusGroup2	JPT	G/A	A/A	484	357	24	3	0.169	0.051	0.566	2.25E-03	9.32E-03	40
3DL3	502	cohortMinusGroup2	JPT	G/A	A/A	1098	691	45	54	1.910	1.270	2.870	2.29E-03	9.56E-03	41
2DP1	448	cohortMinusGroup2	KHV	G/C	C/C	823	874	30	64	2.010	1.290	3.130	2.47E-03	9.79E-03	42
2DL4	412	cohortMinusGroup2	LWK	G/A	A/A	991	469	36	36	2.110	1.310	3.390	2.51E-03	1.00E-02	43
2DL4	625	cohortMinusGroup2	GBR	C/G	G/G	894	436	34	3	0.181	0.055	0.593	2.77E-03	1.03E-02	44
2DP1	448	cohortMinusGroup2	FIN	G/C	C/C	806	913	47	25	0.470	0.287	0.771	3.28E-03	1.05E-02	45
3DL2	474	cohortMinusGroup2	PEL	G/T	T/T	701	212	43	28	2.150	1.300	3.550	3.48E-03	1.07E-02	46
2DL4	625	cohortMinusGroup2	CEU	C/G	G/G	903	438	25	1	0.083	0.011	0.611	3.67E-03	1.10E-02	47
3DL3	961	cohortMinusGroup2	JPT	C/A	A/A	343	237	24	3	0.181	0.054	0.608	3.86E-03	1.12E-02	48
2DL4	412	cohortMinusGroup2	IBS	G/A	A/A	992	501	35	4	0.226	0.080	0.639	3.94E-03	1.14E-02	49
3DL3	502	cohortMinusGroup2	GWD	G/A	A/A	1101	735	42	10	0.357	0.178	0.716	3.94E-03	1.17E-02	50
3DL1	732	cohortMinusGroup2	PEL	T/C	C/C	252	106	13	17	3.110	1.460	6.630	4.30E-03	1.19E-02	51
2DL4	412	cohortMinusGroup2	STU	G/A	A/A	989	500	38	5	0.260	0.102	0.665	4.31E-03	1.21E-02	52
3DL3	961	cohortMinusGroup2	TSI	C/A	A/A	345	209	22	31	2.330	1.310	4.130	5.00E-03	1.24E-02	53
2DP1	448	cohortMinusGroup2	BEB	G/C	C/C	814	918	39	20	0.455	0.263	0.786	5.84E-03	1.26E-02	54
2DL3	953	cohortMinusGroup2	GBR	G/A	A/A	487	328	21	32	2.260	1.280	3.990	6.17E-03	1.28E-02	55
3DL3	502	cohortMinusGroup2	ITU	G/A	A/A	1104	699	39	46	1.860	1.200	2.880	6.61E-03	1.31E-02	56
2DL4	412	cohortMinusGroup2	PEL	G/A	A/A	989	470	38	35	1.940	1.210	3.110	7.75E-03	1.33E-02	57
3DL3	961	cohortMinusGroup2	GBR	C/A	A/A	345	210	22	30	2.240	1.260	3.990	8.01E-03	1.35E-02	58
3DL2	474	cohortMinusGroup2	GBR	G/T	T/T	708	238	36	2	0.165	0.039	0.690	9.12E-03	1.38E-02	59
3DL3	502	cohortMinusGroup2	ASW	G/A	A/A	1109	737	34	8	0.354	0.163	0.769	9.95E-03	1.40E-02	60
2DL4	625	cohortMinusGroup2	MSL	C/G	G/G	892	407	36	32	1.950	1.190	3.180	1.00E-02	1.42E-02	61
2DP1	471	cohortMinusGroup2	PJL	A/G	G/G	430	163	19	18	2.500	1.280	4.880	1.01E-02	1.45E-02	62
2DL4	625	cohortMinusGroup2	GIH	C/G	G/G	903	437	25	2	0.165	0.039	0.700	1.02E-02	1.47E-02	63
2DL5	517	cohortMinusGroup2	CHB	A/G	G/G	252	416	1	17	10.300	1.360	77.900	1.10E-02	1.49E-02	64
3DL2	474	cohortMinusGroup2	JPT	G/T	T/T	694	211	50	29	1.910	1.180	3.100	1.17E-02	1.52E-02	65
3DP1	479	cohortMinusGroup2	TSI	A/C	C/C	494	46	44	11	2.680	1.300	5.540	1.19E-02	1.54E-02	66
2DL5	583	cohortMinusGroup2	CHB	G/A	A/A	251	394	1	16	10.200	1.340	77.400	1.19E-02	1.56E-02	67
3DL1	732	cohortMinusGroup2	GBR	T/C	C/C	249	123	16	0	0.000	0.000	NaN	1.21E-02	1.59E-02	68
2DL4	625	cohortMinusGroup2	STU	C/G	G/G	890	433	38	6	0.325	0.136	0.775	1.23E-02	1.61E-02	69
3DL1	607	cohortMinusGroup2	CEU	C/T	T/T	477	246	26	28	2.090	1.200	3.640	1.25E-02	1.63E-02	70
2DL4	762	cohortMinusGroup2	CHS	C/T	T/T	937	262	34	1	0.105	0.014	0.771	1.26E-02	1.66E-02	71
2DL4	625	cohortMinusGroup2	IBS	C/G	G/G	904	437	24	2	0.172	0.041	0.731	1.31E-02	1.68E-02	72
2DL3	953	cohortMinusGroup2	TSI	G/A	A/A	483	326	25	34	2.010	1.180	3.430	1.35E-02	1.70E-02	73
3DL2	474	cohortMinusGroup2	ITU	G/T	T/T	716	239	28	1	0.107	0.015	0.791	1.44E-02	1.73E-02	74
2DL4	762	cohortMinusGroup2	JPT	C/T	T/T	945	263	26	0	0.000	0.000	NaN	1.47E-02	1.75E-02	75
2DL4	1023	cohortMinusGroup2	GBR	G/A	A/A	638	196	36	2	0.181	0.043	0.759	1.52E-02	1.77E-02	76
2DL4	1023	cohortMinusGroup2	TSI	G/A	A/A	644	197	30	1	0.109	0.015	0.804	1.56E-02	1.80E-02	77
2DL4	412	cohortMinusGroup2	MSL	G/A	A/A	991	473	36	32	1.860	1.140	3.030	1.65E-02	1.82E-02	78
2DL4	412	cohortMinusGroup2	CEU	G/A	A/A	998	501	29	4	0.275	0.096	0.787	1.70E-02	1.84E-02	79
3DL2	474	cohortMinusGroup2	KHV	G/T	T/T	697	213	47	27	1.880	1.140	3.090	1.74E-02	1.87E-02	80
3DL1	607	cohortMinusGroup2	ACB	C/T	T/T	480	271	23	3	0.231	0.069	0.776	1.79E-02	1.89E-02	81
3DL1	1180	cohortMinusGroup2	GWD	G/C	C/C	374	154	39	5	0.311	0.120	0.804	1.84E-02	1.91E-02	82
2DL4	625	cohortMinusGroup2	LWK	C/G	G/G	904	416	24	23	2.080	1.160	3.730	1.85E-02	1.94E-02	83
2DP1	471	cohortMinusGroup2	STU	A/G	G/G	423	160	26	21	2.140	1.170	3.910	1.90E-02	1.96E-02	84
3DL3	502	cohortMinusGroup2	ESN	G/A	A/A	1105	734	38	11	0.436	0.221	0.858	2.03E-02	1.98E-02	85
3DL3	804	cohortMinusGroup2	GWD	G/A	A/A	662	111	41	15	2.180	1.170	4.070	2.10E-02	2.01E-02	86
3DL3	502	cohortMinusGroup2	MXL	G/A	A/A	1103	733	40	12	0.451	0.235	0.865	2.10E-02	2.03E-02	87
2DL5	517	cohortMinusGroup2	CHS	A/G	G/G	250	412	3	21	4.250	1.250	14.400	2.12E-02	2.05E-02	88
2DL5	583	cohortMinusGroup2	CHS	G/A	A/A	249	390	3	20	4.260	1.250	14.500	2.16E-02	2.08E-02	89
2DL5	583	cohortMinusGroup2	YRI	G/A	A/A	249	390	3	20	4.260	1.250	14.500	2.16E-02	2.08E-02	89
2DP1	766	cohortMinusGroup2	PJL	G/C	C/C	321	75	15	10	2.850	1.230	6.590	2.22E-02	2.10E-02	90
3DL3	502	cohortMinusGroup2	PUR	G/A	A/A	1091	727	52	18	0.519	0.301	0.894	2.30E-02	2.12E-02	91
2DL4	412	cohortMinusGroup2	TSI	G/A	A/A	994	499	33	6	0.362	0.151	0.870	2.83E-02	2.15E-02	92
2DL5	517	cohortMinusGroup2	YRI	A/G	G/G	250	413	3	20	4.040	1.190	13.700	2.85E-02	2.17E-02	93
2DP1	1313	cohortMinusGroup2	GIH	A/C	C/C	532	188	28	20	2.020	1.110	3.670	2.92E-02	2.19E-02	94
2DL3	953	cohortMinusGroup2	CDX	G/A	A/A	489	356	19	4	0.289	0.098	0.857	3.07E-02	2.21E-02	95
3DL3	502	cohortMinusGroup2	CDX	G/A	A/A	1101	701	42	44	1.650	1.070	2.540	3.08E-02	2.24E-02	96
3DL2	474	cohortMinusGroup2	TSI	G/T	T/T	715	238	29	2	0.207	0.049	0.874	3.15E-02	2.26E-02	97
2DP1	1313	cohortMinusGroup2	CLM	A/C	C/C	545	195	15	13	2.420	1.130	5.180	3.32E-02	2.28E-02	98
2DL5	583	cohortMinusGroup2	GWD	G/A	A/A	246	384	6	26	2.780	1.130	6.850	3.40E-02	2.31E-02	99
3DP1	774	cohortMinusGroup2	FIN	G/C	C/C	713	144	37	1	0.134	0.018	0.985	3.62E-02	2.33E-02	100
3DL2	474	cohortMinusGroup2	STU	G/T	T/T	716	238	28	2	0.215	0.051	0.909	3.75E-02	2.35E-02	101
2DL3	953	cohortMinusGroup2	PEL	G/A	A/A	497	359	11	1	0.126	0.016	0.980	4.02E-02	2.38E-02	102
3DL3	502	cohortMinusGroup2	GIH	G/A	A/A	1101	702	42	43	1.610	1.040	2.490	4.19E-02	2.40E-02	103
2DP1	448	cohortMinusGroup2	ASW	G/C	C/C	826	923	27	15	0.497	0.263	0.941	4.22E-02	2.42E-02	104
2DL5	583	cohortMinusGroup2	PJL	G/A	A/A	228	389	24	21	0.513	0.279	0.942	4.28E-02	2.45E-02	105
2DP1	1313	cohortMinusGroup2	FIN	A/C	C/C	532	205	28	3	0.278	0.084	0.924	4.34E-02	2.47E-02	106

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL2	474	cohortMinusGroup2	GIH	G/T	T/T	722	239	22	1	0.137	0.018	1.020	4.35E-02	2.49E-02	107
3DL3	906	cohortMinusGroup2	TSI	C/T	T/T	474	61	43	12	2.170	1.080	4.340	4.35E-02	2.52E-02	108
2DL3	953	cohortMinusGroup2	KHV	G/A	A/A	488	355	20	5	0.344	0.128	0.925	4.49E-02	2.54E-02	109
3DL3	961	cohortMinusGroup2	KHV	C/A	A/A	348	236	19	4	0.310	0.104	0.923	4.58E-02	2.56E-02	110
2DL5	517	cohortMinusGroup2	GWD	A/G	G/G	247	407	6	26	2.630	1.070	6.480	4.66E-02	2.59E-02	111
2DL4	762	cohortMinusGroup2	GIH	C/T	T/T	926	242	45	21	1.790	1.050	3.060	4.68E-02	2.61E-02	112
2DP1	448	cohortMinusGroup2	ESN	G/C	C/C	810	909	43	29	0.601	0.372	0.972	4.80E-02	2.63E-02	113
2DP1	522	cohortMinusGroup2	MXL	T/C	C/C	520	219	17	1	0.140	0.019	1.060	5.00E-02	2.66E-02	114
2DL4	625	cohortMinusGroup2	CLM	C/G	G/G	891	431	37	8	0.447	0.206	0.968	5.33E-02	2.68E-02	115
2DL4	625	cohortMinusGroup2	FIN	C/G	G/G	891	431	37	8	0.447	0.206	0.968	5.33E-02	2.68E-02	115
3DL1	607	cohortMinusGroup2	YRI	C/T	T/T	484	271	19	3	0.282	0.083	0.962	5.39E-02	2.70E-02	116
3DL3	502	cohortMinusGroup2	LWK	G/A	A/A	1101	730	42	15	0.539	0.297	0.979	5.43E-02	2.73E-02	117
2DL5	583	cohortMinusGroup2	JPT	G/A	A/A	249	393	3	17	3.590	1.040	12.400	5.44E-02	2.75E-02	118
3DL3	502	cohortMinusGroup2	IBS	G/A	A/A	1084	721	59	24	0.612	0.377	0.993	5.81E-02	2.77E-02	119
3DL1	607	cohortMinusGroup2	IBS	C/T	T/T	466	242	37	32	1.670	1.010	2.750	5.85E-02	2.80E-02	120
2DL5	517	cohortMinusGroup2	PJL	A/G	G/G	230	411	23	22	0.535	0.292	0.981	5.92E-02	2.82E-02	121
2DP1	471	cohortMinusGroup2	CLM	A/G	G/G	439	171	10	10	2.570	1.050	6.280	5.94E-02	2.84E-02	122
2DL3	953	cohortMinusGroup2	ESN	G/A	A/A	481	351	27	9	0.457	0.212	0.984	6.06E-02	2.87E-02	123
3DL2	474	cohortMinusGroup2	CEU	G/T	T/T	719	238	25	2	0.242	0.057	1.030	6.34E-02	2.89E-02	124
2DL4	412	cohortMinusGroup2	CLM	G/A	A/A	987	495	40	10	0.498	0.247	1.000	6.73E-02	2.91E-02	125
3DL3	502	cohortMinusGroup2	ACB	G/A	A/A	1104	731	39	14	0.542	0.292	1.010	6.75E-02	2.94E-02	126
3DL3	502	cohortMinusGroup2	MSL	G/A	A/A	1108	733	35	12	0.518	0.267	1.000	6.77E-02	2.96E-02	127
2DL5	517	cohortMinusGroup2	JPT	A/G	G/G	250	416	3	17	3.410	0.989	11.800	6.83E-02	2.98E-02	128
2DL5	583	cohortMinusGroup2	CEU	G/A	A/A	240	402	12	8	0.398	0.160	0.988	6.91E-02	3.01E-02	129
2DP1	522	cohortMinusGroup2	STU	T/C	C/C	507	199	30	21	1.780	0.995	3.180	6.98E-02	3.03E-02	130
2DL4	1023	cohortMinusGroup2	GIH	G/A	A/A	653	197	21	1	0.158	0.021	1.180	7.16E-02	3.05E-02	131
3DL3	961	cohortMinusGroup2	GIH	C/A	A/A	353	222	14	18	2.040	0.995	4.180	7.17E-02	3.08E-02	132
3DP1	796	cohortMinusGroup2	LWK	T/C	C/C	712	133	40	14	1.870	0.990	3.530	7.63E-02	3.10E-02	133
3DL2	474	cohortMinusGroup2	PUR	G/T	T/T	711	236	33	4	0.365	0.128	1.040	7.75E-02	3.12E-02	134
2DL3	953	cohortMinusGroup2	CHB	G/A	A/A	494	357	14	3	0.297	0.085	1.040	7.75E-02	3.15E-02	135
3DL1	732	cohortMinusGroup2	CHB	T/C	C/C	253	111	12	12	2.280	0.994	5.230	7.80E-02	3.17E-02	136
2DP1	448	cohortMinusGroup2	ACB	G/C	C/C	813	910	40	28	0.625	0.382	1.020	7.82E-02	3.19E-02	137
2DL4	762	cohortMinusGroup2	PEL	C/T	T/T	943	261	28	2	0.258	0.061	1.090	7.88E-02	3.22E-02	138
2DL4	762	cohortMinusGroup2	PUR	C/T	T/T	926	243	45	20	1.690	0.980	2.920	7.89E-02	3.24E-02	139
2DL4	412	cohortMinusGroup2	FIN	G/A	A/A	988	495	39	10	0.512	0.253	1.030	8.08E-02	3.26E-02	140
2DL4	625	cohortMinusGroup2	PEL	C/G	G/G	892	412	36	27	1.620	0.970	2.700	8.33E-02	3.29E-02	141
3DL1	607	cohortMinusGroup2	FIN	C/T	T/T	472	247	31	27	1.660	0.969	2.840	8.41E-02	3.31E-02	142
3DL2	474	cohortMinusGroup2	IBS	G/T	T/T	716	237	28	3	0.324	0.098	1.080	8.44E-02	3.33E-02	143
3DL1	607	cohortMinusGroup2	JPT	C/T	T/T	483	270	20	4	0.358	0.121	1.060	8.54E-02	3.36E-02	144
2DP1	448	cohortMinusGroup2	CLM	G/C	C/C	831	899	22	39	1.640	0.964	2.790	8.74E-02	3.38E-02	145
2DL4	1023	cohortMinusGroup2	CEU	G/A	A/A	649	196	25	2	0.265	0.062	1.130	9.02E-02	3.40E-02	146
3DP1	774	cohortMinusGroup2	LWK	G/C	C/C	712	132	38	13	1.850	0.959	3.570	9.73E-02	3.43E-02	147
3DL3	906	cohortMinusGroup2	IBS	C/T	T/T	474	62	43	11	1.960	0.961	4.000	9.78E-02	3.45E-02	148
2DL4	412	cohortMinusGroup2	ASW	G/A	A/A	1000	483	27	22	1.690	0.953	3.000	9.86E-02	3.47E-02	149
2DL4	625	cohortMinusGroup2	TSI	C/G	G/G	903	434	25	5	0.416	0.158	1.090	1.02E-01	3.50E-02	150
2DP1	1313	cohortMinusGroup2	ESN	A/C	C/C	529	203	31	5	0.420	0.161	1.100	1.03E-01	3.52E-02	151
2DP1	471	cohortMinusGroup2	FIN	A/G	G/G	431	179	18	2	0.268	0.062	1.170	1.03E-01	3.54E-02	152
2DP1	522	cohortMinusGroup2	GIH	T/C	C/C	513	203	24	17	1.790	0.942	3.400	1.05E-01	3.57E-02	153
3DL3	961	cohortMinusGroup2	CHB	C/A	A/A	353	237	14	3	0.319	0.091	1.120	1.05E-01	3.59E-02	154
2DL4	1023	cohortMinusGroup2	IBS	G/A	A/A	645	195	29	3	0.342	0.103	1.130	1.05E-01	3.61E-02	155
2DL5	517	cohortMinusGroup2	GIH	A/G	G/G	233	413	20	20	0.564	0.297	1.070	1.09E-01	3.64E-02	156
2DL4	762	cohortMinusGroup2	TSI	C/T	T/T	921	242	50	21	1.600	0.943	2.720	1.09E-01	3.66E-02	157
2DL5	583	cohortMinusGroup2	GBR	G/A	A/A	240	401	12	9	0.449	0.186	1.080	1.09E-01	3.68E-02	158
2DP1	448	cohortMinusGroup2	MSL	G/C	C/C	821	916	32	22	0.616	0.355	1.070	1.10E-01	3.71E-02	159
2DP1	1313	cohortMinusGroup2	MXL	A/C	C/C	541	206	19	2	0.276	0.064	1.200	1.12E-01	3.73E-02	160
2DL4	625	cohortMinusGroup2	KHV	C/G	G/G	879	425	49	14	0.591	0.323	1.080	1.13E-01	3.75E-02	161
3DL3	777	cohortMinusGroup2	IBS	A/G	G/G	525	68	45	11	1.890	0.933	3.830	1.15E-01	3.78E-02	162
2DL4	1023	cohortMinusGroup2	JPT	G/A	A/A	619	174	55	24	1.550	0.933	2.580	1.17E-01	3.80E-02	163
3DL3	961	cohortMinusGroup2	CDX	C/A	A/A	349	235	18	5	0.413	0.151	1.130	1.18E-01	3.82E-02	164
2DL4	625	cohortMinusGroup2	ASW	C/G	G/G	904	420	24	19	1.700	0.921	3.140	1.20E-01	3.85E-02	165
3DL3	502	cohortMinusGroup2	PJL	G/A	A/A	1090	722	53	23	0.655	0.398	1.080	1.20E-01	3.87E-02	166
2DP1	1313	cohortMinusGroup2	STU	A/C	C/C	526	188	34	20	1.650	0.927	2.940	1.22E-01	3.89E-02	167
3DP1	796	cohortMinusGroup2	MSL	T/C	C/C	717	135	35	12	1.820	0.921	3.600	1.22E-01	3.92E-02	168
2DL5	517	cohortMinusGroup2	GBR	A/G	G/G	241	423	12	10	0.475	0.202	1.120	1.28E-01	3.94E-02	169
2DP1	1313	cohortMinusGroup2	GBR	A/C	C/C	534	204	26	4	0.403	0.139	1.170	1.29E-01	3.96E-02	170
2DP1	522	cohortMinusGroup2	FIN	T/C	C/C	517	217	20	3	0.357	0.105	1.210	1.38E-01	3.99E-02	171
2DP1	522	cohortMinusGroup2	GBR	T/C	C/C	517	217	20	3	0.357	0.105	1.210	1.38E-01	3.99E-02	171
3DL1	1180	cohortMinusGroup2	TSI	G/C	C/C	390	144	23	15	1.770	0.899	3.490	1.40E-01	4.01E-02	172
2DL4	762	cohortMinusGroup2	IBS	C/T	T/T	913	240	58	23	1.510	0.913	2.500	1.42E-01	4.03E-02	173
2DL5	517	cohortMinusGroup2	FIN	A/G	G/G	248	414	5	19	2.280	0.841	6.180	1.49E-01	4.06E-02	174
2DL4	412	cohortMinusGroup2	ITU	G/A	A/A	989	494	38	11	0.580	0.294	1.140	1.51E-01	4.08E-02	175
2DL5	583	cohortMinusGroup2	FIN	G/A	A/A	247	392	5	18	2.270	0.832	6.190	1.55E-01	4.10E-02	176
3DL1	607	cohortMinusGroup2	ESN	C/T	T/T	488	271	15	3	0.360	0.103	1.250	1.55E-01	4.13E-02	177
2DL4	1023	cohortMinusGroup2	PUR	G/A	A/A	643	194	31	4	0.428	0.149	1.230	1.56E-01	4.15E-02	178
3DL3	502	cohortMinusGroup2	KHV	G/A	A/A	1096	703	47	42	1.390	0.907	2.130	1.56E-01	4.17E-02	179
3DL3	777	cohortMinusGroup2	TSI	A/G	G/G	528	69	42	10	1.820	0.874	3.790	1.61E-01	4.20E-02	180
2DL4	625	cohortMinusGroup2	BEB	C/G	G/G	897	431	31	8	0.537	0.245	1.180	1.61E-01	4.22E-02	181
2DL4	1023	cohortMinusGroup2	STU	G/A	A/A	648	195	26	3	0.383	0.115	1.280	1.64E-01	4.24E-02	182
2DP1	522	cohortMinusGroup2	MSL	T/C	C/C	509	202	28	18	1.620	0.877	2.990	1.66E-01	4.27E-02	183
3DL3	961	cohortMinusGroup2	ITU	C/A	A/A	348	220	19	20	1.670	0.872	3.200	1.67E-01	4.29E-02	184
2DL5	517	cohortMinusGroup2	ITU	A/G	G/G	232	410	21	23	0.620	0.336	1.140	1.68E-01	4.31E-02	185
3DL1	1180	cohortMinusGroup2	ESN	G/C	C/C	386	154	27	5	0.464	0.175	1.230	1.68E-01	4.34E-02	186
3DL1	732	cohortMinusGroup2	CDX	T/C	C/C	254	113	11	10	2.040	0.842	4.940	1.70E-01	4.36E-02	187
2DL5	517	cohortMinusGroup2	CEU	A/G	G/G	241	422	12	11	0.523	0.227	1.200	1.85E-01	4.38E-02	188
2DP1	471	cohortMinusGroup2	GIH	A/G	G/G	428	167	21	14	1.710	0.850	3.440	1.86E-01	4.41E-02	189
2DP1	522	cohortMinusGroup2	ASW	T/C	C/C	512	215	25	5	0.476	0.180	1.260	1.87E-01	4.43E-02	190
3DL1	1180	cohortMinusGroup2	CEU	G/C	C/C	397	148	16	11	1.840	0.835	4.060	1.88E-01	4.45E-02	191
3DL1	607	cohortMinusGroup2	TSI	C/T	T/T	476	252	27	22	1.540	0.859	2.760	1.92E-01	4.48E-02	192
2DL4	412	cohortMinusGroup2	PJL	G/A	A/A	993	495	34	10	0.590	0.289	1.200	1.93E-01	4.50E-02	193
3DL1	607	cohortMinusGroup2	CDX	C/T	T/T	488	260	15	14	1.750	0.832	3.680	1.95E-01	4.52E-02	194
3DL3	502	cohortMinusGroup2	TSI	G/A	A/A	1093	722	50	23	0.696	0.421	1.150	1.95E-01	4.55E-02	195
3DL1	607	cohortMinusGroup2	MSL	C/T	T/T	489	271	14	3	0.387	0.110	1.360	2.00E-01	4.57E-02	196
2DL3	953	cohortMinusGroup2	GWD	G/A	A/A	483	334	25	26	1.500	0.851	2.640	2.03E-01	4.59E-02	197
2DL4	762	cohortMinusGroup2	PJL	C/T	T/T	935	248	36	15	1.570	0.846	2.910	2.05E-01	4.62E-02	198
2DP1	471	cohortMinusGroup2	ESN	A/G	G/G	418	174	31	7	0.542	0.234	1.250	2.06E-01	4.64E-02	199
2DL4	412	cohortMinusGroup2	MXL	G/A	A/A	996	496	31	9	0.583	0.275	1.230	2.09E-01	4.66E-02	200
2DL4	762	cohortMinusGroup2	KHV	C/T	T/T	935	258	36	5	0.503	0.195	1.290	2.09E-01	4.69E-02	201
2DL4	1023	cohortMinusGroup2	CDX	G/A	A/A	635	181	39	17	1.530	0.846	2.770	2.12E-01	4.71E-02	202
2DL5	583	cohortMinusGroup2	GIH	G/A	A/A	233	390	19	20	0.629	0.329	1.200	2.14E-01	4.73E-02	203
3DL1	1180	cohortMinusGroup2	FIN	G/C	C/C	388	144	25	15	1.620	0.831	3.160	2.16E-01	4.76E-02	204
3DP1	796	cohortMinusGroup2	TSI	T/C	C/C	710	143	42	4	0.473	0.167	1.340	2.16E-01	4.78E-02	205
2DL4	625	cohortMinusGroup2	ITU	C/G	G/G	891	428	37	11	0.619	0.313	1.230	2.18E-01	4.80E-02	206
3DL1	607	cohortMinusGroup2	PUR	C/T	T/T	480	255	23	19	1.550	0.829	2.900	2.21E-01	4.83E-02	207
2DP1	471	cohortMinusGroup2	LWK	A/G	G/G	437	172	12	9	1.910	0.791	4.610	2.26E-01	4.85E-02	208
2DL5	583	cohortMinusGroup2	ITU	G/A	A/A	231	387	21	23	0.654	0.354	1.210	2.28E-01	4.87E-02	209
2DP1	471	cohortMinusGroup2	YRI	A/G	G/G	427	167	22	14	1.630	0.815	3.260	2.31E-01	4.90E-02	210
2DL4	625	cohortMinusGroup2	PJL	C/G	G/G	894	429	34	10	0.613	0.300	1.250	2.33E-01	4.92E-02	211
2DL4	412	cohortMinusGroup2	KHV	G/A	A/A	975	487	52	18	0.693	0.401	1.200	2.34E-01	4.94E-02	212
3DL3	969	cohortMinusGroup2	CHS	C/T	T/T	342	95	58	10	0.621	0.306	1.260	2.42E-01	4.97E-02	213

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL2	474	cohortMinusGroup2	FIN	G/T	T/T	707	233	37	7	0.574	0.252	1.300	2.46E-01	4.99E-02	214
2DP1	448	cohortMinusGroup2	STU	G/C	C/C	819	911	34	27	0.714	0.427	1.190	2.46E-01	5.01E-02	215
3DL1	1180	cohortMinusGroup2	ACB	G/C	C/C	395	156	18	3	0.422	0.123	1.450	2.46E-01	5.04E-02	216
3DL3	502	cohortMinusGroup2	BEB	G/A	A/A	1104	711	39	34	1.350	0.844	2.160	2.52E-01	5.06E-02	217
2DL5	583	cohortMinusGroup2	IBS	G/A	A/A	241	400	11	10	0.548	0.229	1.310	2.52E-01	5.08E-02	218
2DL4	762	cohortMinusGroup2	CEU	C/T	T/T	924	245	47	18	1.440	0.822	2.520	2.56E-01	5.11E-02	219
2DL4	762	cohortMinusGroup2	FIN	C/T	T/T	924	245	47	18	1.440	0.822	2.520	2.56E-01	5.11E-02	219
2DP1	1313	cohortMinusGroup2	TSI	A/C	C/C	525	200	35	8	0.600	0.274	1.320	2.67E-01	5.13E-02	220
3DL1	732	cohortMinusGroup2	KHV	T/C	C/C	249	111	16	12	1.680	0.769	3.670	2.69E-01	5.15E-02	221
2DL3	953	cohortMinusGroup2	CLM	G/A	A/A	496	346	12	14	1.670	0.763	3.650	2.72E-01	5.18E-02	222
2DL4	762	cohortMinusGroup2	BEB	C/T	T/T	924	255	47	8	0.617	0.288	1.320	2.78E-01	5.20E-02	223
3DL1	607	cohortMinusGroup2	KHV	C/T	T/T	481	267	22	7	0.573	0.242	1.360	2.80E-01	5.22E-02	224
2DL4	762	cohortMinusGroup2	ESN	C/T	T/T	948	253	23	10	1.630	0.766	3.470	2.88E-01	5.25E-02	225
3DL1	607	cohortMinusGroup2	ITU	C/T	T/T	491	263	12	11	1.710	0.744	3.930	2.90E-01	5.27E-02	226
2DP1	448	cohortMinusGroup2	GBR	G/C	C/C	824	915	29	23	0.714	0.410	1.240	2.93E-01	5.29E-02	227
2DP1	766	cohortMinusGroup2	GIH	G/C	C/C	314	76	22	9	1.690	0.748	3.820	2.97E-01	5.32E-02	228
2DP1	448	cohortMinusGroup2	CEU	G/C	C/C	820	911	33	27	0.736	0.439	1.230	3.02E-01	5.34E-02	229
3DL1	732	cohortMinusGroup2	JPT	T/C	C/C	252	113	13	10	1.720	0.732	4.040	3.07E-01	5.36E-02	230
2DP1	448	cohortMinusGroup2	ITU	G/C	C/C	815	906	38	32	0.758	0.469	1.220	3.10E-01	5.39E-02	231
2DL4	625	cohortMinusGroup2	ACB	C/G	G/G	892	416	36	23	1.370	0.802	2.340	3.11E-01	5.41E-02	232
3DL3	969	cohortMinusGroup2	CHB	C/T	T/T	359	90	41	15	1.460	0.774	2.750	3.19E-01	5.43E-02	233
3DL1	732	cohortMinusGroup2	CHS	T/C	C/C	250	112	15	11	1.640	0.730	3.680	3.25E-01	5.46E-02	234
2DL4	412	cohortMinusGroup2	CHB	G/A	A/A	974	472	53	33	1.280	0.818	2.000	3.27E-01	5.48E-02	235
3DL1	607	cohortMinusGroup2	LWK	C/T	T/T	491	271	12	3	0.453	0.127	1.620	3.29E-01	5.50E-02	236
3DP1	796	cohortMinusGroup2	CEU	T/C	C/C	721	144	31	3	0.485	0.146	1.610	3.30E-01	5.52E-02	237
2DL4	762	cohortMinusGroup2	CDX	C/T	T/T	939	258	32	5	0.569	0.219	1.470	3.31E-01	5.55E-02	238
3DP1	796	cohortMinusGroup2	IBS	T/C	C/C	715	143	37	4	0.541	0.190	1.540	3.41E-01	5.57E-02	239
2DL4	625	cohortMinusGroup2	MXL	C/G	G/G	899	430	29	9	0.649	0.305	1.380	3.41E-01	5.59E-02	240
2DL4	412	cohortMinusGroup2	PUR	G/A	A/A	985	490	42	15	0.718	0.394	1.310	3.45E-01	5.62E-02	241
2DP1	522	cohortMinusGroup2	TSI	T/C	C/C	507	212	30	8	0.638	0.288	1.410	3.51E-01	5.64E-02	242
2DL4	1023	cohortMinusGroup2	FIN	G/A	A/A	637	191	37	7	0.631	0.277	1.440	3.58E-01	5.66E-02	243
2DL4	762	cohortMinusGroup2	GWD	C/T	T/T	931	256	40	7	0.636	0.282	1.440	3.61E-01	5.69E-02	244
2DP1	1313	cohortMinusGroup2	MSL	A/C	C/C	531	193	29	15	1.420	0.745	2.710	3.67E-01	5.71E-02	245
2DP1	1313	cohortMinusGroup2	YRI	A/C	C/C	531	193	29	15	1.420	0.745	2.710	3.67E-01	5.71E-02	245
3DL3	804	cohortMinusGroup2	TSI	G/A	A/A	660	115	43	11	1.470	0.736	2.930	3.69E-01	5.73E-02	246
2DP1	471	cohortMinusGroup2	IBS	A/G	G/G	434	178	15	3	0.488	0.140	1.710	3.77E-01	5.76E-02	247
2DL5	517	cohortMinusGroup2	ASW	A/G	G/G	248	418	5	15	1.780	0.639	4.960	3.78E-01	5.78E-02	248
3DL1	607	cohortMinusGroup2	STU	C/T	T/T	493	265	10	9	1.670	0.670	4.160	3.82E-01	5.80E-02	249
2DL4	1023	cohortMinusGroup2	CHS	G/A	A/A	615	176	59	22	1.300	0.775	2.180	3.87E-01	5.83E-02	250
2DP1	522	cohortMinusGroup2	CLM	T/C	C/C	521	210	16	10	1.550	0.692	3.470	3.93E-01	5.85E-02	251
2DL5	583	cohortMinusGroup2	MSL	G/A	A/A	245	392	7	18	1.610	0.663	3.910	3.97E-01	5.87E-02	252
2DL4	1023	cohortMinusGroup2	CLM	G/A	A/A	646	193	28	5	0.598	0.228	1.570	3.98E-01	5.90E-02	253
2DL5	583	cohortMinusGroup2	ASW	G/A	A/A	247	396	5	14	1.750	0.623	4.920	4.06E-01	5.92E-02	254
3DL3	969	cohortMinusGroup2	KHV	C/T	T/T	367	93	33	12	1.430	0.711	2.880	4.09E-01	5.94E-02	255
2DL3	953	cohortMinusGroup2	CEU	G/A	A/A	482	336	26	24	1.320	0.745	2.340	4.14E-01	5.97E-02	256
3DL3	804	cohortMinusGroup2	PJL	G/A	A/A	672	123	31	3	0.529	0.159	1.760	4.16E-01	5.99E-02	257
2DL4	625	cohortMinusGroup2	PUR	C/G	G/G	886	424	42	15	0.746	0.409	1.360	4.16E-01	6.01E-02	258
3DL3	961	cohortMinusGroup2	CEU	C/A	A/A	344	220	23	20	1.360	0.730	2.530	4.19E-01	6.04E-02	259
3DP1	774	cohortMinusGroup2	MSL	G/C	C/C	718	136	32	9	1.480	0.691	3.170	4.20E-01	6.06E-02	260
3DL3	969	cohortMinusGroup2	JPT	C/T	T/T	348	95	52	10	0.704	0.345	1.440	4.24E-01	6.08E-02	261
3DL3	408	cohortMinusGroup2	ACB	G/A	A/A	611	79	41	8	1.510	0.683	3.340	4.27E-01	6.11E-02	262
3DL2	474	cohortMinusGroup2	MXL	G/T	T/T	719	235	25	5	0.612	0.232	1.620	4.33E-01	6.13E-02	263
3DL2	474	cohortMinusGroup2	PJL	G/T	T/T	719	235	25	5	0.612	0.232	1.620	4.33E-01	6.13E-02	263
2DP1	522	cohortMinusGroup2	BEB	T/C	C/C	512	206	25	14	1.390	0.708	2.730	4.33E-01	6.15E-02	264
2DP1	471	cohortMinusGroup2	ITU	A/G	G/G	423	174	26	7	0.655	0.279	1.540	4.34E-01	6.18E-02	265
2DP1	522	cohortMinusGroup2	ACB	T/C	C/C	503	210	34	10	0.704	0.342	1.450	4.34E-01	6.20E-02	266
3DL3	804	cohortMinusGroup2	MSL	G/A	A/A	668	117	35	9	1.470	0.689	3.140	4.34E-01	6.22E-02	267
2DL4	412	cohortMinusGroup2	BEB	G/A	A/A	996	494	31	11	0.715	0.356	1.430	4.35E-01	6.25E-02	268
2DL3	953	cohortMinusGroup2	ITU	G/A	A/A	493	345	15	15	1.430	0.690	2.960	4.38E-01	6.27E-02	269
3DL1	607	cohortMinusGroup2	PJL	C/T	T/T	494	266	9	8	1.650	0.629	4.330	4.40E-01	6.29E-02	270
2DP1	448	cohortMinusGroup2	IBS	G/C	C/C	816	905	37	33	0.804	0.498	1.300	4.40E-01	6.32E-02	271
3DL3	804	cohortMinusGroup2	IBS	G/A	A/A	658	115	45	11	1.400	0.703	2.790	4.43E-01	6.34E-02	272
2DL4	762	cohortMinusGroup2	LWK	C/T	T/T	945	253	26	10	1.440	0.685	3.030	4.50E-01	6.36E-02	273
3DL2	474	cohortMinusGroup2	CLM	G/T	T/T	716	234	28	6	0.656	0.268	1.600	4.66E-01	6.39E-02	274
2DL5	517	cohortMinusGroup2	MSL	A/G	G/G	246	415	7	18	1.520	0.626	3.690	4.68E-01	6.41E-02	275
3DL3	804	cohortMinusGroup2	FIN	G/A	A/A	667	122	36	4	0.607	0.212	1.740	4.76E-01	6.43E-02	276
2DL5	517	cohortMinusGroup2	IBS	A/G	G/G	242	420	11	13	0.681	0.300	1.540	4.78E-01	6.46E-02	277
2DL4	762	cohortMinusGroup2	ACB	C/T	T/T	934	256	37	7	0.690	0.304	1.570	4.82E-01	6.48E-02	278
3DL1	607	cohortMinusGroup2	PEL	C/T	T/T	484	267	19	7	0.668	0.277	1.610	4.86E-01	6.50E-02	279
2DL4	762	cohortMinusGroup2	ITU	C/T	T/T	926	254	45	9	0.729	0.352	1.510	4.95E-01	6.53E-02	280
3DL3	969	cohortMinusGroup2	CDX	C/T	T/T	354	96	46	9	0.721	0.341	1.530	4.96E-01	6.55E-02	281
3DL3	777	cohortMinusGroup2	CEU	A/G	G/G	535	72	35	7	1.490	0.638	3.480	4.98E-01	6.57E-02	282
2DL4	762	cohortMinusGroup2	YRI	C/T	T/T	943	258	28	5	0.653	0.250	1.710	5.09E-01	6.60E-02	283
2DL3	953	cohortMinusGroup2	GIH	G/A	A/A	491	344	17	16	1.340	0.668	2.690	5.14E-01	6.62E-02	284
3DL1	1180	cohortMinusGroup2	ITU	G/C	C/C	401	152	12	7	1.540	0.595	3.980	5.26E-01	6.64E-02	285
3DL3	906	cohortMinusGroup2	CEU	C/T	T/T	482	66	35	7	1.460	0.623	3.420	5.26E-01	6.67E-02	286
3DP1	774	cohortMinusGroup2	GBR	G/C	C/C	712	140	38	5	0.669	0.259	1.730	5.34E-01	6.69E-02	287
3DP1	774	cohortMinusGroup2	CEU	G/C	C/C	718	141	32	4	0.637	0.222	1.830	5.38E-01	6.71E-02	288
3DL3	804	cohortMinusGroup2	PUR	G/A	A/A	656	120	47	6	0.698	0.292	1.670	5.38E-01	6.74E-02	289
3DL3	961	cohortMinusGroup2	PJL	C/A	A/A	355	229	12	11	1.420	0.616	3.270	5.41E-01	6.76E-02	290
2DL5	583	cohortMinusGroup2	ACB	G/A	A/A	243	400	9	10	0.675	0.270	1.680	5.43E-01	6.78E-02	291
2DL3	953	cohortMinusGroup2	LWK	G/A	A/A	488	342	20	18	1.280	0.667	2.460	5.58E-01	6.81E-02	292
2DL4	1023	cohortMinusGroup2	MXL	G/A	A/A	649	193	25	5	0.673	0.254	1.780	5.61E-01	6.83E-02	293
2DP1	1313	cohortMinusGroup2	PUR	A/C	C/C	540	203	20	5	0.665	0.246	1.800	5.61E-01	6.85E-02	294
2DL4	762	cohortMinusGroup2	MXL	C/T	T/T	944	258	27	5	0.678	0.259	1.780	5.64E-01	6.88E-02	295
3DL3	961	cohortMinusGroup2	IBS	C/A	A/A	338	217	29	23	1.240	0.699	2.200	5.65E-01	6.90E-02	296
3DL1	732	cohortMinusGroup2	BEB	T/C	C/C	253	115	12	8	1.470	0.585	3.690	5.67E-01	6.92E-02	297
2DL5	517	cohortMinusGroup2	KHV	A/G	G/G	247	418	6	15	1.480	0.567	3.860	5.67E-01	6.95E-02	298
3DP1	796	cohortMinusGroup2	ACB	T/C	C/C	708	136	44	11	1.300	0.655	2.580	5.71E-01	6.97E-02	299
3DL3	961	cohortMinusGroup2	BEB	C/A	A/A	352	227	15	13	1.340	0.626	2.870	5.72E-01	6.99E-02	300
2DP1	1313	cohortMinusGroup2	BEB	A/C	C/C	535	196	25	12	1.310	0.646	2.660	5.75E-01	7.02E-02	301
2DP1	522	cohortMinusGroup2	IBS	T/C	C/C	519	215	18	5	0.671	0.246	1.830	5.81E-01	7.04E-02	302
2DL4	762	cohortMinusGroup2	STU	C/T	T/T	928	254	43	9	0.765	0.368	1.590	5.84E-01	7.06E-02	303
3DP1	796	cohortMinusGroup2	GWD	T/C	C/C	703	135	49	12	1.280	0.663	2.470	5.84E-01	7.09E-02	304
3DL2	474	cohortMinusGroup2	BEB	G/T	T/T	718	234	26	6	0.708	0.288	1.740	5.85E-01	7.11E-02	305
2DL5	517	cohortMinusGroup2	ACB	A/G	G/G	244	422	9	11	0.707	0.289	1.730	5.97E-01	7.13E-02	306
2DL5	583	cohortMinusGroup2	KHV	G/A	A/A	246	396	6	14	1.450	0.550	3.820	6.03E-01	7.16E-02	307
2DP1	448	cohortMinusGroup2	GIH	G/C	C/C	820	907	33	31	0.849	0.515	1.400	6.07E-01	7.18E-02	308
3DP1	774	cohortMinusGroup2	IBS	G/C	C/C	714	140	36	5	0.708	0.273	1.840	6.20E-01	7.20E-02	309
3DL3	502	cohortMinusGroup2	GBR	G/A	A/A	1100	721	43	24	0.852	0.513	1.420	6.22E-01	7.23E-02	310
2DP1	448	cohortMinusGroup2	PJL	G/C	C/C	825	912	28	26	0.840	0.489	1.440	6.22E-01	7.25E-02	311
2DL5	583	cohortMinusGroup2	ESN	G/A	A/A	247	398	5	12	1.490	0.519	4.280	6.23E-01	7.27E-02	312
2DP1	522	cohortMinusGroup2	YRI	T/C	C/C	507	205	30	15	1.240	0.653	2.350	6.30E-01	7.30E-02	313
3DL3	502	cohortMinusGroup2	STU	G/A	A/A	1090	706	53	39	1.140	0.746	1.740	6.31E-01	7.32E-02	314
3DL3	502	cohortMinusGroup2	CLM	G/A	A/A	1097	719	46	26	0.862	0.528	1.410	6.38E-01	7.34E-02	315
2DP1	522	cohortMinusGroup2	ESN	T/C	C/C	509	211	28	9	0.775	0.360	1.670	6.42E-01	7.37E-02	316
3DL1	607	cohortMinusGroup2	MXL	C/T	T/T	489	264	14	10	1.320	0.578	3.010	6.53E-01	7.39E-02	317
3DP1	796	cohortMinusGroup2	ASW	T/C	C/C	725	140	27	7	1.340	0.572	3.140	6.57E-01	7.41E-02	318
2DL4	625	cohortMinusGroup2	CHB	C/G	G/G	882	414	46	25	1.160	0.703	1.910	6.57E-01	7.44E-02	319

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DL4	1023	cohortMinusGroup2	BEB	G/A	A/A	650	189	24	9	1.290	0.590	2.820	6.70E-01	7.46E-02	320
2DL3	953	cohortMinusGroup2	STU	G/A	A/A	496	349	12	11	1.300	0.567	2.980	6.80E-01	7.48E-02	321
3DL3	804	cohortMinusGroup2	GIH	G/A	A/A	672	122	31	4	0.711	0.247	2.050	6.93E-01	7.51E-02	322
2DL5	517	cohortMinusGroup2	ESN	A/G	G/G	248	421	5	12	1.410	0.491	4.050	6.95E-01	7.53E-02	323
3DP1	774	cohortMinusGroup2	TSI	G/C	C/C	710	139	40	6	0.766	0.319	1.840	6.96E-01	7.55E-02	324
2DL5	517	cohortMinusGroup2	BEB	A/G	G/G	237	410	16	23	0.831	0.430	1.600	7.03E-01	7.58E-02	325
2DP1	766	cohortMinusGroup2	BEB	G/C	C/C	311	77	25	8	1.290	0.560	2.970	7.05E-01	7.60E-02	326
3DL3	408	cohortMinusGroup2	YRI	G/A	A/A	603	82	49	5	0.750	0.290	1.940	7.07E-01	7.62E-02	327
2DL4	412	cohortMinusGroup2	ACB	G/A	A/A	982	480	45	25	1.140	0.691	1.880	7.11E-01	7.65E-02	328
3DL3	502	cohortMinusGroup2	CEU	G/A	A/A	1099	713	44	32	1.120	0.704	1.780	7.17E-01	7.67E-02	329
3DL3	502	cohortMinusGroup2	PEL	G/A	A/A	1099	713	44	32	1.120	0.704	1.780	7.17E-01	7.67E-02	329
3DL1	1180	cohortMinusGroup2	YRI	G/C	C/C	390	152	23	7	0.781	0.328	1.860	7.25E-01	7.69E-02	330
2DP1	766	cohortMinusGroup2	STU	G/C	C/C	307	76	29	9	1.250	0.568	2.750	7.26E-01	7.72E-02	331
3DL1	607	cohortMinusGroup2	GBR	C/T	T/T	471	254	32	20	1.160	0.650	2.070	7.27E-01	7.74E-02	332
2DL5	583	cohortMinusGroup2	TSI	G/A	A/A	238	391	14	19	0.826	0.407	1.680	7.30E-01	7.76E-02	333
3DL3	408	cohortMinusGroup2	TSI	G/A	A/A	610	80	42	7	1.270	0.552	2.920	7.37E-01	7.79E-02	334
3DL3	804	cohortMinusGroup2	YRI	G/A	A/A	655	119	48	7	0.803	0.355	1.820	7.38E-01	7.81E-02	335
2DL4	1023	cohortMinusGroup2	ITU	G/A	A/A	648	192	26	6	0.779	0.316	1.920	7.42E-01	7.83E-02	336
2DL5	583	cohortMinusGroup2	CDX	G/A	A/A	242	397	10	13	0.792	0.342	1.830	7.45E-01	7.86E-02	337
3DL3	804	cohortMinusGroup2	ACB	G/A	A/A	661	117	42	9	1.210	0.574	2.550	7.63E-01	7.88E-02	338
2DL4	1023	cohortMinusGroup2	KHV	G/A	A/A	626	182	48	16	1.150	0.638	2.070	7.64E-01	7.90E-02	339
2DP1	1313	cohortMinusGroup2	GWD	A/C	C/C	517	194	43	14	0.868	0.464	1.620	7.72E-01	7.93E-02	340
3DL1	607	cohortMinusGroup2	CHS	C/T	T/T	485	266	18	8	0.810	0.348	1.890	7.80E-01	7.95E-02	341
2DL3	953	cohortMinusGroup2	MXL	G/A	A/A	494	352	14	8	0.802	0.333	1.930	7.84E-01	7.97E-02	342
3DL1	1180	cohortMinusGroup2	CHS	G/C	C/C	399	155	14	4	0.735	0.238	2.270	7.88E-01	8.00E-02	343
3DL1	1180	cohortMinusGroup2	JPT	G/C	C/C	401	153	12	6	1.310	0.483	3.550	7.91E-01	8.02E-02	344
3DL3	969	cohortMinusGroup2	CLM	C/T	T/T	382	99	18	6	1.290	0.499	3.340	7.93E-01	8.04E-02	345
3DL1	607	cohortMinusGroup2	ASW	C/T	T/T	489	268	14	6	0.782	0.297	2.060	7.93E-01	8.07E-02	346
3DL3	804	cohortMinusGroup2	LWK	G/A	A/A	668	121	35	5	0.789	0.303	2.050	7.94E-01	8.09E-02	347
3DL3	961	cohortMinusGroup2	CLM	C/A	A/A	352	232	15	8	0.809	0.338	1.940	7.96E-01	8.11E-02	348
2DL3	953	cohortMinusGroup2	PUR	G/A	A/A	487	343	21	17	1.150	0.598	2.210	8.03E-01	8.14E-02	349
3DL1	1180	cohortMinusGroup2	GBR	G/C	C/C	391	149	22	10	1.190	0.550	2.570	8.06E-01	8.16E-02	350
3DL1	1180	cohortMinusGroup2	PUR	G/C	C/C	391	149	22	10	1.190	0.550	2.570	8.06E-01	8.16E-02	350
2DL3	953	cohortMinusGroup2	ASW	G/A	A/A	495	349	13	11	1.200	0.531	2.710	8.19E-01	8.18E-02	351
2DL3	953	cohortMinusGroup2	IBS	G/A	A/A	480	338	28	22	1.120	0.630	1.990	8.22E-01	8.21E-02	352
3DL3	777	cohortMinusGroup2	PUR	A/G	G/G	526	74	44	5	0.808	0.310	2.100	8.33E-01	8.23E-02	353
3DL1	1180	cohortMinusGroup2	CLM	G/C	C/C	394	153	19	6	0.813	0.319	2.070	8.37E-01	8.25E-02	354
2DL4	1023	cohortMinusGroup2	PJL	G/A	A/A	651	190	23	8	1.190	0.524	2.700	8.41E-01	8.28E-02	355
3DL3	906	cohortMinusGroup2	PUR	C/T	T/T	474	68	43	5	0.811	0.310	2.120	8.41E-01	8.30E-02	356
3DL1	732	cohortMinusGroup2	FIN	T/C	C/C	247	116	18	7	0.828	0.336	2.040	8.50E-01	8.32E-02	357
2DP1	471	cohortMinusGroup2	PUR	A/G	G/G	431	175	18	6	0.821	0.321	2.100	8.56E-01	8.35E-02	358
2DL5	517	cohortMinusGroup2	CLM	A/G	G/G	244	420	9	13	0.839	0.353	1.990	8.62E-01	8.37E-02	359
2DL5	517	cohortMinusGroup2	TSI	A/G	G/G	238	410	15	23	0.890	0.456	1.740	8.67E-01	8.39E-02	360
3DL1	1180	cohortMinusGroup2	MSL	G/C	C/C	397	154	16	5	0.806	0.290	2.240	8.67E-01	8.42E-02	361
3DL3	804	cohortMinusGroup2	GBR	G/A	A/A	675	120	28	6	1.210	0.491	2.980	8.71E-01	8.44E-02	362
2DL3	953	cohortMinusGroup2	ACB	G/A	A/A	485	342	23	18	1.110	0.590	2.090	8.72E-01	8.46E-02	363
3DP1	796	cohortMinusGroup2	GBR	T/C	C/C	716	141	36	6	0.846	0.350	2.050	8.75E-01	8.49E-02	364
2DP1	471	cohortMinusGroup2	BEB	A/G	G/G	421	171	28	10	0.879	0.418	1.850	8.77E-01	8.51E-02	365
2DP1	1313	cohortMinusGroup2	ASW	A/C	C/C	538	201	22	7	0.852	0.358	2.030	8.80E-01	8.53E-02	366
2DP1	1313	cohortMinusGroup2	CEU	A/C	C/C	538	201	22	7	0.852	0.358	2.030	8.80E-01	8.53E-02	366
2DL4	625	cohortMinusGroup2	CDX	C/G	G/G	895	422	33	17	1.090	0.600	1.980	8.91E-01	8.56E-02	367
3DL1	607	cohortMinusGroup2	CLM	C/T	T/T	478	259	25	15	1.110	0.575	2.140	8.93E-01	8.58E-02	368
3DL1	1180	cohortMinusGroup2	IBS	G/C	C/C	390	149	23	10	1.140	0.530	2.450	8.96E-01	8.60E-02	369
2DL4	412	cohortMinusGroup2	CHS	G/A	A/A	969	478	58	27	0.944	0.590	1.510	9.02E-01	8.63E-02	370
3DL3	961	cohortMinusGroup2	FIN	C/A	A/A	331	218	36	22	0.928	0.532	1.620	9.03E-01	8.65E-02	371
2DL5	517	cohortMinusGroup2	CDX	A/G	G/G	243	418	10	15	0.872	0.386	1.970	9.06E-01	8.67E-02	372
2DP1	1313	cohortMinusGroup2	ITU	A/C	C/C	536	198	24	10	1.130	0.531	2.410	9.08E-01	8.70E-02	373
3DL3	502	cohortMinusGroup2	FIN	G/A	A/A	1093	714	50	31	0.949	0.600	1.500	9.14E-01	8.72E-02	374
3DP1	774	cohortMinusGroup2	ACB	G/C	C/C	703	135	47	10	1.110	0.547	2.250	9.21E-01	8.74E-02	375
2DP1	471	cohortMinusGroup2	GWD	A/G	G/G	409	166	40	15	0.924	0.497	1.720	9.25E-01	8.77E-02	376
2DL5	583	cohortMinusGroup2	BEB	G/A	A/A	236	386	16	24	0.917	0.477	1.760	9.27E-01	8.79E-02	377
2DP1	448	cohortMinusGroup2	MXL	G/C	C/C	826	910	27	28	0.941	0.550	1.610	9.33E-01	8.81E-02	378
3DP1	774	cohortMinusGroup2	PUR	G/C	C/C	720	140	30	5	0.857	0.327	2.250	9.36E-01	8.83E-02	379
3DL1	732	cohortMinusGroup2	CLM	T/C	C/C	250	117	15	6	0.855	0.324	2.260	9.40E-01	8.86E-02	380
3DL1	607	cohortMinusGroup2	CHB	C/T	T/T	492	269	11	5	0.831	0.286	2.420	9.40E-01	8.88E-02	381
2DL4	762	cohortMinusGroup2	MSL	C/T	T/T	942	256	29	7	0.888	0.385	2.050	9.43E-01	8.90E-02	382
2DP1	522	cohortMinusGroup2	GWD	T/C	C/C	493	203	44	17	0.938	0.524	1.680	9.47E-01	8.93E-02	383
3DL3	804	cohortMinusGroup2	CEU	G/A	A/A	668	119	35	7	1.120	0.486	2.580	9.59E-01	8.95E-02	384
2DP1	471	cohortMinusGroup2	MSL	A/G	G/G	419	168	30	13	1.080	0.550	2.120	9.59E-01	8.97E-02	385
2DL3	953	cohortMinusGroup2	YRI	G/A	A/A	481	342	27	18	0.938	0.508	1.730	9.59E-01	9.00E-02	386
2DP1	471	cohortMinusGroup2	ACB	A/G	G/G	427	173	22	8	0.898	0.392	2.060	9.61E-01	9.02E-02	387
2DL4	762	cohortMinusGroup2	CLM	C/T	T/T	926	250	45	13	1.070	0.568	2.010	9.64E-01	9.04E-02	388
2DL4	625	cohortMinusGroup2	CHS	C/G	G/G	871	413	57	26	0.962	0.596	1.550	9.70E-01	9.07E-02	389
3DL1	1180	cohortMinusGroup2	KHV	G/C	C/C	398	154	15	5	0.861	0.308	2.410	9.76E-01	9.09E-02	390
2DP1	522	cohortMinusGroup2	PUR	T/C	C/C	518	213	19	7	0.896	0.371	2.160	9.80E-01	9.11E-02	391
3DP1	774	cohortMinusGroup2	GWD	G/C	C/C	700	136	50	9	0.926	0.445	1.930	9.83E-01	9.14E-02	392
2DL4	762	cohortMinusGroup2	CHB	C/T	T/T	950	258	21	5	0.877	0.328	2.350	9.84E-01	9.16E-02	393
2DP1	766	cohortMinusGroup2	ITU	G/C	C/C	311	78	25	7	1.120	0.467	2.680	9.86E-01	9.18E-02	394
2DL4	762	cohortMinusGroup2	GBR	C/T	T/T	913	248	58	15	0.952	0.530	1.710	9.86E-01	9.21E-02	395
2DP1	522	cohortMinusGroup2	ITU	T/C	C/C	512	209	25	11	1.080	0.522	2.230	9.89E-01	9.23E-02	396
3DL3	961	cohortMinusGroup2	STU	C/A	A/A	350	228	17	12	1.080	0.506	2.300	9.90E-01	9.25E-02	397
2DP1	448	cohortMinusGroup2	LWK	G/C	C/C	822	905	31	33	0.967	0.587	1.590	9.96E-01	9.28E-02	398
2DP1	1313	cohortMinusGroup2	ACB	A/C	C/C	532	198	28	10	0.960	0.458	2.010	1.00E+00	9.30E-02	399
3DL3	804	cohortMinusGroup2	CLM	G/A	A/A	673	121	30	5	0.927	0.353	2.440	1.00E+00	9.30E-02	399
2DL4	412	cohortMinusGroup2	JPT	G/A	A/A	972	478	55	27	0.998	0.622	1.600	1.00E+00	9.32E-02	400
2DL4	625	cohortMinusGroup2	JPT	C/G	G/G	879	416	49	23	0.992	0.596	1.650	1.00E+00	9.35E-02	401
2DL4	412	cohortMinusGroup2	CDX	G/A	A/A	988	486	39	19	0.990	0.566	1.730	1.00E+00	9.37E-02	402
2DP1	471	cohortMinusGroup2	TSI	A/G	G/G	431	174	18	7	0.963	0.395	2.350	1.00E+00	9.37E-02	402
3DP1	774	cohortMinusGroup2	ASW	G/C	C/C	722	139	28	6	1.110	0.451	2.730	1.00E+00	9.39E-02	403
2DL3	953	cohortMinusGroup2	BEB	G/A	A/A	493	350	15	10	0.939	0.417	2.110	1.00E+00	9.42E-02	404
2DL3	953	cohortMinusGroup2	MSL	G/A	A/A	493	350	15	10	0.939	0.417	2.110	1.00E+00	9.42E-02	404
3DP1	796	cohortMinusGroup2	ITU	T/C	C/C	725	142	27	5	0.945	0.358	2.500	1.00E+00	9.42E-02	404
2DL3	953	cohortMinusGroup2	FIN	G/A	A/A	476	338	32	22	0.968	0.553	1.700	1.00E+00	9.44E-02	405
3DL3	804	cohortMinusGroup2	ESN	G/A	A/A	668	120	35	6	0.954	0.393	2.320	1.00E+00	9.44E-02	405
3DL3	969	cohortMinusGroup2	MXL	C/T	T/T	374	98	26	7	1.030	0.434	2.440	1.00E+00	9.44E-02	405
2DL3	953	cohortMinusGroup2	PJL	G/A	A/A	498	353	10	7	0.988	0.372	2.620	1.00E+00	9.46E-02	406
2DL5	583	cohortMinusGroup2	CLM	G/A	A/A	244	398	8	12	0.920	0.371	2.280	1.00E+00	9.46E-02	406
2DP1	448	cohortMinusGroup2	PUR	G/C	C/C	823	906	30	32	0.969	0.584	1.610	1.00E+00	9.46E-02	406
2DP1	522	cohortMinusGroup2	CEU	T/C	C/C	521	214	16	6	0.913	0.353	2.360	1.00E+00	9.46E-02	406
2DP1	522	cohortMinusGroup2	LWK	T/C	C/C	514	210	23	10	1.060	0.496	2.270	1.00E+00	9.46E-02	406
3DL3	961	cohortMinusGroup2	PUR	C/A	A/A	349	228	18	12	1.020	0.482	2.160	1.00E+00	9.46E-02	406
2DP1	1313	cohortMinusGroup2	IBS	A/C	C/C	542	202	18	6	0.894	0.350	2.280	1.00E+00	9.49E-02	407
2DP1	1313	cohortMinusGroup2	LWK	A/C	C/C	538	200	22	8	0.978	0.428	2.230	1.00E+00	9.49E-02	407
3DL1	1180	cohortMinusGroup2	ASW	G/C	C/C	399	154	14	5	0.925	0.328	2.610	1.00E+00	9.49E-02	407

Table A8c Chi square significance tests for KIR variants within the 1000 Genomes populations, reference homozygous versus alternate homozygous

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL2	474	cohortMinusGroup2	CHB	G/G	T/T	1531	204	15	36	18.000	9.680	33.500	7.96E-33	2.09E-04	1
2DL4	1023	cohortMinusGroup2	CHB	G/G	A/A	1536	165	19	33	16.200	9.010	29.100	2.36E-32	4.18E-04	2
2DL4	1023	cohortMinusGroup2	PEL	G/G	A/A	1540	168	15	30	18.300	9.650	34.700	2.30E-31	6.26E-04	3
3DL2	474	cohortMinusGroup2	CHS	G/G	T/T	1527	205	19	35	13.700	7.690	24.400	2.50E-28	8.35E-04	4
3DL2	474	cohortMinusGroup2	PEL	G/G	T/T	1532	212	14	28	14.500	7.510	28.000	1.43E-23	1.04E-03	5
3DL2	474	cohortMinusGroup2	CDX	G/G	T/T	1524	209	22	31	10.300	5.850	18.100	1.20E-21	1.25E-03	6
2DS5	535	cohortMinusGroup2	LWK	G/G	A/A	105	701	26	11	0.063	0.030	0.132	4.92E-20	1.46E-03	7
3DL2	474	cohortMinusGroup2	JPT	G/G	T/T	1522	211	24	29	8.720	4.980	15.300	2.32E-18	1.67E-03	8
2DL4	1023	cohortMinusGroup2	JPT	G/G	A/A	1530	174	25	24	8.440	4.720	15.100	1.97E-16	1.88E-03	9
3DL1	607	cohortMinusGroup2	IBS	C/C	T/T	1539	242	29	32	7.020	4.170	11.800	2.28E-16	2.09E-03	10
3DP1	774	cohortMinusGroup2	ESN	G/G	C/C	1583	122	40	23	7.460	4.330	12.900	5.30E-16	2.30E-03	11
3DP1	796	cohortMinusGroup2	ESN	T/T	C/C	1587	125	38	22	7.350	4.220	12.800	3.61E-15	2.51E-03	12
3DL2	474	cohortMinusGroup2	KHV	G/G	T/T	1519	213	27	27	7.130	4.100	12.400	6.34E-15	2.71E-03	13
3DP1	796	cohortMinusGroup2	YRI	T/T	C/C	1583	125	42	22	6.630	3.840	11.500	7.79E-14	2.92E-03	14
3DP1	774	cohortMinusGroup2	YRI	G/G	C/C	1579	123	44	22	6.420	3.730	11.100	1.90E-13	3.13E-03	15
2DL4	1023	cohortMinusGroup2	CHS	G/G	A/A	1528	176	27	22	7.070	3.940	12.700	2.70E-13	3.34E-03	16
2DP1	448	cohortMinusGroup2	CHB	G/G	C/C	635	857	3	81	20.000	6.290	63.600	3.19E-12	3.55E-03	17
3DL3	502	cohortMinusGroup2	GWD	G/G	A/A	586	735	61	10	0.131	0.067	0.258	1.86E-11	3.76E-03	18
3DL3	961	cohortMinusGroup2	GBR	C/C	A/A	975	210	24	30	5.800	3.320	10.100	2.03E-11	3.97E-03	19
3DL1	607	cohortMinusGroup2	CEU	C/C	T/T	1534	246	34	28	5.140	3.060	8.630	3.23E-11	4.18E-03	20
3DL3	502	cohortMinusGroup2	CHB	G/G	A/A	643	683	4	62	14.600	5.280	40.400	3.61E-11	4.38E-03	21
2DP1	448	cohortMinusGroup2	JPT	G/G	C/C	635	864	3	74	18.100	5.680	57.700	4.48E-11	4.59E-03	22
2DL4	412	cohortMinusGroup2	GWD	G/G	A/A	965	458	18	47	5.500	3.160	9.580	5.88E-11	4.80E-03	23
2DP1	448	cohortMinusGroup2	CHS	G/G	C/C	635	865	3	73	17.900	5.620	57.100	6.52E-11	5.01E-03	24
2DL4	625	cohortMinusGroup2	GWD	C/C	G/G	853	393	18	46	5.550	3.180	9.700	6.53E-11	5.22E-03	25
3DL3	961	cohortMinusGroup2	TSI	C/C	A/A	969	209	30	31	4.790	2.840	8.090	5.37E-10	5.43E-03	26
2DP1	448	cohortMinusGroup2	GWD	G/G	C/C	584	921	54	17	0.200	0.115	0.348	9.05E-10	5.64E-03	27
3DL3	502	cohortMinusGroup2	YRI	G/G	A/A	593	735	54	10	0.149	0.075	0.295	1.10E-09	5.85E-03	28
3DL1	732	cohortMinusGroup2	PEL	T/T	C/C	389	106	4	17	15.600	5.140	47.300	1.85E-09	6.05E-03	29
2DL4	762	cohortMinusGroup2	IBS	C/C	T/T	1117	240	18	23	5.950	3.160	11.200	2.00E-09	6.26E-03	30
3DL1	607	cohortMinusGroup2	FIN	C/C	T/T	1530	247	38	27	4.400	2.640	7.340	2.33E-09	6.47E-03	31
3DL3	502	cohortMinusGroup2	JPT	G/G	A/A	642	691	5	54	10.000	3.980	25.200	4.98E-09	6.68E-03	32
2DL4	412	cohortMinusGroup2	PEL	G/G	A/A	971	470	12	35	6.030	3.100	11.700	6.37E-09	6.89E-03	33
2DP1	1313	cohortMinusGroup2	PJL	A/A	C/C	1397	187	32	21	4.900	2.770	8.670	7.84E-09	7.10E-03	34
2DP1	448	cohortMinusGroup2	PEL	G/G	C/C	635	878	3	60	14.500	4.530	46.400	8.21E-09	7.31E-03	35
2DP1	471	cohortMinusGroup2	STU	A/A	G/G	1727	160	51	21	4.440	2.600	7.570	9.35E-09	7.52E-03	36
2DL3	953	cohortMinusGroup2	GBR	G/G	A/A	1347	328	32	32	4.110	2.480	6.810	9.62E-09	7.72E-03	37
2DL3	953	cohortMinusGroup2	TSI	G/G	A/A	1342	326	37	34	3.780	2.340	6.120	1.87E-08	7.93E-03	38
3DL3	502	cohortMinusGroup2	ESN	G/G	A/A	597	734	50	11	0.179	0.092	0.347	2.83E-08	8.14E-03	39
2DP1	448	cohortMinusGroup2	TSI	G/G	C/C	594	924	44	14	0.205	0.111	0.377	4.85E-08	8.35E-03	40
2DP1	448	cohortMinusGroup2	KHV	G/G	C/C	632	874	6	64	7.710	3.320	17.900	5.34E-08	8.56E-03	41
2DL4	412	cohortMinusGroup2	GIH	G/G	A/A	917	503	66	2	0.055	0.014	0.226	6.86E-08	8.77E-03	42
2DL4	625	cohortMinusGroup2	PEL	C/C	G/G	863	412	8	27	7.070	3.180	15.700	8.25E-08	8.98E-03	43
3DL3	502	cohortMinusGroup2	CHS	G/G	A/A	638	689	9	56	5.760	2.830	11.700	1.32E-07	9.19E-03	44
2DP1	522	cohortMinusGroup2	PJL	T/T	C/C	1666	198	47	22	3.940	2.330	6.680	1.38E-07	9.40E-03	45
2DL4	412	cohortMinusGroup2	IBS	G/G	A/A	915	501	68	4	0.107	0.039	0.295	3.65E-07	9.60E-03	46
2DL4	412	cohortMinusGroup2	ESN	G/G	A/A	959	463	24	42	3.620	2.170	6.050	3.79E-07	9.81E-03	47
2DL4	625	cohortMinusGroup2	GIH	C/C	G/G	811	437	60	2	0.062	0.015	0.254	4.70E-07	1.00E-02	48
2DL4	412	cohortMinusGroup2	CEU	G/G	A/A	918	501	65	4	0.113	0.041	0.312	8.43E-07	1.02E-02	49
2DP1	522	cohortMinusGroup2	STU	T/T	C/C	1665	199	48	21	3.660	2.150	6.240	1.05E-06	1.04E-02	50
2DP1	448	cohortMinusGroup2	CDX	G/G	C/C	630	877	8	61	5.480	2.600	11.500	1.09E-06	1.07E-02	51
2DL4	412	cohortMinusGroup2	YRI	G/G	A/A	959	465	24	40	3.440	2.050	5.770	1.60E-06	1.09E-02	52
2DP1	471	cohortMinusGroup2	PJL	A/A	G/G	1728	163	50	18	3.820	2.180	6.700	1.74E-06	1.11E-02	53
2DL4	625	cohortMinusGroup2	ESN	C/C	G/G	847	400	24	39	3.440	2.040	5.800	1.97E-06	1.13E-02	54
2DP1	522	cohortMinusGroup2	MSL	T/T	C/C	1675	202	38	18	3.930	2.200	7.020	2.02E-06	1.15E-02	55
2DL4	412	cohortMinusGroup2	TSI	G/G	A/A	914	499	69	6	0.159	0.069	0.369	2.10E-06	1.17E-02	56
2DL4	412	cohortMinusGroup2	CHB	G/G	A/A	966	472	17	33	3.970	2.190	7.200	2.37E-06	1.19E-02	57
2DP1	1313	cohortMinusGroup2	GIH	A/A	C/C	1389	188	40	20	3.690	2.110	6.450	2.73E-06	1.21E-02	58
2DP1	1313	cohortMinusGroup2	STU	A/A	C/C	1389	188	40	20	3.690	2.110	6.450	2.73E-06	1.21E-02	58
2DL4	625	cohortMinusGroup2	CEU	C/C	G/G	822	438	49	1	0.038	0.005	0.278	3.16E-06	1.23E-02	59
2DL4	625	cohortMinusGroup2	MSL	C/C	G/G	854	407	17	32	3.950	2.170	7.200	3.30E-06	1.25E-02	60
2DL4	625	cohortMinusGroup2	IBS	C/C	G/G	819	437	52	2	0.072	0.018	0.297	4.39E-06	1.27E-02	61
2DL4	625	cohortMinusGroup2	YRI	C/C	G/G	848	402	23	37	3.390	1.990	5.780	4.44E-06	1.29E-02	62
2DL4	412	cohortMinusGroup2	MSL	G/G	A/A	966	473	17	32	3.840	2.110	6.990	5.06E-06	1.32E-02	63
2DL4	762	cohortMinusGroup2	GBR	C/C	T/T	1122	248	13	15	5.220	2.450	11.100	6.49E-06	1.34E-02	64
2DL4	762	cohortMinusGroup2	CEU	C/C	T/T	1116	245	19	18	4.320	2.230	8.350	7.01E-06	1.36E-02	65
3DL1	607	cohortMinusGroup2	GBR	C/C	T/T	1534	254	34	20	3.550	2.010	6.270	8.54E-06	1.38E-02	66
3DL3	502	cohortMinusGroup2	ACB	G/G	A/A	604	731	43	14	0.269	0.146	0.496	1.42E-05	1.40E-02	67
2DL4	412	cohortMinusGroup2	STU	G/G	A/A	925	500	58	5	0.159	0.063	0.399	1.57E-05	1.42E-02	68
3DL3	502	cohortMinusGroup2	LWK	G/G	A/A	603	730	44	15	0.282	0.155	0.512	1.80E-05	1.44E-02	69
2DL4	625	cohortMinusGroup2	TSI	C/C	G/G	813	434	58	5	0.161	0.064	0.404	1.95E-05	1.46E-02	70
3DL3	961	cohortMinusGroup2	FIN	C/C	A/A	970	218	29	22	3.380	1.910	6.000	2.61E-05	1.48E-02	71
3DL1	1180	cohortMinusGroup2	TSI	G/G	C/C	1484	144	42	15	3.680	1.990	6.800	2.62E-05	1.50E-02	72
2DL4	1023	cohortMinusGroup2	KHV	G/G	A/A	1518	182	37	16	3.610	1.970	6.620	2.76E-05	1.52E-02	73
3DL3	961	cohortMinusGroup2	PEL	C/C	A/A	926	240	73	0	0.000	0.000	NaN	3.12E-05	1.55E-02	74
3DL3	961	cohortMinusGroup2	CHS	C/C	A/A	918	239	81	1	0.047	0.007	0.342	3.19E-05	1.57E-02	75
3DL3	502	cohortMinusGroup2	MSL	G/G	A/A	609	733	38	12	0.262	0.136	0.506	3.82E-05	1.59E-02	76
2DL3	953	cohortMinusGroup2	CHS	G/G	A/A	1297	358	82	2	0.088	0.022	0.361	3.95E-05	1.61E-02	77
2DL3	953	cohortMinusGroup2	PEL	G/G	A/A	1306	359	73	1	0.050	0.007	0.360	5.08E-05	1.63E-02	78
2DL4	1023	cohortMinusGroup2	CDX	G/G	A/A	1512	181	43	17	3.300	1.840	5.910	5.45E-05	1.65E-02	79
3DL1	607	cohortMinusGroup2	TSI	C/C	T/T	1523	252	45	22	2.950	1.740	5.000	5.49E-05	1.67E-02	80
3DL3	804	cohortMinusGroup2	GWD	G/G	A/A	1447	111	57	15	3.430	1.880	6.250	5.52E-05	1.69E-02	81
2DL3	953	cohortMinusGroup2	CHB	G/G	A/A	1293	357	86	3	0.126	0.040	0.401	6.11E-05	1.71E-02	82
2DL4	625	cohortMinusGroup2	STU	C/C	G/G	814	433	57	6	0.198	0.085	0.463	6.40E-05	1.73E-02	83
2DL4	762	cohortMinusGroup2	TSI	C/C	T/T	1105	242	30	21	3.200	1.800	5.690	6.87E-05	1.75E-02	84
2DL5	517	cohortMinusGroup2	LWK	A/A	G/G	582	427	41	6	0.199	0.084	0.473	1.07E-04	1.78E-02	85
2DL4	412	cohortMinusGroup2	LWK	G/G	A/A	956	469	27	36	2.720	1.630	4.530	1.24E-04	1.80E-02	86
2DL4	762	cohortMinusGroup2	JPT	C/C	T/T	1070	263	65	0	0.000	0.000	NaN	1.38E-04	1.82E-02	87
3DL3	961	cohortMinusGroup2	CHB	C/C	A/A	914	237	85	3	0.136	0.043	0.434	1.50E-04	1.84E-02	88
2DL3	953	cohortMinusGroup2	CEU	G/G	A/A	1345	336	34	24	2.830	1.660	4.840	1.52E-04	1.86E-02	89
2DL4	625	cohortMinusGroup2	CHB	C/C	G/G	856	414	15	25	3.450	1.800	6.610	1.60E-04	1.88E-02	90
2DL4	762	cohortMinusGroup2	GIH	C/C	T/T	1103	242	32	21	2.990	1.690	5.280	1.61E-04	1.90E-02	91
3DL1	1180	cohortMinusGroup2	FIN	G/G	C/C	1478	144	48	15	3.210	1.750	5.880	1.71E-04	1.92E-02	92
2DL4	625	cohortMinusGroup2	LWK	C/C	G/G	858	416	13	23	3.650	1.830	7.280	1.87E-04	1.94E-02	93
2DL4	1023	cohortMinusGroup2	GWD	G/G	A/A	1444	198	111	0	0.000	0.000	NaN	1.92E-04	1.96E-02	94
2DL4	762	cohortMinusGroup2	CHS	C/C	T/T	1064	262	71	1	0.057	0.008	0.414	1.92E-04	1.98E-02	95
2DP1	1313	cohortMinusGroup2	CHS	A/A	C/C	1333	208	96	0	0.000	0.000	NaN	2.20E-04	2.00E-02	96
2DL3	953	cohortMinusGroup2	JPT	G/G	A/A	1302	357	77	3	0.142	0.045	0.453	2.24E-04	2.03E-02	97
3DL2	474	cohortMinusGroup2	ESN	G/G	T/T	1457	240	89	0	0.000	0.000	NaN	2.58E-04	2.05E-02	98
2DL4	1023	cohortMinusGroup2	YRI	G/G	A/A	1448	198	107	0	0.000	0.000	NaN	2.61E-04	2.07E-02	99
2DP1	1313	cohortMinusGroup2	CHB	A/A	C/C	1335	208	94	0	0.000	0.000	NaN	2.62E-04	2.09E-02	100
2DP1	1313	cohortMinusGroup2	JPT	A/A	C/C	1337	208	92	0	0.000	0.000	NaN	3.11E-04	2.11E-02	101
2DP1	1313	cohortMinusGroup2	MSL	A/A	C/C	1395	193	34	15	3.190	1.710	5.970	3.14E-04	2.13E-02	102
3DP1	774	cohortMinusGroup2	LWK	G/G	C/C	1575	132	48	13	3.230	1.710	6.110	3.70E-04	2.15E-02	103
3DL1	607	cohortMinusGroup2	GWD	C/C	T/T	1492	274	76	0	0.000	0.000	NaN	3.75E-04	2.17E-02	104
3DL2	474	cohortMinusGroup2	ACB	G/G	T/T	1462	240	84	0	0.000	0.000	NaN	4.07E-04	2.19E-02	105
3DL3	502	cohortMinusGroup2	CDX	G/G	A/A	634	701	13	44	3.060	1.630	5.730	4.26E-04	2.21E-02	106

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DL4	625	cohortMinusGroup2	GBR	C/C	G/G	832	436	39	3	0.147	0.045	0.478	4.42E-04	2.23E-02	107
3DL3	502	cohortMinusGroup2	KHV	G/G	A/A	635	703	12	42	3.160	1.650	6.060	4.54E-04	2.26E-02	108
2DL4	762	cohortMinusGroup2	FIN	C/C	T/T	1108	245	27	18	3.010	1.630	5.550	4.60E-04	2.28E-02	109
2DP1	522	cohortMinusGroup2	JPT	T/T	C/C	1614	220	99	0	0.000	0.000	NaN	4.68E-04	2.30E-02	110
2DL4	1023	cohortMinusGroup2	LWK	G/G	A/A	1456	198	99	0	0.000	0.000	NaN	4.80E-04	2.32E-02	111
2DL4	412	cohortMinusGroup2	GBR	G/G	A/A	938	500	45	5	0.208	0.082	0.527	4.93E-04	2.34E-02	112
3DL2	474	cohortMinusGroup2	LWK	G/G	T/T	1452	239	94	1	0.065	0.009	0.466	4.96E-04	2.36E-02	113
3DL3	961	cohortMinusGroup2	ITU	C/C	A/A	968	220	31	20	2.840	1.590	5.080	4.99E-04	2.38E-02	114
2DP1	522	cohortMinusGroup2	CHB	T/T	C/C	1615	220	98	0	0.000	0.000	NaN	5.05E-04	2.40E-02	115
3DL3	961	cohortMinusGroup2	ACB	C/C	A/A	923	237	76	3	0.154	0.048	0.492	5.15E-04	2.42E-02	116
3DL3	961	cohortMinusGroup2	JPT	C/C	A/A	923	237	76	3	0.154	0.048	0.492	5.15E-04	2.42E-02	116
3DL2	474	cohortMinusGroup2	GWD	G/G	T/T	1453	239	93	1	0.065	0.009	0.471	5.43E-04	2.44E-02	117
2DP1	471	cohortMinusGroup2	GWD	A/A	G/G	1724	166	54	15	2.880	1.590	5.220	5.84E-04	2.46E-02	118
2DP1	1313	cohortMinusGroup2	KHV	A/A	C/C	1345	208	84	0	0.000	0.000	NaN	6.22E-04	2.48E-02	119
2DL4	762	cohortMinusGroup2	PUR	C/C	T/T	1102	243	33	20	2.750	1.550	4.870	6.39E-04	2.51E-02	120
3DL3	502	cohortMinusGroup2	STU	G/G	A/A	636	706	11	39	3.190	1.620	6.280	6.98E-04	2.53E-02	121
2DP1	522	cohortMinusGroup2	GWD	T/T	C/C	1661	203	52	17	2.670	1.520	4.710	8.44E-04	2.55E-02	122
2DL4	1023	cohortMinusGroup2	ACB	G/G	A/A	1465	198	90	0	0.000	0.000	NaN	9.51E-04	2.57E-02	123
3DL2	474	cohortMinusGroup2	MSL	G/G	T/T	1474	240	72	0	0.000	0.000	NaN	1.21E-03	2.59E-02	124
3DL1	732	cohortMinusGroup2	YRI	T/T	C/C	358	123	35	0	0.000	0.000	NaN	1.27E-03	2.61E-02	125
3DL2	474	cohortMinusGroup2	GIH	G/G	T/T	1463	239	83	1	0.074	0.010	0.533	1.34E-03	2.63E-02	126
2DL4	1023	cohortMinusGroup2	MSL	G/G	A/A	1471	198	84	0	0.000	0.000	NaN	1.50E-03	2.65E-02	127
2DP1	522	cohortMinusGroup2	CHS	T/T	C/C	1615	219	98	1	0.075	0.010	0.542	1.51E-03	2.67E-02	128
2DP1	448	cohortMinusGroup2	GBR	G/G	C/C	602	915	36	23	0.420	0.246	0.716	1.69E-03	2.69E-02	129
3DL3	961	cohortMinusGroup2	KHV	C/C	A/A	925	236	74	4	0.212	0.077	0.586	1.69E-03	2.71E-02	130
2DL3	953	cohortMinusGroup2	CDX	G/G	A/A	1310	356	69	4	0.213	0.077	0.588	1.74E-03	2.74E-02	131
2DS5	535	cohortMinusGroup2	ITU	G/G	A/A	131	656	0	56	Inf	NaN	Inf	1.74E-03	2.76E-02	132
2DL3	953	cohortMinusGroup2	KHV	G/G	A/A	1304	355	75	5	0.245	0.098	0.610	1.78E-03	2.78E-02	133
3DL3	961	cohortMinusGroup2	IBS	C/C	A/A	956	217	43	23	2.360	1.390	4.000	1.87E-03	2.80E-02	134
2DS5	535	cohortMinusGroup2	PJL	G/G	A/A	131	657	0	55	Inf	NaN	Inf	1.95E-03	2.82E-02	135
2DS5	535	cohortMinusGroup2	STU	G/G	A/A	131	657	0	55	Inf	NaN	Inf	1.95E-03	2.82E-02	135
3DL3	502	cohortMinusGroup2	ASW	G/G	A/A	623	737	24	8	0.282	0.126	0.632	1.98E-03	2.84E-02	136
3DL3	961	cohortMinusGroup2	CEU	C/C	A/A	964	220	35	20	2.500	1.420	4.410	2.02E-03	2.86E-02	137
2DP1	471	cohortMinusGroup2	CHB	A/A	G/G	1679	181	99	0	0.000	0.000	NaN	2.07E-03	2.88E-02	138
2DP1	471	cohortMinusGroup2	JPT	A/A	G/G	1679	181	99	0	0.000	0.000	NaN	2.07E-03	2.88E-02	138
2DL4	412	cohortMinusGroup2	JPT	G/G	A/A	961	478	22	27	2.470	1.390	4.380	2.46E-03	2.90E-02	139
2DP1	522	cohortMinusGroup2	KHV	T/T	C/C	1623	219	90	1	0.082	0.011	0.594	2.75E-03	2.92E-02	140
2DL4	412	cohortMinusGroup2	ASW	G/G	A/A	967	483	16	22	2.750	1.430	5.280	2.83E-03	2.94E-02	141
3DL2	474	cohortMinusGroup2	ITU	G/G	T/T	1472	239	74	1	0.083	0.012	0.601	3.00E-03	2.97E-02	142
3DL1	607	cohortMinusGroup2	YRI	C/C	T/T	1483	271	85	3	0.193	0.061	0.615	3.24E-03	2.99E-02	143
2DL4	625	cohortMinusGroup2	CHS	C/C	G/G	849	413	22	26	2.430	1.360	4.340	3.36E-03	3.01E-02	144
2DS5	535	cohortMinusGroup2	GIH	G/G	A/A	131	662	0	50	Inf	NaN	Inf	3.43E-03	3.03E-02	145
2DP1	471	cohortMinusGroup2	KHV	A/A	G/G	1688	181	90	0	0.000	0.000	NaN	3.58E-03	3.05E-02	146
2DL4	412	cohortMinusGroup2	CHS	G/G	A/A	960	478	23	27	2.360	1.340	4.160	3.78E-03	3.07E-02	147
2DP1	522	cohortMinusGroup2	GIH	T/T	C/C	1654	203	59	17	2.350	1.340	4.110	3.82E-03	3.09E-02	148
2DL4	412	cohortMinusGroup2	PJL	G/G	A/A	931	495	52	10	0.362	0.182	0.718	3.87E-03	3.11E-02	149
3DL3	502	cohortMinusGroup2	ITU	G/G	A/A	629	699	18	46	2.300	1.320	4.010	3.90E-03	3.13E-02	150
3DL1	732	cohortMinusGroup2	MSL	T/T	C/C	364	123	29	0	0.000	0.000	NaN	4.02E-03	3.15E-02	151
3DP1	796	cohortMinusGroup2	GWD	T/T	C/C	1573	135	52	12	2.690	1.400	5.160	4.27E-03	3.17E-02	152
3DL3	804	cohortMinusGroup2	CHS	G/G	A/A	1401	126	103	0	0.000	0.000	NaN	4.45E-03	3.19E-02	153
3DL3	804	cohortMinusGroup2	JPT	G/G	A/A	1401	126	103	0	0.000	0.000	NaN	4.45E-03	3.19E-02	153
3DL1	732	cohortMinusGroup2	KHV	T/T	C/C	381	111	12	12	3.430	1.500	7.850	4.58E-03	3.22E-02	154
3DL3	502	cohortMinusGroup2	PEL	G/G	A/A	637	713	10	32	2.860	1.390	5.860	4.60E-03	3.24E-02	155
2DL4	625	cohortMinusGroup2	PJL	C/C	G/G	819	429	52	10	0.367	0.185	0.729	4.61E-03	3.26E-02	156
2DL3	953	cohortMinusGroup2	GWD	G/G	A/A	1329	334	50	26	2.070	1.270	3.370	4.69E-03	3.28E-02	157
2DL4	762	cohortMinusGroup2	CHB	C/C	T/T	1060	258	75	5	0.274	0.110	0.684	4.90E-03	3.30E-02	158
2DL4	625	cohortMinusGroup2	JPT	C/C	G/G	852	416	19	23	2.480	1.340	4.600	5.12E-03	3.32E-02	159
2DL4	1023	cohortMinusGroup2	GIH	G/G	A/A	1473	197	82	1	0.091	0.013	0.659	5.15E-03	3.34E-02	160
2DL4	625	cohortMinusGroup2	ITU	C/C	G/G	817	428	54	11	0.389	0.201	0.752	5.58E-03	3.36E-02	161
3DL3	502	cohortMinusGroup2	PUR	G/G	A/A	612	727	35	18	0.433	0.243	0.772	5.60E-03	3.38E-02	162
2DL4	412	cohortMinusGroup2	ITU	G/G	A/A	930	494	53	11	0.391	0.202	0.755	5.81E-03	3.40E-02	163
2DP1	448	cohortMinusGroup2	STU	G/G	C/C	601	911	37	27	0.481	0.290	0.798	5.89E-03	3.42E-02	164
2DL4	412	cohortMinusGroup2	FIN	G/G	A/A	933	495	50	10	0.377	0.190	0.750	6.05E-03	3.45E-02	165
2DP1	471	cohortMinusGroup2	CHS	A/A	G/G	1679	180	99	1	0.094	0.013	0.679	6.08E-03	3.47E-02	166
2DL5	583	cohortMinusGroup2	LWK	G/G	A/A	525	405	25	5	0.259	0.098	0.682	6.10E-03	3.49E-02	167
3DL2	474	cohortMinusGroup2	TSI	G/G	T/T	1469	238	77	2	0.160	0.039	0.656	6.17E-03	3.51E-02	168
2DP1	448	cohortMinusGroup2	YRI	G/G	C/C	604	914	34	24	0.466	0.274	0.794	6.31E-03	3.53E-02	169
3DL1	607	cohortMinusGroup2	ESN	C/C	T/T	1490	271	78	3	0.211	0.066	0.673	6.33E-03	3.55E-02	170
3DL1	607	cohortMinusGroup2	LWK	C/C	T/T	1490	271	78	3	0.211	0.066	0.673	6.33E-03	3.55E-02	170
2DP1	471	cohortMinusGroup2	GIH	A/A	G/G	1718	167	60	14	2.400	1.310	4.390	6.40E-03	3.57E-02	171
3DL3	804	cohortMinusGroup2	KHV	G/G	A/A	1408	126	96	0	0.000	0.000	NaN	6.40E-03	3.59E-02	172
2DL4	762	cohortMinusGroup2	PEL	C/C	T/T	1083	261	52	2	0.160	0.039	0.661	6.53E-03	3.61E-02	173
2DP1	522	cohortMinusGroup2	BEB	T/T	C/C	1666	206	47	14	2.410	1.300	4.450	7.22E-03	3.63E-02	174
2DL3	953	cohortMinusGroup2	FIN	G/G	A/A	1338	338	41	22	2.120	1.250	3.610	7.38E-03	3.65E-02	175
2DL4	625	cohortMinusGroup2	BEB	C/C	G/G	827	431	44	8	0.349	0.163	0.748	7.45E-03	3.67E-02	176
2DL4	625	cohortMinusGroup2	FIN	C/C	G/G	827	431	44	8	0.349	0.163	0.748	7.45E-03	3.67E-02	176
2DL4	1023	cohortMinusGroup2	TSI	G/G	A/A	1478	197	77	1	0.097	0.014	0.704	7.47E-03	3.70E-02	177
3DL3	961	cohortMinusGroup2	CDX	C/C	A/A	931	235	68	5	0.291	0.116	0.730	8.34E-03	3.72E-02	178
3DL3	961	cohortMinusGroup2	MXL	C/C	A/A	958	239	41	1	0.098	0.013	0.715	8.39E-03	3.74E-02	179
3DL2	474	cohortMinusGroup2	STU	G/G	T/T	1473	238	73	2	0.170	0.041	0.697	8.76E-03	3.76E-02	180
2DL4	625	cohortMinusGroup2	ASW	C/C	G/G	856	420	15	19	2.580	1.300	5.130	8.90E-03	3.78E-02	181
2DP1	1313	cohortMinusGroup2	CDX	A/A	C/C	1352	206	77	2	0.170	0.041	0.697	9.05E-03	3.80E-02	182
3DL3	804	cohortMinusGroup2	TSI	G/G	A/A	1450	115	54	11	2.570	1.310	5.050	9.45E-03	3.82E-02	183
3DL2	474	cohortMinusGroup2	CEU	G/G	T/T	1474	238	72	2	0.172	0.042	0.706	9.56E-03	3.84E-02	184
3DL2	474	cohortMinusGroup2	YRI	G/G	T/T	1454	236	92	4	0.268	0.098	0.736	9.76E-03	3.86E-02	185
3DL1	607	cohortMinusGroup2	GIH	C/C	T/T	1495	271	73	3	0.227	0.071	0.725	1.02E-02	3.88E-02	186
2DS5	535	cohortMinusGroup2	CDX	G/G	A/A	131	672	0	40	Inf	NaN	Inf	1.06E-02	3.90E-02	187
3DL1	732	cohortMinusGroup2	ESN	T/T	C/C	358	121	35	2	0.169	0.040	0.713	1.14E-02	3.93E-02	188
2DL4	625	cohortMinusGroup2	ACB	C/C	G/G	850	416	21	23	2.240	1.230	4.090	1.18E-02	3.95E-02	189
2DL4	1023	cohortMinusGroup2	ASW	G/G	A/A	1499	198	56	0	0.000	0.000	NaN	1.24E-02	3.97E-02	190
3DL1	607	cohortMinusGroup2	PUR	C/C	T/T	1513	255	55	19	2.050	1.200	3.510	1.25E-02	3.99E-02	191
3DL1	1180	cohortMinusGroup2	CEU	G/G	C/C	1482	148	44	11	2.500	1.260	4.940	1.28E-02	4.01E-02	192
2DL5	517	cohortMinusGroup2	MXL	A/A	G/G	601	429	22	4	0.255	0.087	0.745	1.29E-02	4.03E-02	193
3DL3	502	cohortMinusGroup2	BEB	G/G	A/A	634	711	13	34	2.330	1.220	4.450	1.30E-02	4.05E-02	194
2DP1	448	cohortMinusGroup2	PJL	G/G	C/C	604	912	34	26	0.506	0.301	0.852	1.35E-02	4.07E-02	195
2DL5	583	cohortMinusGroup2	MXL	G/G	A/A	530	406	20	4	0.261	0.089	0.770	1.63E-02	4.09E-02	196
3DL1	607	cohortMinusGroup2	ACB	C/C	T/T	1500	271	68	3	0.244	0.076	0.781	1.63E-02	4.11E-02	197
3DL2	474	cohortMinusGroup2	IBS	G/G	T/T	1470	237	76	3	0.245	0.077	0.783	1.63E-02	4.13E-02	198
2DS5	535	cohortMinusGroup2	BEB	G/G	A/A	131	676	0	36	Inf	NaN	Inf	1.66E-02	4.15E-02	199
2DP1	1313	cohortMinusGroup2	PEL	A/A	C/C	1371	207	58	1	0.114	0.016	0.827	1.70E-02	4.18E-02	200
3DL1	607	cohortMinusGroup2	MSL	C/C	T/T	1501	271	67	3	0.248	0.077	0.794	1.79E-02	4.20E-02	201
3DL3	804	cohortMinusGroup2	PEL	G/G	A/A	1428	126	76	0	0.000	0.000	NaN	1.81E-02	4.22E-02	202
3DL1	607	cohortMinusGroup2	CHB	C/C	T/T	1484	269	84	5	0.328	0.132	0.816	1.81E-02	4.24E-02	203
2DP1	471	cohortMinusGroup2	YRI	A/A	G/G	1711	167	67	14	2.140	1.180	3.890	1.84E-02	4.26E-02	204
3DL3	969	cohortMinusGroup2	YRI	C/C	T/T	1541	105	97	0	0.000	0.000	NaN	1.90E-02	4.28E-02	205
3DL1	607	cohortMinusGroup2	JPT	C/C	T/T	1493	270	75	4	0.295	0.107	0.813	1.91E-02	4.30E-02	206
2DP1	522	cohortMinusGroup2	PEL	T/T	C/C	1638	218	75	2	0.200	0.049	0.820	2.18E-02	4.32E-02	207
2DL4	412	cohortMinusGroup2	ACB	G/G	A/A	958	480	25	25	2.000	1.140	3.520	2.21E-02	4.34E-02	208
3DL3	969	cohortMinusGroup2	IBS	C/C	T/T	1546	105	92	0	0.000	0.000	NaN	2.32E-02	4.36E-02	209

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	969	cohortMinusGroup2	ESN	C/C	T/T	1548	105	90	0	0.000	0.000	NaN	2.52E-02	4.38E-02	210
3DP1	796	cohortMinusGroup2	CHS	T/T	C/C	1541	146	84	1	0.126	0.017	0.912	2.53E-02	4.41E-02	211
2DS5	535	cohortMinusGroup2	IBS	G/G	A/A	131	680	0	32	Inf	NaN	Inf	2.61E-02	4.43E-02	212
3DL3	969	cohortMinusGroup2	ACB	C/C	T/T	1549	105	89	0	0.000	0.000	NaN	2.62E-02	4.45E-02	213
2DL4	412	cohortMinusGroup2	CLM	G/G	A/A	940	495	43	10	0.442	0.220	0.887	2.70E-02	4.47E-02	214
2DL4	1023	cohortMinusGroup2	CEU	G/G	A/A	1483	196	72	2	0.210	0.051	0.863	2.79E-02	4.49E-02	215
3DP1	774	cohortMinusGroup2	CHS	G/G	C/C	1540	144	83	1	0.129	0.018	0.933	2.81E-02	4.51E-02	216
3DL3	969	cohortMinusGroup2	TSI	C/C	T/T	1551	105	87	0	0.000	0.000	NaN	2.84E-02	4.53E-02	217
2DL3	953	cohortMinusGroup2	IBS	G/G	A/A	1332	338	47	22	1.840	1.090	3.100	2.87E-02	4.55E-02	218
2DL4	762	cohortMinusGroup2	YRI	C/C	T/T	1075	258	60	5	0.347	0.138	0.873	2.88E-02	4.57E-02	219
2DP1	1313	cohortMinusGroup2	YRI	A/A	C/C	1376	193	53	15	2.020	1.120	3.650	2.93E-02	4.59E-02	220
3DP1	796	cohortMinusGroup2	JPT	T/T	C/C	1544	146	81	1	0.131	0.018	0.948	2.97E-02	4.61E-02	221
3DP1	796	cohortMinusGroup2	PJL	T/T	C/C	1545	146	80	1	0.132	0.018	0.956	3.14E-02	4.64E-02	222
2DL4	762	cohortMinusGroup2	CDX	C/C	T/T	1076	258	59	5	0.353	0.140	0.888	3.22E-02	4.66E-02	223
3DL3	408	cohortMinusGroup2	JPT	G/G	A/A	1587	87	103	0	0.000	0.000	NaN	3.26E-02	4.68E-02	224
2DP1	448	cohortMinusGroup2	GIH	G/G	C/C	602	907	36	31	0.572	0.350	0.935	3.31E-02	4.70E-02	225
3DL3	969	cohortMinusGroup2	FIN	C/C	T/T	1555	105	83	0	0.000	0.000	NaN	3.34E-02	4.72E-02	226
2DP1	448	cohortMinusGroup2	MSL	G/G	C/C	610	916	28	22	0.523	0.296	0.923	3.36E-02	4.74E-02	227
3DL3	408	cohortMinusGroup2	CHS	G/G	A/A	1588	87	102	0	0.000	0.000	NaN	3.37E-02	4.76E-02	228
3DL3	502	cohortMinusGroup2	GIH	G/G	A/A	626	702	21	43	1.830	1.070	3.120	3.43E-02	4.78E-02	229
3DP1	774	cohortMinusGroup2	PJL	G/G	C/C	1544	144	79	1	0.136	0.019	0.985	3.48E-02	4.80E-02	230
2DP1	522	cohortMinusGroup2	YRI	T/T	C/C	1651	205	62	15	1.950	1.090	3.490	3.57E-02	4.82E-02	231
2DL4	762	cohortMinusGroup2	KHV	C/C	T/T	1077	258	58	5	0.360	0.143	0.907	3.61E-02	4.84E-02	232
2DL4	412	cohortMinusGroup2	BEB	G/G	A/A	939	494	44	11	0.475	0.243	0.928	3.76E-02	4.86E-02	233
3DL1	1180	cohortMinusGroup2	BEB	G/G	C/C	1460	158	66	1	0.140	0.019	1.020	3.97E-02	4.89E-02	234
3DL1	607	cohortMinusGroup2	CLM	C/C	T/T	1523	259	45	15	1.960	1.080	3.570	3.97E-02	4.91E-02	235
3DL3	961	cohortMinusGroup2	GIH	C/C	A/A	958	222	41	18	1.890	1.070	3.350	4.04E-02	4.93E-02	236
2DL4	762	cohortMinusGroup2	CLM	C/C	T/T	1108	250	27	13	2.130	1.080	4.190	4.11E-02	4.95E-02	237
2DL4	625	cohortMinusGroup2	CLM	C/C	G/G	835	431	36	8	0.431	0.199	0.935	4.25E-02	4.97E-02	238
3DL3	502	cohortMinusGroup2	TSI	G/G	A/A	612	722	35	23	0.557	0.326	0.953	4.25E-02	4.99E-02	239
3DP1	774	cohortMinusGroup2	CLM	G/G	C/C	1548	144	75	1	0.143	0.020	1.040	4.31E-02	5.01E-02	240
3DP1	796	cohortMinusGroup2	CLM	T/T	C/C	1551	146	74	1	0.144	0.020	1.040	4.34E-02	5.03E-02	241
2DP1	471	cohortMinusGroup2	GBR	A/A	G/G	1712	180	66	1	0.144	0.020	1.040	4.41E-02	5.05E-02	242
3DL2	474	cohortMinusGroup2	GBR	G/G	T/T	1492	238	54	2	0.232	0.056	0.958	4.54E-02	5.07E-02	243
2DP1	1313	cohortMinusGroup2	BEB	A/A	C/C	1388	196	41	12	2.070	1.070	4.010	4.57E-02	5.09E-02	244
3DL3	969	cohortMinusGroup2	GWD	C/C	T/T	1537	104	101	1	0.146	0.020	1.060	4.64E-02	5.12E-02	245
3DL1	607	cohortMinusGroup2	BEB	C/C	T/T	1503	270	65	4	0.343	0.124	0.949	4.69E-02	5.14E-02	246
2DP1	522	cohortMinusGroup2	FIN	T/T	C/C	1637	217	76	3	0.298	0.093	0.953	4.70E-02	5.16E-02	247
3DP1	796	cohortMinusGroup2	PEL	T/T	C/C	1554	146	71	1	0.150	0.021	1.090	5.10E-02	5.18E-02	248
2DL4	1023	cohortMinusGroup2	IBS	G/G	A/A	1480	195	75	3	0.304	0.095	0.973	5.20E-02	5.20E-02	249
3DP1	774	cohortMinusGroup2	PEL	G/G	C/C	1552	144	71	1	0.152	0.021	1.100	5.34E-02	5.22E-02	250
2DP1	1313	cohortMinusGroup2	GWD	A/A	C/C	1377	194	52	14	1.910	1.040	3.510	5.37E-02	5.24E-02	251
3DL2	474	cohortMinusGroup2	ASW	G/G	T/T	1494	238	52	2	0.241	0.058	0.996	5.40E-02	5.26E-02	252
3DP1	796	cohortMinusGroup2	CHB	T/T	C/C	1538	145	87	2	0.244	0.059	1.000	5.41E-02	5.28E-02	253
2DP1	522	cohortMinusGroup2	CDX	T/T	C/C	1628	216	85	4	0.355	0.129	0.977	5.44E-02	5.30E-02	254
2DL4	762	cohortMinusGroup2	GWD	C/C	T/T	1069	256	66	7	0.443	0.201	0.977	5.52E-02	5.32E-02	255
2DP1	448	cohortMinusGroup2	CEU	G/G	C/C	607	911	31	27	0.580	0.343	0.982	5.57E-02	5.34E-02	256
2DP1	471	cohortMinusGroup2	BEB	A/A	G/G	1730	171	48	10	2.110	1.050	4.250	5.66E-02	5.37E-02	257
3DP1	796	cohortMinusGroup2	CDX	T/T	C/C	1556	146	69	1	0.154	0.021	1.120	5.69E-02	5.39E-02	258
2DP1	471	cohortMinusGroup2	PEL	A/A	G/G	1701	179	77	2	0.247	0.060	1.010	5.70E-02	5.41E-02	259
3DP1	774	cohortMinusGroup2	CHB	G/G	C/C	1536	143	87	2	0.247	0.060	1.010	5.71E-02	5.43E-02	260
2DL4	1023	cohortMinusGroup2	STU	G/G	A/A	1482	195	73	3	0.312	0.097	0.999	5.96E-02	5.45E-02	261
2DP1	471	cohortMinusGroup2	FIN	A/A	G/G	1702	179	76	2	0.250	0.061	1.030	6.04E-02	5.47E-02	262
2DL5	517	cohortMinusGroup2	STU	A/A	G/G	604	409	19	24	1.870	1.010	3.460	6.32E-02	5.49E-02	263
2DP1	522	cohortMinusGroup2	MXL	T/T	C/C	1665	219	48	1	0.158	0.022	1.150	6.32E-02	5.51E-02	264
2DP1	448	cohortMinusGroup2	MXL	G/G	C/C	629	910	9	28	2.150	1.010	4.590	6.33E-02	5.53E-02	265
2DP1	448	cohortMinusGroup2	ASW	G/G	C/C	618	923	20	15	0.502	0.255	0.988	6.34E-02	5.55E-02	266
3DL1	1180	cohortMinusGroup2	CDX	G/G	C/C	1453	157	73	2	0.254	0.062	1.040	6.44E-02	5.57E-02	267
3DL2	474	cohortMinusGroup2	PUR	G/G	T/T	1478	236	68	4	0.368	0.133	1.020	6.79E-02	5.60E-02	268
2DS5	535	cohortMinusGroup2	TSI	G/G	A/A	130	680	1	32	6.120	0.829	45.200	7.53E-02	5.62E-02	269
2DP1	471	cohortMinusGroup2	CDX	A/A	G/G	1693	178	85	3	0.336	0.105	1.070	8.11E-02	5.64E-02	270
2DP1	471	cohortMinusGroup2	IBS	A/A	G/G	1694	178	84	3	0.340	0.106	1.090	8.57E-02	5.66E-02	271
2DL5	583	cohortMinusGroup2	PEL	G/G	A/A	531	404	19	6	0.415	0.164	1.050	8.70E-02	5.68E-02	272
3DP1	774	cohortMinusGroup2	KHV	G/G	C/C	1545	143	78	2	0.277	0.067	1.140	9.04E-02	5.70E-02	273
3DP1	796	cohortMinusGroup2	KHV	T/T	C/C	1548	145	77	2	0.277	0.067	1.140	9.07E-02	5.72E-02	274
3DP1	774	cohortMinusGroup2	FIN	G/G	C/C	1562	144	61	1	0.178	0.025	1.290	9.12E-02	5.74E-02	275
2DL5	517	cohortMinusGroup2	PEL	A/A	G/G	601	426	22	7	0.449	0.190	1.060	9.27E-02	5.76E-02	276
2DP1	1313	cohortMinusGroup2	FIN	A/A	C/C	1371	205	58	3	0.346	0.107	1.110	9.58E-02	5.78E-02	277
2DP1	522	cohortMinusGroup2	GBR	T/T	C/C	1648	217	65	3	0.351	0.109	1.130	9.94E-02	5.80E-02	278
3DP1	796	cohortMinusGroup2	PUR	T/T	C/C	1550	145	75	2	0.285	0.069	1.170	1.01E-01	5.83E-02	279
2DL4	1023	cohortMinusGroup2	GBR	G/G	A/A	1501	196	54	2	0.284	0.069	1.170	1.01E-01	5.85E-02	280
3DL3	961	cohortMinusGroup2	BEB	C/C	A/A	969	227	30	13	1.850	0.950	3.600	1.01E-01	5.87E-02	281
2DL5	583	cohortMinusGroup2	STU	G/G	A/A	531	386	19	24	1.740	0.940	3.220	1.05E-01	5.89E-02	282
2DL5	517	cohortMinusGroup2	GWD	A/A	G/G	600	407	23	26	1.670	0.940	2.970	1.08E-01	5.91E-02	283
2DP1	448	cohortMinusGroup2	BEB	G/G	C/C	615	918	23	20	0.583	0.317	1.070	1.09E-01	5.93E-02	284
3DP1	796	cohortMinusGroup2	FIN	T/T	C/C	1553	145	72	2	0.298	0.072	1.230	1.17E-01	5.95E-02	285
2DP1	448	cohortMinusGroup2	FIN	G/G	C/C	611	913	27	25	0.620	0.356	1.080	1.17E-01	5.97E-02	286
3DP1	774	cohortMinusGroup2	GWD	G/G	C/C	1569	136	54	9	1.920	0.928	3.970	1.19E-01	5.99E-02	287
2DL5	517	cohortMinusGroup2	PUR	A/A	G/G	597	405	26	28	1.590	0.919	2.750	1.28E-01	6.01E-02	288
2DP1	522	cohortMinusGroup2	IBS	T/T	C/C	1631	215	82	5	0.463	0.186	1.150	1.28E-01	6.03E-02	289
2DL4	412	cohortMinusGroup2	PUR	G/G	A/A	936	490	47	15	0.610	0.338	1.100	1.29E-01	6.05E-02	290
2DL3	953	cohortMinusGroup2	PJL	G/G	A/A	1328	353	51	7	0.516	0.232	1.150	1.37E-01	6.08E-02	291
2DP1	448	cohortMinusGroup2	LWK	G/G	C/C	605	905	33	33	0.669	0.408	1.100	1.39E-01	6.10E-02	292
3DL1	1180	cohortMinusGroup2	CHB	G/G	C/C	1453	156	73	3	0.383	0.119	1.230	1.40E-01	6.12E-02	293
3DP1	774	cohortMinusGroup2	CDX	G/G	C/C	1554	143	69	2	0.315	0.076	1.300	1.42E-01	6.14E-02	294
2DL4	625	cohortMinusGroup2	PUR	C/C	G/G	824	424	47	15	0.620	0.343	1.120	1.46E-01	6.16E-02	295
3DL2	474	cohortMinusGroup2	PJL	G/G	T/T	1480	235	66	5	0.477	0.190	1.200	1.51E-01	6.18E-02	296
2DP1	1313	cohortMinusGroup2	ACB	A/A	C/C	1390	198	39	10	1.800	0.885	3.660	1.54E-01	6.20E-02	297
2DP1	1313	cohortMinusGroup2	MXL	A/A	C/C	1387	206	42	2	0.321	0.077	1.340	1.56E-01	6.22E-02	298
2DL5	583	cohortMinusGroup2	CDX	G/G	A/A	521	397	29	13	0.588	0.302	1.150	1.57E-01	6.24E-02	299
2DL4	1023	cohortMinusGroup2	PUR	G/G	A/A	1486	194	69	4	0.444	0.160	1.230	1.57E-01	6.26E-02	300
3DP1	774	cohortMinusGroup2	JPT	G/G	C/C	1541	142	82	3	0.397	0.124	1.270	1.60E-01	6.28E-02	301
3DL1	1180	cohortMinusGroup2	CHS	G/G	C/C	1443	155	83	4	0.449	0.162	1.240	1.62E-01	6.31E-02	302
2DL5	517	cohortMinusGroup2	BEB	A/A	G/G	602	410	21	23	1.610	0.879	2.950	1.63E-01	6.33E-02	303
3DP1	796	cohortMinusGroup2	STU	T/T	C/C	1545	144	80	3	0.402	0.125	1.290	1.68E-01	6.35E-02	304
2DL5	583	cohortMinusGroup2	GWD	G/G	A/A	527	384	23	26	1.550	0.871	2.760	1.75E-01	6.37E-02	305
3DP1	774	cohortMinusGroup2	STU	G/G	C/C	1543	142	80	3	0.407	0.127	1.310	1.75E-01	6.39E-02	306
2DS5	535	cohortMinusGroup2	CLM	G/G	A/A	129	680	2	32	3.040	0.720	12.800	1.79E-01	6.41E-02	307
3DL3	961	cohortMinusGroup2	STU	C/C	A/A	969	228	30	12	1.700	0.857	3.370	1.81E-01	6.43E-02	308
3DL1	607	cohortMinusGroup2	CHS	C/C	T/T	1490	266	78	8	0.575	0.275	1.200	1.83E-01	6.45E-02	309
2DP1	1313	cohortMinusGroup2	CLM	A/A	C/C	1372	195	57	13	1.600	0.860	2.980	1.86E-01	6.47E-02	310
2DL5	583	cohortMinusGroup2	BEB	G/G	A/A	529	386	21	24	1.570	0.861	2.860	1.86E-01	6.49E-02	311
3DL1	732	cohortMinusGroup2	IBS	T/T	C/C	374	121	19	2	0.325	0.075	1.420	1.90E-01	6.51E-02	312
2DL5	583	cohortMinusGroup2	ACB	G/G	A/A	527	400	23	10	0.573	0.270	1.220	1.98E-01	6.53E-02	313
2DL3	953	cohortMinusGroup2	ACB	G/G	A/A	1332	342	47	18	1.490	0.854	2.600	2.07E-01	6.56E-02	314
2DL5	517	cohortMinusGroup2	TSI	A/A	G/G	601	410	22	23	1.530	0.842	2.780	2.10E-01	6.58E-02	315
3DP1	774	cohortMinusGroup2	BEB	G/G	C/C	1562	143	61	2	0.358	0.087	1.480	2.12E-01	6.60E-02	316
3DL3	502	cohortMinusGroup2	FIN	G/G	A/A	629	714	18	31	1.520	0.842	2.740	2.13E-01	6.62E-02	317
2DL5	583	cohortMinusGroup2	TSI	G/G	A/A	534	391	16	19	1.620	0.823	3.190	2.16E-01	6.64E-02	318

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DL4	762	cohortMinusGroup2	PJL	C/C	T/T	1092	248	43	15	1.540	0.842	2.820	2.18E-01	6.66E-02	319
3DP1	796	cohortMinusGroup2	BEB	T/T	C/C	1566	145	59	2	0.366	0.089	1.510	2.26E-01	6.68E-02	320
2DP1	448	cohortMinusGroup2	IBS	G/G	C/C	607	905	31	33	0.714	0.433	1.180	2.33E-01	6.70E-02	321
2DP1	471	cohortMinusGroup2	CEU	A/A	G/G	1701	177	77	4	0.499	0.180	1.380	2.42E-01	6.72E-02	322
3DL1	1180	cohortMinusGroup2	PUR	G/G	C/C	1465	149	61	10	1.610	0.808	3.210	2.45E-01	6.74E-02	323
2DL5	583	cohortMinusGroup2	KHV	G/G	A/A	539	396	11	14	1.730	0.777	3.850	2.47E-01	6.76E-02	324
2DL4	762	cohortMinusGroup2	ESN	C/C	T/T	1069	253	66	10	0.640	0.325	1.260	2.52E-01	6.79E-02	325
3DL1	1180	cohortMinusGroup2	ACB	G/G	C/C	1464	156	62	3	0.454	0.141	1.460	2.54E-01	6.81E-02	326
3DL1	1180	cohortMinusGroup2	PEL	G/G	C/C	1464	156	62	3	0.454	0.141	1.460	2.54E-01	6.81E-02	326
3DL1	607	cohortMinusGroup2	KHV	C/C	T/T	1502	267	66	7	0.597	0.271	1.320	2.60E-01	6.83E-02	327
3DL3	804	cohortMinusGroup2	STU	G/G	A/A	1428	123	76	3	0.458	0.142	1.470	2.60E-01	6.85E-02	328
2DL5	517	cohortMinusGroup2	ACB	A/A	G/G	598	422	25	11	0.624	0.304	1.280	2.61E-01	6.87E-02	329
2DL5	583	cohortMinusGroup2	PUR	G/G	A/A	524	383	26	27	1.420	0.816	2.470	2.70E-01	6.89E-02	330
2DP1	522	cohortMinusGroup2	ACB	T/T	C/C	1663	210	50	10	1.580	0.789	3.160	2.70E-01	6.91E-02	331
3DL3	804	cohortMinusGroup2	ITU	G/G	A/A	1429	123	75	3	0.465	0.145	1.500	2.72E-01	6.93E-02	332
2DL5	517	cohortMinusGroup2	CLM	A/A	G/G	595	420	28	13	0.658	0.337	1.290	2.83E-01	6.95E-02	333
2DP1	1313	cohortMinusGroup2	GBR	A/A	C/C	1377	204	52	4	0.519	0.186	1.450	2.86E-01	6.97E-02	334
2DL4	762	cohortMinusGroup2	ACB	C/C	T/T	1086	256	49	7	0.606	0.271	1.350	2.90E-01	6.99E-02	335
2DL3	953	cohortMinusGroup2	LWK	G/G	A/A	1329	342	50	18	1.400	0.806	2.430	2.96E-01	7.02E-02	336
2DP1	448	cohortMinusGroup2	ITU	G/G	C/C	609	906	29	32	0.742	0.444	1.240	3.11E-01	7.04E-02	337
2DP1	448	cohortMinusGroup2	PUR	G/G	C/C	609	906	29	32	0.742	0.444	1.240	3.11E-01	7.04E-02	337
2DL5	583	cohortMinusGroup2	CLM	G/G	A/A	526	398	24	12	0.661	0.327	1.340	3.23E-01	7.06E-02	338
3DL1	607	cohortMinusGroup2	MXL	C/C	T/T	1530	264	38	10	1.530	0.753	3.110	3.32E-01	7.08E-02	339
2DL4	412	cohortMinusGroup2	MXL	G/G	A/A	956	496	27	9	0.642	0.300	1.380	3.33E-01	7.10E-02	340
3DP1	796	cohortMinusGroup2	CEU	T/T	C/C	1560	144	65	3	0.500	0.155	1.610	3.37E-01	7.12E-02	341
2DL3	953	cohortMinusGroup2	PUR	G/G	A/A	1331	343	48	17	1.370	0.778	2.410	3.42E-01	7.14E-02	342
2DL4	762	cohortMinusGroup2	MSL	C/C	T/T	1088	256	47	7	0.633	0.283	1.420	3.45E-01	7.16E-02	343
3DP1	774	cohortMinusGroup2	GIH	G/G	C/C	1545	141	78	4	0.562	0.203	1.560	3.59E-01	7.18E-02	344
2DL5	517	cohortMinusGroup2	CDX	A/A	G/G	593	418	30	15	0.709	0.377	1.330	3.61E-01	7.20E-02	345
2DL3	953	cohortMinusGroup2	YRI	G/G	A/A	1327	342	52	18	1.340	0.774	2.320	3.65E-01	7.22E-02	346
2DP1	522	cohortMinusGroup2	CEU	T/T	C/C	1640	214	73	6	0.630	0.271	1.470	3.68E-01	7.24E-02	347
3DL1	607	cohortMinusGroup2	CDX	C/C	T/T	1509	260	59	14	1.380	0.759	2.510	3.75E-01	7.27E-02	348
2DP1	471	cohortMinusGroup2	CLM	A/A	G/G	1709	171	69	10	1.450	0.733	2.870	3.83E-01	7.29E-02	349
3DL2	474	cohortMinusGroup2	CLM	G/G	T/T	1486	234	60	6	0.635	0.271	1.490	3.84E-01	7.31E-02	350
2DL5	583	cohortMinusGroup2	JPT	G/G	A/A	534	393	16	17	1.440	0.719	2.890	3.89E-01	7.33E-02	351
3DL3	961	cohortMinusGroup2	CLM	C/C	A/A	951	232	48	8	0.683	0.319	1.460	4.17E-01	7.35E-02	352
2DP1	522	cohortMinusGroup2	ITU	T/T	C/C	1650	209	63	11	1.380	0.716	2.660	4.38E-01	7.37E-02	353
2DL4	1023	cohortMinusGroup2	ITU	G/G	A/A	1485	192	70	6	0.663	0.284	1.550	4.40E-01	7.39E-02	354
3DP1	774	cohortMinusGroup2	ITU	G/G	C/C	1550	141	73	4	0.602	0.217	1.670	4.41E-01	7.41E-02	355
2DL5	517	cohortMinusGroup2	CHS	A/A	G/G	600	412	23	21	1.330	0.726	2.430	4.41E-01	7.43E-02	356
3DL1	607	cohortMinusGroup2	PEL	C/C	T/T	1510	267	58	7	0.683	0.308	1.510	4.41E-01	7.45E-02	357
3DL3	961	cohortMinusGroup2	PJL	C/C	A/A	966	229	33	11	1.410	0.702	2.830	4.43E-01	7.47E-02	358
3DL3	502	cohortMinusGroup2	MXL	G/G	A/A	632	733	15	12	0.690	0.321	1.490	4.47E-01	7.50E-02	359
2DP1	1313	cohortMinusGroup2	ASW	A/A	C/C	1397	201	32	7	1.520	0.662	3.490	4.52E-01	7.52E-02	360
2DP1	1313	cohortMinusGroup2	ESN	A/A	C/C	1376	203	53	5	0.639	0.252	1.620	4.53E-01	7.54E-02	361
3DL1	607	cohortMinusGroup2	PJL	C/C	T/T	1504	266	64	8	0.707	0.335	1.490	4.55E-01	7.56E-02	362
2DP1	448	cohortMinusGroup2	ESN	G/G	C/C	613	909	25	29	0.782	0.454	1.350	4.56E-01	7.58E-02	363
3DL1	732	cohortMinusGroup2	BEB	T/T	C/C	376	115	17	8	1.540	0.648	3.660	4.58E-01	7.60E-02	364
2DL4	1023	cohortMinusGroup2	CLM	G/G	A/A	1495	193	60	5	0.646	0.256	1.630	4.62E-01	7.62E-02	365
2DL5	517	cohortMinusGroup2	CEU	A/A	G/G	601	422	22	11	0.712	0.342	1.480	4.65E-01	7.64E-02	366
3DL3	804	cohortMinusGroup2	PJL	G/G	A/A	1442	123	62	3	0.567	0.175	1.830	4.70E-01	7.66E-02	367
2DL3	953	cohortMinusGroup2	MXL	G/G	A/A	1336	352	43	8	0.706	0.329	1.520	4.70E-01	7.68E-02	368
2DL3	953	cohortMinusGroup2	ESN	G/G	A/A	1332	351	47	9	0.727	0.353	1.500	4.83E-01	7.70E-02	369
2DL4	625	cohortMinusGroup2	MXL	C/C	G/G	846	430	25	9	0.708	0.328	1.530	4.86E-01	7.72E-02	370
2DL4	762	cohortMinusGroup2	ASW	C/C	T/T	1107	259	28	4	0.611	0.212	1.760	4.87E-01	7.75E-02	371
2DP1	1313	cohortMinusGroup2	IBS	A/A	C/C	1370	202	59	6	0.690	0.294	1.620	5.04E-01	7.77E-02	372
2DL5	517	cohortMinusGroup2	KHV	A/A	G/G	607	418	16	15	1.360	0.665	2.780	5.07E-01	7.79E-02	373
2DP1	471	cohortMinusGroup2	ACB	A/A	G/G	1721	173	57	8	1.400	0.657	2.980	5.15E-01	7.81E-02	374
2DL4	1023	cohortMinusGroup2	BEB	G/G	A/A	1502	189	53	9	1.350	0.655	2.780	5.41E-01	7.83E-02	375
2DL3	953	cohortMinusGroup2	STU	G/G	A/A	1325	349	54	11	0.773	0.400	1.490	5.42E-01	7.85E-02	376
3DL2	474	cohortMinusGroup2	BEB	G/G	T/T	1492	234	54	6	0.708	0.301	1.660	5.47E-01	7.87E-02	377
2DL5	517	cohortMinusGroup2	JPT	A/A	G/G	604	416	19	17	1.300	0.668	2.530	5.49E-01	7.89E-02	378
3DP1	796	cohortMinusGroup2	IBS	T/T	C/C	1559	143	66	4	0.661	0.237	1.840	5.63E-01	7.91E-02	379
2DP1	1313	cohortMinusGroup2	ITU	A/A	C/C	1376	198	53	10	1.310	0.656	2.620	5.64E-01	7.93E-02	380
3DL3	804	cohortMinusGroup2	GIH	G/G	A/A	1433	122	71	4	0.662	0.238	1.840	5.66E-01	7.95E-02	381
3DL3	502	cohortMinusGroup2	CEU	G/G	A/A	624	713	23	32	1.220	0.706	2.110	5.69E-01	7.98E-02	382
2DL3	953	cohortMinusGroup2	GIH	G/G	A/A	1329	344	50	16	1.240	0.698	2.200	5.69E-01	8.00E-02	383
3DP1	796	cohortMinusGroup2	GIH	T/T	C/C	1547	142	78	5	0.698	0.278	1.750	5.72E-01	8.02E-02	384
2DP1	448	cohortMinusGroup2	ACB	G/G	C/C	615	910	23	28	0.823	0.470	1.440	5.91E-01	8.04E-02	385
2DL5	517	cohortMinusGroup2	ASW	A/A	G/G	606	418	17	15	1.280	0.632	2.590	6.15E-01	8.06E-02	386
3DL3	502	cohortMinusGroup2	GBR	G/G	A/A	622	721	25	24	0.828	0.468	1.460	6.15E-01	8.08E-02	387
3DL1	1180	cohortMinusGroup2	GWD	G/G	C/C	1460	154	66	5	0.718	0.285	1.810	6.19E-01	8.10E-02	388
2DS5	590	cohortMinusGroup2	LWK	G/G	C/C	199	30	40	4	0.663	0.221	1.990	6.25E-01	8.12E-02	389
2DL4	762	cohortMinusGroup2	STU	C/C	T/T	1086	254	49	9	0.785	0.381	1.620	6.28E-01	8.14E-02	390
2DP1	1313	cohortMinusGroup2	PUR	A/A	C/C	1382	203	47	5	0.724	0.285	1.840	6.39E-01	8.16E-02	391
3DL1	607	cohortMinusGroup2	STU	C/C	T/T	1504	265	64	9	0.798	0.392	1.620	6.48E-01	8.18E-02	392
3DP1	774	cohortMinusGroup2	CEU	G/G	C/C	1560	141	63	4	0.702	0.252	1.960	6.52E-01	8.21E-02	393
3DP1	796	cohortMinusGroup2	TSI	T/T	C/C	1563	143	62	4	0.705	0.253	1.970	6.57E-01	8.23E-02	394
2DP1	471	cohortMinusGroup2	LWK	A/A	G/G	1707	172	71	9	1.260	0.619	2.570	6.62E-01	8.25E-02	395
3DL1	607	cohortMinusGroup2	ASW	C/C	T/T	1523	268	45	6	0.758	0.320	1.790	6.65E-01	8.27E-02	396
2DL3	953	cohortMinusGroup2	MSL	G/G	A/A	1332	350	47	10	0.810	0.405	1.620	6.66E-01	8.29E-02	397
2DL5	583	cohortMinusGroup2	ESN	G/G	A/A	530	398	20	12	0.799	0.386	1.650	6.72E-01	8.31E-02	398
2DL5	583	cohortMinusGroup2	GBR	G/G	A/A	541	401	9	9	1.350	0.531	3.430	6.96E-01	8.33E-02	399
2DL5	583	cohortMinusGroup2	CEU	G/G	A/A	536	402	14	8	0.762	0.317	1.830	6.96E-01	8.35E-02	400
3DL1	1180	cohortMinusGroup2	ESN	G/G	C/C	1463	154	63	5	0.754	0.299	1.900	6.98E-01	8.37E-02	401
2DL4	762	cohortMinusGroup2	LWK	C/C	T/T	1083	253	52	10	0.823	0.413	1.640	6.99E-01	8.39E-02	402
2DP1	1313	cohortMinusGroup2	LWK	A/A	C/C	1385	200	44	8	1.260	0.585	2.720	7.06E-01	8.41E-02	403
2DL3	953	cohortMinusGroup2	BEB	G/G	A/A	1333	350	46	10	0.828	0.414	1.660	7.14E-01	8.43E-02	404
2DL5	517	cohortMinusGroup2	MSL	A/A	G/G	601	415	22	18	1.180	0.625	2.230	7.19E-01	8.46E-02	405
2DL5	583	cohortMinusGroup2	CHS	G/G	A/A	527	390	23	20	1.180	0.639	2.180	7.20E-01	8.48E-02	406
2DP1	522	cohortMinusGroup2	LWK	T/T	C/C	1648	210	65	10	1.210	0.612	2.390	7.21E-01	8.50E-02	407
3DL1	1180	cohortMinusGroup2	KHV	G/G	C/C	1464	154	62	5	0.767	0.304	1.940	7.26E-01	8.52E-02	408
3DL3	502	cohortMinusGroup2	IBS	G/G	A/A	623	721	24	24	0.864	0.486	1.540	7.26E-01	8.54E-02	409
2DP1	522	cohortMinusGroup2	PUR	T/T	C/C	1646	213	67	7	0.807	0.366	1.780	7.31E-01	8.56E-02	410
3DL2	474	cohortMinusGroup2	FIN	G/G	T/T	1491	233	55	7	0.814	0.366	1.810	7.53E-01	8.58E-02	411
2DP1	522	cohortMinusGroup2	CLM	T/T	C/C	1647	210	66	10	1.190	0.603	2.350	7.54E-01	8.60E-02	412
3DL1	1180	cohortMinusGroup2	GIH	G/G	C/C	1465	154	61	5	0.780	0.309	1.970	7.55E-01	8.62E-02	413
2DL5	517	cohortMinusGroup2	IBS	A/A	G/G	601	420	22	13	0.846	0.421	1.700	7.66E-01	8.64E-02	414
2DP1	522	cohortMinusGroup2	ESN	T/T	C/C	1654	211	59	9	1.200	0.587	2.460	7.67E-01	8.66E-02	415
3DP1	796	cohortMinusGroup2	ITU	T/T	C/C	1556	142	69	5	0.794	0.315	2.000	7.83E-01	8.69E-02	416
3DL1	1180	cohortMinusGroup2	JPT	G/G	C/C	1456	153	70	6	0.816	0.349	1.910	7.87E-01	8.71E-02	417
2DL4	412	cohortMinusGroup2	KHV	G/G	A/A	952	487	31	18	1.140	0.631	2.060	7.89E-01	8.73E-02	418
2DL5	583	cohortMinusGroup2	ASW	G/G	A/A	534	396	16	14	1.180	0.569	2.450	7.97E-01	8.75E-02	419
2DP1	448	cohortMinusGroup2	CLM	G/G	C/C	609	899	29	39	0.911	0.557	1.490	8.06E-01	8.77E-02	420
2DL5	517	cohortMinusGroup2	GIH	A/A	G/G	591	413	32	20	0.894	0.504	1.590	8.12E-01	8.79E-02	421
3DL1	1180	cohortMinusGroup2	MSL	G/G	C/C	1467	154	59	5	0.807	0.319	2.040	8.14E-01	8.81E-02	422
2DL5	517	cohortMinusGroup2	ESN	A/A	G/G	603	421	20	12	0.859	0.415	1.780	8.21E-01	8.83E-02	423
2DL5	517	cohortMinusGroup2	GBR	A/A	G/G	611	423	12	10	1.200	0.514	2.800	8.34E-01	8.85E-02	424
2DL3	953	cohortMinusGroup2	ASW	G/G	A/A	1342	349	37	11	1.140	0.576	2.260	8.39E-01	8.87E-02	425

gene	pos	group1	group2	genotype1	genotype2	group1 genotype1 ObservedCount	group1 genotype2 ObservedCount	group2 genotype1 ObservedCount	group2 genotype2 ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DP1	774	cohortMinusGroup2	PUR	G/G	C/C	1556	140	67	5	0.829	0.329	2.090	8.59E-01	8.89E-02	426
2DP1	471	cohortMinusGroup2	PUR	A/A	G/G	1709	175	69	6	0.849	0.363	1.980	8.61E-01	8.91E-02	427
2DP1	471	cohortMinusGroup2	ESN	A/A	G/G	1719	174	59	7	1.170	0.526	2.600	8.62E-01	8.94E-02	428
2DL5	517	cohortMinusGroup2	PJL	A/A	G/G	594	411	29	22	1.100	0.623	1.940	8.64E-01	8.96E-02	429
2DL4	762	cohortMinusGroup2	ITU	C/C	T/T	1091	254	44	9	0.879	0.424	1.820	8.66E-01	8.98E-02	430
2DL4	625	cohortMinusGroup2	KHV	C/C	G/G	846	425	25	14	1.110	0.571	2.160	8.82E-01	9.00E-02	431
2DL4	762	cohortMinusGroup2	BEB	C/C	T/T	1105	255	30	8	1.160	0.526	2.560	8.82E-01	9.02E-02	432
2DL4	412	cohortMinusGroup2	CDX	G/G	A/A	943	486	40	19	0.922	0.528	1.610	8.83E-01	9.04E-02	433
2DL5	517	cohortMinusGroup2	FIN	A/A	G/G	598	414	25	19	1.100	0.598	2.020	8.86E-01	9.06E-02	434
3DP1	774	cohortMinusGroup2	IBS	G/G	C/C	1557	140	66	5	0.843	0.334	2.130	8.87E-01	9.08E-02	435
2DL5	583	cohortMinusGroup2	MSL	G/G	A/A	528	392	22	18	1.100	0.582	2.080	8.92E-01	9.10E-02	436
3DL1	1180	cohortMinusGroup2	STU	G/G	C/C	1460	153	66	6	0.867	0.370	2.030	9.04E-01	9.12E-02	437
3DL1	1180	cohortMinusGroup2	PJL	G/G	C/C	1461	153	65	6	0.881	0.376	2.070	9.34E-01	9.14E-02	438
2DL3	953	cohortMinusGroup2	CLM	G/G	A/A	1329	346	50	14	1.080	0.590	1.980	9.37E-01	9.17E-02	439
2DL5	583	cohortMinusGroup2	IBS	G/G	A/A	535	400	15	10	0.892	0.397	2.010	9.42E-01	9.19E-02	440
2DL5	517	cohortMinusGroup2	YRI	A/A	G/G	596	413	27	20	1.070	0.592	1.930	9.45E-01	9.21E-02	441
3DL2	474	cohortMinusGroup2	MXL	G/G	T/T	1509	235	37	5	0.868	0.338	2.230	9.47E-01	9.23E-02	442
2DL3	953	cohortMinusGroup2	ITU	G/G	A/A	1325	345	54	15	1.070	0.597	1.920	9.48E-01	9.25E-02	443
2DP1	1313	cohortMinusGroup2	TSI	A/A	C/C	1379	200	50	8	1.100	0.514	2.350	9.58E-01	9.27E-02	444
2DL5	517	cohortMinusGroup2	CHB	A/A	G/G	597	416	26	17	0.938	0.503	1.750	9.67E-01	9.29E-02	445
3DL1	607	cohortMinusGroup2	ITU	C/C	T/T	1501	263	67	11	0.937	0.489	1.800	9.73E-01	9.31E-02	446
3DL1	1180	cohortMinusGroup2	CLM	G/G	C/C	1474	153	52	6	1.110	0.469	2.630	9.90E-01	9.33E-02	447
2DL4	762	cohortMinusGroup2	MXL	C/C	T/T	1113	258	22	5	0.980	0.368	2.610	1.00E+00	9.35E-02	448
2DP1	1313	cohortMinusGroup2	CEU	A/A	C/C	1379	201	50	7	0.960	0.429	2.150	1.00E+00	9.37E-02	449
3DL3	804	cohortMinusGroup2	LWK	G/G	A/A	1443	121	61	5	0.978	0.386	2.480	1.00E+00	9.40E-02	450
2DP1	471	cohortMinusGroup2	ITU	A/A	G/G	1714	174	64	7	1.080	0.487	2.390	1.00E+00	9.42E-02	451
2DL4	1023	cohortMinusGroup2	FIN	G/G	A/A	1500	191	55	7	1.000	0.449	2.230	1.00E+00	9.44E-02	452
2DL4	625	cohortMinusGroup2	CDX	C/C	G/G	837	422	34	17	0.992	0.548	1.800	1.00E+00	9.46E-02	453
2DL5	583	cohortMinusGroup2	CHB	G/G	A/A	528	394	22	16	0.975	0.505	1.880	1.00E+00	9.48E-02	454
2DL5	583	cohortMinusGroup2	GIH	G/G	A/A	524	390	26	20	1.030	0.567	1.870	1.00E+00	9.48E-02	454
3DL3	502	cohortMinusGroup2	CLM	G/G	A/A	625	719	22	26	1.030	0.578	1.840	1.00E+00	9.48E-02	454
2DL5	517	cohortMinusGroup2	ITU	A/A	G/G	591	410	32	23	1.040	0.600	1.800	1.00E+00	9.50E-02	455
2DL5	583	cohortMinusGroup2	PJL	G/G	A/A	521	389	29	21	0.970	0.545	1.730	1.00E+00	9.50E-02	455
2DL5	583	cohortMinusGroup2	YRI	G/G	A/A	523	390	27	20	0.993	0.549	1.800	1.00E+00	9.50E-02	455
3DL3	502	cohortMinusGroup2	PJL	G/G	A/A	627	722	20	23	0.999	0.544	1.840	1.00E+00	9.52E-02	456
2DP1	471	cohortMinusGroup2	TSI	A/A	G/G	1704	174	74	7	0.926	0.420	2.040	1.00E+00	9.54E-02	457
3DP1	774	cohortMinusGroup2	TSI	G/G	C/C	1561	139	62	6	1.090	0.463	2.560	1.00E+00	9.54E-02	457
2DL5	583	cohortMinusGroup2	FIN	G/G	A/A	527	392	23	18	1.050	0.559	1.970	1.00E+00	9.56E-02	458
2DL5	583	cohortMinusGroup2	ITU	G/G	A/A	518	387	32	23	0.962	0.554	1.670	1.00E+00	9.58E-02	459
3DL1	1180	cohortMinusGroup2	ITU	G/G	C/C	1461	152	65	7	1.040	0.469	2.310	1.00E+00	9.58E-02	459
2DP1	522	cohortMinusGroup2	TSI	T/T	C/C	1647	212	66	8	0.942	0.446	1.990	1.00E+00	9.60E-02	460
3DL1	1180	cohortMinusGroup2	YRI	G/G	C/C	1460	152	66	7	1.020	0.460	2.260	1.00E+00	9.60E-02	460
3DL1	732	cohortMinusGroup2	CLM	T/T	C/C	375	117	18	6	1.070	0.415	2.760	1.00E+00	9.62E-02	461
2DL4	1023	cohortMinusGroup2	PJL	G/G	A/A	1490	190	65	8	0.965	0.456	2.040	1.00E+00	9.65E-02	462
3DL3	961	cohortMinusGroup2	PUR	C/C	A/A	948	228	51	12	0.978	0.513	1.860	1.00E+00	9.65E-02	462

Table A9 KIR genotypes for 5489 samples from the TCGA Project na = not available = ambiguous

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-HT-A617-10A-01D-A29Q-08	LGG	AmerIndian	na																	
TCGA-A2-A0T1-10A-01D-A099-09	BRCA	AmerIndian	NO																	
TCGA-EK-A2RD-10A-01D-A20U-09	CESC	AmerIndian	NO																	
TCGA-DQ-7592-10A-01D-2078-08	HNSC	AmerIndian	NO																	
TCGA-A4-8515-10A-01D-2396-08	KIRP	AmerIndian	NO																	
TCGA-G3-A3CJ-10A-01D-A20W-10	LIHC	AmerIndian	NO																	
TCGA-42-2593-10A-01D-1764-09	OV	AmerIndian	NO																	
TCGA-DE-A4MC-10A-01D-A25A-08	THCA	AmerIndian	NO																	
TCGA-AX-A06H-10A-01D-A122-09	UCEC	AmerIndian	NO																	
TCGA-EK-A2RO-10A-01D-A18J-09	CESC	AmerIndian	YES																	
TCGA-JW-A5VG-10A-01D-A28E-09	CESC	AmerIndian	YES																	
TCGA-JW-A5VH-10A-01D-A28E-09	CESC	AmerIndian	YES																	
TCGA-JW-A5VI-10A-01D-A28E-09	CESC	AmerIndian	YES																	
TCGA-JW-A5VJ-10A-01D-A28E-09	CESC	AmerIndian	YES																	
TCGA-JW-A5VL-10A-01D-A28E-09	CESC	AmerIndian	YES																	
TCGA-CV-A45Y-10A-01D-A25E-08	HNSC	AmerIndian	YES																	
TCGA-DI-A2QT-10A-01D-A19Y-09	UCEC	AmerIndian	YES																	
TCGA-AR-A1AS-10A-01D-A12Q-09	BRCA	ASIAN	na																	
TCGA-AD-6889-10A-01D-1924-10	COAD	ASIAN	na																	
TCGA-HV-A5A3-10A-01D-A26I-08	PAAD	ASIAN	na																	
TCGA-HV-A5A4-10A-01D-A26I-08	PAAD	ASIAN	na																	
TCGA-EE-A17Y-10B-01D-A198-08	SKCM	ASIAN	na																	
TCGA-EO-A3B0-10A-01D-A19Y-09	UCEC	ASIAN	na																	
TCGA-PK-A5H9-10A-01D-A29L-10	ACC	ASIAN	NO																	
TCGA-CF-A1HR-10A-01D-A13W-08	BLCA	ASIAN	NO																	
TCGA-CF-A1HS-10A-01D-A13W-08	BLCA	ASIAN	NO																	
TCGA-CF-A27C-10A-01D-A16O-08	BLCA	ASIAN	NO																	
TCGA-CF-A3MF-10A-01D-A21A-08	BLCA	ASIAN	NO																	
TCGA-CF-A3MG-10A-01D-A20D-08	BLCA	ASIAN	NO																	
TCGA-CF-A3MH-10A-01D-A20D-08	BLCA	ASIAN	NO																	
TCGA-CF-A3MI-10A-01D-A20D-08	BLCA	ASIAN	NO																	
TCGA-CF-A47S-10A-01D-A23U-08	BLCA	ASIAN	NO																	
TCGA-CF-A47T-10A-01D-A23U-08	BLCA	ASIAN	NO																	
TCGA-CF-A47V-10A-01D-A23U-08	BLCA	ASIAN	NO																	
TCGA-CF-A47W-10A-01D-A23U-08	BLCA	ASIAN	NO																	
TCGA-CF-A47X-10A-01D-A23U-08	BLCA	ASIAN	NO																	
TCGA-CF-A47Y-10A-01D-A23U-08	BLCA	ASIAN	NO																	
TCGA-CF-A5U8-10A-01D-A289-08	BLCA	ASIAN	NO																	
TCGA-CF-A5UA-10A-01D-A289-08	BLCA	ASIAN	NO																	
TCGA-DK-A6AV-10A-01D-A30H-08	BLCA	ASIAN	NO																	
TCGA-E7-A4IJ-10A-01D-A26K-08	BLCA	ASIAN	NO																	
TCGA-E7-A4XJ-10A-01D-A26K-08	BLCA	ASIAN	NO																	
TCGA-E7-A5KE-10A-01D-A289-08	BLCA	ASIAN	NO																	
TCGA-E7-A5KF-10A-01D-A289-08	BLCA	ASIAN	NO																	
TCGA-E7-A677-10A-01D-A30H-08	BLCA	ASIAN	NO																	
TCGA-E7-A678-10A-01D-A30H-08	BLCA	ASIAN	NO																	
TCGA-E7-A6ME-10B-01D-A329-08	BLCA	ASIAN	NO																	
TCGA-E7-A6MF-10B-01D-A329-08	BLCA	ASIAN	NO																	
TCGA-FD-A62N-10A-01D-A30H-08	BLCA	ASIAN	NO																	
TCGA-G2-A3VY-10A-01D-A22Z-08	BLCA	ASIAN	NO																	
TCGA-A1-A0SK-10A-03D-A099-09	BRCA	ASIAN	NO																	
TCGA-A2-A0CR-10A-01D-A22A-09	BRCA	ASIAN	NO																	
TCGA-A2-A0CV-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-AO-A126-10A-01D-A10M-09	BRCA	ASIAN	NO																	
TCGA-C8-A12K-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A12L-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A12M-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A12N-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A12O-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A12P-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A12Q-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A12T-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A12U-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A12V-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A12W-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A12X-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A12Y-10A-01D-A12B-09	BRCA	ASIAN	NO																	
TCGA-C8-A12Z-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A130-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A131-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A132-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A134-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A135-10A-02D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A137-10A-02D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A138-10A-01D-A110-09	BRCA	ASIAN	NO																	
TCGA-C8-A1HE-10A-01D-A13O-09	BRCA	ASIAN	NO																	
TCGA-C8-A1HF-10A-01D-A135-09	BRCA	ASIAN	NO																	
TCGA-C8-A1HG-10A-01D-A135-09	BRCA	ASIAN	NO																	
TCGA-C8-A1HI-10A-01D-A135-09	BRCA	ASIAN	NO																	
TCGA-C8-A1HJ-10A-01D-A13O-09	BRCA	ASIAN	NO																	
TCGA-C8-A1HK-10A-01D-A13O-09	BRCA	ASIAN	NO																	
TCGA-C8-A1HL-10A-01D-A135-09	BRCA	ASIAN	NO																	
TCGA-C8-A1HM-10A-01D-A135-09	BRCA	ASIAN	NO																	
TCGA-C8-A1HN-10A-01D-A135-09	BRCA	ASIAN	NO																	
TCGA-C8-A1HO-10A-01D-A188-09	BRCA	ASIAN	NO																	
TCGA-C8-A26V-10A-01D-A16D-09	BRCA	ASIAN	NO																	
TCGA-C8-A26W-10A-01D-A16D-09	BRCA	ASIAN	NO																	
TCGA-C8-A26X-10A-01D-A16D-09	BRCA	ASIAN	NO																	
TCGA-C8-A26Y-10A-01D-A16D-09	BRCA	ASIAN	NO																	
TCGA-C8-A26Z-10A-01D-A16D-09	BRCA	ASIAN	NO																	
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TCGA-C8-A27B-10A-01D-A167-09	BRCA	ASIAN	NO																	
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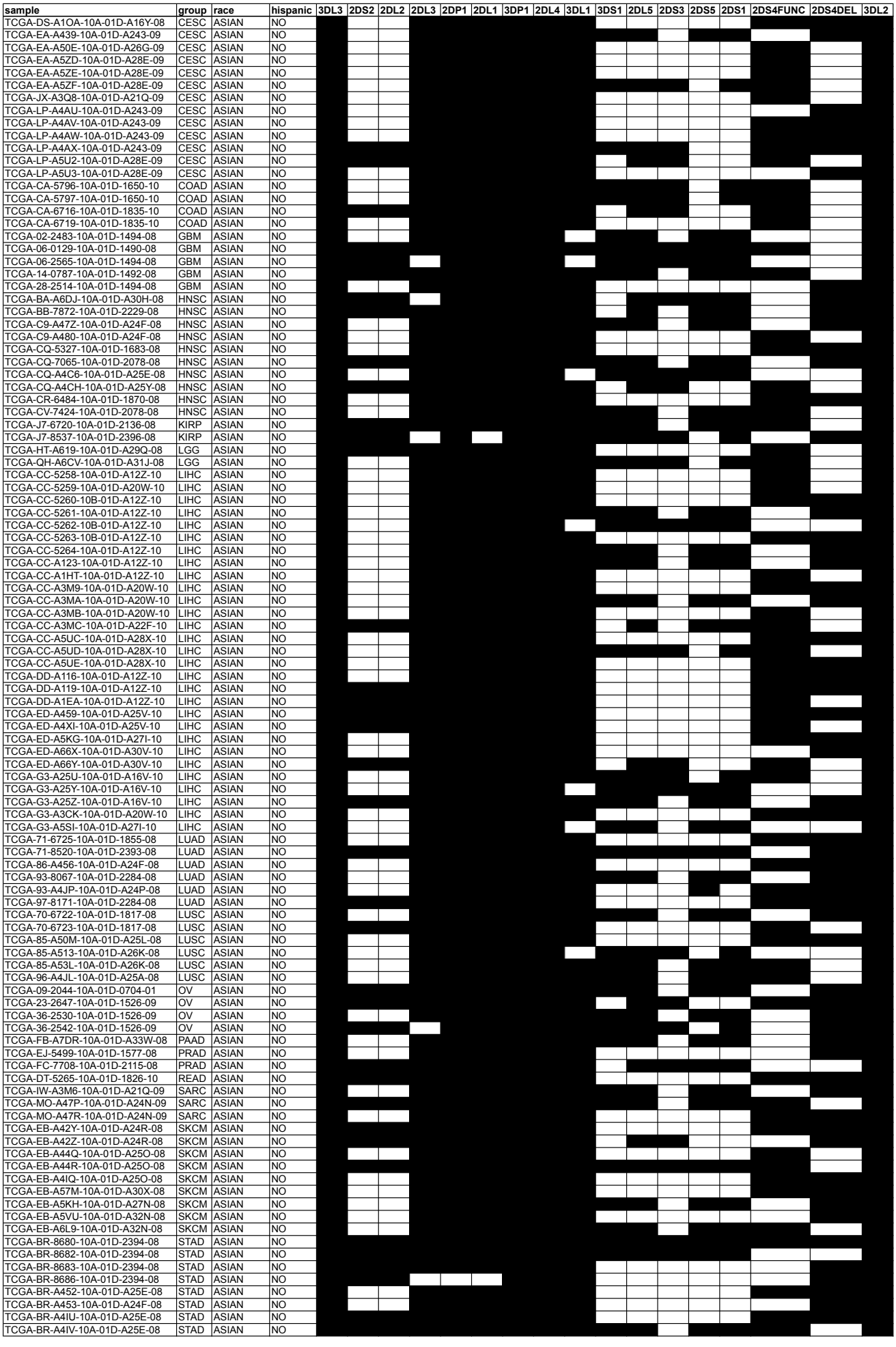
TCGA-C8-A3M8-10A-01D-A20S-09	BRCA	ASIAN	NO																	
TCGA-EW-A1IY-10A-01D-A13O-09	BRCA	ASIAN	NO																	
TCGA-JL-A3YW-10B-01D-A23C-09	BRCA	ASIAN	NO																	
TCGA-JL-A3YX-10A-01D-A22X-09	BRCA	ASIAN	NO																	
TCGA-PE-A5DD-10A-01D-A27P-09	BRCA	ASIAN	NO																	
TCGA-DR-A0ZL-10A-01D-A10S-08	CESC	ASIAN	NO																	



sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DS-A1OA-10A-01D-A16Y-08	CESC	ASIAN	NO																	
TCGA-EA-A439-10A-01D-A243-09	CESC	ASIAN	NO																	
TCGA-EA-A50E-10A-01D-A26G-09	CESC	ASIAN	NO																	
TCGA-EA-A5ZD-10A-01D-A28E-09	CESC	ASIAN	NO																	
TCGA-EA-A5ZE-10A-01D-A28E-09	CESC	ASIAN	NO																	
TCGA-EA-A5ZF-10A-01D-A28E-09	CESC	ASIAN	NO																	
TCGA-JX-A3Q8-10A-01D-A21Q-09	CESC	ASIAN	NO																	
TCGA-LP-A4AU-10A-01D-A243-09	CESC	ASIAN	NO																	
TCGA-LP-A4AV-10A-01D-A243-09	CESC	ASIAN	NO																	
TCGA-LP-A4AW-10A-01D-A243-09	CESC	ASIAN	NO																	
TCGA-LP-A4AX-10A-01D-A243-09	CESC	ASIAN	NO																	
TCGA-LP-A5U2-10A-01D-A28E-09	CESC	ASIAN	NO																	
TCGA-LP-A5U3-10A-01D-A28E-09	CESC	ASIAN	NO																	
TCGA-CA-5796-10A-01D-1650-10	COAD	ASIAN	NO																	
TCGA-CA-5797-10A-01D-1650-10	COAD	ASIAN	NO																	
TCGA-CA-6716-10A-01D-1835-10	COAD	ASIAN	NO																	
TCGA-CA-6719-10A-01D-1835-10	COAD	ASIAN	NO																	
TCGA-02-2483-10A-01D-1494-08	GBM	ASIAN	NO																	
TCGA-06-0129-10A-01D-1490-08	GBM	ASIAN	NO																	
TCGA-06-2565-10A-01D-1494-08	GBM	ASIAN	NO																	
TCGA-14-0787-10A-01D-1492-08	GBM	ASIAN	NO																	
TCGA-28-2514-10A-01D-1494-08	GBM	ASIAN	NO																	
TCGA-BA-A6DJ-10A-01D-A30H-08	HNSC	ASIAN	NO																	
TCGA-BB-7872-10A-01D-2229-08	HNSC	ASIAN	NO																	
TCGA-C9-A47Z-10A-01D-A24F-08	HNSC	ASIAN	NO																	
TCGA-C9-A480-10A-01D-A24F-08	HNSC	ASIAN	NO																	
TCGA-CQ-5327-10A-01D-1683-08	HNSC	ASIAN	NO																	
TCGA-CQ-7065-10A-01D-2078-08	HNSC	ASIAN	NO																	
TCGA-CQ-A4C6-10A-01D-A25E-08	HNSC	ASIAN	NO																	
TCGA-CQ-A4CH-10A-01D-A25Y-08	HNSC	ASIAN	NO																	
TCGA-CR-6484-10A-01D-1870-08	HNSC	ASIAN	NO																	
TCGA-CV-7424-10A-01D-2078-08	HNSC	ASIAN	NO																	
TCGA-J7-6720-10A-01D-2136-08	KIRP	ASIAN	NO																	
TCGA-J7-8537-10A-01D-2396-08	KIRP	ASIAN	NO																	
TCGA-HT-A619-10A-01D-A29Q-08	LGG	ASIAN	NO																	
TCGA-QH-A6CV-10A-01D-A31J-08	LGG	ASIAN	NO																	
TCGA-CC-5258-10A-01D-A12Z-10	LIHC	ASIAN	NO																	
TCGA-CC-5259-10A-01D-A20W-10	LIHC	ASIAN	NO																	
TCGA-CC-5260-10B-01D-A12Z-10	LIHC	ASIAN	NO																	
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TCGA-CC-5263-10B-01D-A12Z-10	LIHC	ASIAN	NO																	
TCGA-CC-5264-10A-01D-A12Z-10	LIHC	ASIAN	NO																	
TCGA-CC-A123-10A-01D-A12Z-10	LIHC	ASIAN	NO																	
TCGA-CC-A1HT-10A-01D-A12Z-10	LIHC	ASIAN	NO																	
TCGA-CC-A3M9-10A-01D-A20W-10	LIHC	ASIAN	NO																	
TCGA-CC-A3MA-10A-01D-A20W-10	LIHC	ASIAN	NO																	
TCGA-CC-A3MB-10A-01D-A20W-10	LIHC	ASIAN	NO																	
TCGA-CC-A3MC-10A-01D-A22F-10	LIHC	ASIAN	NO																	
TCGA-CC-A5UC-10A-01D-A28X-10	LIHC	ASIAN	NO																	
TCGA-CC-A5UD-10A-01D-A28X-10	LIHC	ASIAN	NO																	
TCGA-CC-A5UE-10A-01D-A28X-10	LIHC	ASIAN	NO																	
TCGA-DD-A116-10A-01D-A12Z-10	LIHC	ASIAN	NO																	
TCGA-DD-A119-10A-01D-A12Z-10	LIHC	ASIAN	NO																	
TCGA-DD-A1EA-10A-01D-A12Z-10	LIHC	ASIAN	NO																	
TCGA-ED-A459-10A-01D-A25V-10	LIHC	ASIAN	NO																	
TCGA-ED-A4XI-10A-01D-A25V-10	LIHC	ASIAN	NO																	
TCGA-ED-A5KG-10A-01D-A27I-10	LIHC	ASIAN	NO																	
TCGA-ED-A66X-10A-01D-A30V-10	LIHC	ASIAN	NO																	
TCGA-ED-A66Y-10A-01D-A30V-10	LIHC	ASIAN	NO																	
TCGA-G3-A25U-10A-01D-A16V-10	LIHC	ASIAN	NO																	
TCGA-G3-A25Y-10A-01D-A16V-10	LIHC	ASIAN	NO																	
TCGA-G3-A25Z-10A-01D-A16V-10	LIHC	ASIAN	NO																	
TCGA-G3-A3CK-10A-01D-A20W-10	LIHC	ASIAN	NO																	
TCGA-G3-A5SI-10A-01D-A27I-10	LIHC	ASIAN	NO																	
TCGA-71-6725-10A-01D-1855-08	LUAD	ASIAN	NO																	
TCGA-71-8520-10A-01D-2393-08	LUAD	ASIAN	NO																	
TCGA-86-A456-10A-01D-A24F-08	LUAD	ASIAN	NO																	
TCGA-93-8067-10A-01D-2284-08	LUAD	ASIAN	NO																	
TCGA-93-A4JP-10A-01D-A24P-08	LUAD	ASIAN	NO																	
TCGA-97-8171-10A-01D-2284-08	LUAD	ASIAN	NO																	
TCGA-70-6722-10A-01D-1817-08	LUSC	ASIAN	NO																	
TCGA-70-6723-10A-01D-1817-08	LUSC	ASIAN	NO																	
TCGA-85-A50M-10A-01D-A25L-08	LUSC	ASIAN	NO																	
TCGA-85-A513-10A-01D-A26K-08	LUSC	ASIAN	NO																	
TCGA-85-A53L-10A-01D-A26K-08	LUSC	ASIAN	NO																	
TCGA-96-A4JL-10A-01D-A25A-08	LUSC	ASIAN	NO																	
TCGA-09-2044-10A-01D-0704-01	OV	ASIAN	NO																	
TCGA-23-2647-10A-01D-1526-09	OV	ASIAN	NO																	
TCGA-36-2530-10A-01D-1526-09	OV	ASIAN	NO																	
TCGA-36-2542-10A-01D-1526-09	OV	ASIAN	NO																	
TCGA-FB-A7DR-10A-01D-A33W-08	PAAD	ASIAN	NO																	
TCGA-EJ-5499-10A-01D-1577-08	PRAD	ASIAN	NO																	
TCGA-FC-7708-10A-01D-2115-08	PRAD	ASIAN	NO																	
TCGA-DT-5265-10A-01D-1826-10	READ	ASIAN	NO																	
TCGA-IW-A3M6-10A-01D-A21Q-09	SARC	ASIAN	NO																	
TCGA-MO-A47P-10A-01D-A24N-09	SARC	ASIAN	NO																	
TCGA-MO-A47R-10A-01D-A24N-09	SARC	ASIAN	NO																	
TCGA-EB-A42Y-10A-01D-A24R-08	SKCM	ASIAN	NO																	
TCGA-EB-A42Z-10A-01D-A24R-08	SKCM	ASIAN	NO																	
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TCGA-EB-A44R-10A-01D-A25O-08	SKCM	ASIAN	NO																	
TCGA-EB-A4IQ-10A-01D-A25O-08	SKCM	ASIAN	NO																	
TCGA-EB-A57M-10A-01D-A30X-08	SKCM	ASIAN	NO																	
TCGA-EB-A5KH-10A-01D-A27N-08	SKCM	ASIAN	NO																	
TCGA-EB-A5VU-10A-01D-A32N-08	SKCM	ASIAN	NO																	
TCGA-EB-A6L9-10A-01D-A32N-08	SKCM	ASIAN	NO																	
TCGA-BR-8680-10A-01D-2394-08	STAD	ASIAN	NO																	
TCGA-BR-8682-10A-01D-2394-08	STAD	ASIAN	NO																	
TCGA-BR-8683-10A-01D-2394-08	STAD	ASIAN	NO																	
TCGA-BR-8686-10A-01D-2394-08	STAD	ASIAN	NO																	
TCGA-BR-A452-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-BR-A453-10A-01D-A24F-08	STAD	ASIAN	NO																	
TCGA-BR-A4IU-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-BR-A4IV-10A-01D-A25E-08	STAD	ASIAN	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BR-A4IY-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-BR-A4IZ-10A-01D-A25E-08	STAD	ASIAN	NO																	
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TCGA-BR-A4J4-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-BR-A4J5-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-BR-A4J7-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-CD-5798-10A-01D-1600-08	STAD	ASIAN	NO																	
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TCGA-CD-5803-10A-01D-1600-08	STAD	ASIAN	NO																	
TCGA-CD-5804-10A-01D-2053-08	STAD	ASIAN	NO																	
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TCGA-CD-A4MG-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-CD-A4MH-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-CD-A4MI-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-CD-A4MJ-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-F1-A72C-10A-01D-A33W-08	STAD	ASIAN	NO																	
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TCGA-HU-8238-10A-01D-2341-08	STAD	ASIAN	NO																	
TCGA-HU-8243-10A-01D-2341-08	STAD	ASIAN	NO																	
TCGA-HU-8244-10A-01D-2341-08	STAD	ASIAN	NO																	
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TCGA-HU-8608-10A-01D-2394-08	STAD	ASIAN	NO																	
TCGA-HU-8610-10A-01D-2394-08	STAD	ASIAN	NO																	
TCGA-HU-A4G2-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-HU-A4G3-10A-01D-A24F-08	STAD	ASIAN	NO																	
TCGA-HU-A4G6-10A-01D-A24F-08	STAD	ASIAN	NO																	
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TCGA-HU-A4GQ-10A-01D-A25E-08	STAD	ASIAN	NO																	
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TCGA-HU-A4GU-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-HU-A4GX-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-HU-A4GY-10A-01D-A24F-08	STAD	ASIAN	NO																	
TCGA-HU-A4H2-10A-01D-A25E-08	STAD	ASIAN	NO																	
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TCGA-HU-A4H8-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-HU-A4HB-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-HU-A4HD-10A-01D-A25E-08	STAD	ASIAN	NO																	
TCGA-IN-A6RO-10A-01D-A33W-08	STAD	ASIAN	NO																	
TCGA-MX-A5UG-10A-01D-A31J-08	STAD	ASIAN	NO																	
TCGA-CE-A13K-10A-01D-A10S-08	THCA	ASIAN	NO																	
TCGA-CE-A27D-10A-01D-A17V-08	THCA	ASIAN	NO																	
TCGA-CE-A3MD-10A-01D-A20C-08	THCA	ASIAN	NO																	
TCGA-CE-A3ME-10A-01D-A20C-08	THCA	ASIAN	NO																	
TCGA-CE-A481-10A-01D-A23U-08	THCA	ASIAN	NO																	
TCGA-CE-A482-10A-01D-A23U-08	THCA	ASIAN	NO																	
TCGA-CE-A483-10A-01D-A23U-08	THCA	ASIAN	NO																	
TCGA-CE-A484-10A-01D-A23U-08	THCA	ASIAN	NO																	
TCGA-CE-A485-10A-01D-A23U-08	THCA	ASIAN	NO																	
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TCGA-DJ-A2PR-10A-01D-A19M-08	THCA	ASIAN	NO																	
TCGA-DJ-A2Q3-10A-01D-A18F-08	THCA	ASIAN	NO																	
TCGA-DJ-A2Q7-10A-01D-A18F-08	THCA	ASIAN	NO																	
TCGA-DJ-A2QA-10A-01D-A18F-08	THCA	ASIAN	NO																	
TCGA-DJ-A2QB-10A-01D-A19M-08	THCA	ASIAN	NO																	
TCGA-DJ-A3UM-10A-01D-A22D-08	THCA	ASIAN	NO																	
TCGA-DJ-A3UQ-10A-01D-A22D-08	THCA	ASIAN	NO																	
TCGA-DJ-A3V3-10A-01D-A22Z-08	THCA	ASIAN	NO																	
TCGA-DJ-A4UQ-10A-01D-A25A-08	THCA	ASIAN	NO																	
TCGA-DJ-A4UR-10A-01D-A25A-08	THCA	ASIAN	NO																	
TCGA-DJ-A4UW-10A-01D-A25A-08	THCA	ASIAN	NO																	
TCGA-DJ-A4V0-10A-01D-A25A-08	THCA	ASIAN	NO																	
TCGA-E8-A413-10A-01D-A23K-08	THCA	ASIAN	NO																	
TCGA-E8-A414-10A-01D-A23K-08	THCA	ASIAN	NO																	
TCGA-E8-A415-10A-01D-A23K-08	THCA	ASIAN	NO																	
TCGA-E8-A416-10A-01D-A23K-08	THCA	ASIAN	NO																	
TCGA-E8-A417-10A-01D-A23K-08	THCA	ASIAN	NO																	
TCGA-E8-A432-10A-01D-A23K-08	THCA	ASIAN	NO																	
TCGA-E8-A433-10A-01D-A23K-08	THCA	ASIAN	NO																	
TCGA-E8-A434-10A-01D-A23K-08	THCA	ASIAN	NO																	
TCGA-E8-A436-10A-01D-A23U-08	THCA	ASIAN	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-E8-A44K-10A-01D-A23U-08	THCA	ASIAN	NO																	
TCGA-E8-A44M-10A-01D-A23U-08	THCA	ASIAN	NO																	
TCGA-EL-A3D1-10A-01D-A19M-08	THCA	ASIAN	NO																	
TCGA-EM-A22M-10A-01D-A17V-08	THCA	ASIAN	NO																	
TCGA-EM-A22O-10A-01D-A17V-08	THCA	ASIAN	NO																	
TCGA-EM-A2OV-10A-01D-A202-08	THCA	ASIAN	NO																	
TCGA-ET-A2N1-10A-01D-A18F-08	THCA	ASIAN	NO																	
TCGA-ET-A3BN-10A-01D-A19M-08	THCA	ASIAN	NO																	
TCGA-ET-A3BS-10A-01D-A202-08	THCA	ASIAN	NO																	
TCGA-FK-A3SB-10A-01D-A22D-08	THCA	ASIAN	NO																	
TCGA-FK-A3SE-10A-01D-A22D-08	THCA	ASIAN	NO																	
TCGA-L6-A4EP-10A-01D-A25A-08	THCA	ASIAN	NO																	
TCGA-A5-A1OG-10A-01D-A14G-09	UCEC	ASIAN	NO																	
TCGA-A5-A1OJ-10A-01D-A14G-09	UCEC	ASIAN	NO																	
TCGA-AX-A2HJ-10A-01D-A17D-09	UCEC	ASIAN	NO																	
TCGA-BS-A0TC-10A-01D-A10B-09	UCEC	ASIAN	NO																	
TCGA-BS-A0TD-10A-01D-A10B-09	UCEC	ASIAN	NO																	
TCGA-BS-A0TE-10A-01D-A10B-09	UCEC	ASIAN	NO																	
TCGA-BS-A0TJ-10A-01D-A10B-09	UCEC	ASIAN	NO																	
TCGA-BS-A0UF-10A-01D-A10B-09	UCEC	ASIAN	NO																	
TCGA-BS-A0UJ-10A-01D-A127-09	UCEC	ASIAN	NO																	
TCGA-BS-A0UT-10A-01D-A10B-09	UCEC	ASIAN	NO																	
TCGA-BS-A0V6-10A-01D-A122-09	UCEC	ASIAN	NO																	
TCGA-BS-A0WQ-10A-01D-A10G-09	UCEC	ASIAN	NO																	
TCGA-EO-A2CG-10A-01D-A17W-09	UCEC	ASIAN	NO																	
TCGA-EW-A1IX-10A-01D-A142-09	BRCA	ASIAN	YES																	
TCGA-AR-A0TT-10A-01D-A099-09	BRCA	BLACK	na																	
TCGA-BH-A0AV-10A-01D-A110-09	BRCA	BLACK	na																	
TCGA-BH-A0B0-10A-01D-A110-09	BRCA	BLACK	na																	
TCGA-OL-A5RU-10A-01D-A28E-09	BRCA	BLACK	na																	
TCGA-OL-A5RV-10A-01D-A28E-09	BRCA	BLACK	na																	
TCGA-OL-A5RW-10A-01D-A28E-09	BRCA	BLACK	na																	
TCGA-OL-A5RX-10A-01D-A28E-09	BRCA	BLACK	na																	
TCGA-OL-A5RY-10A-01D-A28E-09	BRCA	BLACK	na																	
TCGA-OL-A5RZ-10A-01D-A28E-09	BRCA	BLACK	na																	
TCGA-OL-A5S0-10A-01D-A28E-09	BRCA	BLACK	na																	
TCGA-C5-A1BM-10A-01D-A13W-08	CESC	BLACK	na																	
TCGA-EK-A2PG-10A-01D-A18J-09	CESC	BLACK	na																	
TCGA-IR-A3LH-10A-01D-A20U-09	CESC	BLACK	na																	
TCGA-A6-A565-10A-01D-A28G-10	COAD	BLACK	na																	
TCGA-A6-A567-10A-01D-A28G-10	COAD	BLACK	na																	
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TCGA-14-0781-10A-01D-1696-08	GBM	BLACK	na																	
TCGA-14-1450-10B-01D-1845-08	GBM	BLACK	na																	
TCGA-14-1829-10A-01D-1494-08	GBM	BLACK	na																	
TCGA-14-4157-10A-01D-1353-08	GBM	BLACK	na																	
TCGA-28-5211-10B-01D-1845-08	GBM	BLACK	na																	
TCGA-BA-A6D8-10A-01D-A31J-08	HNSC	BLACK	na																	
TCGA-CV-6954-10A-01D-1912-08	HNSC	BLACK	na																	
TCGA-CV-6960-10A-01D-2013-08	HNSC	BLACK	na																	
TCGA-CV-7263-10A-01D-2013-08	HNSC	BLACK	na																	
TCGA-F9-A4JJ-10A-01D-A25F-10	KIRP	BLACK	na																	
TCGA-CS-4942-10A-01D-1468-08	LGG	BLACK	na																	
TCGA-CS-5395-10A-01D-1468-08	LGG	BLACK	na																	
TCGA-44-6778-10A-01D-1855-08	LUAD	BLACK	na																	
TCGA-13-2065-10A-01D-1526-09	OV	BLACK	na																	
TCGA-AP-A0LM-10A-01D-A122-09	UCEC	BLACK	na																	
TCGA-AP-A1DR-10A-01D-A135-09	UCEC	BLACK	na																	
TCGA-AP-A5FX-10A-01D-A27P-09	UCEC	BLACK	na																	
TCGA-B5-A0JN-10A-01D-A10O-09	UCEC	BLACK	na																	
TCGA-B5-A0JU-10A-01D-A14G-09	UCEC	BLACK	na																	
TCGA-B5-A0KB-10A-01D-A14G-09	UCEC	BLACK	na																	
TCGA-B5-A11G-10A-01D-A122-09	UCEC	BLACK	na																	
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TCGA-B5-A11R-10A-01D-A122-09	UCEC	BLACK	na																	
TCGA-B5-A11U-10A-01D-A122-09	UCEC	BLACK	na																	
TCGA-B5-A11V-10A-01D-A10M-09	UCEC	BLACK	na																	
TCGA-B5-A11X-10A-01D-A10M-09	UCEC	BLACK	na																	
TCGA-B5-A1MY-10A-01D-A142-09	UCEC	BLACK	na																	
TCGA-B5-A1N2-10A-01D-A142-09	UCEC	BLACK	na																	
TCGA-B5-A3F9-10A-01D-A22A-09	UCEC	BLACK	na																	
TCGA-B5-A3FB-10A-01D-A19Y-09	UCEC	BLACK	na																	
TCGA-B5-A3FD-10A-01D-A19Y-09	UCEC	BLACK	na																	
TCGA-B5-A3FH-10A-01D-A19Y-09	UCEC	BLACK	na																	
TCGA-B5-A5OC-10A-01D-A27P-09	UCEC	BLACK	na																	
TCGA-B5-A5OD-10A-01D-A31U-09	UCEC	BLACK	na																	
TCGA-B5-A5OE-10A-01D-A31U-09	UCEC	BLACK	na																	
TCGA-EY-A1GM-10A-01D-A14G-09	UCEC	BLACK	na																	
TCGA-FI-A2EW-10A-01D-A17D-09	UCEC	BLACK	na																	
TCGA-FD-A3B4-10A-01D-A202-08	BLCA	BLACK	NO																	
TCGA-FD-A3B5-10A-01D-A20D-08	BLCA	BLACK	NO																	
TCGA-FD-A3B7-10A-01D-A20D-08	BLCA	BLACK	NO																	
TCGA-FD-A3N5-10A-01D-A21A-08	BLCA	BLACK	NO																	
TCGA-FD-A3N6-10A-01D-A21A-08	BLCA	BLACK	NO																	
TCGA-FD-A43P-10A-01D-A23U-08	BLCA	BLACK	NO																	
TCGA-FD-A5BU-10A-01D-A26K-08	BLCA	BLACK	NO																	
TCGA-FD-A62S-10A-01D-A30H-08	BLCA	BLACK	NO																	
TCGA-G2-A2EC-10A-01D-A17V-08	BLCA	BLACK	NO																	
TCGA-G2-A3IB-10A-01D-A20D-08	BLCA	BLACK	NO																	
TCGA-GC-A6I3-10A-01D-A31J-08	BLCA	BLACK	NO																	
TCGA-H4-A2HQ-10A-01D-A17V-08	BLCA	BLACK	NO																	
TCGA-KQ-A41N-10D-01D-A339-08	BLCA	BLACK	NO																	
TCGA-A1-A0SJ-10A-02D-A099-09	BRCA	BLACK	NO																	
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TCGA-A2-A0YF-10A-01D-A10G-09	BRCA	BLACK	NO																	
TCGA-A2-A259-10A-01D-A16D-09	BRCA	BLACK	NO																	
TCGA-A2-A25B-10A-01D-A167-09	BRCA	BLACK	NO																	
TCGA-A2-A25E-10A-01D-A167-09	BRCA	BLACK	NO																	
TCGA-A2-A3KC-10A-01D-A20S-09	BRCA	BLACK	NO																	
TCGA-A2-A3XS-10A-01D-A22X-09	BRCA	BLACK	NO																	
TCGA-A2-A3XT-10A-01D-A22X-09	BRCA	BLACK	NO																	
TCGA-A2-A3XU-10A-01D-A22X-09	BRCA	BLACK	NO																	
TCGA-A2-A3XV-10A-01D-A23C-09	BRCA	BLACK	NO																	
TCGA-A2-A3XW-10A-01D-A23C-09	BRCA	BLACK	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-A2-A3XX-10A-01D-A23C-09	BRCA	BLACK	NO																	
TCGA-A2-A3XY-10A-01D-A23C-09	BRCA	BLACK	NO																	
TCGA-A2-A3XZ-10A-01D-A23C-09	BRCA	BLACK	NO																	
TCGA-A2-A3Y0-10A-01D-A23C-09	BRCA	BLACK	NO																	
TCGA-A2-A4RX-10A-01D-A25Q-09	BRCA	BLACK	NO																	
TCGA-A2-A4S3-10A-01D-A25Q-09	BRCA	BLACK	NO																	
TCGA-A7-A13D-10A-02D-A12Q-09	BRCA	BLACK	NO																	
TCGA-A7-A26G-10A-01D-A167-09	BRCA	BLACK	NO																	
TCGA-A7-A2KD-10A-01D-A21Q-09	BRCA	BLACK	NO																	
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TCGA-A7-A4SE-10A-01D-A25Q-09	BRCA	BLACK	NO																	
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TCGA-A6-A5ZU-10A-01D-A28G-10	COAD	BLACK	NO																	
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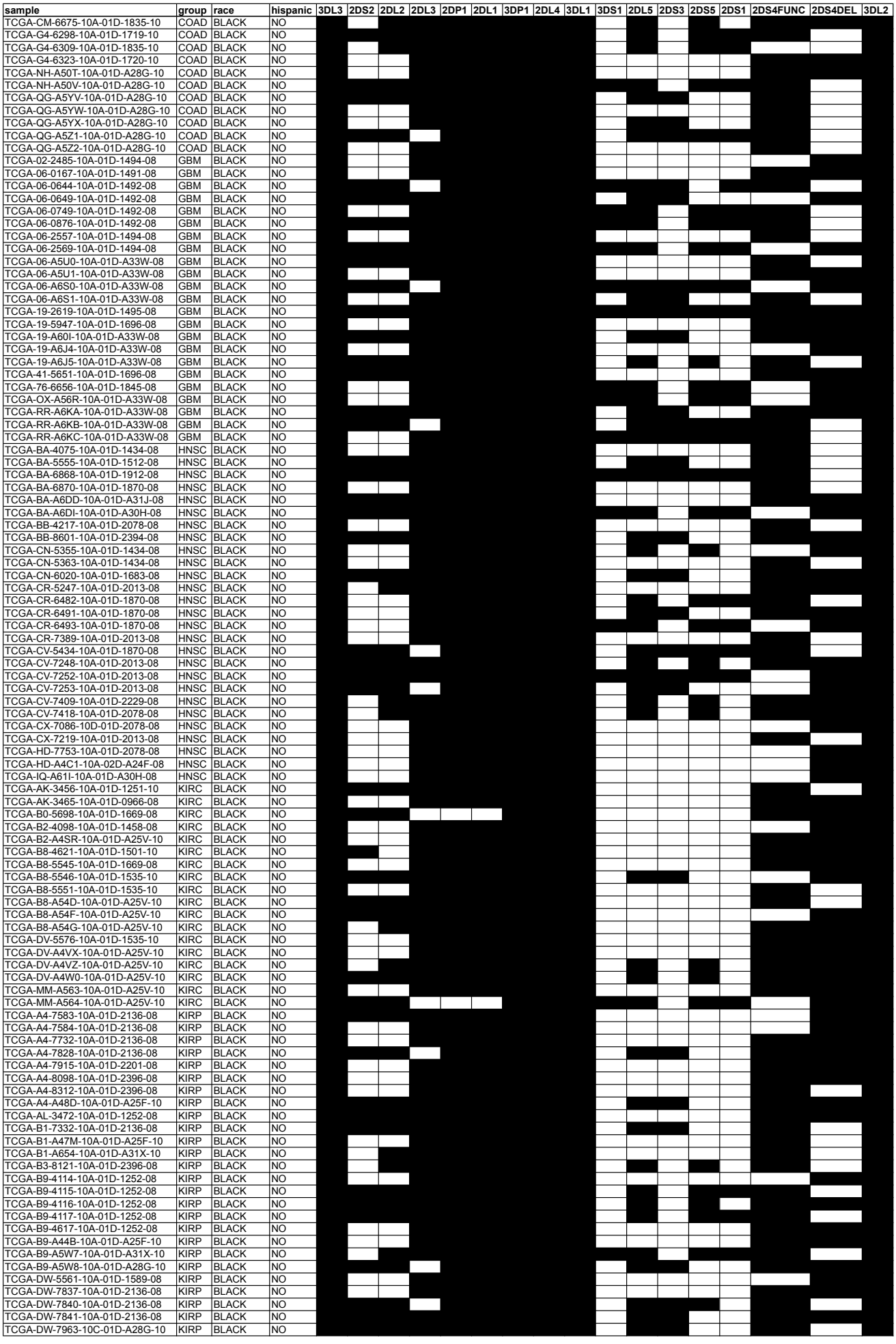

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CM-6675-10A-01D-1835-10	COAD	BLACK	NO																	
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sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
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TCGA-G7-A4TM-10B-01D-A31X-10	KIRP	BLACK	NO																	
TCGA-IA-A40X-10A-01D-A25F-10	KIRP	BLACK	NO																	
TCGA-IZ-A6M8-10A-01D-A31X-10	KIRP	BLACK	NO																	
TCGA-MH-A55W-10A-01D-A26P-10	KIRP	BLACK	NO																	
TCGA-MH-A55Z-10A-01D-A26P-10	KIRP	BLACK	NO																	
TCGA-MH-A562-10A-01D-A26P-10	KIRP	BLACK	NO																	
TCGA-Q2-A5QZ-10A-01D-A28G-10	KIRP	BLACK	NO																	
TCGA-DU-5872-10A-01D-1705-08	LGG	BLACK	NO																	
TCGA-DU-7012-10A-01D-2024-08	LGG	BLACK	NO																	
TCGA-DU-7298-10A-01D-2024-08	LGG	BLACK	NO																	
TCGA-DU-A5TS-10A-01D-A289-08	LGG	BLACK	NO																	
TCGA-DU-A5TW-10A-01D-A289-08	LGG	BLACK	NO																	
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TCGA-FG-6688-10A-01D-1893-08	LGG	BLACK	NO																	
TCGA-HT-7604-10A-01D-2086-08	LGG	BLACK	NO																	
TCGA-HT-7608-10A-01D-2086-08	LGG	BLACK	NO																	
TCGA-HT-7881-10A-01D-2396-08	LGG	BLACK	NO																	
TCGA-HT-8113-10A-01D-2396-08	LGG	BLACK	NO																	
TCGA-BW-A5NO-10A-01D-A27I-10	LIHC	BLACK	NO																	
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TCGA-EP-A2KC-10A-01D-A20W-10	LIHC	BLACK	NO																	
TCGA-K7-A5RG-10A-01D-A28X-10	LIHC	BLACK	NO																	
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TCGA-67-3771-10A-01D-1040-01	LUAD	BLACK	NO																	
TCGA-69-7765-10A-01D-2167-08	LUAD	BLACK	NO																	
TCGA-69-8253-10A-01D-2284-08	LUAD	BLACK	NO																	
TCGA-69-A59K-10A-01D-A25L-08	LUAD	BLACK	NO																	
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TCGA-MN-A4N1-10A-01D-A24P-08	LUAD	BLACK	NO																	
TCGA-NJ-A4YF-10A-01D-A25L-08	LUAD	BLACK	NO																	
TCGA-21-5787-10A-01D-1632-08	LUSC	BLACK	NO																	
TCGA-34-5232-10A-01D-1817-08	LUSC	BLACK	NO																	
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TCGA-98-8020-10A-01D-2244-08	LUSC	BLACK	NO																	
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TCGA-O2-A52W-10A-01D-A26K-08	LUSC	BLACK	NO																	
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TCGA-DE-A4MA-10A-01D-A25A-08	THCA	BLACK	NO																	
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TCGA-EL-A3CP-10A-01D-A19M-08	THCA	BLACK	NO																	
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TCGA-FK-A3S3-10A-01D-A22D-08	THCA	BLACK	NO																	
TCGA-FY-A2QD-10A-01D-A19M-08	THCA	BLACK	NO																	
TCGA-L6-A4EU-10A-01D-A25A-08	THCA	BLACK	NO																	
TCGA-A5-A0GG-10A-01D-A122-09	UCEC	BLACK	NO																	
TCGA-A5-A0GR-10A-01D-A122-09	UCEC	BLACK	NO																	
TCGA-AJ-A3QS-10A-01D-A22A-09	UCEC	BLACK	NO																	
TCGA-AJ-A5DV-10A-01D-A27P-09	UCEC	BLACK	NO																	
TCGA-AJ-A5DW-10A-01D-A27P-09	UCEC	BLACK	NO																	
TCGA-AX-A0IU-10A-01D-A10B-09	UCEC	BLACK	NO																	
TCGA-AX-A1CA-10A-01D-A135-09	UCEC	BLACK	NO																	
TCGA-AX-A3GI-10A-01D-A20S-09	UCEC	BLACK	NO																	
TCGA-B5-A3FC-10A-01D-A22A-09	UCEC	BLACK	NO																	
TCGA-BG-A0MK-10A-01D-A19Y-09	UCEC	BLACK	NO																	
TCGA-BG-A186-10A-01D-A12J-09	UCEC	BLACK	NO																	
TCGA-BK-A13B-10A-01D-A22A-09	UCEC	BLACK	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BK-A13C-10A-01D-A122-09	UCEC	BLACK	NO																	
TCGA-BK-A4ZD-10A-01D-A27P-09	UCEC	BLACK	NO																	
TCGA-BK-A56F-10A-01D-A27P-09	UCEC	BLACK	NO																	
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TCGA-E6-A2P8-10B-01D-A19Y-09	UCEC	BLACK	NO																	
TCGA-EY-A1GD-10A-01D-A13O-09	UCEC	BLACK	NO																	
TCGA-EY-A1GF-10A-01D-A13O-09	UCEC	BLACK	NO																	
TCGA-EY-A1GJ-10A-01D-A142-09	UCEC	BLACK	NO																	
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TCGA-EY-A1GU-10A-01D-A13O-09	UCEC	BLACK	NO																	
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TCGA-EY-A210-10A-01D-A159-09	UCEC	BLACK	NO																	
TCGA-EY-A2ON-10A-01D-A18P-09	UCEC	BLACK	NO																	
TCGA-EY-A3L3-10A-01D-A22A-09	UCEC	BLACK	NO																	
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TCGA-FI-A2CY-10A-01D-A17D-09	UCEC	BLACK	NO																	
TCGA-FI-A2F4-10B-01D-A17D-09	UCEC	BLACK	NO																	
TCGA-FI-A3PV-10A-01D-A22A-09	UCEC	BLACK	NO																	
TCGA-H5-A2HR-10A-01D-A17W-09	UCEC	BLACK	NO																	
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TCGA-PG-A6IB-10A-01D-A31U-09	UCEC	BLACK	NO																	
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TCGA-QS-A5YR-10A-01D-A31U-09	UCEC	BLACK	NO																	
TCGA-SL-A6J9-10A-01D-A31U-09	UCEC	BLACK	NO																	
TCGA-SL-A6JA-10A-01D-A31U-09	UCEC	BLACK	NO																	
TCGA-AQ-A54N-10A-01D-A25Q-09	BRCA	BLACK	YES																	
TCGA-B8-A54E-10A-01D-A25V-10	KIRC	BLACK	YES																	
TCGA-MW-A4EC-10A-01D-A25V-10	KIRC	BLACK	YES																	
TCGA-BK-A0CC-10A-02D-A272-09	UCEC	BLACK	YES																	
TCGA-OR-A5LK-10A-01D-A29L-10	ACC	na	na																	
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TCGA-HQ-A2OF-10B-01D-A26K-08	BLCA	na	na																	
TCGA-HQ-A5ND-10A-01D-A26K-08	BLCA	na	na																	
TCGA-HQ-A5NE-10A-01D-A289-08	BLCA	na	na																	
TCGA-A8-A075-10B-01D-A099-09	BRCA	na	na																	
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TCGA-A8-A097-10A-01D-A047-09	BRCA	na	na																	
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TCGA-E2-A1BC-10A-01D-A12Q-09	BRCA	na	na																	
TCGA-HN-A2NL-10A-01D-A18P-09	BRCA	na	na																	
TCGA-HN-A2OB-10B-01D-A27P-09	BRCA	na	na																	
TCGA-OK-A5Q2-10A-01D-A27P-09	BRCA	na	na																	
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TCGA-DG-A2KK-10A-01D-A17W-09	CESC	na	na																	
TCGA-DG-A2KL-10A-01D-A17W-09	CESC	na	na																	
TCGA-DG-A2KM-10A-01D-A17W-09	CESC	na	na																	
TCGA-DS-A3LQ-10A-01D-A21Q-09	CESC	na	na																	
TCGA-EK-A2RC-10A-01D-A18J-09	CESC	na	na																	
TCGA-FU-A3TX-10A-01D-A22X-09	CESC	na	na																	
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TCGA-HE-A5NK-10A-01D-A26P-10	KIRP	na	na																	
TCGA-HE-A5NL-10A-01D-A26P-10	KIRP	na	na																	
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TCGA-DB-A64Q-10A-01D-A29Q-08	LGG	na	na																	
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TCGA-DD-A1EB-10A-01D-A12Z-10	LIHC	na	na																	
TCGA-HP-A5MZ-10A-01D-A27I-10	LIHC	na	na																	
TCGA-HP-A5N0-10A-01D-A28X-10	LIHC	na	na																	
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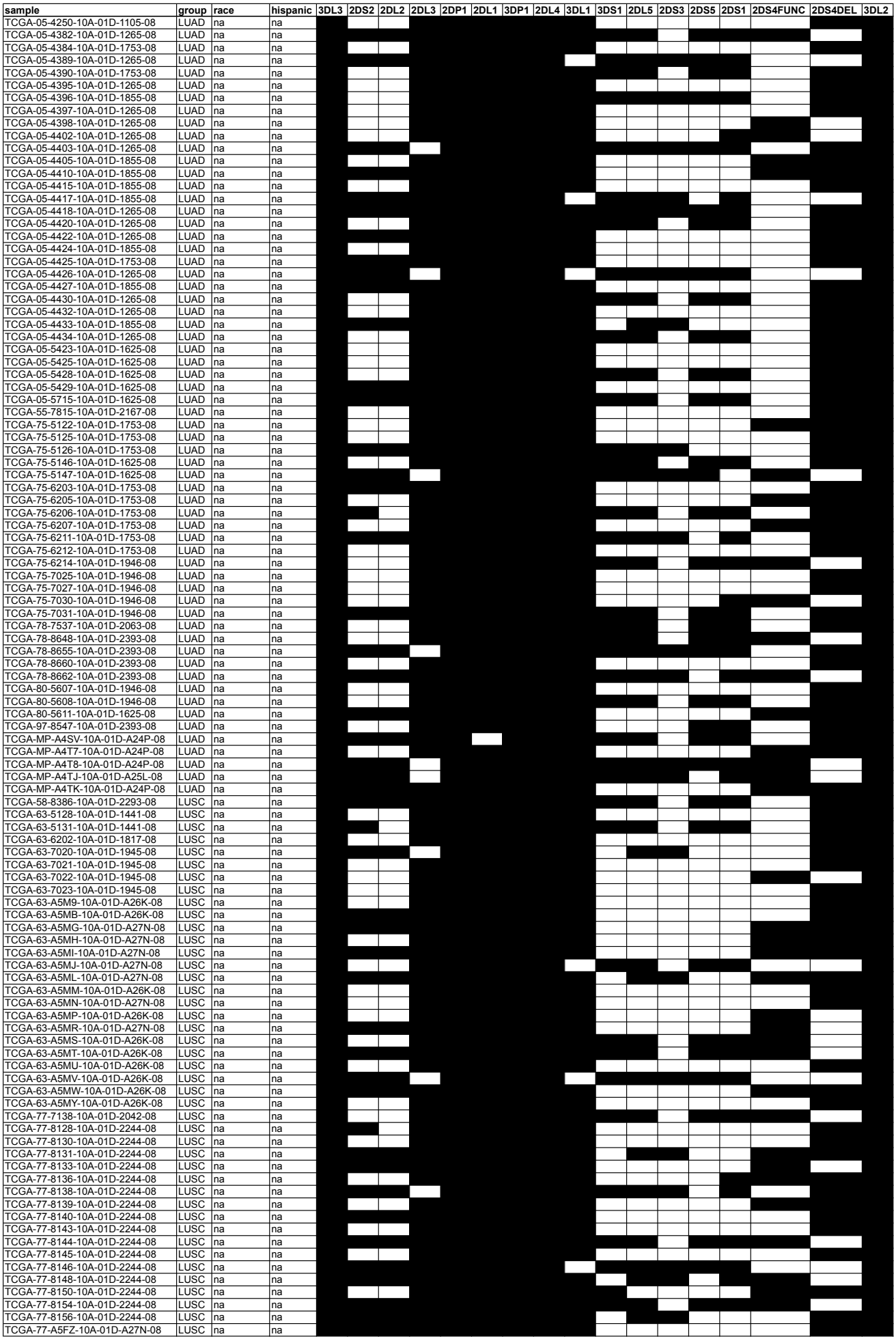
TCGA-05-4249-10A-01D-1105-08	LUAD	na	na																	


sample
group
race
hispanic
3DL3
2DS2
2DL2
2DL3
2DP1
2DL1
3DP1
2DL4
3DL1
3DS1
2DL5
2DS3
2DS5
2DS1
2DS4FUNC
2DS4DEL
3DL2
TCGA-05-4250-10A-01D-1105-08 LUAD na na
TCGA-05-4382-10A-01D-1265-08 LUAD na na
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TCGA-75-7027-10A-01D-1946-08 LUAD na na
TCGA-75-7030-10A-01D-1946-08 LUAD na na
TCGA-75-7031-10A-01D-1946-08 LUAD na na
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TCGA-78-8648-10A-01D-2393-08 LUAD na na
TCGA-78-8655-10A-01D-2393-08 LUAD na na
TCGA-78-8660-10A-01D-2393-08 LUAD na na
TCGA-78-8662-10A-01D-2393-08 LUAD na na
TCGA-80-5607-10A-01D-1946-08 LUAD na na
TCGA-80-5608-10A-01D-1946-08 LUAD na na
TCGA-80-5611-10A-01D-1625-08 LUAD na na
TCGA-97-8547-10A-01D-2393-08 LUAD na na
TCGA-MP-A4SV-10A-01D-A24P-08 LUAD na na
TCGA-MP-A4T7-10A-01D-A24P-08 LUAD na na
TCGA-MP-A4T8-10A-01D-A24P-08 LUAD na na
TCGA-MP-A4TJ-10A-01D-A25L-08 LUAD na na
TCGA-MP-A4TK-10A-01D-A24P-08 LUAD na na
TCGA-58-8386-10A-01D-2293-08 LUSC na na
TCGA-63-5128-10A-01D-1441-08 LUSC na na
TCGA-63-5131-10A-01D-1441-08 LUSC na na
TCGA-63-6202-10A-01D-1817-08 LUSC na na
TCGA-63-7020-10A-01D-1945-08 LUSC na na
TCGA-63-7021-10A-01D-1945-08 LUSC na na
TCGA-63-7022-10A-01D-1945-08 LUSC na na
TCGA-63-7023-10A-01D-1945-08 LUSC na na
TCGA-63-A5M9-10A-01D-A26K-08 LUSC na na
TCGA-63-A5MB-10A-01D-A26K-08 LUSC na na
TCGA-63-A5MG-10A-01D-A27N-08 LUSC na na
TCGA-63-A5MH-10A-01D-A27N-08 LUSC na na
TCGA-63-A5MI-10A-01D-A27N-08 LUSC na na
TCGA-63-A5MJ-10A-01D-A27N-08 LUSC na na
TCGA-63-A5ML-10A-01D-A27N-08 LUSC na na
TCGA-63-A5MM-10A-01D-A26K-08 LUSC na na
TCGA-63-A5MN-10A-01D-A27N-08 LUSC na na
TCGA-63-A5MP-10A-01D-A26K-08 LUSC na na
TCGA-63-A5MR-10A-01D-A27N-08 LUSC na na
TCGA-63-A5MS-10A-01D-A26K-08 LUSC na na
TCGA-63-A5MT-10A-01D-A26K-08 LUSC na na
TCGA-63-A5MU-10A-01D-A26K-08 LUSC na na
TCGA-63-A5MV-10A-01D-A26K-08 LUSC na na
TCGA-63-A5MW-10A-01D-A26K-08 LUSC na na
TCGA-63-A5MY-10A-01D-A26K-08 LUSC na na
TCGA-77-7138-10A-01D-2042-08 LUSC na na
TCGA-77-8128-10A-01D-2244-08 LUSC na na
TCGA-77-8130-10A-01D-2244-08 LUSC na na
TCGA-77-8131-10A-01D-2244-08 LUSC na na
TCGA-77-8133-10A-01D-2244-08 LUSC na na
TCGA-77-8136-10A-01D-2244-08 LUSC na na
TCGA-77-8138-10A-01D-2244-08 LUSC na na
TCGA-77-8139-10A-01D-2244-08 LUSC na na
TCGA-77-8140-10A-01D-2244-08 LUSC na na
TCGA-77-8143-10A-01D-2244-08 LUSC na na
TCGA-77-8144-10A-01D-2244-08 LUSC na na
TCGA-77-8145-10A-01D-2244-08 LUSC na na
TCGA-77-8146-10A-01D-2244-08 LUSC na na
TCGA-77-8148-10A-01D-2244-08 LUSC na na
TCGA-77-8150-10A-01D-2244-08 LUSC na na
TCGA-77-8154-10A-01D-2244-08 LUSC na na
TCGA-77-8156-10A-01D-2244-08 LUSC na na
TCGA-77-A5FZ-10A-01D-A27N-08 LUSC na na

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-77-A5G1-10A-01D-A27N-08	LUSC	na	na																	
TCGA-77-A5G3-10A-01D-A27N-08	LUSC	na	na																	
TCGA-77-A5G6-10A-01D-A27N-08	LUSC	na	na																	
TCGA-77-A5G7-10A-01D-A27N-08	LUSC	na	na																	
TCGA-77-A5G8-10A-01D-A27N-08	LUSC	na	na																	
TCGA-77-A5GA-10A-01D-A27N-08	LUSC	na	na																	
TCGA-77-A5GB-10A-01D-A27N-08	LUSC	na	na																	
TCGA-77-A5GF-10A-01D-A27N-08	LUSC	na	na																	
TCGA-77-A5GH-10A-01D-A27N-08	LUSC	na	na																	
TCGA-79-5596-10A-01D-1945-08	LUSC	na	na																	
TCGA-36-2532-10A-01D-1526-09	OV	na	na																	
TCGA-36-2533-10A-01D-1526-09	OV	na	na																	
TCGA-36-2537-10A-01D-1526-09	OV	na	na																	
TCGA-36-2538-10A-01D-1526-09	OV	na	na																	
TCGA-36-2543-10A-01D-1526-09	OV	na	na																	
TCGA-36-2544-10A-01D-1526-09	OV	na	na																	
TCGA-36-2545-10A-01D-1526-09	OV	na	na																	
TCGA-36-2547-10A-01D-1526-09	OV	na	na																	
TCGA-36-2548-10A-01D-1526-09	OV	na	na																	
TCGA-36-2552-10A-01D-1526-09	OV	na	na																	
TCGA-EJ-5502-10A-01D-1577-08	PRAD	na	na																	
TCGA-EJ-7218-10A-01D-A329-08	PRAD	na	na																	
TCGA-EJ-7312-10A-01D-A329-08	PRAD	na	na																	
TCGA-EJ-7318-10A-01D-A329-08	PRAD	na	na																	
TCGA-EJ-7325-10A-01D-A329-08	PRAD	na	na																	
TCGA-EJ-8468-10A-01D-2395-08	PRAD	na	na																	
TCGA-EJ-8469-10A-01D-2395-08	PRAD	na	na																	
TCGA-EJ-8470-10A-01D-2395-08	PRAD	na	na																	
TCGA-EJ-8472-10A-01D-2395-08	PRAD	na	na																	
TCGA-EJ-8474-10A-01D-2395-08	PRAD	na	na																	
TCGA-EJ-A46B-10A-01D-A25A-08	PRAD	na	na																	
TCGA-EJ-A46D-10A-01D-A25A-08	PRAD	na	na																	
TCGA-EJ-A46E-10A-01D-A25A-08	PRAD	na	na																	
TCGA-EJ-A46F-10A-01D-A25A-08	PRAD	na	na																	
TCGA-EJ-A46G-10A-01D-A26K-08	PRAD	na	na																	
TCGA-EJ-A46H-10A-01D-A26K-08	PRAD	na	na																	
TCGA-EJ-A46I-10A-01D-A26K-08	PRAD	na	na																	
TCGA-EJ-A65B-10A-01D-A30H-08	PRAD	na	na																	
TCGA-EJ-A65D-10A-01D-A30H-08	PRAD	na	na																	
TCGA-EJ-A65E-10A-01D-A29Q-08	PRAD	na	na																	
TCGA-EJ-A65F-10A-01D-A30X-08	PRAD	na	na																	
TCGA-EJ-A65G-10A-01D-A29Q-08	PRAD	na	na																	
TCGA-EJ-A65J-10A-01D-A30X-08	PRAD	na	na																	
TCGA-EJ-A65M-10A-01D-A29Q-08	PRAD	na	na																	
TCGA-EJ-A6RA-10A-01D-A33W-08	PRAD	na	na																	
TCGA-EJ-A6RC-10A-01D-A329-08	PRAD	na	na																	
TCGA-EJ-A7NF-10A-01D-A33W-08	PRAD	na	na																	
TCGA-EJ-A7NG-10A-01D-A33W-08	PRAD	na	na																	
TCGA-EJ-A7NH-10A-01D-A33W-08	PRAD	na	na																	
TCGA-EJ-A7NM-10A-01D-A33W-08	PRAD	na	na																	
TCGA-EJ-A7NN-10A-01D-A33W-08	PRAD	na	na																	
TCGA-FC-A4JI-10A-01D-A25A-08	PRAD	na	na																	
TCGA-FC-A5OB-10A-01D-A29Q-08	PRAD	na	na																	
TCGA-FC-A66V-10A-01D-A30H-08	PRAD	na	na																	
TCGA-FC-A6HD-10A-01D-A31J-08	PRAD	na	na																	
TCGA-G9-6339-10A-01D-A30X-08	PRAD	na	na																	
TCGA-G9-6347-10A-01D-A31J-08	PRAD	na	na																	
TCGA-G9-6354-10A-01D-A30X-08	PRAD	na	na																	
TCGA-G9-6379-10A-01D-A31J-08	PRAD	na	na																	
TCGA-G9-6498-10A-01D-A30X-08	PRAD	na	na																	
TCGA-G9-7510-10A-01D-2260-08	PRAD	na	na																	
TCGA-G9-7519-10A-01D-2260-08	PRAD	na	na																	
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TCGA-G9-7523-10A-01D-2260-08	PRAD	na	na																	
TCGA-G9-7525-10A-01D-2260-08	PRAD	na	na																	
TCGA-H9-A6BX-10A-01D-A30X-08	PRAD	na	na																	
TCGA-H9-A6BY-10A-01D-A30H-08	PRAD	na	na																	
TCGA-HC-7817-10A-01D-A29Q-08	PRAD	na	na																	
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TCGA-HC-8216-10A-01D-A29Q-08	PRAD	na	na																	
TCGA-HC-8256-10A-01D-2260-08	PRAD	na	na																	
TCGA-HC-8257-10A-01D-2260-08	PRAD	na	na																	
TCGA-HC-8258-10A-01D-2260-08	PRAD	na	na																	
TCGA-HC-8259-10A-01D-2260-08	PRAD	na	na																	
TCGA-HC-8260-10A-01D-2260-08	PRAD	na	na																	
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TCGA-HC-8264-10A-01D-2395-08	PRAD	na	na																	
TCGA-HC-8265-10A-01D-2260-08	PRAD	na	na																	
TCGA-HC-8266-10A-01D-2260-08	PRAD	na	na																	
TCGA-HC-A48F-10A-01D-A25A-08	PRAD	na	na																	
TCGA-HC-A4ZV-10A-01D-A26K-08	PRAD	na	na																	
TCGA-HC-A631-10A-01D-A29Q-08	PRAD	na	na																	
TCGA-HC-A632-10A-01D-A29Q-08	PRAD	na	na																	
TCGA-HC-A6AL-10A-01D-A30H-08	PRAD	na	na																	
TCGA-HC-A6AN-10A-01D-A30H-08	PRAD	na	na																	
TCGA-HC-A6AO-10A-01D-A30H-08	PRAD	na	na																	
TCGA-HC-A6AP-10A-01D-A30H-08	PRAD	na	na																	
TCGA-HC-A6AQ-10A-01D-A30H-08	PRAD	na	na																	
TCGA-HC-A6AS-10A-01D-A30H-08	PRAD	na	na																	
TCGA-HC-A6HX-10A-01D-A31J-08	PRAD	na	na																	
TCGA-HC-A6HY-10A-01D-A31J-08	PRAD	na	na																	
TCGA-HC-A76W-10A-01D-A33W-08	PRAD	na	na																	
TCGA-HC-A76X-10A-01D-A33W-08	PRAD	na	na																	
TCGA-J4-8198-10A-01D-2260-08	PRAD	na	na																	
TCGA-J4-8200-10A-01D-A29Q-08	PRAD	na	na																	
TCGA-J4-A67K-10A-01D-A30H-08	PRAD	na	na																	
TCGA-J4-A67L-10A-01D-A30H-08	PRAD	na	na																	
TCGA-J4-A67M-10A-01D-A30H-08	PRAD	na	na																	
TCGA-J4-A67N-10A-01D-A30H-08	PRAD	na	na																	
TCGA-J4-A67O-10A-01D-A30H-08	PRAD	na	na																	
TCGA-J4-A67Q-10A-01D-A30H-08	PRAD	na	na																	
TCGA-J4-A67R-10A-01D-A30H-08	PRAD	na	na																	
TCGA-J4-A67S-10A-01D-A30H-08	PRAD	na	na																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-J4-A67T-10A-01D-A30X-08	PRAD	na	na																	
TCGA-J4-A6G1-10A-01D-A30X-08	PRAD	na	na																	
TCGA-J4-A6G3-10A-01D-A30X-08	PRAD	na	na																	
TCGA-J4-A6M7-10A-01D-A31J-08	PRAD	na	na																	
TCGA-J9-A52B-10A-01D-A26K-08	PRAD	na	na																	
TCGA-J9-A52C-10A-01D-A26K-08	PRAD	na	na																	
TCGA-J9-A52D-10A-01D-A29Q-08	PRAD	na	na																	
TCGA-J9-A52E-10A-01D-A26K-08	PRAD	na	na																	
TCGA-KC-A4BL-10A-01D-A25A-08	PRAD	na	na																	
TCGA-KC-A4BN-10A-01D-A25A-08	PRAD	na	na																	
TCGA-KC-A4BO-10A-01D-A25A-08	PRAD	na	na																	
TCGA-KC-A4BR-10A-01D-A25A-08	PRAD	na	na																	
TCGA-KC-A4BV-10A-01D-A26K-08	PRAD	na	na																	
TCGA-KC-A7F3-10A-01D-A33W-08	PRAD	na	na																	
TCGA-KC-A7F5-10A-01D-A33W-08	PRAD	na	na																	
TCGA-KC-A7F6-10A-01D-A33W-08	PRAD	na	na																	
TCGA-KC-A7FA-10A-01D-A33W-08	PRAD	na	na																	
TCGA-KC-A7FD-10A-01D-A33W-08	PRAD	na	na																	
TCGA-KC-A7FE-10A-01D-A33W-08	PRAD	na	na																	
TCGA-M7-A71Y-10A-01D-A329-08	PRAD	na	na																	
TCGA-M7-A71Z-10A-01D-A329-08	PRAD	na	na																	
TCGA-M7-A720-10A-01D-A329-08	PRAD	na	na																	
TCGA-M7-A721-10A-01D-A329-08	PRAD	na	na																	
TCGA-M7-A723-10A-01D-A329-08	PRAD	na	na																	
TCGA-M7-A724-10A-01D-A329-08	PRAD	na	na																	
TCGA-M7-A725-10A-01D-A329-08	PRAD	na	na																	
TCGA-QU-A6IL-10A-01D-A31J-08	PRAD	na	na																	
TCGA-QU-A6IM-10A-01D-A31J-08	PRAD	na	na																	
TCGA-QU-A6IN-10A-01D-A31J-08	PRAD	na	na																	
TCGA-QU-A6IO-10A-01D-A31J-08	PRAD	na	na																	
TCGA-QU-A6IP-10A-01D-A31J-08	PRAD	na	na																	
TCGA-SU-A7E7-10A-01D-A33W-08	PRAD	na	na																	
TCGA-AG-3591-10A-01D-1733-10	READ	na	na																	
TCGA-AG-3592-10A-01D-1733-10	READ	na	na																	
TCGA-AG-4021-10A-01D-1733-10	READ	na	na																	
TCGA-DX-A3U8-10A-01D-A29N-09	SARC	na	na																	
TCGA-HS-A5N7-10A-01D-A26G-09	SARC	na	na																	
TCGA-HS-A5N8-10A-01D-A26G-09	SARC	na	na																	
TCGA-HS-A5N9-10A-01D-A26G-09	SARC	na	na																	
TCGA-KD-A5QT-10A-01D-A27P-09	SARC	na	na																	
TCGA-HR-A2OG-10A-01D-A199-08	SKCM	na	na																	
TCGA-HR-A2OH-10A-01D-A199-08	SKCM	na	na																	
TCGA-HR-A5NC-10A-01D-A27N-08	SKCM	na	na																	
TCGA-CG-4300-10A-01D-1158-08	STAD	na	na																	
TCGA-CG-4301-10A-01D-1158-08	STAD	na	na																	
TCGA-CG-4304-10A-01D-1158-08	STAD	na	na																	
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TCGA-CG-4306-10A-01D-1158-08	STAD	na	na																	
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TCGA-CG-4438-10A-01D-1158-08	STAD	na	na																	
TCGA-CG-4440-10A-01D-1158-08	STAD	na	na																	
TCGA-CG-4441-10A-01D-1800-08	STAD	na	na																	
TCGA-CG-4442-10A-01D-1158-08	STAD	na	na																	
TCGA-CG-4443-10A-01D-1158-08	STAD	na	na																	
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TCGA-CG-4449-10A-01D-1158-08	STAD	na	na																	
TCGA-CG-4455-10A-01D-1158-08	STAD	na	na																	
TCGA-CG-4460-10A-01D-1158-08	STAD	na	na																	
TCGA-CG-4462-10A-01D-1158-08	STAD	na	na																	
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TCGA-CG-5716-10A-01D-1800-08	STAD	na	na																	
TCGA-CG-5717-10A-01D-1600-08	STAD	na	na																	
TCGA-CG-5718-10A-01D-1600-08	STAD	na	na																	
TCGA-CG-5719-10A-01D-1600-08	STAD	na	na																	
TCGA-HF-7131-10A-01D-2053-08	STAD	na	na																	
TCGA-HF-7132-10A-01D-2053-08	STAD	na	na																	
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TCGA-HF-7134-10A-01D-2053-08	STAD	na	na																	
TCGA-HF-7136-10A-01D-2053-08	STAD	na	na																	
TCGA-HF-A5NB-10A-01D-A31J-08	STAD	na	na																	
TCGA-KB-A6F5-10A-01D-A33W-08	STAD	na	na																	
TCGA-KB-A6F7-10A-01D-A32N-08	STAD	na	na																	
TCGA-EM-A1CS-10A-01D-A13W-08	THCA	na	na																	
TCGA-EM-A1CT-10A-01D-A13W-08	THCA	na	na																	
TCGA-EM-A1CU-10A-02D-A13W-08	THCA	na	na																	
TCGA-EM-A1CV-10A-01D-A13W-08	THCA	na	na																	
TCGA-EM-A1CW-10A-01D-A13W-08	THCA	na	na																	
TCGA-EM-A1YA-10A-01D-A14W-08	THCA	na	na																	
TCGA-EM-A1YB-10A-01D-A14W-08	THCA	na	na																	
TCGA-EM-A22I-10A-01D-A17V-08	THCA	na	na																	
TCGA-EM-A22J-10A-01D-A17V-08	THCA	na	na																	
TCGA-EM-A22K-10A-01D-A17V-08	THCA	na	na																	
TCGA-EM-A22L-10A-01D-A17V-08	THCA	na	na																	
TCGA-EM-A22N-10A-01D-A17V-08	THCA	na	na																	
TCGA-EM-A22P-10A-01D-A19M-08	THCA	na	na																	
TCGA-EM-A22Q-10A-01D-A17V-08	THCA	na	na																	
TCGA-EM-A2CJ-10A-01D-A17V-08	THCA	na	na																	
TCGA-EM-A2CK-10A-01D-A17V-08	THCA	na	na																	
TCGA-EM-A2CL-10A-01D-A17V-08	THCA	na	na																	
TCGA-EM-A2CM-10A-01D-A17V-08	THCA	na	na																	
TCGA-EM-A2CN-10B-01D-A19M-08	THCA	na	na																	
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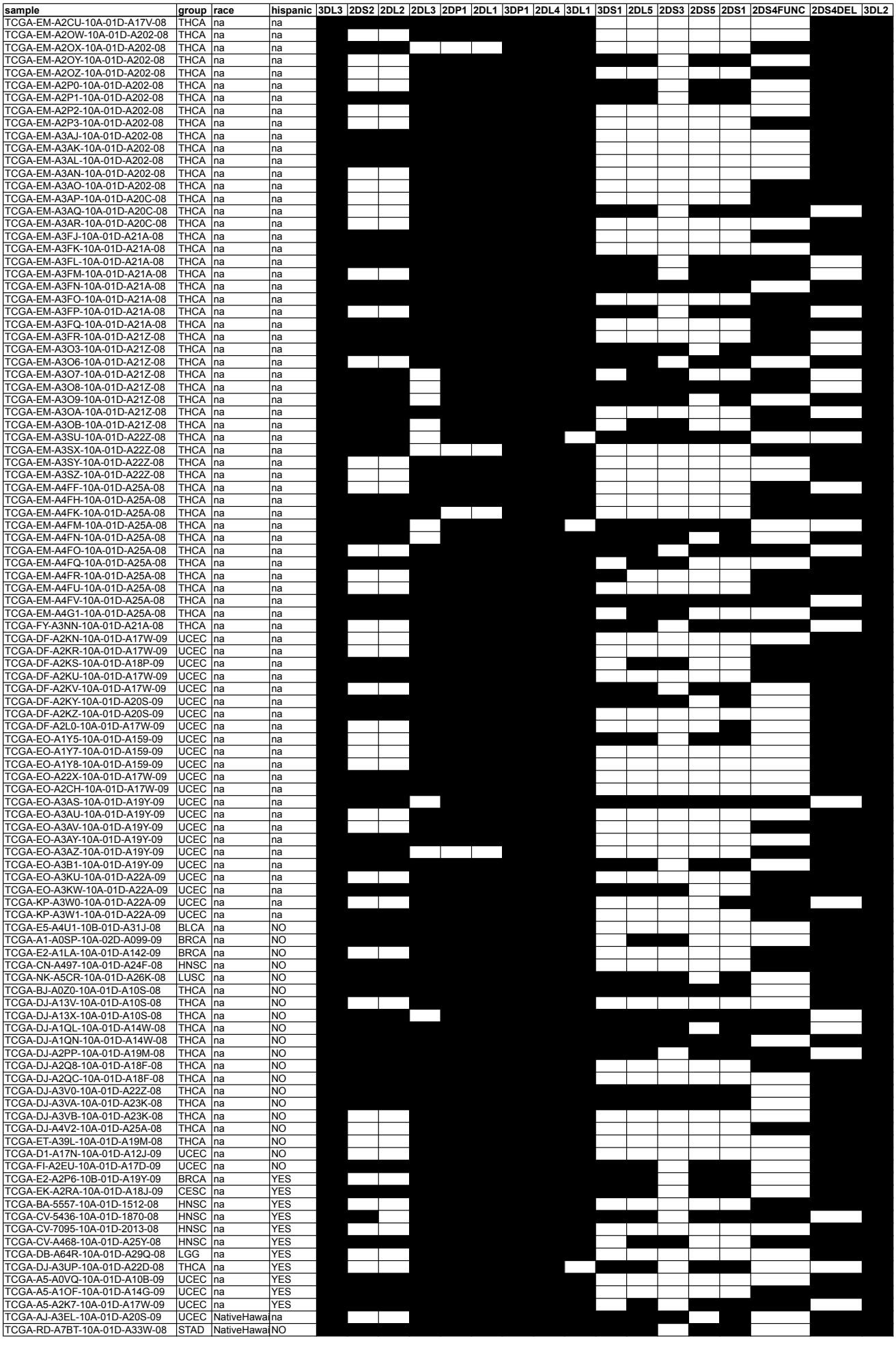
TCGA-EM-A2CR-10A-01D-A17V-08	THCA	na	na																	
TCGA-EM-A2CS-10A-01D-A19M-08	THCA	na	na																	
TCGA-EM-A2CT-10A-01D-A17V-08	THCA	na	na																	



sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EM-A2CU-10A-01D-A17V-08	THCA	na	na																	
TCGA-EM-A2OW-10A-01D-A202-08	THCA	na	na																	
TCGA-EM-A2OX-10A-01D-A202-08	THCA	na	na																	
TCGA-EM-A2OY-10A-01D-A202-08	THCA	na	na																	
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TCGA-EM-A3FJ-10A-01D-A21A-08	THCA	na	na																	
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TCGA-EM-A3OB-10A-01D-A21Z-08	THCA	na	na																	
TCGA-EM-A3SU-10A-01D-A22Z-08	THCA	na	na																	
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TCGA-EM-A4FN-10A-01D-A25A-08	THCA	na	na																	
TCGA-EM-A4FO-10A-01D-A25A-08	THCA	na	na																	
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TCGA-EO-A3AV-10A-01D-A19Y-09	UCEC	na	na																	
TCGA-EO-A3AY-10A-01D-A19Y-09	UCEC	na	na																	
TCGA-EO-A3AZ-10A-01D-A19Y-09	UCEC	na	na																	
TCGA-EO-A3B1-10A-01D-A19Y-09	UCEC	na	na																	
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TCGA-NK-A5CR-10A-01D-A26K-08	LUSC	na	NO																	
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TCGA-FI-A2EU-10A-01D-A17D-09	UCEC	na	NO																	
TCGA-E2-A2P6-10B-01D-A19Y-09	BRCA	na	YES																	
TCGA-EK-A2RA-10A-01D-A18J-09	CESC	na	YES																	
TCGA-BA-5557-10A-01D-1512-08	HNSC	na	YES																	
TCGA-CV-5436-10A-01D-1870-08	HNSC	na	YES																	
TCGA-CV-7095-10A-01D-2013-08	HNSC	na	YES																	
TCGA-CV-A468-10A-01D-A25Y-08	HNSC	na	YES																	
TCGA-DB-A64R-10A-01D-A29Q-08	LGG	na	YES																	
TCGA-DJ-A3UP-10A-01D-A22D-08	THCA	na	YES																	
TCGA-A5-A0VQ-10A-01D-A10B-09	UCEC	na	YES																	
TCGA-A5-A1OF-10A-01D-A14G-09	UCEC	na	YES																	
TCGA-A5-A2K7-10A-01D-A17W-09	UCEC	na	YES																	
TCGA-AJ-A3EL-10A-01D-A20S-09	UCEC	NativeHawai	na																	
TCGA-RD-A7BT-10A-01D-A33W-08	STAD	NativeHawai	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-AX-A3G4-10A-01D-A20S-09	UCEC	NativeHawai	NO																	
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TCGA-BS-A0UL-10A-01D-A10G-09	UCEC	NativeHawai	NO																	
TCGA-BS-A0UV-10A-01D-A10B-09	UCEC	NativeHawai	NO																	
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TCGA-BS-A0V8-10A-01D-A122-09	UCEC	NativeHawai	NO																	
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TCGA-AR-A24Q-10A-01D-A167-09	BRCA	WHITE	na																	
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TCGA-BH-A0DH-10A-01D-A099-09	BRCA	WHITE	na																	
TCGA-BH-A0DQ-10A-01D-A099-09	BRCA	WHITE	na																	
TCGA-BH-A0E9-10A-01D-A110-09	BRCA	WHITE	na																	
TCGA-BH-A0HI-10A-01D-A099-09	BRCA	WHITE	na																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BH-A0HN-10A-01D-A099-09	BRCA	WHITE	na																	
TCGA-BH-A0HP-10A-01D-A099-09	BRCA	WHITE	na																	
TCGA-BH-A0RX-10A-01D-A099-09	BRCA	WHITE	na																	
TCGA-PE-A5DE-10A-01D-A27P-09	BRCA	WHITE	na																	
TCGA-C5-A1BE-10A-01D-A13W-08	CESC	WHITE	na																	
TCGA-C5-A1BF-10A-01D-A13W-08	CESC	WHITE	na																	
TCGA-C5-A1BJ-10A-01D-A13W-08	CESC	WHITE	na																	
TCGA-C5-A1M6-10A-01D-A13W-08	CESC	WHITE	na																	
TCGA-C5-A1MJ-10A-01D-A14W-08	CESC	WHITE	na																	
TCGA-C5-A1ML-10A-01D-A14W-08	CESC	WHITE	na																	
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TCGA-FU-A23K-10A-01D-A16O-08	CESC	WHITE	na																	
TCGA-FU-A23L-10A-01D-A16O-08	CESC	WHITE	na																	
TCGA-IR-A3L7-10A-01D-A20U-09	CESC	WHITE	na																	
TCGA-IR-A3LA-10A-01D-A22X-09	CESC	WHITE	na																	
TCGA-IR-A3LC-10A-01D-A20U-09	CESC	WHITE	na																	
TCGA-IR-A3LF-10A-01D-A22X-09	CESC	WHITE	na																	
TCGA-IR-A3LI-10A-01D-A20U-09	CESC	WHITE	na																	
TCGA-IR-A3LK-10A-01D-A20U-09	CESC	WHITE	na																	
TCGA-IR-A3LL-10A-01D-A20U-09	CESC	WHITE	na																	
TCGA-JX-A3PZ-10A-01D-A21Q-09	CESC	WHITE	na																	
TCGA-MU-A51Y-10A-01D-A26G-09	CESC	WHITE	na																	
TCGA-AD-6890-10A-01D-1924-10	COAD	WHITE	na																	
TCGA-AD-6899-10A-01D-1924-10	COAD	WHITE	na																	
TCGA-AD-6901-10A-01D-1924-10	COAD	WHITE	na																	
TCGA-AD-6963-10A-01D-1924-10	COAD	WHITE	na																	
TCGA-02-0033-10A-01D-1490-08	GBM	WHITE	na																	
TCGA-14-0740-10B-01D-1845-08	GBM	WHITE	na																	
TCGA-14-0786-10A-01D-1492-08	GBM	WHITE	na																	
TCGA-14-0789-10A-01D-1492-08	GBM	WHITE	na																	
TCGA-14-0790-10A-01D-1494-08	GBM	WHITE	na																	
TCGA-14-0813-10A-01D-1492-08	GBM	WHITE	na																	
TCGA-14-0817-10A-01D-1492-08	GBM	WHITE	na																	
TCGA-14-0862-10C-01D-1845-08	GBM	WHITE	na																	
TCGA-14-0871-10A-01D-1492-08	GBM	WHITE	na																	
TCGA-14-1043-10A-01D-1845-08	GBM	WHITE	na																	
TCGA-14-1395-10A-01D-1845-08	GBM	WHITE	na																	
TCGA-14-1456-10A-01D-1494-08	GBM	WHITE	na																	
TCGA-14-1823-10A-01D-1494-08	GBM	WHITE	na																	
TCGA-14-2554-10A-01D-1494-08	GBM	WHITE	na																	
TCGA-14-3476-10A-01D-1353-08	GBM	WHITE	na																	
TCGA-16-0861-10A-01D-1492-08	GBM	WHITE	na																	
TCGA-28-2499-10A-01D-1494-08	GBM	WHITE	na																	
TCGA-28-5204-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-28-5207-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-28-5208-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-28-5209-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-28-5213-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-28-5214-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-28-5215-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-28-5216-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-28-5218-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-28-5219-10A-01D-1486-08	GBM	WHITE	na																	
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TCGA-28-6450-10A-01D-1696-08	GBM	WHITE	na																	
TCGA-32-1970-10A-01D-1494-08	GBM	WHITE	na																	
TCGA-76-4926-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-76-4927-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-76-4928-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-76-4931-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-76-4932-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-76-4934-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-76-4935-10A-01D-1486-08	GBM	WHITE	na																	
TCGA-76-6191-10A-01D-1696-08	GBM	WHITE	na																	
TCGA-76-6285-10A-01D-1696-08	GBM	WHITE	na																	
TCGA-76-6661-10A-01D-1845-08	GBM	WHITE	na																	
TCGA-76-6663-10A-01D-1845-08	GBM	WHITE	na																	
TCGA-76-6664-10A-01D-1845-08	GBM	WHITE	na																	
TCGA-81-5910-10A-01D-1696-08	GBM	WHITE	na																	
TCGA-81-5911-10A-01D-1845-08	GBM	WHITE	na																	
TCGA-BA-6871-10A-01D-1870-08	HNSC	WHITE	na																	
TCGA-CN-4740-10A-01D-1434-08	HNSC	WHITE	na																	
TCGA-CV-6939-10A-01D-1912-08	HNSC	WHITE	na																	
TCGA-CV-7099-10A-01D-2013-08	HNSC	WHITE	na																	
TCGA-CV-7100-10A-01D-2013-08	HNSC	WHITE	na																	
TCGA-DQ-7593-10D-01D-2229-08	HNSC	WHITE	na																	
TCGA-EU-5904-10A-01D-1669-08	KIRC	WHITE	na																	
TCGA-EU-5905-10A-01D-1669-08	KIRC	WHITE	na																	
TCGA-DZ-6133-10A-01D-1962-08	KIRP	WHITE	na																	
TCGA-DZ-6134-10A-01D-1962-08	KIRP	WHITE	na																	
TCGA-EV-5901-10A-01D-1589-08	KIRP	WHITE	na																	
TCGA-EV-5902-10A-01D-1589-08	KIRP	WHITE	na																	
TCGA-CS-4943-10A-01D-1468-08	LGG	WHITE	na																	
TCGA-CS-4944-10A-01D-1468-08	LGG	WHITE	na																	
TCGA-CS-5390-10A-01D-1468-08	LGG	WHITE	na																	
TCGA-CS-5393-10A-01D-1468-08	LGG	WHITE	na																	
TCGA-CS-5394-10A-01D-1468-08	LGG	WHITE	na																	
TCGA-CS-6669-10A-01D-1893-08	LGG	WHITE	na																	
TCGA-HW-7491-10A-01D-2024-08	LGG	WHITE	na																	
TCGA-HW-A5KJ-10A-01D-A27N-08	LGG	WHITE	na																	
TCGA-HW-A5KK-10A-01D-A27N-08	LGG	WHITE	na																	
TCGA-HW-A5KL-10A-01D-A27N-08	LGG	WHITE	na																	
TCGA-HW-A5KM-10A-01D-A27N-08	LGG	WHITE	na																	
TCGA-BC-A217-10A-01D-A152-10	LIHC	WHITE	na																	
TCGA-BC-A3KF-10A-01D-A20W-10	LIHC	WHITE	na																	
TCGA-BC-A69I-10A-01D-A30V-10	LIHC	WHITE	na																	
TCGA-DD-A115-10A-01D-A12Z-10	LIHC	WHITE	na																	
TCGA-44-6776-10A-01D-1855-08	LUAD	WHITE	na																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-44-6777-10A-01D-1855-08	LUAD	WHITE	na																	
TCGA-50-5941-10A-01D-1753-08	LUAD	WHITE	na																	
TCGA-50-5944-10A-01D-1753-08	LUAD	WHITE	na																	
TCGA-50-5946-10A-01D-1753-08	LUAD	WHITE	na																	
TCGA-55-6543-10A-01D-1753-08	LUAD	WHITE	na																	
TCGA-55-6712-10A-01D-1855-08	LUAD	WHITE	na																	
TCGA-55-7281-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-55-8302-10A-01D-2323-08	LUAD	WHITE	na																	
TCGA-78-7143-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7145-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7146-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7147-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7148-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7149-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7150-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7152-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7153-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7154-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7155-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7156-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7158-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7159-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7160-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7161-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7220-10A-01D-2036-08	LUAD	WHITE	na																	
TCGA-78-7535-10A-01D-2063-08	LUAD	WHITE	na																	
TCGA-78-7536-10A-01D-2063-08	LUAD	WHITE	na																	
TCGA-78-7539-10A-01D-2063-08	LUAD	WHITE	na																	
TCGA-78-7633-10A-01D-2063-08	LUAD	WHITE	na																	
TCGA-95-A4VP-10A-01D-A25L-08	LUAD	WHITE	na																	
TCGA-MP-A4SW-10A-01D-A24P-08	LUAD	WHITE	na																	
TCGA-MP-A4T4-10A-01D-A25L-08	LUAD	WHITE	na																	
TCGA-MP-A4TD-10A-01D-A25L-08	LUAD	WHITE	na																	
TCGA-NJ-A4YG-10A-01D-A25L-08	LUAD	WHITE	na																	
TCGA-NJ-A4YI-10A-01D-A25L-08	LUAD	WHITE	na																	
TCGA-34-5927-10A-01D-1817-08	LUSC	WHITE	na																	
TCGA-43-6771-10A-01D-1817-08	LUSC	WHITE	na																	
TCGA-43-6773-10A-01D-1945-08	LUSC	WHITE	na																	
TCGA-43-7658-10A-01D-2122-08	LUSC	WHITE	na																	
TCGA-56-6545-10A-01D-1817-08	LUSC	WHITE	na																	
TCGA-56-7221-10A-01D-2042-08	LUSC	WHITE	na																	
TCGA-56-8304-10A-01D-2323-08	LUSC	WHITE	na																	
TCGA-56-A49D-10A-01D-A24F-08	LUSC	WHITE	na																	
TCGA-77-6842-10A-01D-1945-08	LUSC	WHITE	na																	
TCGA-77-6843-10A-01D-1945-08	LUSC	WHITE	na																	
TCGA-77-6844-10A-01D-1945-08	LUSC	WHITE	na																	
TCGA-77-6845-10A-01D-1945-08	LUSC	WHITE	na																	
TCGA-77-7139-10A-01D-2042-08	LUSC	WHITE	na																	
TCGA-77-7140-10A-01D-2042-08	LUSC	WHITE	na																	
TCGA-77-7463-10A-01D-2042-08	LUSC	WHITE	na																	
TCGA-77-7465-10A-01D-2042-08	LUSC	WHITE	na																	
TCGA-94-8491-10A-01D-2323-08	LUSC	WHITE	na																	
TCGA-MF-A522-10A-01D-A25L-08	LUSC	WHITE	na																	
TCGA-NC-A5HD-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HE-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HF-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HG-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HH-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HI-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HJ-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HK-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HL-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HM-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HN-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HO-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HP-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HQ-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HR-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-NC-A5HT-10A-01D-A26K-08	LUSC	WHITE	na																	
TCGA-13-2057-10A-01D-1526-09	OV	WHITE	na																	
TCGA-24-1430-10A-01D-0472-01	OV	WHITE	na																	
TCGA-24-1431-10A-01D-0472-01	OV	WHITE	na																	
TCGA-29-2429-10A-01D-1526-09	OV	WHITE	na																	
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TCGA-29-2432-10A-01D-1526-09	OV	WHITE	na																	
TCGA-29-2436-10A-01D-1526-09	OV	WHITE	na																	
TCGA-36-2534-10A-01D-1526-09	OV	WHITE	na																	
TCGA-HC-7081-10A-01D-1962-08	PRAD	WHITE	na																	
TCGA-HC-7231-10A-01D-2115-08	PRAD	WHITE	na																	
TCGA-HC-7233-10A-01D-2115-08	PRAD	WHITE	na																	
TCGA-AH-6544-10A-01D-1826-10	READ	WHITE	na																	
TCGA-DX-A3UB-10A-01D-A307-09	SARC	WHITE	na																	
TCGA-DX-A48R-10A-01D-A307-09	SARC	WHITE	na																	
TCGA-DX-A48U-10A-01D-A307-09	SARC	WHITE	na																	
TCGA-DX-A6B8-10A-01D-A307-09	SARC	WHITE	na																	
TCGA-DX-A6BK-10A-01D-A307-09	SARC	WHITE	na																	
TCGA-IS-A3K6-10A-01D-A21Q-09	SARC	WHITE	na																	
TCGA-IS-A3K7-10A-01D-A21Q-09	SARC	WHITE	na																	
TCGA-IS-A3K8-10A-01D-A21Q-09	SARC	WHITE	na																	
TCGA-IW-A3M5-10A-01D-A21Q-09	SARC	WHITE	na																	
TCGA-BF-A1PU-10A-01D-A19A-08	SKCM	WHITE	na																	
TCGA-BF-A1PV-10A-01D-A19A-08	SKCM	WHITE	na																	
TCGA-BF-A3DJ-10A-02D-A20D-08	SKCM	WHITE	na																	
TCGA-EE-A17X-10A-01D-A199-08	SKCM	WHITE	na																	
TCGA-EE-A29A-10A-01D-A198-08	SKCM	WHITE	na																	
TCGA-FR-A2OS-10B-01D-A21A-08	SKCM	WHITE	na																	
TCGA-FS-A4F4-10B-01D-A25O-08	SKCM	WHITE	na																	
TCGA-BJ-A192-10A-01D-A13W-08	THCA	WHITE	na																	
TCGA-DJ-A13T-10A-01D-A10S-08	THCA	WHITE	na																	
TCGA-DJ-A1QE-10A-01D-A14W-08	THCA	WHITE	na																	
TCGA-DJ-A1QF-10A-01D-A14W-08	THCA	WHITE	na																	
TCGA-E8-A437-10A-01D-A23U-08	THCA	WHITE	na																	
TCGA-ET-A4KN-10A-01D-A25A-08	THCA	WHITE	na																	
TCGA-ET-A4KQ-10A-01D-A25A-08	THCA	WHITE	na																	
TCGA-J8-A3YD-10A-01D-A22Z-08	THCA	WHITE	na																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-J8-A3YE-10A-01D-A23K-08	THCA	WHITE	na																	
TCGA-J8-A3YG-10A-01D-A22Z-08	THCA	WHITE	na																	
TCGA-J8-A3YH-10A-01D-A22Z-08	THCA	WHITE	na																	
TCGA-J8-A42S-10A-01D-A23K-08	THCA	WHITE	na																	
TCGA-J8-A4HW-10A-01D-A25A-08	THCA	WHITE	na																	
TCGA-A5-A1OH-10A-01D-A22A-09	UCEC	WHITE	na																	
TCGA-A5-A2K4-10B-01D-A18P-09	UCEC	WHITE	na																	
TCGA-AJ-A23M-10A-01D-A159-09	UCEC	WHITE	na																	
TCGA-AJ-A23N-10A-01D-A22A-09	UCEC	WHITE	na																	
TCGA-AJ-A2QN-10A-01D-A18P-09	UCEC	WHITE	na																	
TCGA-AJ-A2QO-10A-01D-A18P-09	UCEC	WHITE	na																	
TCGA-AJ-A3NC-10A-01D-A22A-09	UCEC	WHITE	na																	
TCGA-AJ-A3OK-10A-01D-A22A-09	UCEC	WHITE	na																	
TCGA-AP-A05O-10A-01D-A122-09	UCEC	WHITE	na																	
TCGA-AP-A0LE-10A-01D-A10B-09	UCEC	WHITE	na																	
TCGA-AP-A0LL-10A-01D-A10B-09	UCEC	WHITE	na																	
TCGA-AP-A0LP-10A-01D-A10B-09	UCEC	WHITE	na																	
TCGA-AP-A0LQ-10A-01D-A10B-09	UCEC	WHITE	na																	
TCGA-AP-A0LS-10B-01D-A14G-09	UCEC	WHITE	na																	
TCGA-AP-A1DH-10A-01D-A135-09	UCEC	WHITE	na																	
TCGA-AP-A1DK-10A-01D-A135-09	UCEC	WHITE	na																	
TCGA-AP-A1DM-10A-01D-A135-09	UCEC	WHITE	na																	
TCGA-AP-A1DP-10A-01D-A135-09	UCEC	WHITE	na																	
TCGA-AP-A1DQ-10A-01D-A135-09	UCEC	WHITE	na																	
TCGA-AP-A1E0-10A-01D-A135-09	UCEC	WHITE	na																	
TCGA-AP-A1E1-10A-01D-A135-09	UCEC	WHITE	na																	
TCGA-AP-A1E3-10A-01D-A135-09	UCEC	WHITE	na																	
TCGA-AP-A1E4-10A-01D-A135-09	UCEC	WHITE	na																	
TCGA-AX-A06D-10A-01D-A122-09	UCEC	WHITE	na																	
TCGA-AX-A06L-10A-01D-A122-09	UCEC	WHITE	na																	
TCGA-AX-A2HK-10A-01D-A17D-09	UCEC	WHITE	na																	
TCGA-AX-A2IN-10A-01D-A17W-09	UCEC	WHITE	na																	
TCGA-AX-A2IO-10A-01D-A17W-09	UCEC	WHITE	na																	
TCGA-AX-A3G3-10A-01D-A20S-09	UCEC	WHITE	na																	
TCGA-AX-A3G8-10A-01D-A22A-09	UCEC	WHITE	na																	
TCGA-B5-A0JS-10A-01D-A10O-09	UCEC	WHITE	na																	
TCGA-B5-A0JT-10A-01D-A122-09	UCEC	WHITE	na																	
TCGA-B5-A0JX-10B-01D-A14K-09	UCEC	WHITE	na																	
TCGA-B5-A0JY-10A-01D-A10O-09	UCEC	WHITE	na																	
TCGA-B5-A0K2-10A-01D-A10B-09	UCEC	WHITE	na																	
TCGA-B5-A0K7-10A-02D-A10B-09	UCEC	WHITE	na																	
TCGA-B5-A0K8-10B-01D-A14K-09	UCEC	WHITE	na																	
TCGA-B5-A0K9-10A-02D-A10B-09	UCEC	WHITE	na																	
TCGA-B5-A11E-10A-01D-A10M-09	UCEC	WHITE	na																	
TCGA-B5-A11F-10A-01D-A10M-09	UCEC	WHITE	na																	
TCGA-B5-A11H-10B-01D-A122-09	UCEC	WHITE	na																	
TCGA-B5-A11J-10A-01D-A122-09	UCEC	WHITE	na																	
TCGA-B5-A11L-10A-01D-A13O-09	UCEC	WHITE	na																	
TCGA-B5-A11M-10A-01D-A122-09	UCEC	WHITE	na																	
TCGA-B5-A11N-10A-01D-A122-09	UCEC	WHITE	na																	
TCGA-B5-A11O-10A-01D-A122-09	UCEC	WHITE	na																	
TCGA-B5-A11P-10A-01D-A14G-09	UCEC	WHITE	na																	
TCGA-B5-A11Q-10A-01D-A122-09	UCEC	WHITE	na																	
TCGA-B5-A11S-10A-01D-A122-09	UCEC	WHITE	na																	
TCGA-B5-A11W-10A-01D-A122-09	UCEC	WHITE	na																	
TCGA-B5-A11Y-10A-01D-A10M-09	UCEC	WHITE	na																	
TCGA-B5-A11Z-10A-01D-A10M-09	UCEC	WHITE	na																	
TCGA-B5-A121-10A-01D-A122-09	UCEC	WHITE	na																	
TCGA-B5-A1MR-10A-01D-A14G-09	UCEC	WHITE	na																	
TCGA-B5-A1MU-10A-01D-A13O-09	UCEC	WHITE	na																	
TCGA-B5-A1MV-10A-01D-A14G-09	UCEC	WHITE	na																	
TCGA-B5-A1MW-10A-01D-A17D-09	UCEC	WHITE	na																	
TCGA-B5-A1MX-10A-01D-A142-09	UCEC	WHITE	na																	
TCGA-B5-A1MZ-10A-01D-A142-09	UCEC	WHITE	na																	
TCGA-B5-A3FA-10A-01D-A19Y-09	UCEC	WHITE	na																	
TCGA-B5-A3S1-10A-01D-A22A-09	UCEC	WHITE	na																	
TCGA-EO-A22U-10B-01D-A17W-09	UCEC	WHITE	na																	
TCGA-EY-A1GL-10A-01D-A13O-09	UCEC	WHITE	na																	
TCGA-EY-A214-10A-01D-A159-09	UCEC	WHITE	na																	
TCGA-FI-A2D4-10A-01D-A17D-09	UCEC	WHITE	na																	
TCGA-OR-A5K6-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5K8-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5KP-10A-01D-A30A-10	ACC	WHITE	NO																	
TCGA-OR-A5KQ-10A-01D-A30A-10	ACC	WHITE	NO																	
TCGA-OR-A5KS-10A-01D-A30A-10	ACC	WHITE	NO																	
TCGA-OR-A5KT-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5KU-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5KV-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5KW-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5KX-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5KY-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5KZ-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5L1-10A-01D-A30A-10	ACC	WHITE	NO																	
TCGA-OR-A5L2-10A-01D-A30A-10	ACC	WHITE	NO																	
TCGA-OR-A5L3-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5L4-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5L6-10C-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5L8-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5L9-10B-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5LA-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5LB-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5LC-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5LD-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5LE-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5LF-10A-01D-A30A-10	ACC	WHITE	NO																	
TCGA-OR-A5LG-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5LH-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OR-A5LI-10A-01D-A30A-10	ACC	WHITE	NO																	
TCGA-OR-A5LJ-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-OU-A5PI-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-P6-A5OF-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-P6-A5OG-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-PA-A5YG-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-PK-A5H8-10A-01D-A29L-10	ACC	WHITE	NO																	
TCGA-BL-A0C8-10A-01D-A10S-08	BLCA	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-BL-A13I-10A-01D-A271-08	BLCA	WHITE	NO																	
TCGA-BL-A13J-10A-01D-A271-08	BLCA	WHITE	NO																	
TCGA-BL-A5ZZ-10A-01D-A30H-08	BLCA	WHITE	NO																	
TCGA-BT-A0S7-10A-01D-A10S-08	BLCA	WHITE	NO																	
TCGA-BT-A0YX-10A-01D-A10S-08	BLCA	WHITE	NO																	
TCGA-BT-A2LB-10A-01D-A18F-08	BLCA	WHITE	NO																	
TCGA-BT-A2LD-10A-01D-A20D-08	BLCA	WHITE	NO																	
TCGA-BT-A3PH-10A-01D-A21Z-08	BLCA	WHITE	NO																	
TCGA-BT-A3PJ-10A-01D-A21Z-08	BLCA	WHITE	NO																	
TCGA-BT-A3PK-10A-01D-A21Z-08	BLCA	WHITE	NO																	
TCGA-BT-A42B-10A-01D-A23K-08	BLCA	WHITE	NO																	
TCGA-BT-A42C-10A-01D-A23K-08	BLCA	WHITE	NO																	
TCGA-BT-A42E-10A-01D-A23U-08	BLCA	WHITE	NO																	
TCGA-BT-A42F-10A-01D-A23U-08	BLCA	WHITE	NO																	
TCGA-CU-A0YO-10A-01D-A10S-08	BLCA	WHITE	NO																	
TCGA-CU-A0YR-10A-01D-A10S-08	BLCA	WHITE	NO																	
TCGA-CU-A3KJ-10A-01D-A21A-08	BLCA	WHITE	NO																	
TCGA-CU-A3QU-10B-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-CU-A3YL-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-CU-A5W6-10A-01D-A289-08	BLCA	WHITE	NO																	
TCGA-CU-A72E-10A-01D-A339-08	BLCA	WHITE	NO																	
TCGA-DK-A1A3-10A-01D-A13W-08	BLCA	WHITE	NO																	
TCGA-DK-A1A5-10A-01D-A13W-08	BLCA	WHITE	NO																	
TCGA-DK-A1A7-10A-01D-A13W-08	BLCA	WHITE	NO																	
TCGA-DK-A1AA-10A-01D-A13W-08	BLCA	WHITE	NO																	
TCGA-DK-A1AB-10A-01D-A13W-08	BLCA	WHITE	NO																	
TCGA-DK-A1AE-10A-01D-A13W-08	BLCA	WHITE	NO																	
TCGA-DK-A1AF-10A-01D-A13W-08	BLCA	WHITE	NO																	
TCGA-DK-A1AG-10A-01D-A13W-08	BLCA	WHITE	NO																	
TCGA-DK-A2HX-10A-01D-A18F-08	BLCA	WHITE	NO																	
TCGA-DK-A2I1-10A-01D-A17V-08	BLCA	WHITE	NO																	
TCGA-DK-A2I2-10A-01D-A17V-08	BLCA	WHITE	NO																	
TCGA-DK-A2I4-10A-01D-A21A-08	BLCA	WHITE	NO																	
TCGA-DK-A2I6-10A-01D-A18F-08	BLCA	WHITE	NO																	
TCGA-DK-A3IK-10A-01D-A21A-08	BLCA	WHITE	NO																	
TCGA-DK-A3IL-10A-01D-A20D-08	BLCA	WHITE	NO																	
TCGA-DK-A3IM-10A-01D-A20D-08	BLCA	WHITE	NO																	
TCGA-DK-A3IN-10A-01D-A20D-08	BLCA	WHITE	NO																	
TCGA-DK-A3IQ-10A-01D-A20D-08	BLCA	WHITE	NO																	
TCGA-DK-A3IS-10A-01D-A21A-08	BLCA	WHITE	NO																	
TCGA-DK-A3IT-10A-01D-A20D-08	BLCA	WHITE	NO																	
TCGA-DK-A3IU-10A-01D-A20D-08	BLCA	WHITE	NO																	
TCGA-DK-A3IV-10A-01D-A21A-08	BLCA	WHITE	NO																	
TCGA-DK-A3WW-10A-01D-A23K-08	BLCA	WHITE	NO																	
TCGA-DK-A3WX-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-DK-A3WY-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-DK-A3X1-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-DK-A3X2-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-DK-A6AW-10A-01D-A30H-08	BLCA	WHITE	NO																	
TCGA-DK-A6B0-10A-01D-A31J-08	BLCA	WHITE	NO																	
TCGA-DK-A6B1-10A-01D-A30H-08	BLCA	WHITE	NO																	
TCGA-DK-A6B2-10A-01D-A30H-08	BLCA	WHITE	NO																	
TCGA-DK-A6B5-10A-01D-A31J-08	BLCA	WHITE	NO																	
TCGA-DK-A6B6-10A-01D-A30H-08	BLCA	WHITE	NO																	
TCGA-E5-A2PC-10B-01D-A202-08	BLCA	WHITE	NO																	
TCGA-E5-A4TZ-10B-01D-A31J-08	BLCA	WHITE	NO																	
TCGA-E7-A3X6-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-E7-A3Y1-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-E7-A519-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-E7-A541-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-E7-A7DU-10A-01D-A329-08	BLCA	WHITE	NO																	
TCGA-E7-A7DV-10A-01D-A339-08	BLCA	WHITE	NO																	
TCGA-FD-A3B3-10A-01D-A202-08	BLCA	WHITE	NO																	
TCGA-FD-A3B6-10A-01D-A20D-08	BLCA	WHITE	NO																	
TCGA-FD-A3NA-10A-01D-A21A-08	BLCA	WHITE	NO																	
TCGA-FD-A3SJ-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-FD-A3SL-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-FD-A3SM-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-FD-A3SO-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-FD-A3SP-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-FD-A3SQ-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-FD-A3SR-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-FD-A3SS-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-FD-A43N-10A-01D-A23U-08	BLCA	WHITE	NO																	
TCGA-FD-A43S-10A-01D-A23U-08	BLCA	WHITE	NO																	
TCGA-FD-A43U-10A-01D-A23U-08	BLCA	WHITE	NO																	
TCGA-FD-A43X-10A-01D-A23U-08	BLCA	WHITE	NO																	
TCGA-FD-A43Y-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-FD-A5BR-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-FD-A5BS-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-FD-A5BT-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-FD-A5BV-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-FD-A5BX-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-FD-A5BY-10A-01D-A289-08	BLCA	WHITE	NO																	
TCGA-FD-A5BZ-10A-01D-A289-08	BLCA	WHITE	NO																	
TCGA-FD-A5C0-10A-01D-A289-08	BLCA	WHITE	NO																	
TCGA-FD-A5C1-10A-01D-A289-08	BLCA	WHITE	NO																	
TCGA-FD-A62O-10A-01D-A30H-08	BLCA	WHITE	NO																	
TCGA-FD-A62P-10A-01D-A30H-08	BLCA	WHITE	NO																	
TCGA-FD-A6TA-10A-21D-A339-08	BLCA	WHITE	NO																	
TCGA-FD-A6TB-10A-21D-A339-08	BLCA	WHITE	NO																	
TCGA-FD-A6TC-10A-21D-A339-08	BLCA	WHITE	NO																	
TCGA-FD-A6TD-10A-21D-A339-08	BLCA	WHITE	NO																	
TCGA-FD-A6TE-10A-21D-A339-08	BLCA	WHITE	NO																	
TCGA-FD-A6TF-10A-21D-A329-08	BLCA	WHITE	NO																	
TCGA-FD-A6TG-10A-01D-A329-08	BLCA	WHITE	NO																	
TCGA-FD-A6TH-10A-01D-A329-08	BLCA	WHITE	NO																	
TCGA-FD-A6TI-10A-01D-A329-08	BLCA	WHITE	NO																	
TCGA-FD-A6TK-10A-21D-A339-08	BLCA	WHITE	NO																	
TCGA-FJ-A3Z7-10A-01D-A23K-08	BLCA	WHITE	NO																	
TCGA-FJ-A3Z9-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-FJ-A3ZE-10A-01D-A23K-08	BLCA	WHITE	NO																	
TCGA-FJ-A3ZF-10A-01D-A23K-08	BLCA	WHITE	NO																	
TCGA-FT-A3EE-10A-01D-A202-08	BLCA	WHITE	NO																	
TCGA-FT-A61P-10A-01D-A30H-08	BLCA	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-G2-A2EF-10A-01D-A18F-08	BLCA	WHITE	NO																	
TCGA-G2-A2EJ-10A-01D-A17V-08	BLCA	WHITE	NO																	
TCGA-G2-A2EK-10A-01D-A18F-08	BLCA	WHITE	NO																	
TCGA-G2-A2EL-10A-01D-A18F-08	BLCA	WHITE	NO																	
TCGA-G2-A3IE-10A-01D-A20D-08	BLCA	WHITE	NO																	
TCGA-GC-A3BM-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-GC-A3I6-10A-01D-A20D-08	BLCA	WHITE	NO																	
TCGA-GC-A3OO-10C-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-GC-A3RB-10A-01D-A21Z-08	BLCA	WHITE	NO																	
TCGA-GC-A3RC-10B-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-GC-A3RD-10B-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-GC-A3WC-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-GC-A3YS-10A-01D-A23K-08	BLCA	WHITE	NO																	
TCGA-GC-A4ZW-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-GC-A6I1-10A-01D-A31J-08	BLCA	WHITE	NO																	
TCGA-GD-A2C5-10A-01D-A17V-08	BLCA	WHITE	NO																	
TCGA-GD-A3OP-10A-01D-A21Z-08	BLCA	WHITE	NO																	
TCGA-GD-A3OQ-10A-01D-A21Z-08	BLCA	WHITE	NO																	
TCGA-GD-A3OS-10A-01D-A21Z-08	BLCA	WHITE	NO																	
TCGA-GD-A6C6-10A-01D-A31J-08	BLCA	WHITE	NO																	
TCGA-GD-A76B-10A-01D-A329-08	BLCA	WHITE	NO																	
TCGA-GU-A42P-10A-01D-A23U-08	BLCA	WHITE	NO																	
TCGA-GU-A42Q-10A-01D-A23U-08	BLCA	WHITE	NO																	
TCGA-GU-A42R-10A-01D-A23K-08	BLCA	WHITE	NO																	
TCGA-GU-A762-10A-01D-A339-08	BLCA	WHITE	NO																	
TCGA-GU-A763-10A-01D-A329-08	BLCA	WHITE	NO																	
TCGA-GU-A766-10A-01D-A329-08	BLCA	WHITE	NO																	
TCGA-GU-A767-10A-01D-A329-08	BLCA	WHITE	NO																	
TCGA-GV-A3JV-10B-01D-A21Z-08	BLCA	WHITE	NO																	
TCGA-GV-A3JW-10A-01D-A20D-08	BLCA	WHITE	NO																	
TCGA-GV-A3JX-10A-01D-A20D-08	BLCA	WHITE	NO																	
TCGA-GV-A3JZ-10A-01D-A21A-08	BLCA	WHITE	NO																	
TCGA-GV-A3QF-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-GV-A3QG-10A-01D-A21Z-08	BLCA	WHITE	NO																	
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TCGA-GV-A3QI-10A-01D-A21Z-08	BLCA	WHITE	NO																	
TCGA-GV-A3QK-10A-01D-A23K-08	BLCA	WHITE	NO																	
TCGA-GV-A40E-10A-01D-A23K-08	BLCA	WHITE	NO																	
TCGA-GV-A40G-10A-01D-A23K-08	BLCA	WHITE	NO																	
TCGA-GV-A6ZA-10A-01D-A339-08	BLCA	WHITE	NO																	
TCGA-H4-A2HO-10A-01D-A17V-08	BLCA	WHITE	NO																	
TCGA-K4-A3WS-10A-01D-A22Z-08	BLCA	WHITE	NO																	
TCGA-K4-A3WU-10A-01D-A23K-08	BLCA	WHITE	NO																	
TCGA-K4-A4AB-10A-01D-A289-08	BLCA	WHITE	NO																	
TCGA-K4-A4AC-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-K4-A54R-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-K4-A5RH-10A-01D-A30H-08	BLCA	WHITE	NO																	
TCGA-K4-A5RI-10A-01D-A289-08	BLCA	WHITE	NO																	
TCGA-K4-A5RJ-10A-01D-A289-08	BLCA	WHITE	NO																	
TCGA-K4-A6FZ-10A-01D-A31J-08	BLCA	WHITE	NO																	
TCGA-K4-A6MB-10A-01D-A31J-08	BLCA	WHITE	NO																	
TCGA-KQ-A41P-10F-01D-A339-08	BLCA	WHITE	NO																	
TCGA-KQ-A41Q-10D-01D-A339-08	BLCA	WHITE	NO																	
TCGA-LC-A66R-10A-01D-A30H-08	BLCA	WHITE	NO																	
TCGA-LT-A5Z6-10A-01D-A289-08	BLCA	WHITE	NO																	
TCGA-MV-A51V-10A-01D-A26K-08	BLCA	WHITE	NO																	
TCGA-PQ-A6FI-10A-01D-A31J-08	BLCA	WHITE	NO																	
TCGA-PQ-A6FN-10A-01D-A31J-08	BLCA	WHITE	NO																	
TCGA-R3-A69X-10A-01D-A30H-08	BLCA	WHITE	NO																	
TCGA-S5-A6DX-10A-01D-A31J-08	BLCA	WHITE	NO																	
TCGA-UY-A78K-10A-01D-A339-08	BLCA	WHITE	NO																	
TCGA-UY-A78L-10A-01D-A339-08	BLCA	WHITE	NO																	
TCGA-UY-A78N-10A-01D-A339-08	BLCA	WHITE	NO																	
TCGA-UY-A78O-10A-01D-A339-08	BLCA	WHITE	NO																	
TCGA-A1-A0SB-10B-01D-A142-09	BRCA	WHITE	NO																	
TCGA-A1-A0SD-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-A1-A0SE-10A-03D-A099-09	BRCA	WHITE	NO																	
TCGA-A1-A0SF-10B-01D-A142-09	BRCA	WHITE	NO																	
TCGA-A1-A0SG-10B-01D-A17G-09	BRCA	WHITE	NO																	
TCGA-A1-A0SH-10A-03D-A099-09	BRCA	WHITE	NO																	
TCGA-A1-A0SI-10B-01D-A142-09	BRCA	WHITE	NO																	
TCGA-A1-A0SM-10A-02D-A10G-09	BRCA	WHITE	NO																	
TCGA-A1-A0SN-10B-01D-A142-09	BRCA	WHITE	NO																	
TCGA-A1-A0SO-10A-03D-A099-09	BRCA	WHITE	NO																	
TCGA-A2-A04U-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-A2-A04W-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-A2-A0CK-10A-01D-A22A-09	BRCA	WHITE	NO																	
TCGA-A2-A0CO-10A-01D-A22A-09	BRCA	WHITE	NO																	
TCGA-A2-A0CS-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-A2-A0CW-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-A2-A0D3-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-A2-A0EN-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-A2-A0EP-10A-01D-A22X-09	BRCA	WHITE	NO																	
TCGA-A2-A0ES-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-A2-A0EW-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-A2-A0ST-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-A2-A0SU-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-A2-A0SX-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-A2-A0SY-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-A2-A0T0-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-A2-A0T2-10A-01D-A099-09	BRCA	WHITE	NO																	
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TCGA-A2-A0T4-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-A2-A0T5-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-A2-A0T6-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-A2-A0T7-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-A2-A0YC-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-A2-A0YD-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-A2-A0YE-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-A2-A0YG-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-A2-A0YH-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-A2-A0YI-10A-01D-A10M-09	BRCA	WHITE	NO																	
TCGA-A2-A0YJ-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-A2-A0YK-10A-01D-A117-09	BRCA	WHITE	NO																	
TCGA-A2-A0YL-10A-01D-A10G-09	BRCA	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-A2-A0YM-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-A2-A0YT-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-A2-A1FV-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-A2-A1FW-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-A2-A1FX-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-A2-A1FZ-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-A2-A1G0-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-A2-A1G1-10A-01D-A13O-09	BRCA	WHITE	NO																	
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TCGA-A2-A25A-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-A2-A25C-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-A2-A25D-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-A2-A25F-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-A2-A3KD-10A-01D-A20S-09	BRCA	WHITE	NO																	
TCGA-A2-A4RW-10A-01D-A25Q-09	BRCA	WHITE	NO																	
TCGA-A2-A4RY-10A-01D-A25Q-09	BRCA	WHITE	NO																	
TCGA-A2-A4S0-10A-01D-A25Q-09	BRCA	WHITE	NO																	
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TCGA-A2-A4S2-10A-01D-A25Q-09	BRCA	WHITE	NO																	
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TCGA-A7-A0DB-10A-02D-A272-09	BRCA	WHITE	NO																	
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TCGA-A7-A13F-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-A7-A13H-10A-01D-A22A-09	BRCA	WHITE	NO																	
TCGA-A7-A26E-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-A7-A26F-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-A7-A26H-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-A7-A26I-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-A7-A26J-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-A7-A3IY-10A-01D-A21Q-09	BRCA	WHITE	NO																	
TCGA-A7-A3IZ-10A-01D-A20S-09	BRCA	WHITE	NO																	
TCGA-A7-A3J0-10A-01D-A20S-09	BRCA	WHITE	NO																	
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TCGA-A7-A3RF-10A-01D-A22A-09	BRCA	WHITE	NO																	
TCGA-A7-A425-10A-01D-A243-09	BRCA	WHITE	NO																	
TCGA-A7-A426-10A-01D-A243-09	BRCA	WHITE	NO																	
TCGA-A7-A4SA-10A-01D-A25Q-09	BRCA	WHITE	NO																	
TCGA-A7-A4SB-10A-01D-A25Q-09	BRCA	WHITE	NO																	
TCGA-A7-A4SC-10A-01D-A25Q-09	BRCA	WHITE	NO																	
TCGA-A7-A5ZX-10A-01D-A29N-09	BRCA	WHITE	NO																	
TCGA-AC-A2B8-10A-01D-A17D-09	BRCA	WHITE	NO																	
TCGA-AC-A2QH-10A-01D-A18P-09	BRCA	WHITE	NO																	
TCGA-AC-A2QI-10A-01D-A19Y-09	BRCA	WHITE	NO																	
TCGA-AC-A3HN-10A-01D-A20S-09	BRCA	WHITE	NO																	
TCGA-AC-A3QP-10B-01D-A22X-09	BRCA	WHITE	NO																	
TCGA-AC-A3TM-10A-01D-A22A-09	BRCA	WHITE	NO																	
TCGA-AC-A3TN-10A-01D-A22A-09	BRCA	WHITE	NO																	
TCGA-AC-A3W6-10A-01D-A22A-09	BRCA	WHITE	NO																	
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TCGA-AC-A5XS-10A-01D-A29N-09	BRCA	WHITE	NO																	
TCGA-AC-A62Y-10A-01D-A29N-09	BRCA	WHITE	NO																	
TCGA-AN-A04C-10A-01D-A047-09	BRCA	WHITE	NO																	
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TCGA-AN-A0XL-10A-01D-A10M-09	BRCA	WHITE	NO																	
TCGA-AN-A0XN-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-AN-A0XO-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-AN-A0XP-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-AN-A0XR-10A-01D-A117-09	BRCA	WHITE	NO																	
TCGA-AN-A0XS-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-AN-A0XT-10A-01D-A10G-09	BRCA	WHITE	NO																	
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TCGA-AO-A03N-10A-01D-A10M-09	BRCA	WHITE	NO																	
TCGA-AO-A03U-10A-01D-A10M-09	BRCA	WHITE	NO																	
TCGA-AO-A03V-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-AO-A0JG-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-AO-A124-10A-01D-A10M-09	BRCA	WHITE	NO																	
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TCGA-AO-A12F-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-AO-A12G-10A-01D-A10M-09	BRCA	WHITE	NO																	
TCGA-AO-A1KO-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-AO-A1KR-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-AO-A1KT-10A-01D-A188-09	BRCA	WHITE	NO																	
TCGA-AQ-A04H-10A-01D-A10M-09	BRCA	WHITE	NO																	
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TCGA-AQ-A0Y5-10A-01D-A17G-09	BRCA	WHITE	NO																	
TCGA-AQ-A1H2-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-AQ-A1H3-10A-01D-A188-09	BRCA	WHITE	NO																	
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TCGA-AR-A0TQ-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-AR-A0TR-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-AR-A0TS-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-AR-A0TW-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-AR-A0TY-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-AR-A0TZ-10A-01D-A099-09	BRCA	WHITE	NO																	
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TCGA-AR-A0U4-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-AR-A1AH-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-AR-A1AI-10A-01D-A12Q-09	BRCA	WHITE	NO																	
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TCGA-AR-A1AM-10A-01D-A22A-09	BRCA	WHITE	NO																	
TCGA-AR-A1AO-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-AR-A1AP-10A-01D-A12Q-09	BRCA	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-AR-A1AQ-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-AR-A1AR-10A-01D-A135-09	BRCA	WHITE	NO																	
TCGA-AR-A1AT-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-AR-A1AU-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-AR-A1AW-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-AR-A1AX-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-AR-A1AY-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-AR-A24H-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-AR-A24L-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-AR-A24M-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-AR-A24N-10A-01D-A167-09	BRCA	WHITE	NO																	
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TCGA-AR-A24P-10A-01D-A167-09	BRCA	WHITE	NO																	
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TCGA-AR-A24T-10A-01D-A167-09	BRCA	WHITE	NO																	
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TCGA-AR-A255-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-AR-A2LE-10A-01D-A17W-09	BRCA	WHITE	NO																	
TCGA-AR-A2LH-10A-01D-A18P-09	BRCA	WHITE	NO																	
TCGA-AR-A2LJ-10A-01D-A19Y-09	BRCA	WHITE	NO																	
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TCGA-AR-A2LN-10A-01D-A18P-09	BRCA	WHITE	NO																	
TCGA-AR-A2LO-10A-01D-A18P-09	BRCA	WHITE	NO																	
TCGA-AR-A2LQ-10A-01D-A18P-09	BRCA	WHITE	NO																	
TCGA-AR-A2LR-10A-01D-A18P-09	BRCA	WHITE	NO																	
TCGA-AR-A5QM-10A-01D-A27P-09	BRCA	WHITE	NO																	
TCGA-AR-A5QN-10A-01D-A28E-09	BRCA	WHITE	NO																	
TCGA-AR-A5QP-10A-01D-A28E-09	BRCA	WHITE	NO																	
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TCGA-B6-A0RP-10A-01D-A099-09	BRCA	WHITE	NO																	
TCGA-B6-A0RQ-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-B6-A0RT-10A-01D-A099-09	BRCA	WHITE	NO																	
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TCGA-B6-A0WY-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-B6-A0X0-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-B6-A0X1-10A-01D-A117-09	BRCA	WHITE	NO																	
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TCGA-B6-A0X7-10A-01D-A10M-09	BRCA	WHITE	NO																	
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TCGA-BH-A0B7-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-BH-A0BG-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-BH-A0BL-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-BH-A0BO-10A-01D-A12B-09	BRCA	WHITE	NO																	
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TCGA-BH-A0BQ-10A-01D-A110-09	BRCA	WHITE	NO																	
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TCGA-BH-A0C1-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-BH-A0C7-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-BH-A0DE-10A-02D-A110-09	BRCA	WHITE	NO																	
TCGA-BH-A0DL-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-BH-A0DX-10A-02D-A110-09	BRCA	WHITE	NO																	
TCGA-BH-A0EA-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-BH-A0EI-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-BH-A0H5-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-BH-A0W4-10A-01D-A10G-09	BRCA	WHITE	NO																	
TCGA-BH-A0W5-10A-01D-A117-09	BRCA	WHITE	NO																	
TCGA-BH-A0W7-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-BH-A0WA-10A-01D-A117-09	BRCA	WHITE	NO																	
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TCGA-BH-A18I-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-BH-A201-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-BH-A202-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-BH-A28O-10A-01D-A22A-09	BRCA	WHITE	NO																	
TCGA-BH-A28Q-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-BH-A2L8-10A-01D-A18P-09	BRCA	WHITE	NO																	
TCGA-C8-A133-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-D8-A13Y-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-D8-A13Z-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-D8-A140-10A-01D-A110-09	BRCA	WHITE	NO																	
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TCGA-D8-A1JC-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-D8-A1JD-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-D8-A1JE-10A-01D-A188-09	BRCA	WHITE	NO																	
TCGA-D8-A1JF-10A-01D-A17G-09	BRCA	WHITE	NO																	
TCGA-D8-A1JG-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-D8-A1JH-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-D8-A1JI-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-D8-A1JJ-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1JK-10A-01D-A13O-09	BRCA	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-D8-A1JL-10A-01D-A188-09	BRCA	WHITE	NO																	
TCGA-D8-A1JM-10A-01D-A188-09	BRCA	WHITE	NO																	
TCGA-D8-A1JN-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-D8-A1JP-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-D8-A1JS-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-D8-A1JT-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-D8-A1JU-10A-01D-A188-09	BRCA	WHITE	NO																	
TCGA-D8-A1X5-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-D8-A1X6-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1X7-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1X9-10A-01D-A17G-09	BRCA	WHITE	NO																	
TCGA-D8-A1XA-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-D8-A1XB-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-D8-A1XC-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-D8-A1XF-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-D8-A1XG-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-D8-A1XK-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1XL-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1XM-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1XO-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1XQ-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1XR-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1XS-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1XT-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1XU-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1XV-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1XW-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1XY-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1XZ-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1Y0-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1Y1-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-D8-A1Y2-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-D8-A1Y3-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-D8-A27E-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-D8-A27F-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-D8-A27G-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-D8-A27H-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-D8-A27I-10A-02D-A16D-09	BRCA	WHITE	NO																	
TCGA-D8-A27K-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-D8-A27L-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-D8-A27M-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-D8-A27N-10A-01D-A16D-09	BRCA	WHITE	NO																	
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TCGA-D8-A27R-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-D8-A27T-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-D8-A27V-10A-01D-A17D-09	BRCA	WHITE	NO																	
TCGA-D8-A27W-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-D8-A3Z5-10A-01D-A243-09	BRCA	WHITE	NO																	
TCGA-D8-A3Z6-10A-01D-A23C-09	BRCA	WHITE	NO																	
TCGA-D8-A4Z1-10A-01D-A25Q-09	BRCA	WHITE	NO																	
TCGA-E2-A105-10A-01D-A10M-09	BRCA	WHITE	NO																	
TCGA-E2-A107-10A-01D-A10M-09	BRCA	WHITE	NO																	
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TCGA-E2-A109-10A-01D-A10M-09	BRCA	WHITE	NO																	
TCGA-E2-A10A-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-E2-A10B-10A-01D-A10M-09	BRCA	WHITE	NO																	
TCGA-E2-A10C-10A-01D-A10M-09	BRCA	WHITE	NO																	
TCGA-E2-A10F-10A-01D-A10M-09	BRCA	WHITE	NO																	
TCGA-E2-A14N-10A-01D-A135-09	BRCA	WHITE	NO																	
TCGA-E2-A14O-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-E2-A14P-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A14Q-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A14R-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-E2-A14S-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A14T-10A-01D-A110-09	BRCA	WHITE	NO																	
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TCGA-E2-A14V-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A14W-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A14Y-10A-01D-A12B-09	BRCA	WHITE	NO																	
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TCGA-E2-A153-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A154-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-E2-A155-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A156-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A158-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A159-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-E2-A15A-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A15C-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A15D-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-E2-A15E-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A15F-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-E2-A15G-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A15H-10A-01D-A12B-09	BRCA	WHITE	NO																	
TCGA-E2-A15I-10A-01D-A135-09	BRCA	WHITE	NO																	
TCGA-E2-A15J-10A-01D-A12Q-09	BRCA	WHITE	NO																	
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TCGA-E2-A15R-10A-01D-A110-09	BRCA	WHITE	NO																	
TCGA-E2-A15S-10A-01D-A110-09	BRCA	WHITE	NO																	
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TCGA-E2-A1B0-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-E2-A1B1-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-E2-A1B4-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-E2-A1B5-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-E2-A1B6-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-E2-A1BD-10A-01D-A12Q-09	BRCA	WHITE	NO																	
TCGA-E2-A1IE-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-E2-A1IF-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-E2-A1IG-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-E2-A1IH-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-E2-A1II-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-E2-A1IJ-10A-01D-A142-09	BRCA	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-E2-A1IK-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-E2-A1IL-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-E2-A1IN-10A-01D-A188-09	BRCA	WHITE	NO																	
TCGA-E2-A1IO-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-E2-A1L6-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-E2-A1L7-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-E2-A1L9-10A-01D-A188-09	BRCA	WHITE	NO																	
TCGA-E2-A3DX-10A-01D-A20S-09	BRCA	WHITE	NO																	
TCGA-E9-A1N3-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-E9-A1N4-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-E9-A1N5-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-E9-A1N8-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-E9-A1N9-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-E9-A1NA-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-E9-A1NC-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-E9-A1NE-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-E9-A1NF-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-E9-A1NG-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-E9-A1NI-10A-01D-A17G-09	BRCA	WHITE	NO																	
TCGA-E9-A1QZ-10A-01D-A167-09	BRCA	WHITE	NO																	
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TCGA-E9-A1R3-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-E9-A1R4-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-E9-A1R5-10A-01D-A14K-09	BRCA	WHITE	NO																	
TCGA-E9-A1R6-10A-01D-A14G-09	BRCA	WHITE	NO																	
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TCGA-E9-A1RD-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-E9-A1RE-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-E9-A1RF-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-E9-A1RG-10A-01D-A14G-09	BRCA	WHITE	NO																	
TCGA-E9-A1RH-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-E9-A1RI-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-E9-A226-10A-01D-A159-09	BRCA	WHITE	NO																	
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TCGA-E9-A228-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-E9-A229-10B-01D-A159-09	BRCA	WHITE	NO																	
TCGA-E9-A22A-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-E9-A22B-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-E9-A22D-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-E9-A22E-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-E9-A22G-10A-01D-A159-09	BRCA	WHITE	NO																	
TCGA-E9-A22H-10A-01D-A17G-09	BRCA	WHITE	NO																	
TCGA-E9-A243-10A-01D-A17G-09	BRCA	WHITE	NO																	
TCGA-E9-A244-10A-01D-A167-09	BRCA	WHITE	NO																	
TCGA-E9-A245-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-E9-A247-10A-01D-A167-09	BRCA	WHITE	NO																	
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TCGA-E9-A249-10A-01D-A167-09	BRCA	WHITE	NO																	
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TCGA-E9-A295-10A-01D-A16D-09	BRCA	WHITE	NO																	
TCGA-E9-A2JS-10A-01D-A17W-09	BRCA	WHITE	NO																	
TCGA-E9-A2JT-10A-01D-A18P-09	BRCA	WHITE	NO																	
TCGA-E9-A3HO-10A-02D-A20S-09	BRCA	WHITE	NO																	
TCGA-E9-A3Q9-10A-01D-A21Q-09	BRCA	WHITE	NO																	
TCGA-E9-A3QA-10A-01D-A22A-09	BRCA	WHITE	NO																	
TCGA-E9-A3X8-10B-01D-A22X-09	BRCA	WHITE	NO																	
TCGA-E9-A54X-10A-01D-A25Q-09	BRCA	WHITE	NO																	
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TCGA-E9-A5FK-10A-01D-A27P-09	BRCA	WHITE	NO																	
TCGA-E9-A5FL-10A-01D-A27P-09	BRCA	WHITE	NO																	
TCGA-E9-A5UO-10A-01D-A28E-09	BRCA	WHITE	NO																	
TCGA-E9-A5UP-10A-01D-A28E-09	BRCA	WHITE	NO																	
TCGA-E9-A6HE-10A-01D-A31U-09	BRCA	WHITE	NO																	
TCGA-EW-A1IZ-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-EW-A1J5-10A-01D-A13O-09	BRCA	WHITE	NO																	
TCGA-EW-A1P0-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-EW-A1P3-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-EW-A1P5-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-EW-A1P8-10A-01D-A142-09	BRCA	WHITE	NO																	
TCGA-GM-A2DA-10C-01D-A18P-09	BRCA	WHITE	NO																	
TCGA-GM-A2DB-10C-01D-A18P-09	BRCA	WHITE	NO																	
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TCGA-GM-A2DL-10C-01D-A18P-09	BRCA	WHITE	NO																	
TCGA-GM-A2DN-10C-01D-A17W-09	BRCA	WHITE	NO																	
TCGA-GM-A3NW-10A-01D-A22A-09	BRCA	WHITE	NO																	
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TCGA-GM-A3XG-10A-01D-A243-09	BRCA	WHITE	NO																	
TCGA-GM-A3XN-10A-01D-A22X-09	BRCA	WHITE	NO																	
TCGA-GM-A4E0-10A-01D-A25Q-09	BRCA	WHITE	NO																	
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TCGA-GM-A5PX-10A-01D-A28E-09	BRCA	WHITE	NO																	
TCGA-LD-A66U-10A-01D-A31U-09	BRCA	WHITE	NO																	
TCGA-LL-A440-10A-01D-A243-09	BRCA	WHITE	NO																	
TCGA-LL-A50Y-10A-01D-A25Q-09	BRCA	WHITE	NO																	
TCGA-LL-A5YL-10A-01D-A29N-09	BRCA	WHITE	NO																	
TCGA-LL-A6FP-10A-01D-A31U-09	BRCA	WHITE	NO																	
TCGA-LQ-A4E4-10A-01D-A25Q-09	BRCA	WHITE	NO																	
TCGA-MS-A51U-10A-01D-A25Q-09	BRCA	WHITE	NO																	
TCGA-OL-A5DA-10A-01D-A27P-09	BRCA	WHITE	NO																	
TCGA-OL-A66J-10A-01D-A29N-09	BRCA	WHITE	NO																	
TCGA-OL-A66K-10A-01D-A29N-09	BRCA	WHITE	NO																	
TCGA-OL-A66N-10A-01D-A31U-09	BRCA	WHITE	NO																	
TCGA-PE-A5DC-10A-01D-A27P-09	BRCA	WHITE	NO																	
TCGA-BI-A0VR-10A-01D-A10S-08	CESC	WHITE	NO																	
TCGA-BI-A0VS-10A-01D-A10S-08	CESC	WHITE	NO																	
TCGA-BI-A20A-10A-01D-A14W-08	CESC	WHITE	NO																	
TCGA-C5-A1BI-10A-01D-A13W-08	CESC	WHITE	NO																	
TCGA-C5-A1BL-10A-01D-A13W-08	CESC	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-C5-A1BN-10A-01D-A14W-08	CESC	WHITE	NO																	
TCGA-C5-A1BQ-10A-01D-A20U-09	CESC	WHITE	NO																	
TCGA-C5-A1M5-10A-01D-A13W-08	CESC	WHITE	NO																	
TCGA-C5-A1M7-10A-01D-A13W-08	CESC	WHITE	NO																	
TCGA-C5-A1M8-10A-01D-A13W-08	CESC	WHITE	NO																	
TCGA-C5-A1M9-10A-01D-A13W-08	CESC	WHITE	NO																	
TCGA-C5-A1ME-10A-01D-A13W-08	CESC	WHITE	NO																	
TCGA-C5-A1MF-10A-01D-A13W-08	CESC	WHITE	NO																	
TCGA-C5-A1MH-10A-01D-A14W-08	CESC	WHITE	NO																	
TCGA-C5-A1MI-10A-01D-A14W-08	CESC	WHITE	NO																	
TCGA-C5-A1MK-10A-01D-A14W-08	CESC	WHITE	NO																	
TCGA-C5-A1MN-10A-01D-A14W-08	CESC	WHITE	NO																	
TCGA-C5-A1MQ-10A-01D-A14W-08	CESC	WHITE	NO																	
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TCGA-C5-A3HD-10A-01D-A20U-09	CESC	WHITE	NO																	
TCGA-C5-A3HF-10A-01D-A20U-09	CESC	WHITE	NO																	
TCGA-C5-A3HL-10A-01D-A20U-09	CESC	WHITE	NO																	
TCGA-DR-A0ZM-10A-01D-A10S-08	CESC	WHITE	NO																	
TCGA-DS-A0VK-10A-01D-A10S-08	CESC	WHITE	NO																	
TCGA-DS-A0VM-10A-01D-A10S-08	CESC	WHITE	NO																	
TCGA-DS-A0VN-10A-01D-A10S-08	CESC	WHITE	NO																	
TCGA-DS-A1OB-10A-01D-A14W-08	CESC	WHITE	NO																	
TCGA-DS-A1OD-10A-01D-A14W-08	CESC	WHITE	NO																	
TCGA-DS-A5RQ-10A-01D-A28E-09	CESC	WHITE	NO																	
TCGA-EA-A1QS-10A-01D-A22X-09	CESC	WHITE	NO																	
TCGA-EA-A1QT-10A-01D-A14W-08	CESC	WHITE	NO																	
TCGA-EA-A3HQ-10A-01D-A20U-09	CESC	WHITE	NO																	
TCGA-EA-A3HR-10A-01D-A20U-09	CESC	WHITE	NO																	
TCGA-EA-A3HS-10B-01D-A20U-09	CESC	WHITE	NO																	
TCGA-EA-A3HT-10A-01D-A21Q-09	CESC	WHITE	NO																	
TCGA-EA-A3HU-10B-01D-A20U-09	CESC	WHITE	NO																	
TCGA-EA-A3QD-10A-01D-A22X-09	CESC	WHITE	NO																	
TCGA-EA-A3QE-10A-01D-A21Q-09	CESC	WHITE	NO																	
TCGA-EA-A3Y4-10A-01D-A243-09	CESC	WHITE	NO																	
TCGA-EA-A410-10A-01D-A243-09	CESC	WHITE	NO																	
TCGA-EA-A411-10A-01D-A243-09	CESC	WHITE	NO																	
TCGA-EA-A43B-10A-01D-A243-09	CESC	WHITE	NO																	
TCGA-EA-A44S-10A-01D-A26G-09	CESC	WHITE	NO																	
TCGA-EA-A4BA-10A-01D-A26G-09	CESC	WHITE	NO																	
TCGA-EA-A556-10A-01D-A26G-09	CESC	WHITE	NO																	
TCGA-EA-A5FO-10A-01D-A28E-09	CESC	WHITE	NO																	
TCGA-EA-A5O9-10A-01D-A28E-09	CESC	WHITE	NO																	
TCGA-EK-A2PK-10A-01D-A18J-09	CESC	WHITE	NO																	
TCGA-EK-A2R7-10A-01D-A18J-09	CESC	WHITE	NO																	
TCGA-EK-A2R8-10A-01D-A18J-09	CESC	WHITE	NO																	
TCGA-EK-A2R9-10A-01D-A18J-09	CESC	WHITE	NO																	
TCGA-EK-A2RB-10A-01D-A18J-09	CESC	WHITE	NO																	
TCGA-EK-A2RE-10A-01D-A18J-09	CESC	WHITE	NO																	
TCGA-EK-A2RJ-10A-01D-A18J-09	CESC	WHITE	NO																	
TCGA-EK-A2RK-10A-01D-A18J-09	CESC	WHITE	NO																	
TCGA-EK-A2RN-10A-01D-A20U-09	CESC	WHITE	NO																	
TCGA-EK-A3GK-10A-01D-A20U-09	CESC	WHITE	NO																	
TCGA-EK-A3GN-10A-01D-A20U-09	CESC	WHITE	NO																	
TCGA-EX-A3L1-10A-01D-A21Q-09	CESC	WHITE	NO																	
TCGA-EX-A449-10A-01D-A243-09	CESC	WHITE	NO																	
TCGA-FU-A2QG-10A-01D-A18J-09	CESC	WHITE	NO																	
TCGA-FU-A3HY-10A-01D-A21Q-09	CESC	WHITE	NO																	
TCGA-FU-A3HZ-10A-01D-A20U-09	CESC	WHITE	NO																	
TCGA-FU-A3NI-10A-01D-A21Q-09	CESC	WHITE	NO																	
TCGA-FU-A3TQ-10A-01D-A22X-09	CESC	WHITE	NO																	
TCGA-FU-A3WB-10A-01D-A22X-09	CESC	WHITE	NO																	
TCGA-FU-A3YQ-10A-01D-A22X-09	CESC	WHITE	NO																	
TCGA-FU-A40J-10A-01D-A243-09	CESC	WHITE	NO																	
TCGA-FU-A57G-10A-01D-A26G-09	CESC	WHITE	NO																	
TCGA-FU-A5XV-10A-01D-A28E-09	CESC	WHITE	NO																	
TCGA-HG-A2PA-10B-01D-A20U-09	CESC	WHITE	NO																	
TCGA-HM-A3JK-10A-01D-A21Q-09	CESC	WHITE	NO																	
TCGA-HM-A4S6-10A-01D-A26G-09	CESC	WHITE	NO																	
TCGA-IR-A3LB-10A-01D-A243-09	CESC	WHITE	NO																	
TCGA-JX-A5QV-10A-01D-A28E-09	CESC	WHITE	NO																	
TCGA-MY-A5BF-10A-01D-A26G-09	CESC	WHITE	NO																	
TCGA-Q1-A5R1-10A-01D-A28E-09	CESC	WHITE	NO																	
TCGA-Q1-A5R2-10A-01D-A28E-09	CESC	WHITE	NO																	
TCGA-Q1-A5R3-10B-01D-A28E-09	CESC	WHITE	NO																	
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TCGA-A6-4105-10A-01D-1771-10	COAD	WHITE	NO																	
TCGA-A6-5656-10A-01D-A270-10	COAD	WHITE	NO																	
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TCGA-A6-5662-10A-01D-1650-10	COAD	WHITE	NO																	
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TCGA-A6-6651-10A-01D-1835-10	COAD	WHITE	NO																	
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TCGA-A6-6780-10A-01D-A270-10	COAD	WHITE	NO																	
TCGA-A6-6781-10A-01D-1924-10	COAD	WHITE	NO																	
TCGA-A6-6782-10A-01D-1835-10	COAD	WHITE	NO																	
TCGA-AD-5900-10A-01D-1650-10	COAD	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-AD-6548-10A-01D-1835-10	COAD	WHITE	NO																	
TCGA-AD-6888-10A-01D-1924-10	COAD	WHITE	NO																	
TCGA-AD-6895-10A-01D-1924-10	COAD	WHITE	NO																	
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TCGA-AD-6965-10A-01D-1924-10	COAD	WHITE	NO																	
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TCGA-D5-5537-10A-01D-1924-10	COAD	WHITE	NO																	
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TCGA-D5-6929-10A-01D-1924-10	COAD	WHITE	NO																	
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TCGA-D5-7000-10A-01D-1924-10	COAD	WHITE	NO																	
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TCGA-DM-A1D7-10A-01D-A152-10	COAD	WHITE	NO																	
TCGA-DM-A1D8-10A-01D-A152-10	COAD	WHITE	NO																	
TCGA-DM-A1D9-10A-01D-A152-10	COAD	WHITE	NO																	
TCGA-DM-A1DA-10A-01D-A152-10	COAD	WHITE	NO																	
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TCGA-F4-6856-10A-01D-1924-10	COAD	WHITE	NO																	
TCGA-G4-6293-10A-01D-1719-10	COAD	WHITE	NO																	
TCGA-G4-6294-10A-01D-1771-10	COAD	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-G4-6295-10A-01D-1719-10	COAD	WHITE	NO																	
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TCGA-06-0240-10A-01D-1491-08	GBM	WHITE	NO																	
TCGA-06-0241-10A-01D-1491-08	GBM	WHITE	NO																	
TCGA-06-0645-10A-01D-1492-08	GBM	WHITE	NO																	
TCGA-06-0646-10A-01D-1492-08	GBM	WHITE	NO																	
TCGA-06-0648-10A-01D-1492-08	GBM	WHITE	NO																	
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TCGA-06-0744-10A-01D-1492-08	GBM	WHITE	NO																	
TCGA-06-0745-10A-01D-1492-08	GBM	WHITE	NO																	
TCGA-06-0747-10A-01D-1492-08	GBM	WHITE	NO																	
TCGA-06-0750-10A-01D-1492-08	GBM	WHITE	NO																	
TCGA-06-0875-10A-01D-1492-08	GBM	WHITE	NO																	
TCGA-06-0877-10A-01D-1492-08	GBM	WHITE	NO																	
TCGA-06-0878-10A-01D-1492-08	GBM	WHITE	NO																	
TCGA-06-0879-10A-01D-1492-08	GBM	WHITE	NO																	
TCGA-06-0881-10A-01D-1492-08	GBM	WHITE	NO																	
TCGA-06-0882-10A-01D-1492-08	GBM	WHITE	NO																	
TCGA-06-0939-10A-01D-1353-08	GBM	WHITE	NO																	
TCGA-06-1804-10A-01D-1696-08	GBM	WHITE	NO																	
TCGA-06-1806-10B-01D-1845-08	GBM	WHITE	NO																	
TCGA-06-2558-10A-01D-1494-08	GBM	WHITE	NO																	
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TCGA-06-2561-10A-01D-1494-08	GBM	WHITE	NO																	
TCGA-06-2562-10A-01D-1494-08	GBM	WHITE	NO																	
TCGA-06-2563-10A-01D-1494-08	GBM	WHITE	NO																	
TCGA-06-2564-10A-01D-1494-08	GBM	WHITE	NO																	
TCGA-06-2567-10A-01D-1494-08	GBM	WHITE	NO																	
TCGA-06-2570-10A-01D-1495-08	GBM	WHITE	NO																	
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TCGA-06-5411-10A-01D-1696-08	GBM	WHITE	NO																	
TCGA-06-5412-10A-01D-1696-08	GBM	WHITE	NO																	
TCGA-06-5413-10A-01D-1696-08	GBM	WHITE	NO																	
TCGA-06-5414-10A-01D-1486-08	GBM	WHITE	NO																	
TCGA-06-5415-10A-01D-1486-08	GBM	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-06-5416-10A-01D-1486-08	GBM	WHITE	NO																	
TCGA-06-5417-10A-01D-1486-08	GBM	WHITE	NO																	
TCGA-06-5418-10A-01D-1486-08	GBM	WHITE	NO																	
TCGA-06-5856-10A-01D-1696-08	GBM	WHITE	NO																	
TCGA-06-5858-10A-01D-1696-08	GBM	WHITE	NO																	
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TCGA-32-1991-10C-01D-1353-08	GBM	WHITE	NO																	
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TCGA-32-2495-10B-01D-1353-08	GBM	WHITE	NO																	
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TCGA-32-2638-10A-01D-1495-08	GBM	WHITE	NO																	
TCGA-32-4208-10A-01D-1353-08	GBM	WHITE	NO																	
TCGA-32-4210-10A-01D-1353-08	GBM	WHITE	NO																	
TCGA-32-4211-10A-01D-1353-08	GBM	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-32-4213-10A-01D-1353-08	GBM	WHITE	NO																	
TCGA-32-4719-10A-01D-1353-08	GBM	WHITE	NO																	
TCGA-32-5222-10A-01D-1486-08	GBM	WHITE	NO																	
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TCGA-BA-4077-10A-01D-1434-08	HNSC	WHITE	NO																	
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TCGA-BA-7269-10A-01D-2013-08	HNSC	WHITE	NO																	
TCGA-BA-A4IF-10A-01D-A25Y-08	HNSC	WHITE	NO																	
TCGA-BA-A4IG-10A-01D-A25Y-08	HNSC	WHITE	NO																	
TCGA-BA-A4IH-10A-01D-A25Y-08	HNSC	WHITE	NO																	
TCGA-BA-A4II-10A-01D-A25Y-08	HNSC	WHITE	NO																	
TCGA-BA-A6DA-10A-01D-A31J-08	HNSC	WHITE	NO																	
TCGA-BA-A6DB-10A-01D-A30H-08	HNSC	WHITE	NO																	
TCGA-BA-A6DE-10A-01D-A31J-08	HNSC	WHITE	NO																	
TCGA-BA-A6DF-10A-01D-A30H-08	HNSC	WHITE	NO																	
TCGA-BA-A6DG-10A-01D-A30H-08	HNSC	WHITE	NO																	
TCGA-BA-A6DL-10A-01D-A30H-08	HNSC	WHITE	NO																	
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TCGA-CN-5370-10A-01D-2013-08	HNSC	WHITE	NO																	
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TCGA-CN-5374-10A-01D-1434-08	HNSC	WHITE	NO																	
TCGA-CN-6010-10A-01D-1683-08	HNSC	WHITE	NO																	
TCGA-CN-6011-10A-01D-1683-08	HNSC	WHITE	NO																	
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TCGA-CN-6988-10A-01D-1912-08	HNSC	WHITE	NO																	
TCGA-CN-6989-10A-01D-1912-08	HNSC	WHITE	NO																	
TCGA-CN-6992-10A-01D-1912-08	HNSC	WHITE	NO																	
TCGA-CN-6994-10A-01D-1912-08	HNSC	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CN-6995-10A-01D-2013-08	HNSC	WHITE	NO																	
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TCGA-CN-6997-10A-01D-2013-08	HNSC	WHITE	NO																	
TCGA-CN-6998-10A-01D-2013-08	HNSC	WHITE	NO																	
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TCGA-CN-A499-10A-01D-A24F-08	HNSC	WHITE	NO																	
TCGA-CN-A49A-10A-01D-A24F-08	HNSC	WHITE	NO																	
TCGA-CN-A49B-10A-01D-A24F-08	HNSC	WHITE	NO																	
TCGA-CN-A49C-10B-01D-A24F-08	HNSC	WHITE	NO																	
TCGA-CN-A63U-10A-01D-A30H-08	HNSC	WHITE	NO																	
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TCGA-CN-A63Y-10A-01D-A30H-08	HNSC	WHITE	NO																	
TCGA-CN-A640-10A-01D-A30H-08	HNSC	WHITE	NO																	
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TCGA-CV-6937-10A-01D-2013-08	HNSC	WHITE	NO																	
TCGA-CV-6938-10A-01D-1912-08	HNSC	WHITE	NO																	
TCGA-CV-6940-10A-01D-1912-08	HNSC	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-CV-6941-10A-01D-1912-08	HNSC	WHITE	NO																	
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TCGA-CV-6948-10A-01D-1912-08	HNSC	WHITE	NO																	
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sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
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TCGA-QK-A6IG-10A-01D-A31J-08	HNSC	WHITE	NO																	
TCGA-QK-A6IH-10A-01D-A31J-08	HNSC	WHITE	NO																	
TCGA-QK-A6II-10A-01D-A31J-08	HNSC	WHITE	NO																	
TCGA-QK-A6IJ-10A-01D-A31J-08	HNSC	WHITE	NO																	
TCGA-AK-3426-10A-01D-1251-10	KIRC	WHITE	NO																	
TCGA-AK-3427-10A-01D-0966-08	KIRC	WHITE	NO																	
TCGA-AK-3429-10A-01D-1251-10	KIRC	WHITE	NO																	
TCGA-AK-3430-10A-01D-1251-10	KIRC	WHITE	NO																	
TCGA-AK-3436-10A-01D-1251-10	KIRC	WHITE	NO																	
TCGA-AK-3440-10A-01D-0966-08	KIRC	WHITE	NO																	
TCGA-AK-3443-10A-01D-0966-08	KIRC	WHITE	NO																	
TCGA-AK-3444-10A-01D-0966-08	KIRC	WHITE	NO																	
TCGA-AK-3447-10A-01D-0966-08	KIRC	WHITE	NO																	
TCGA-AK-3451-10A-01D-1251-10	KIRC	WHITE	NO																	
TCGA-AK-3453-10A-01D-0966-08	KIRC	WHITE	NO																	
TCGA-AK-3455-10A-01D-0966-08	KIRC	WHITE	NO																	
TCGA-AK-3458-10A-01D-1501-10	KIRC	WHITE	NO																	
TCGA-AS-3777-10A-01D-0966-08	KIRC	WHITE	NO																	
TCGA-AS-3778-10A-01D-0966-08	KIRC	WHITE	NO																	
TCGA-B0-5399-10A-01D-1501-10	KIRC	WHITE	NO																	
TCGA-B2-3923-10A-01D-1458-08	KIRC	WHITE	NO																	
TCGA-B2-3924-10A-01D-1458-08	KIRC	WHITE	NO																	
TCGA-B2-4099-10A-01D-1458-08	KIRC	WHITE	NO																	
TCGA-B2-5633-10A-01D-1535-10	KIRC	WHITE	NO																	
TCGA-B2-5635-10A-01D-A270-10	KIRC	WHITE	NO																	
TCGA-B2-5636-10A-01D-1535-10	KIRC	WHITE	NO																	
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TCGA-B4-5832-10A-01D-1669-08	KIRC	WHITE	NO																	
TCGA-B4-5834-10A-02D-1669-08	KIRC	WHITE	NO																	
TCGA-B4-5835-10A-01D-1669-08	KIRC	WHITE	NO																	
TCGA-B4-5836-10A-01D-1669-08	KIRC	WHITE	NO																	
TCGA-B4-5838-10A-01D-1669-08	KIRC	WHITE	NO																	
TCGA-B4-5843-10A-01D-1669-08	KIRC	WHITE	NO																	
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TCGA-B8-5159-10A-01D-1421-08	KIRC	WHITE	NO																	
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TCGA-B8-5163-10A-01D-1421-08	KIRC	WHITE	NO																	
TCGA-B8-5164-10A-01D-1421-08	KIRC	WHITE	NO																	
TCGA-B8-5165-10A-01D-1421-08	KIRC	WHITE	NO																	
TCGA-B8-5549-10A-01D-1535-10	KIRC	WHITE	NO																	
TCGA-B8-5550-10A-01D-1535-10	KIRC	WHITE	NO																	
TCGA-B8-5552-10A-01D-1669-08	KIRC	WHITE	NO																	
TCGA-B8-5553-10A-01D-1535-10	KIRC	WHITE	NO																	
TCGA-DV-5565-10A-01D-1535-10	KIRC	WHITE	NO																	
TCGA-DV-5566-10A-01D-1535-10	KIRC	WHITE	NO																	
TCGA-DV-5568-10A-01D-1535-10	KIRC	WHITE	NO																	
TCGA-DV-5569-10A-01D-1535-10	KIRC	WHITE	NO																	
TCGA-DV-5573-10A-01D-1535-10	KIRC	WHITE	NO																	
TCGA-DV-5574-10A-01D-1535-10	KIRC	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DV-5575-10A-01D-1535-10	KIRC	WHITE	NO																	
TCGA-EU-5906-10A-01D-1669-08	KIRC	WHITE	NO																	
TCGA-EU-5907-10A-01D-1669-08	KIRC	WHITE	NO																	
TCGA-A4-7286-10A-01D-2136-08	KIRP	WHITE	NO																	
TCGA-A4-7287-10A-01D-2136-08	KIRP	WHITE	NO																	
TCGA-A4-7734-10A-01D-2136-08	KIRP	WHITE	NO																	
TCGA-A4-7996-10A-01D-2201-08	KIRP	WHITE	NO																	
TCGA-A4-7997-10A-01D-2201-08	KIRP	WHITE	NO																	
TCGA-A4-8310-10A-01D-2396-08	KIRP	WHITE	NO																	
TCGA-A4-8311-10A-01D-2396-08	KIRP	WHITE	NO																	
TCGA-A4-8517-10A-01D-2396-08	KIRP	WHITE	NO																	
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TCGA-A4-8630-10A-01D-2396-08	KIRP	WHITE	NO																	
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TCGA-A4-A57E-10A-01D-A26P-10	KIRP	WHITE	NO																	
TCGA-A4-A5DU-10A-01D-A28G-10	KIRP	WHITE	NO																	
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TCGA-A4-A6HP-10A-01D-A31X-10	KIRP	WHITE	NO																	
TCGA-AL-3466-10A-01D-1252-08	KIRP	WHITE	NO																	
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TCGA-AL-3473-10A-01D-1252-08	KIRP	WHITE	NO																	
TCGA-AL-7173-10A-01D-2136-08	KIRP	WHITE	NO																	
TCGA-AL-A5DJ-10A-01D-A26P-10	KIRP	WHITE	NO																	
TCGA-B1-5398-10A-01D-1589-08	KIRP	WHITE	NO																	
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TCGA-B1-A47O-10A-01D-A25F-10	KIRP	WHITE	NO																	
TCGA-B1-A655-10A-01D-A31X-10	KIRP	WHITE	NO																	
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TCGA-B3-3925-10A-01D-1458-08	KIRP	WHITE	NO																	
TCGA-B3-4103-10A-01D-1458-08	KIRP	WHITE	NO																	
TCGA-B3-4104-10A-01D-1458-08	KIRP	WHITE	NO																	
TCGA-B9-5155-10A-01D-1589-08	KIRP	WHITE	NO																	
TCGA-B9-5156-10A-01D-1589-08	KIRP	WHITE	NO																	
TCGA-B9-7268-10A-01D-2136-08	KIRP	WHITE	NO																	
TCGA-B9-A5W9-10A-01D-A28G-10	KIRP	WHITE	NO																	
TCGA-B9-A69E-10A-01D-A31X-10	KIRP	WHITE	NO																	
TCGA-DW-5560-10A-01D-1589-08	KIRP	WHITE	NO																	
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TCGA-GL-7966-10A-01D-2201-08	KIRP	WHITE	NO																	
TCGA-GL-8500-10A-01D-2396-08	KIRP	WHITE	NO																	
TCGA-GL-A4EM-10A-01D-A25F-10	KIRP	WHITE	NO																	
TCGA-GL-A59R-10A-01D-A26P-10	KIRP	WHITE	NO																	
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TCGA-IA-A40U-10A-01D-A25F-10	KIRP	WHITE	NO																	
TCGA-IA-A40Y-10A-01D-A25F-10	KIRP	WHITE	NO																	
TCGA-IZ-8195-10A-01D-2396-08	KIRP	WHITE	NO																	
TCGA-IZ-8196-10A-01D-2396-08	KIRP	WHITE	NO																	
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TCGA-KV-A6GD-10A-01D-A31X-10	KIRP	WHITE	NO																	
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TCGA-MH-A560-10A-01D-A26P-10	KIRP	WHITE	NO																	
TCGA-PJ-A5Z8-10A-01D-A28G-10	KIRP	WHITE	NO																	
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TCGA-CS-4938-10A-01D-1893-08	LGG	WHITE	NO																	
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TCGA-DB-A4XF-10A-01D-A27N-08	LGG	WHITE	NO																	
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TCGA-DB-A64V-10A-01D-A29Q-08	LGG	WHITE	NO																	
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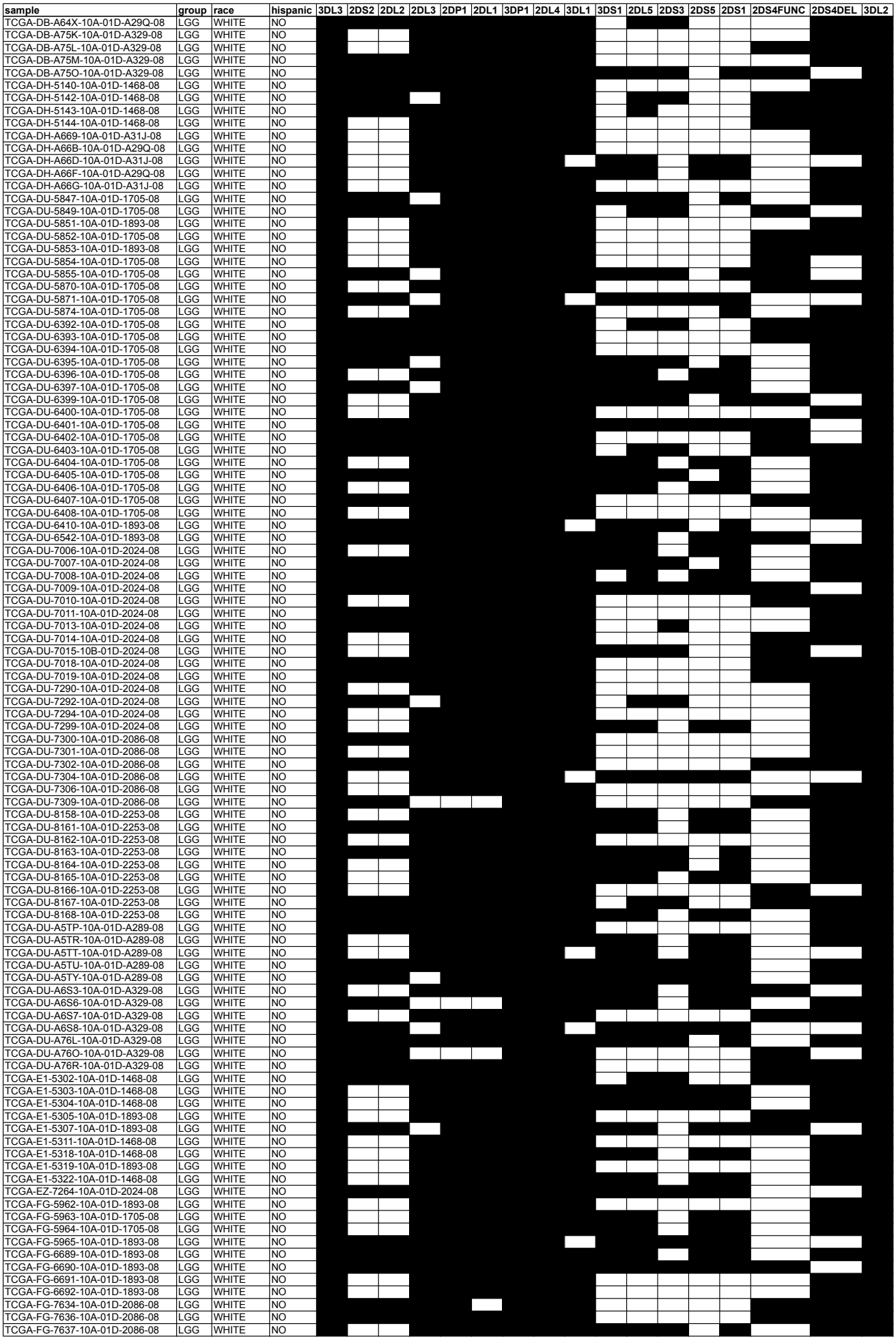

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DB-A64X-10A-01D-A29Q-08	LGG	WHITE	NO																	
TCGA-DB-A75K-10A-01D-A329-08	LGG	WHITE	NO																	
TCGA-DB-A75L-10A-01D-A329-08	LGG	WHITE	NO																	
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TCGA-DU-A76O-10A-01D-A329-08	LGG	WHITE	NO																	
TCGA-DU-A76R-10A-01D-A329-08	LGG	WHITE	NO																	
TCGA-E1-5302-10A-01D-1468-08	LGG	WHITE	NO																	
TCGA-E1-5303-10A-01D-1468-08	LGG	WHITE	NO																	
TCGA-E1-5304-10A-01D-1468-08	LGG	WHITE	NO																	
TCGA-E1-5305-10A-01D-1893-08	LGG	WHITE	NO																	
TCGA-E1-5307-10A-01D-1893-08	LGG	WHITE	NO																	
TCGA-E1-5311-10A-01D-1468-08	LGG	WHITE	NO																	
TCGA-E1-5318-10A-01D-1468-08	LGG	WHITE	NO																	
TCGA-E1-5319-10A-01D-1893-08	LGG	WHITE	NO																	
TCGA-E1-5322-10A-01D-1468-08	LGG	WHITE	NO																	
TCGA-EZ-7264-10A-01D-2024-08	LGG	WHITE	NO																	
TCGA-FG-5962-10A-01D-1893-08	LGG	WHITE	NO																	
TCGA-FG-5963-10A-01D-1705-08	LGG	WHITE	NO																	
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TCGA-FG-6692-10A-01D-1893-08	LGG	WHITE	NO																	
TCGA-FG-7634-10A-01D-2086-08	LGG	WHITE	NO																	
TCGA-FG-7636-10A-01D-2086-08	LGG	WHITE	NO																	
TCGA-FG-7637-10A-01D-2086-08	LGG	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-FG-7638-10A-01D-2086-08	LGG	WHITE	NO																	
TCGA-FG-7641-10A-01D-2253-08	LGG	WHITE	NO																	
TCGA-FG-7643-10A-01D-2086-08	LGG	WHITE	NO																	
TCGA-FG-8181-10A-01D-2253-08	LGG	WHITE	NO																	
TCGA-FG-8182-10A-01D-2253-08	LGG	WHITE	NO																	
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TCGA-FG-8189-10A-01D-A289-08	LGG	WHITE	NO																	
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TCGA-FG-A4MU-10A-01D-A289-08	LGG	WHITE	NO																	
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TCGA-FG-A4MX-10A-01D-A26K-08	LGG	WHITE	NO																	
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TCGA-FG-A60K-10A-01D-A29Q-08	LGG	WHITE	NO																	
TCGA-FG-A60L-10A-01D-A31J-08	LGG	WHITE	NO																	
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TCGA-FG-A6J1-10A-01D-A31J-08	LGG	WHITE	NO																	
TCGA-FG-A6J3-10A-01D-A31J-08	LGG	WHITE	NO																	
TCGA-FG-A713-10A-01D-A329-08	LGG	WHITE	NO																	
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TCGA-HT-A4DV-10A-01D-A26K-08	LGG	WHITE	NO																	
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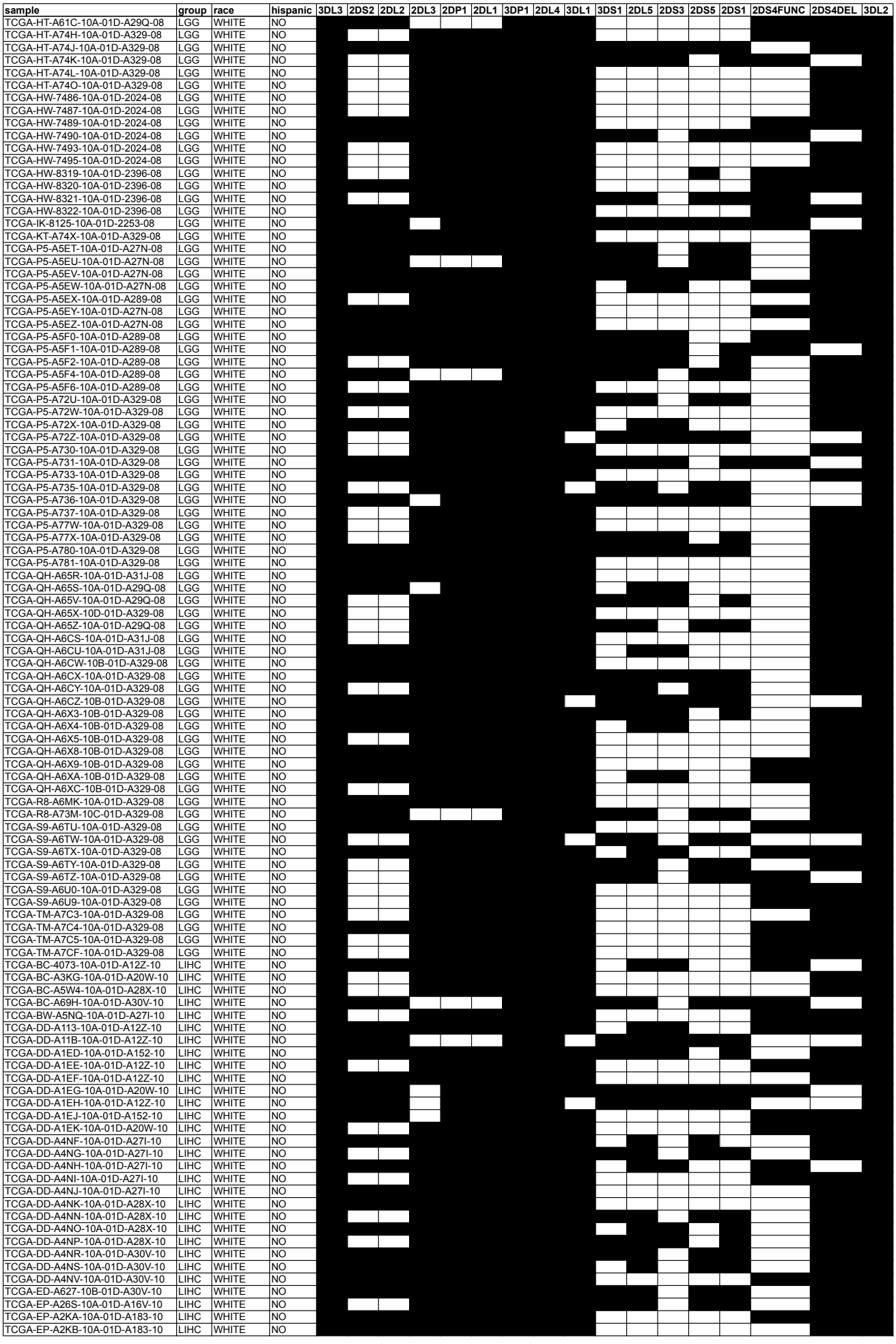
TCGA-HT-A616-10A-01D-A29Q-08	LGG	WHITE	NO																	
TCGA-HT-A618-10A-01D-A29Q-08	LGG	WHITE	NO																	
TCGA-HT-A61A-10A-01D-A29Q-08	LGG	WHITE	NO																	
TCGA-HT-A61B-10A-01D-A29Q-08	LGG	WHITE	NO																	



sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-HT-A61C-10A-01D-A29Q-08	LGG	WHITE	NO																	
TCGA-HT-A74H-10A-01D-A329-08	LGG	WHITE	NO																	
TCGA-HT-A74J-10A-01D-A329-08	LGG	WHITE	NO																	
TCGA-HT-A74K-10A-01D-A329-08	LGG	WHITE	NO																	
TCGA-HT-A74L-10A-01D-A329-08	LGG	WHITE	NO																	
TCGA-HT-A74O-10A-01D-A329-08	LGG	WHITE	NO																	
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TCGA-IK-8125-10A-01D-2253-08	LGG	WHITE	NO																	
TCGA-KT-A74X-10A-01D-A329-08	LGG	WHITE	NO																	
TCGA-P5-A5ET-10A-01D-A27N-08	LGG	WHITE	NO																	
TCGA-P5-A5EU-10A-01D-A27N-08	LGG	WHITE	NO																	
TCGA-P5-A5EV-10A-01D-A27N-08	LGG	WHITE	NO																	
TCGA-P5-A5EW-10A-01D-A27N-08	LGG	WHITE	NO																	
TCGA-P5-A5EX-10A-01D-A289-08	LGG	WHITE	NO																	
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TCGA-P5-A5EZ-10A-01D-A27N-08	LGG	WHITE	NO																	
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TCGA-P5-A5F6-10A-01D-A289-08	LGG	WHITE	NO																	
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TCGA-P5-A72W-10A-01D-A329-08	LGG	WHITE	NO																	
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TCGA-P5-A77X-10A-01D-A329-08	LGG	WHITE	NO																	
TCGA-P5-A780-10A-01D-A329-08	LGG	WHITE	NO																	
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TCGA-QH-A65R-10A-01D-A31J-08	LGG	WHITE	NO																	
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TCGA-QH-A65Z-10A-01D-A29Q-08	LGG	WHITE	NO																	
TCGA-QH-A6CS-10A-01D-A31J-08	LGG	WHITE	NO																	
TCGA-QH-A6CU-10A-01D-A31J-08	LGG	WHITE	NO																	
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TCGA-R8-A73M-10C-01D-A329-08	LGG	WHITE	NO																	
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TCGA-S9-A6TW-10A-01D-A329-08	LGG	WHITE	NO																	
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TCGA-ED-A627-10B-01D-A30V-10	LIHC	WHITE	NO																	
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TCGA-EP-A2KA-10A-01D-A183-10	LIHC	WHITE	NO																	
TCGA-EP-A2KB-10A-01D-A183-10	LIHC	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EP-A3JL-10A-01D-A20W-10	LIHC	WHITE	NO																	
TCGA-EP-A3RK-10A-01D-A22F-10	LIHC	WHITE	NO																	
TCGA-FV-A2QQ-10B-01D-A22F-10	LIHC	WHITE	NO																	
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TCGA-FV-A495-10A-01D-A25V-10	LIHC	WHITE	NO																	
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sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
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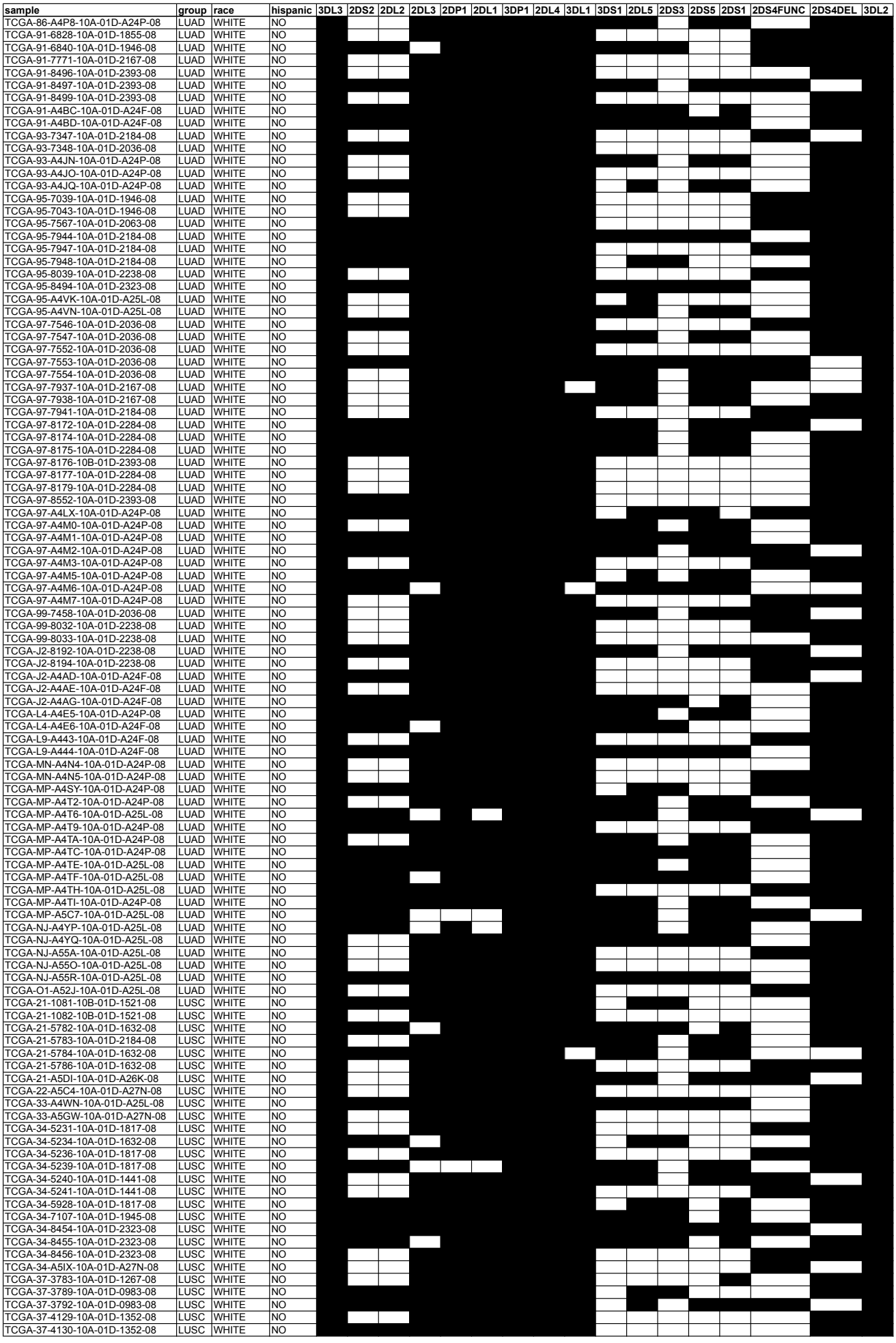

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
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TCGA-97-A4M3-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-97-A4M5-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-97-A4M6-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-97-A4M7-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-99-7458-10A-01D-2036-08	LUAD	WHITE	NO																	
TCGA-99-8032-10A-01D-2238-08	LUAD	WHITE	NO																	
TCGA-99-8033-10A-01D-2238-08	LUAD	WHITE	NO																	
TCGA-J2-8192-10A-01D-2238-08	LUAD	WHITE	NO																	
TCGA-J2-8194-10A-01D-2238-08	LUAD	WHITE	NO																	
TCGA-J2-A4AD-10A-01D-A24F-08	LUAD	WHITE	NO																	
TCGA-J2-A4AE-10A-01D-A24F-08	LUAD	WHITE	NO																	
TCGA-J2-A4AG-10A-01D-A24F-08	LUAD	WHITE	NO																	
TCGA-L4-A4E5-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-L4-A4E6-10A-01D-A24F-08	LUAD	WHITE	NO																	
TCGA-L9-A443-10A-01D-A24F-08	LUAD	WHITE	NO																	
TCGA-L9-A444-10A-01D-A24F-08	LUAD	WHITE	NO																	
TCGA-MN-A4N4-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-MN-A4N5-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-MP-A4SY-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-MP-A4T2-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-MP-A4T6-10A-01D-A25L-08	LUAD	WHITE	NO																	
TCGA-MP-A4T9-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-MP-A4TA-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-MP-A4TC-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-MP-A4TE-10A-01D-A25L-08	LUAD	WHITE	NO																	
TCGA-MP-A4TF-10A-01D-A25L-08	LUAD	WHITE	NO																	
TCGA-MP-A4TH-10A-01D-A25L-08	LUAD	WHITE	NO																	
TCGA-MP-A4TI-10A-01D-A24P-08	LUAD	WHITE	NO																	
TCGA-MP-A5C7-10A-01D-A25L-08	LUAD	WHITE	NO																	
TCGA-NJ-A4YP-10A-01D-A25L-08	LUAD	WHITE	NO																	
TCGA-NJ-A4YQ-10A-01D-A25L-08	LUAD	WHITE	NO																	
TCGA-NJ-A55A-10A-01D-A25L-08	LUAD	WHITE	NO																	
TCGA-NJ-A55O-10A-01D-A25L-08	LUAD	WHITE	NO																	
TCGA-NJ-A55R-10A-01D-A25L-08	LUAD	WHITE	NO																	
TCGA-O1-A52J-10A-01D-A25L-08	LUAD	WHITE	NO																	
TCGA-21-1081-10B-01D-1521-08	LUSC	WHITE	NO																	
TCGA-21-1082-10B-01D-1521-08	LUSC	WHITE	NO																	
TCGA-21-5782-10A-01D-1632-08	LUSC	WHITE	NO																	
TCGA-21-5783-10A-01D-2184-08	LUSC	WHITE	NO																	
TCGA-21-5784-10A-01D-1632-08	LUSC	WHITE	NO																	
TCGA-21-5786-10A-01D-1632-08	LUSC	WHITE	NO																	
TCGA-21-A5DI-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-22-A5C4-10A-01D-A27N-08	LUSC	WHITE	NO																	
TCGA-33-A4WN-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-33-A5GW-10A-01D-A27N-08	LUSC	WHITE	NO																	
TCGA-34-5231-10A-01D-1817-08	LUSC	WHITE	NO																	
TCGA-34-5234-10A-01D-1632-08	LUSC	WHITE	NO																	
TCGA-34-5236-10A-01D-1817-08	LUSC	WHITE	NO																	
TCGA-34-5239-10A-01D-1817-08	LUSC	WHITE	NO																	
TCGA-34-5240-10A-01D-1441-08	LUSC	WHITE	NO																	
TCGA-34-5241-10A-01D-1441-08	LUSC	WHITE	NO																	
TCGA-34-5928-10A-01D-1817-08	LUSC	WHITE	NO																	
TCGA-34-7107-10A-01D-1945-08	LUSC	WHITE	NO																	
TCGA-34-8454-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-34-8455-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-34-8456-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-34-A5IX-10A-01D-A27N-08	LUSC	WHITE	NO																	
TCGA-37-3783-10A-01D-1267-08	LUSC	WHITE	NO																	
TCGA-37-3789-10A-01D-0983-08	LUSC	WHITE	NO																	
TCGA-37-3792-10A-01D-0983-08	LUSC	WHITE	NO																	
TCGA-37-4129-10A-01D-1352-08	LUSC	WHITE	NO																	
TCGA-37-4130-10A-01D-1352-08	LUSC	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-37-4132-10A-01D-1352-08	LUSC	WHITE	NO																	
TCGA-37-4133-10A-01D-1352-08	LUSC	WHITE	NO																	
TCGA-37-4135-10A-01D-1352-08	LUSC	WHITE	NO																	
TCGA-37-4141-10A-01D-1352-08	LUSC	WHITE	NO																	
TCGA-37-5819-10A-01D-1632-08	LUSC	WHITE	NO																	
TCGA-37-A5EL-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-37-A5EM-10A-01D-A27N-08	LUSC	WHITE	NO																	
TCGA-37-A5EN-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-43-3920-10A-01D-0983-08	LUSC	WHITE	NO																	
TCGA-43-5668-10A-01D-1632-08	LUSC	WHITE	NO																	
TCGA-43-5670-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-43-6143-10A-01D-1817-08	LUSC	WHITE	NO																	
TCGA-43-6647-10A-01D-1817-08	LUSC	WHITE	NO																	
TCGA-43-7656-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-43-7657-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-43-8115-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-43-8116-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-43-8118-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-43-A474-10A-01D-A24F-08	LUSC	WHITE	NO																	
TCGA-43-A475-10A-01D-A24F-08	LUSC	WHITE	NO																	
TCGA-43-A56U-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-46-3765-10A-01D-0983-08	LUSC	WHITE	NO																	
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TCGA-46-3767-10A-01D-0983-08	LUSC	WHITE	NO																	
TCGA-46-3768-10A-01D-0983-08	LUSC	WHITE	NO																	
TCGA-46-3769-10A-01D-0983-08	LUSC	WHITE	NO																	
TCGA-46-6025-10A-01D-1817-08	LUSC	WHITE	NO																	
TCGA-46-6026-10A-01D-1817-08	LUSC	WHITE	NO																	
TCGA-52-7809-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-52-7810-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-56-5897-10A-01D-1632-08	LUSC	WHITE	NO																	
TCGA-56-5898-10A-01D-1632-08	LUSC	WHITE	NO																	
TCGA-56-6546-10A-01D-1817-08	LUSC	WHITE	NO																	
TCGA-56-7222-10A-01D-2042-08	LUSC	WHITE	NO																	
TCGA-56-7223-10A-01D-2042-08	LUSC	WHITE	NO																	
TCGA-56-7579-10A-01D-2042-08	LUSC	WHITE	NO																	
TCGA-56-7580-10A-01D-2042-08	LUSC	WHITE	NO																	
TCGA-56-7582-10A-01D-2042-08	LUSC	WHITE	NO																	
TCGA-56-7731-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-56-7823-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-56-8082-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-56-8083-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-56-8201-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-56-8307-10A-01D-2293-08	LUSC	WHITE	NO																	
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TCGA-56-8309-10A-01D-2293-08	LUSC	WHITE	NO																	
TCGA-56-8503-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-56-8504-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-56-8622-10A-01D-2395-08	LUSC	WHITE	NO																	
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TCGA-56-8624-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-56-8625-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-56-8626-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-56-8628-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-56-8629-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-56-A4BW-10A-01D-A24F-08	LUSC	WHITE	NO																	
TCGA-56-A4BX-10A-01D-A24F-08	LUSC	WHITE	NO																	
TCGA-56-A4BY-10A-01D-A24F-08	LUSC	WHITE	NO																	
TCGA-56-A4ZJ-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-56-A4ZK-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-56-A5DR-10A-01D-A27N-08	LUSC	WHITE	NO																	
TCGA-56-A5DS-10A-01D-A27N-08	LUSC	WHITE	NO																	
TCGA-58-8387-10A-01D-2293-08	LUSC	WHITE	NO																	
TCGA-58-8388-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-58-8390-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-58-8391-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-58-8392-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-58-8393-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-58-A46J-10A-01D-A24F-08	LUSC	WHITE	NO																	
TCGA-58-A46K-10A-01D-A24F-08	LUSC	WHITE	NO																	
TCGA-58-A46L-10A-01D-A24F-08	LUSC	WHITE	NO																	
TCGA-58-A46M-10A-01D-A24F-08	LUSC	WHITE	NO																	
TCGA-58-A46N-10A-01D-A24F-08	LUSC	WHITE	NO																	
TCGA-68-7755-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-68-7756-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-68-7757-10A-01D-2293-08	LUSC	WHITE	NO																	
TCGA-68-A59J-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-85-6175-10A-01D-1817-08	LUSC	WHITE	NO																	
TCGA-85-6560-10A-01D-1817-08	LUSC	WHITE	NO																	
TCGA-85-6561-10A-01D-1817-08	LUSC	WHITE	NO																	
TCGA-85-6798-10A-01D-1945-08	LUSC	WHITE	NO																	
TCGA-85-7696-10A-01D-2122-08	LUSC	WHITE	NO																	
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TCGA-85-7698-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-85-7699-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-85-7710-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-85-7843-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-85-7844-10A-01D-2122-08	LUSC	WHITE	NO																	
TCGA-85-7950-10A-01D-2184-08	LUSC	WHITE	NO																	
TCGA-85-8048-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-85-8049-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-85-8052-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-85-8070-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-85-8071-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-85-8072-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-85-8276-10A-01D-2293-08	LUSC	WHITE	NO																	
TCGA-85-8277-10A-01D-2293-08	LUSC	WHITE	NO																	
TCGA-85-8287-10A-01D-2293-08	LUSC	WHITE	NO																	
TCGA-85-8288-10A-01D-2293-08	LUSC	WHITE	NO																	
TCGA-85-8350-10A-01D-2293-08	LUSC	WHITE	NO																	
TCGA-85-8351-10A-01D-2293-08	LUSC	WHITE	NO																	
TCGA-85-8352-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-85-8353-10A-01D-2293-08	LUSC	WHITE	NO																	
TCGA-85-8354-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-85-8355-10A-01D-2293-08	LUSC	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-85-8479-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-85-8481-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-85-8580-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-85-8582-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-85-8584-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-85-8664-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-85-8666-10A-01D-2395-08	LUSC	WHITE	NO																	
TCGA-85-A4CL-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-85-A4CN-10A-01D-A24F-08	LUSC	WHITE	NO																	
TCGA-85-A4JB-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-85-A4JC-10A-01D-A25A-08	LUSC	WHITE	NO																	
TCGA-85-A4PA-10A-01D-A25A-08	LUSC	WHITE	NO																	
TCGA-85-A4QQ-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-85-A4QR-10A-01D-A25A-08	LUSC	WHITE	NO																	
TCGA-85-A50Z-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-85-A510-10A-01D-A26K-08	LUSC	WHITE	NO																	
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TCGA-85-A512-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-85-A5B5-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-90-6837-10A-01D-1945-08	LUSC	WHITE	NO																	
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TCGA-90-7964-10A-01D-2184-08	LUSC	WHITE	NO																	
TCGA-90-A4ED-10A-01D-A25A-08	LUSC	WHITE	NO																	
TCGA-90-A4EE-10B-01D-A25A-08	LUSC	WHITE	NO																	
TCGA-90-A59Q-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-92-7340-10A-01D-2042-08	LUSC	WHITE	NO																	
TCGA-92-7341-10A-01D-2042-08	LUSC	WHITE	NO																	
TCGA-92-8063-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-92-8064-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-92-8065-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-94-7033-10A-01D-1946-08	LUSC	WHITE	NO																	
TCGA-94-7943-10A-01D-2184-08	LUSC	WHITE	NO																	
TCGA-94-8035-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-94-8490-10A-01D-2323-08	LUSC	WHITE	NO																	
TCGA-94-A4VJ-10A-01D-A25A-08	LUSC	WHITE	NO																	
TCGA-94-A5I4-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-94-A5I6-10A-01D-A27N-08	LUSC	WHITE	NO																	
TCGA-96-7544-10A-01D-2042-08	LUSC	WHITE	NO																	
TCGA-96-7545-10A-01D-2042-08	LUSC	WHITE	NO																	
TCGA-96-8169-10A-01D-2293-08	LUSC	WHITE	NO																	
TCGA-96-8170-10A-01D-2293-08	LUSC	WHITE	NO																	
TCGA-96-A4JK-10A-01D-A25A-08	LUSC	WHITE	NO																	
TCGA-98-7454-10A-01D-2042-08	LUSC	WHITE	NO																	
TCGA-98-8021-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-98-8022-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-98-8023-10A-01D-2244-08	LUSC	WHITE	NO																	
TCGA-98-A538-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-98-A539-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-98-A53B-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-98-A53C-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-98-A53D-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-98-A53H-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-98-A53I-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-98-A53J-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-J1-A4AH-10A-01D-A24F-08	LUSC	WHITE	NO																	
TCGA-L3-A4E7-10A-01D-A25A-08	LUSC	WHITE	NO																	
TCGA-L3-A524-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-LA-A446-10A-01D-A25A-08	LUSC	WHITE	NO																	
TCGA-NK-A5CT-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-NK-A5CX-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-NK-A5D1-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-O2-A52N-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-O2-A52Q-10A-01D-A26K-08	LUSC	WHITE	NO																	
TCGA-O2-A52S-10A-01D-A25L-08	LUSC	WHITE	NO																	
TCGA-O2-A5IB-10A-01D-A27N-08	LUSC	WHITE	NO																	
TCGA-13-0751-10A-01D-0446-08	OV	WHITE	NO																	
TCGA-13-0757-10A-01D-0356-01	OV	WHITE	NO																	
TCGA-13-0758-10A-01D-0356-01	OV	WHITE	NO																	
TCGA-13-0883-10A-01D-0399-01	OV	WHITE	NO																	
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TCGA-13-0913-10A-01D-0399-01	OV	WHITE	NO																	
TCGA-13-0916-10A-01D-0399-01	OV	WHITE	NO																	
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TCGA-13-1500-10A-01D-0472-01	OV	WHITE	NO																	
TCGA-13-1505-10A-01D-0472-01	OV	WHITE	NO																	
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TCGA-13-2071-10A-01D-1526-09	OV	WHITE	NO																	
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TCGA-59-2372-10A-01D-1526-09	OV	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-F2-A44G-10A-01D-A26I-08	PAAD	WHITE	NO																	
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TCGA-CH-5740-10A-01D-1576-08	PRAD	WHITE	NO																	
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TCGA-EJ-5495-10A-01D-1577-08	PRAD	WHITE	NO																	
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TCGA-EJ-5503-10A-01D-1577-08	PRAD	WHITE	NO																	
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TCGA-G9-6370-10A-01D-1786-08	PRAD	WHITE	NO																	
TCGA-G9-6371-10A-01D-1786-08	PRAD	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-G9-6373-10A-01D-1786-08	PRAD	WHITE	NO																	
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TCGA-G9-6385-10A-01D-1786-08	PRAD	WHITE	NO																	
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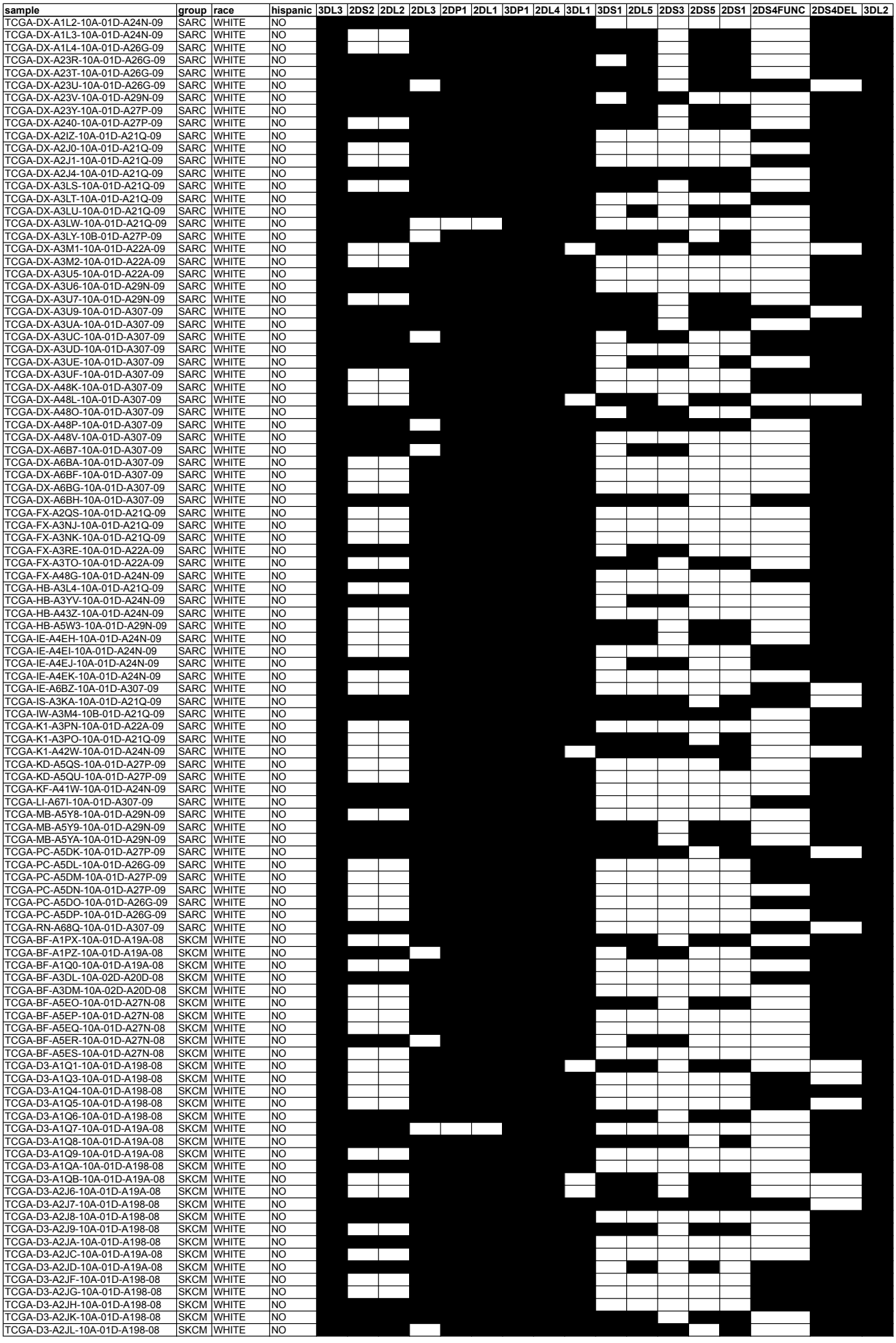
TCGA-DX-A1KZ-10A-01D-A24N-09	SARC	WHITE	NO																	
TCGA-DX-A1L0-10A-01D-A24N-09	SARC	WHITE	NO																	
TCGA-DX-A1L1-10A-01D-A24N-09	SARC	WHITE	NO																	



sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-DX-A1L2-10A-01D-A24N-09	SARC	WHITE	NO																	
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TCGA-DX-A2IZ-10A-01D-A21Q-09	SARC	WHITE	NO																	
TCGA-DX-A2J0-10A-01D-A21Q-09	SARC	WHITE	NO																	
TCGA-DX-A2J1-10A-01D-A21Q-09	SARC	WHITE	NO																	
TCGA-DX-A2J4-10A-01D-A21Q-09	SARC	WHITE	NO																	
TCGA-DX-A3LS-10A-01D-A21Q-09	SARC	WHITE	NO																	
TCGA-DX-A3LT-10A-01D-A21Q-09	SARC	WHITE	NO																	
TCGA-DX-A3LU-10A-01D-A21Q-09	SARC	WHITE	NO																	
TCGA-DX-A3LW-10A-01D-A21Q-09	SARC	WHITE	NO																	
TCGA-DX-A3LY-10B-01D-A27P-09	SARC	WHITE	NO																	
TCGA-DX-A3M1-10A-01D-A22A-09	SARC	WHITE	NO																	
TCGA-DX-A3M2-10A-01D-A22A-09	SARC	WHITE	NO																	
TCGA-DX-A3U5-10A-01D-A22A-09	SARC	WHITE	NO																	
TCGA-DX-A3U6-10A-01D-A29N-09	SARC	WHITE	NO																	
TCGA-DX-A3U7-10A-01D-A29N-09	SARC	WHITE	NO																	
TCGA-DX-A3U9-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A3UA-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A3UC-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A3UD-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A3UE-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A3UF-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A48K-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A48L-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A48O-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A48P-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A48V-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A6B7-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A6BA-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A6BF-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A6BG-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-DX-A6BH-10A-01D-A307-09	SARC	WHITE	NO																	
TCGA-FX-A2QS-10A-01D-A21Q-09	SARC	WHITE	NO																	
TCGA-FX-A3NJ-10A-01D-A21Q-09	SARC	WHITE	NO																	
TCGA-FX-A3NK-10A-01D-A21Q-09	SARC	WHITE	NO																	
TCGA-FX-A3RE-10A-01D-A22A-09	SARC	WHITE	NO																	
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TCGA-HB-A3L4-10A-01D-A21Q-09	SARC	WHITE	NO																	
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TCGA-HB-A5W3-10A-01D-A29N-09	SARC	WHITE	NO																	
TCGA-IE-A4EH-10A-01D-A24N-09	SARC	WHITE	NO																	
TCGA-IE-A4EI-10A-01D-A24N-09	SARC	WHITE	NO																	
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TCGA-IW-A3M4-10B-01D-A21Q-09	SARC	WHITE	NO																	
TCGA-K1-A3PN-10A-01D-A22A-09	SARC	WHITE	NO																	
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TCGA-K1-A42W-10A-01D-A24N-09	SARC	WHITE	NO																	
TCGA-KD-A5QS-10A-01D-A27P-09	SARC	WHITE	NO																	
TCGA-KD-A5QU-10A-01D-A27P-09	SARC	WHITE	NO																	
TCGA-KF-A41W-10A-01D-A24N-09	SARC	WHITE	NO																	
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TCGA-MB-A5YA-10A-01D-A29N-09	SARC	WHITE	NO																	
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TCGA-D3-A2J6-10A-01D-A19A-08	SKCM	WHITE	NO																	
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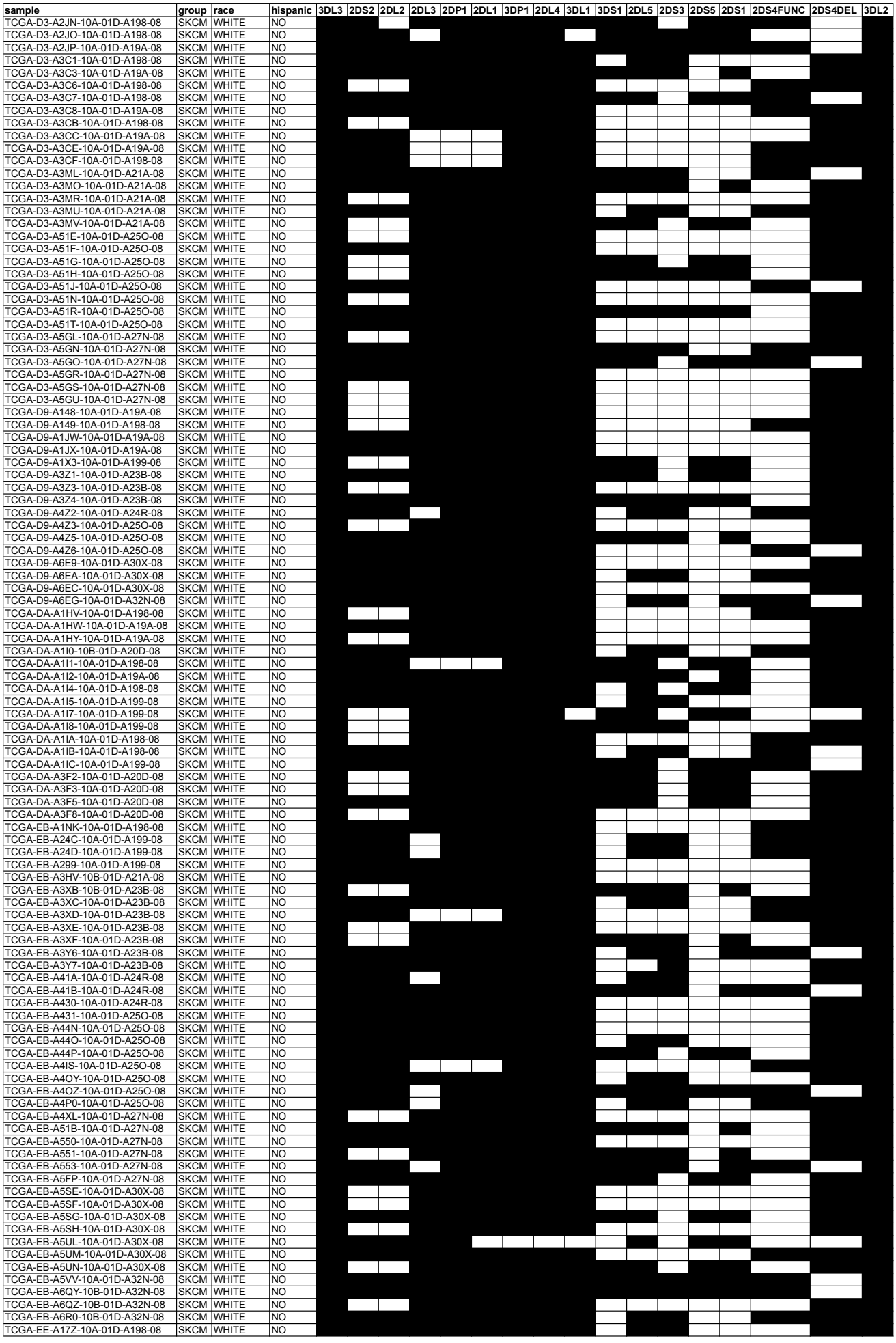
TCGA-D3-A2JA-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-D3-A2JC-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-D3-A2JD-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-D3-A2JF-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-D3-A2JG-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-D3-A2JH-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-D3-A2JK-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-D3-A2JL-10A-01D-A198-08	SKCM	WHITE	NO																	



sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-D3-A2JN-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-D3-A2JO-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-D3-A2JP-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-D3-A3C1-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-D3-A3C3-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-D3-A3C6-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-D3-A3C7-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-D3-A3C8-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-D3-A3CB-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-D3-A3CC-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-D3-A3CE-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-D3-A3CF-10A-01D-A198-08	SKCM	WHITE	NO																	
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TCGA-D3-A3MV-10A-01D-A21A-08	SKCM	WHITE	NO																	
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TCGA-D3-A51F-10A-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-D3-A51G-10A-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-D3-A51H-10A-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-D3-A51J-10A-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-D3-A51N-10A-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-D3-A51R-10A-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-D3-A51T-10A-01D-A25O-08	SKCM	WHITE	NO																	
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TCGA-D3-A5GN-10A-01D-A27N-08	SKCM	WHITE	NO																	
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TCGA-D3-A5GS-10A-01D-A27N-08	SKCM	WHITE	NO																	
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TCGA-D9-A1JX-10A-01D-A19A-08	SKCM	WHITE	NO																	
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TCGA-D9-A3Z3-10A-01D-A23B-08	SKCM	WHITE	NO																	
TCGA-D9-A3Z4-10A-01D-A23B-08	SKCM	WHITE	NO																	
TCGA-D9-A4Z2-10A-01D-A24R-08	SKCM	WHITE	NO																	
TCGA-D9-A4Z3-10A-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-D9-A4Z5-10A-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-D9-A4Z6-10A-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-D9-A6E9-10A-01D-A30X-08	SKCM	WHITE	NO																	
TCGA-D9-A6EA-10A-01D-A30X-08	SKCM	WHITE	NO																	
TCGA-D9-A6EC-10A-01D-A30X-08	SKCM	WHITE	NO																	
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TCGA-DA-A1HW-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-DA-A1HY-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-DA-A1I0-10B-01D-A20D-08	SKCM	WHITE	NO																	
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TCGA-EB-A3HV-10B-01D-A21A-08	SKCM	WHITE	NO																	
TCGA-EB-A3XB-10B-01D-A23B-08	SKCM	WHITE	NO																	
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TCGA-EB-A6R0-10B-01D-A32N-08	SKCM	WHITE	NO																	
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sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
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TCGA-EE-A2GC-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2GD-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2GE-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2GH-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2GI-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2GJ-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2GK-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2GL-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2GM-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2GN-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2GO-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2GP-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2GR-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2GS-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2GT-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2GU-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2M5-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2M6-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2M7-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2M8-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2MC-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2MD-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2ME-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2MF-10B-01D-A21A-08	SKCM	WHITE	NO																	
TCGA-EE-A2MG-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2MH-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2MI-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2MJ-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2MK-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2ML-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2MM-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A2MN-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2MP-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-EE-A2MQ-10A-01D-A199-08	SKCM	WHITE	NO																	
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TCGA-EE-A3AD-10A-01D-A198-08	SKCM	WHITE	NO																	
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TCGA-EE-A3AF-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A3AG-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A3AH-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-EE-A3J3-10A-01D-A20D-08	SKCM	WHITE	NO																	
TCGA-EE-A3J4-10A-01D-A20D-08	SKCM	WHITE	NO																	
TCGA-EE-A3J5-10A-01D-A20D-08	SKCM	WHITE	NO																	
TCGA-EE-A3J7-10A-01D-A20D-08	SKCM	WHITE	NO																	
TCGA-EE-A3J8-10A-01D-A20D-08	SKCM	WHITE	NO																	
TCGA-EE-A3JA-10A-01D-A20D-08	SKCM	WHITE	NO																	
TCGA-EE-A3JB-10A-01D-A21A-08	SKCM	WHITE	NO																	
TCGA-EE-A3JD-10A-01D-A20D-08	SKCM	WHITE	NO																	
TCGA-EE-A3JE-10A-01D-A20D-08	SKCM	WHITE	NO																	
TCGA-EE-A3JH-10A-01D-A21A-08	SKCM	WHITE	NO																	
TCGA-EE-A3JI-10A-01D-A21A-08	SKCM	WHITE	NO																	
TCGA-ER-A193-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-ER-A194-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-ER-A195-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A196-10A-01D-A199-08	SKCM	WHITE	NO																	
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TCGA-ER-A19A-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-ER-A19B-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A19C-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A19D-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-ER-A19E-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-ER-A19F-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A19G-10A-01D-A198-08	SKCM	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-ER-A19H-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A19J-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A19K-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-ER-A19L-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-ER-A19M-10A-01D-A23B-08	SKCM	WHITE	NO																	
TCGA-ER-A19N-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-ER-A19O-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-ER-A19P-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A19Q-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-ER-A19S-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A19T-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-ER-A19W-10A-01D-A23B-08	SKCM	WHITE	NO																	
TCGA-ER-A1A1-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-ER-A2NB-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A2NC-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-ER-A2ND-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A2NE-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A2NF-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-ER-A2NG-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A2NH-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-ER-A3ES-10A-01D-A20D-08	SKCM	WHITE	NO																	
TCGA-ER-A3ET-10A-01D-A20D-08	SKCM	WHITE	NO																	
TCGA-ER-A3EV-10A-01D-A20D-08	SKCM	WHITE	NO																	
TCGA-ER-A3PL-10A-01D-A23B-08	SKCM	WHITE	NO																	
TCGA-ER-A42H-10A-01D-A24R-08	SKCM	WHITE	NO																	
TCGA-ER-A42K-10A-01D-A24R-08	SKCM	WHITE	NO																	
TCGA-ER-A42L-10A-01D-A24R-08	SKCM	WHITE	NO																	
TCGA-FR-A3R1-10B-01D-A23B-08	SKCM	WHITE	NO																	
TCGA-FR-A3YN-10A-01D-A23B-08	SKCM	WHITE	NO																	
TCGA-FR-A3YO-10A-01D-A23B-08	SKCM	WHITE	NO																	
TCGA-FR-A44A-10A-01D-A24R-08	SKCM	WHITE	NO																	
TCGA-FR-A69P-10A-01D-A30X-08	SKCM	WHITE	NO																	
TCGA-FR-A726-10A-01D-A32N-08	SKCM	WHITE	NO																	
TCGA-FR-A728-10A-01D-A32N-08	SKCM	WHITE	NO																	
TCGA-FS-A1YW-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1YX-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1YY-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1Z0-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1Z3-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1Z4-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1Z7-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZA-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZB-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZC-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZD-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZE-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZF-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZG-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZH-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZJ-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZK-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZM-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZN-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZP-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZQ-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZR-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZS-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZT-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZU-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZW-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A1ZY-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-FS-A4F0-10A-01D-A24R-08	SKCM	WHITE	NO																	
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TCGA-FS-A4F5-10B-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-FS-A4F8-10B-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-FS-A4F9-10A-01D-A24R-08	SKCM	WHITE	NO																	
TCGA-FS-A4FB-10B-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-FS-A4FC-10A-01D-A24R-08	SKCM	WHITE	NO																	
TCGA-FS-A4FD-10B-01D-A25O-08	SKCM	WHITE	NO																	
TCGA-FW-A3I3-10A-01D-A21A-08	SKCM	WHITE	NO																	
TCGA-FW-A3R5-10A-01D-A23B-08	SKCM	WHITE	NO																	
TCGA-FW-A3TU-10A-01D-A23B-08	SKCM	WHITE	NO																	
TCGA-FW-A3TV-10A-01D-A23B-08	SKCM	WHITE	NO																	
TCGA-FW-A5DX-10A-01D-A27N-08	SKCM	WHITE	NO																	
TCGA-GF-A2C7-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-GF-A3OT-10A-01D-A23B-08	SKCM	WHITE	NO																	
TCGA-GF-A4EO-10A-01D-A24R-08	SKCM	WHITE	NO																	
TCGA-GF-A6C8-10A-01D-A30X-08	SKCM	WHITE	NO																	
TCGA-GF-A6C9-10A-01D-A30X-08	SKCM	WHITE	NO																	
TCGA-GF-A769-10A-01D-A32N-08	SKCM	WHITE	NO																	
TCGA-GN-A261-10A-01D-A199-08	SKCM	WHITE	NO																	
TCGA-GN-A262-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-GN-A263-10A-01D-A198-08	SKCM	WHITE	NO																	
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TCGA-GN-A267-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-GN-A268-10A-01D-A198-08	SKCM	WHITE	NO																	
TCGA-GN-A269-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-GN-A26A-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-GN-A26C-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-GN-A26D-10A-01D-A19A-08	SKCM	WHITE	NO																	
TCGA-GN-A4U3-10F-01D-A32N-08	SKCM	WHITE	NO																	
TCGA-GN-A4U4-10B-01D-A32N-08	SKCM	WHITE	NO																	
TCGA-GN-A4U5-10B-01D-A32N-08	SKCM	WHITE	NO																	
TCGA-GN-A4U7-10B-01D-A32N-08	SKCM	WHITE	NO																	
TCGA-GN-A4U8-10B-01D-A32N-08	SKCM	WHITE	NO																	
TCGA-GN-A4U9-10B-01D-A32N-08	SKCM	WHITE	NO																	
TCGA-OD-A75X-10A-01D-A32N-08	SKCM	WHITE	NO																	
TCGA-QB-A6FS-10A-01D-A30X-08	SKCM	WHITE	NO																	
TCGA-RP-A690-10A-01D-A30X-08	SKCM	WHITE	NO																	
TCGA-RP-A693-10A-01D-A30X-08	SKCM	WHITE	NO																	
TCGA-RP-A694-10A-01D-A30X-08	SKCM	WHITE	NO																	
TCGA-RP-A695-10A-01D-A30X-08	SKCM	WHITE	NO																	
TCGA-B7-5816-10A-01D-1600-08	STAD	WHITE	NO																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-B7-5818-10A-01D-1600-08	STAD	WHITE	NO																	
TCGA-B7-A5TI-10A-01D-A31J-08	STAD	WHITE	NO																	
TCGA-B7-A5TJ-10A-01D-A31J-08	STAD	WHITE	NO																	
TCGA-B7-A5TK-10A-01D-A31J-08	STAD	WHITE	NO																	
TCGA-B7-A5TN-10A-01D-A31J-08	STAD	WHITE	NO																	
TCGA-BR-6452-10A-01D-1800-08	STAD	WHITE	NO																	
TCGA-BR-6455-10A-01D-1800-08	STAD	WHITE	NO																	
TCGA-BR-6456-10A-01D-1800-08	STAD	WHITE	NO																	
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TCGA-BR-6458-10A-01D-1800-08	STAD	WHITE	NO																	
TCGA-BR-6563-10A-01D-2053-08	STAD	WHITE	NO																	
TCGA-BR-6564-10A-01D-1882-08	STAD	WHITE	NO																	
TCGA-BR-6565-10A-01D-1800-08	STAD	WHITE	NO																	
TCGA-BR-6566-10A-01D-1800-08	STAD	WHITE	NO																	
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TCGA-BR-6803-10A-01D-1882-08	STAD	WHITE	NO																	
TCGA-BR-6852-10A-01D-1882-08	STAD	WHITE	NO																	
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TCGA-BR-7715-10A-01D-2053-08	STAD	WHITE	NO																	
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TCGA-BR-8080-10A-01D-2340-08	STAD	WHITE	NO																	
TCGA-BR-8081-10A-01D-2340-08	STAD	WHITE	NO																	
TCGA-BR-8284-10A-01D-2340-08	STAD	WHITE	NO																	
TCGA-BR-8285-10A-01D-2340-08	STAD	WHITE	NO																	
TCGA-BR-8286-10A-01D-2340-08	STAD	WHITE	NO																	
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TCGA-BR-8384-10A-01D-2394-08	STAD	WHITE	NO																	
TCGA-BR-8483-10A-01D-2394-08	STAD	WHITE	NO																	
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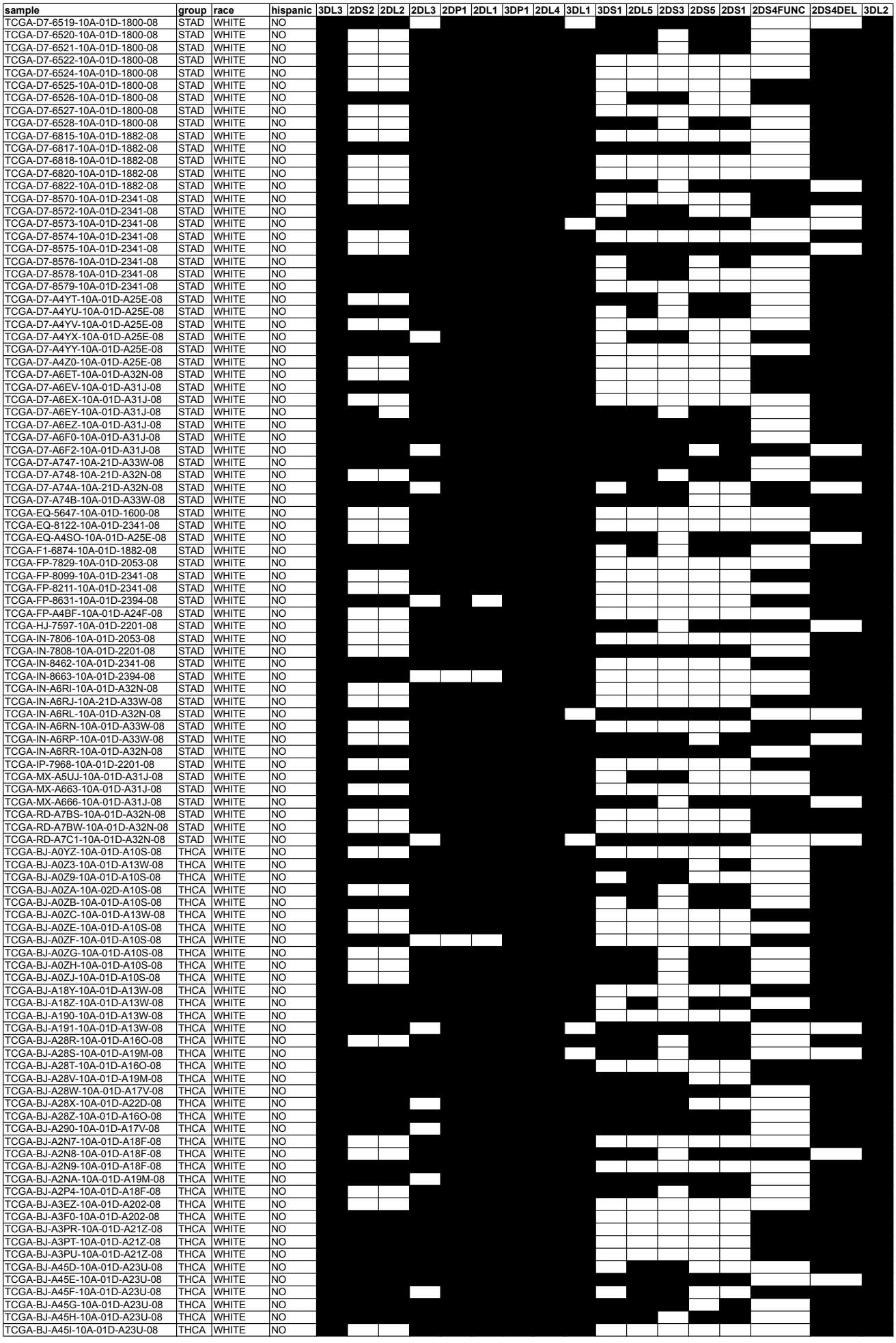

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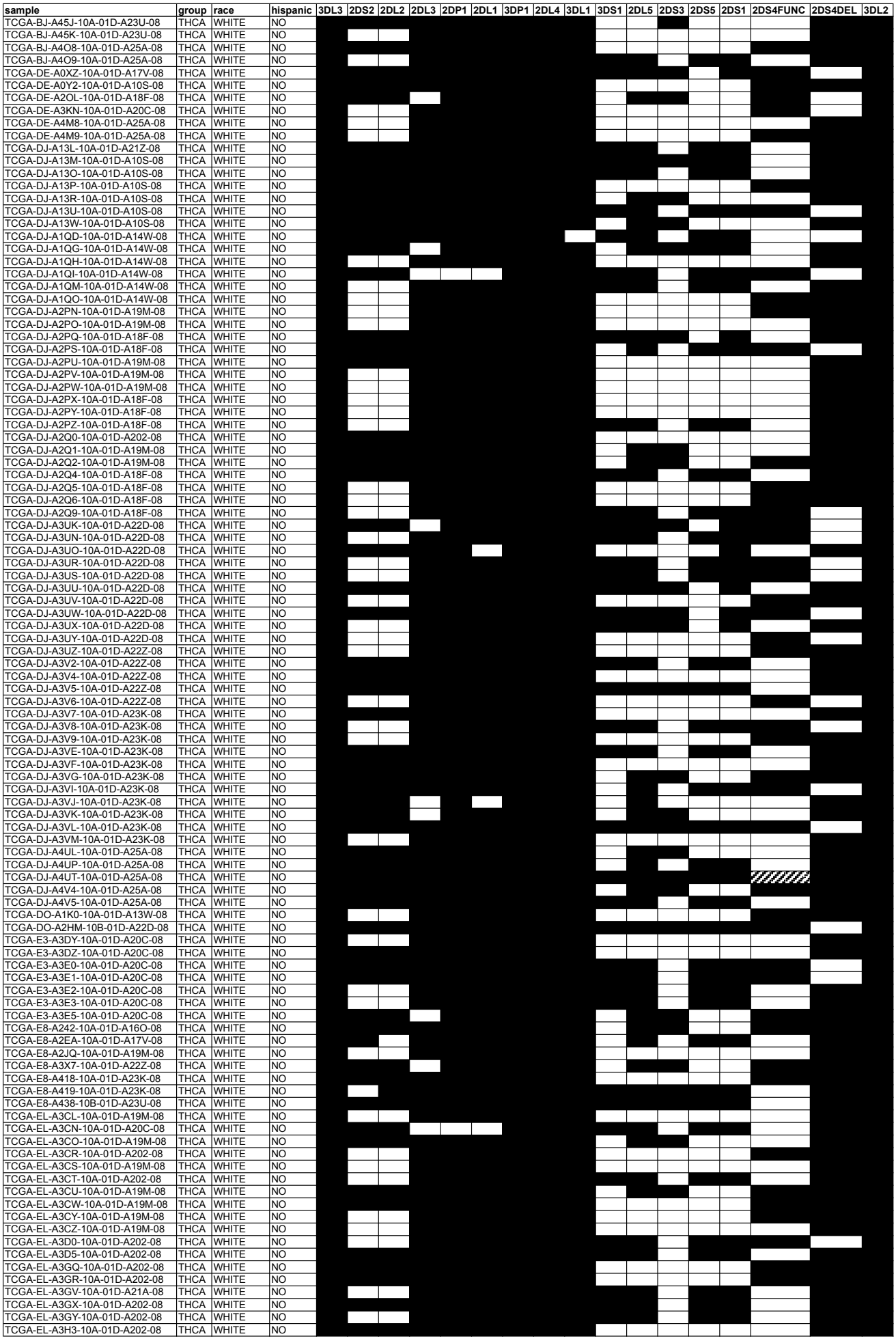

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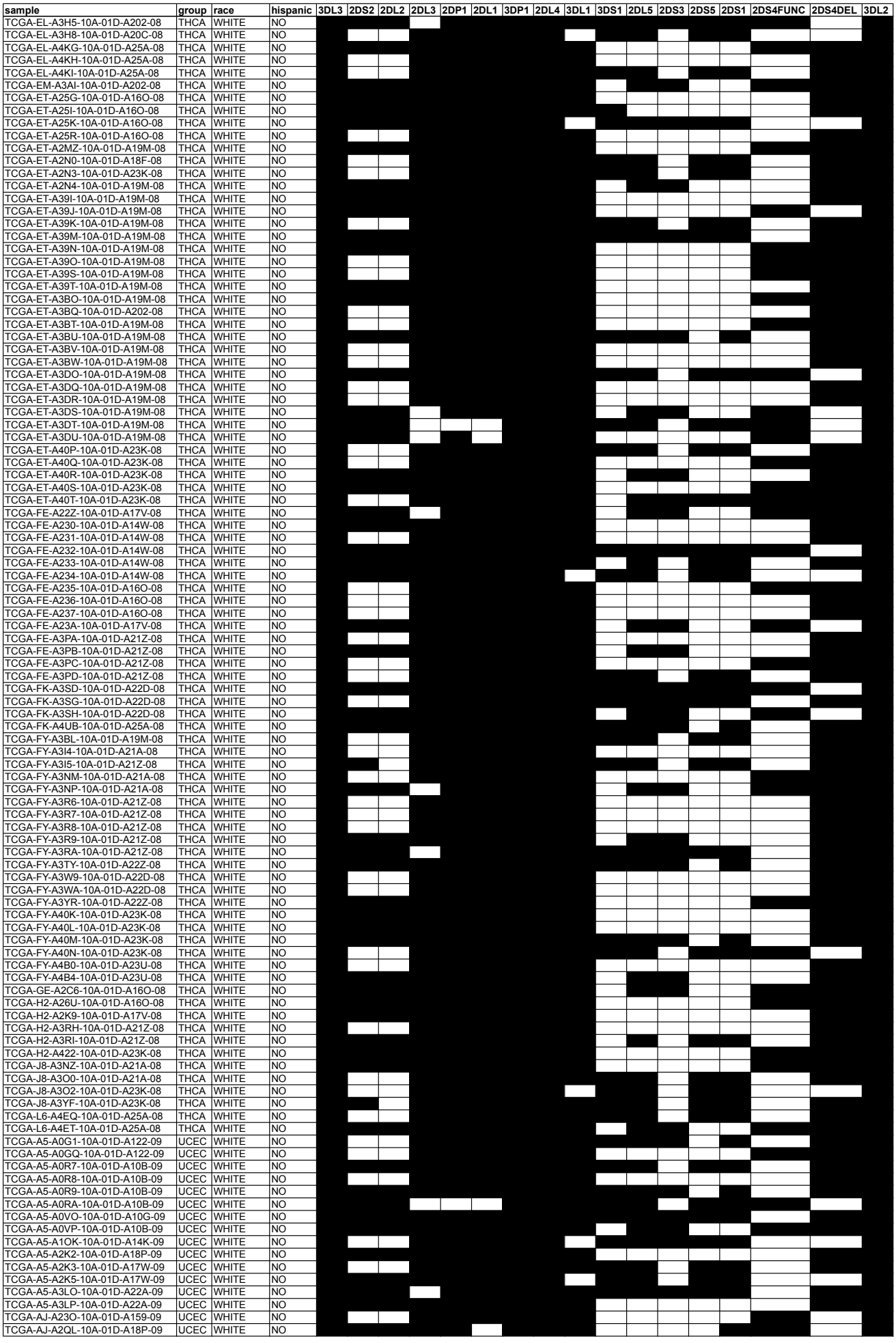

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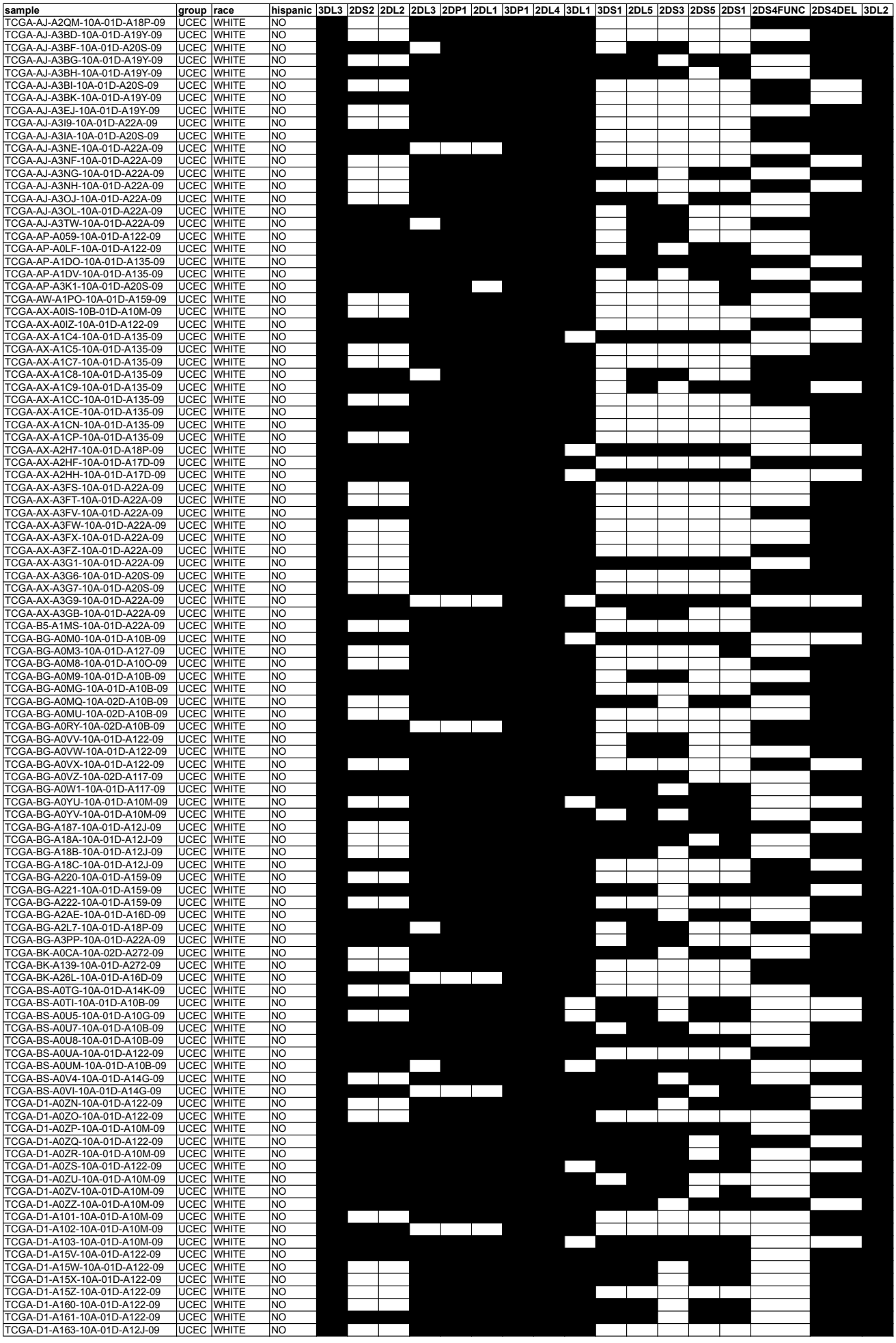

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sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
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TCGA-D1-A16D-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16E-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16F-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16G-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16I-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16J-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16N-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16O-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16Q-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16R-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16S-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16V-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16X-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A16Y-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A174-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A175-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A176-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A177-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17A-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17B-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17C-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17D-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17F-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17H-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17K-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17L-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17M-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17Q-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17R-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17S-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17T-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A17U-10A-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-D1-A1NS-10A-01D-A14G-09	UCEC	WHITE	NO																	
TCGA-D1-A1NU-10A-01D-A14G-09	UCEC	WHITE	NO																	
TCGA-D1-A1NX-10A-01D-A16D-09	UCEC	WHITE	NO																	
TCGA-D1-A1NY-10A-01D-A16D-09	UCEC	WHITE	NO																	
TCGA-D1-A1NZ-10A-01D-A14G-09	UCEC	WHITE	NO																	
TCGA-D1-A1O0-10A-01D-A17D-09	UCEC	WHITE	NO																	
TCGA-D1-A1O5-10A-01D-A14G-09	UCEC	WHITE	NO																	
TCGA-D1-A1O7-10A-01D-A14G-09	UCEC	WHITE	NO																	
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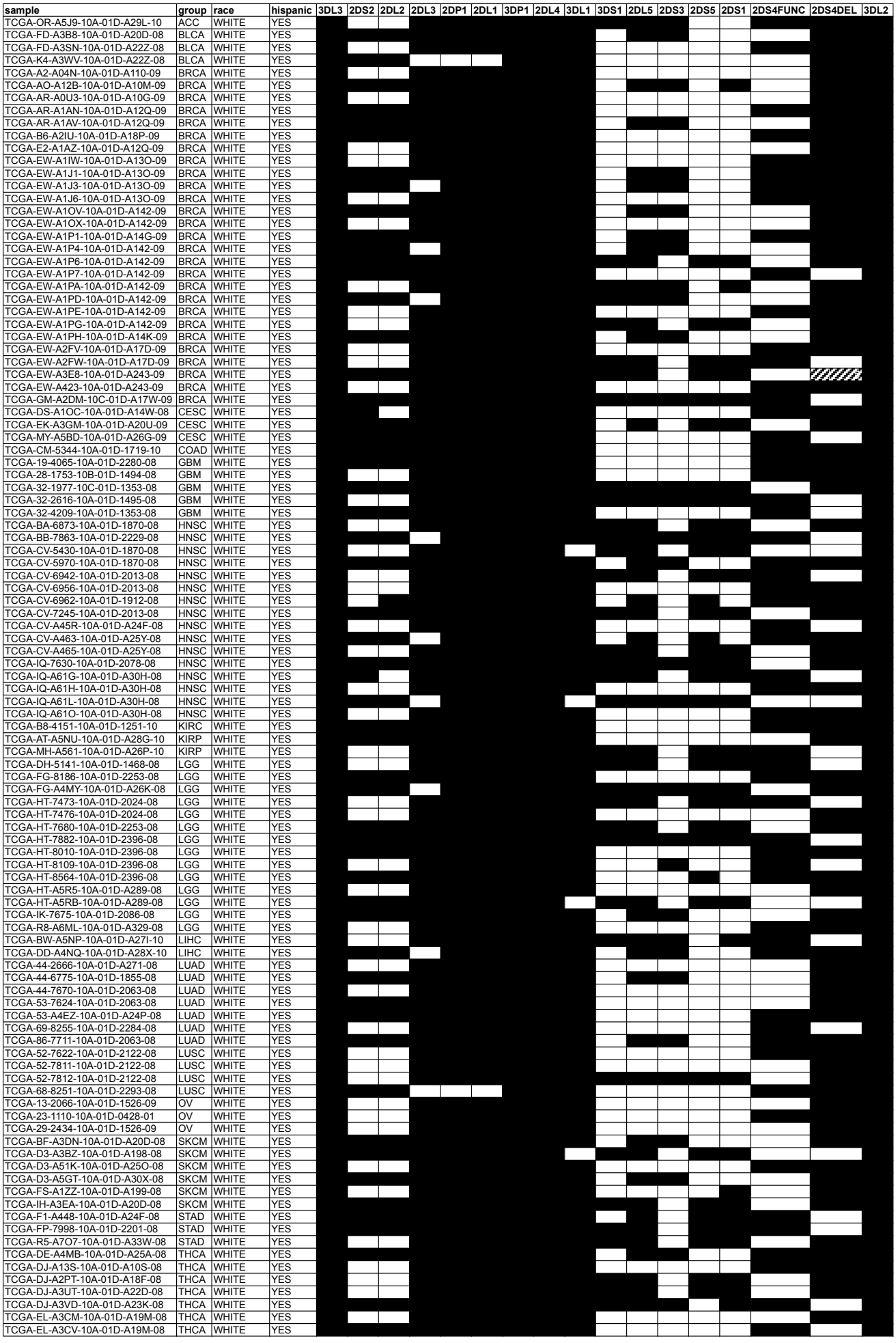
TCGA-D1-A2G6-10A-01D-A17D-09	UCEC	WHITE	NO																	
TCGA-D1-A2G7-10A-01D-A17W-09	UCEC	WHITE	NO																	
TCGA-D1-A3DA-10A-01D-A20S-09	UCEC	WHITE	NO																	
TCGA-D1-A3DG-10A-01D-A19Y-09	UCEC	WHITE	NO																	
TCGA-D1-A3DH-10A-01D-A19Y-09	UCEC	WHITE	NO																	
TCGA-D1-A3JP-10B-01D-A22A-09	UCEC	WHITE	NO																	
TCGA-D1-A3JQ-10B-01D-A22A-09	UCEC	WHITE	NO																	
TCGA-DI-A0WH-10B-01D-A12J-09	UCEC	WHITE	NO																	
TCGA-DI-A1BU-10A-01D-A135-09	UCEC	WHITE	NO																	
TCGA-DI-A1BY-10A-01D-A135-09	UCEC	WHITE	NO																	
TCGA-DI-A1C3-10A-01D-A135-09	UCEC	WHITE	NO																	
TCGA-E6-A1LX-10A-01D-A14G-09	UCEC	WHITE	NO																	
TCGA-E6-A1M0-10A-01D-A142-09	UCEC	WHITE	NO																	
TCGA-E6-A2P9-10B-01D-A19Y-09	UCEC	WHITE	NO																	
TCGA-EC-A1NJ-10A-01D-A14G-09	UCEC	WHITE	NO																	
TCGA-EC-A1QX-10A-01D-A16D-09	UCEC	WHITE	NO																	
TCGA-EC-A24G-10A-01D-A16D-09	UCEC	WHITE	NO																	
TCGA-EO-A22Y-10A-01D-A17W-09	UCEC	WHITE	NO																	
TCGA-EO-A3L0-10A-01D-A22A-09	UCEC	WHITE	NO																	
TCGA-EY-A1G7-10A-01D-A13O-09	UCEC	WHITE	NO																	
TCGA-EY-A1G8-10A-01D-A13O-09	UCEC	WHITE	NO																	
TCGA-EY-A1GC-10A-01D-A13O-09	UCEC	WHITE	NO																	
TCGA-EY-A1GE-10A-01D-A13O-09	UCEC	WHITE	NO																	
TCGA-EY-A1GH-10A-01D-A13O-09	UCEC	WHITE	NO																	
TCGA-EY-A1GI-10A-01D-A13O-09	UCEC	WHITE	NO																	
TCGA-EY-A1GK-10A-01D-A13O-09	UCEC	WHITE	NO																	
TCGA-EY-A1GO-10A-01D-A14G-09	UCEC	WHITE	NO																	
TCGA-EY-A1GQ-10A-01D-A13O-09	UCEC	WHITE	NO																	
TCGA-EY-A1GT-10A-01D-A13O-09	UCEC	WHITE	NO																	
TCGA-EY-A1GV-10A-01D-A13O-09	UCEC	WHITE	NO																	
TCGA-EY-A1GX-10A-01D-A13O-09	UCEC	WHITE	NO																	
TCGA-EY-A212-10A-01D-A14K-09	UCEC	WHITE	NO																	
TCGA-EY-A215-10A-01D-A14K-09	UCEC	WHITE	NO																	
TCGA-EY-A2OM-10A-01D-A18P-09	UCEC	WHITE	NO																	
TCGA-EY-A2OO-10A-01D-A19Y-09	UCEC	WHITE	NO																	
TCGA-EY-A2OP-10A-01D-A19Y-09	UCEC	WHITE	NO																	
TCGA-EY-A2OQ-10A-01D-A19Y-09	UCEC	WHITE	NO																	
TCGA-EY-A3QX-10A-01D-A22A-09	UCEC	WHITE	NO																	
TCGA-FI-A2CX-10A-01D-A17D-09	UCEC	WHITE	NO																	
TCGA-FI-A2D0-10A-01D-A17D-09	UCEC	WHITE	NO																	
TCGA-FI-A2D2-10A-01D-A17D-09	UCEC	WHITE	NO																	
TCGA-FI-A2D5-10A-01D-A17D-09	UCEC	WHITE	NO																	
TCGA-FI-A2D6-10A-01D-A17D-09	UCEC	WHITE	NO																	
TCGA-FI-A2EX-10A-01D-A17D-09	UCEC	WHITE	NO																	
TCGA-FI-A2EY-10A-01D-A18P-09	UCEC	WHITE	NO																	
TCGA-FI-A2F8-10B-01D-A17D-09	UCEC	WHITE	NO																	
TCGA-FI-A2F9-10B-01D-A17D-09	UCEC	WHITE	NO																	
TCGA-FI-A3PX-10A-01D-A22A-09	UCEC	WHITE	NO																	
TCGA-K6-A3WQ-10A-01D-A22A-09	UCEC	WHITE	NO																	
TCGA-KP-A3VZ-10A-01D-A22A-09	UCEC	WHITE	NO																	
TCGA-KP-A3W3-10A-01D-A22A-09	UCEC	WHITE	NO																	
TCGA-KP-A3W4-10A-01D-A22A-09	UCEC	WHITE	NO																	
TCGA-OR-A5J2-10A-01D-A29L-10	ACC	WHITE	YES																	
TCGA-OR-A5J3-10A-01D-A29L-10	ACC	WHITE	YES																	
TCGA-OR-A5J4-10A-01D-A29L-10	ACC	WHITE	YES																	
TCGA-OR-A5J7-10A-01D-A29L-10	ACC	WHITE	YES																	
TCGA-OR-A5J8-10A-01D-A29L-10	ACC	WHITE	YES																	



sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-OR-A5J9-10A-01D-A29L-10	ACC	WHITE	YES																	
TCGA-FD-A3B8-10A-01D-A20D-08	BLCA	WHITE	YES																	
TCGA-FD-A3SN-10A-01D-A22Z-08	BLCA	WHITE	YES																	
TCGA-K4-A3WV-10A-01D-A22Z-08	BLCA	WHITE	YES																	
TCGA-A2-A04N-10A-01D-A110-09	BRCA	WHITE	YES																	
TCGA-AO-A12B-10A-01D-A10M-09	BRCA	WHITE	YES																	
TCGA-AR-A0U3-10A-01D-A10G-09	BRCA	WHITE	YES																	
TCGA-AR-A1AN-10A-01D-A12Q-09	BRCA	WHITE	YES																	
TCGA-AR-A1AV-10A-01D-A12Q-09	BRCA	WHITE	YES																	
TCGA-B6-A2IU-10A-01D-A18P-09	BRCA	WHITE	YES																	
TCGA-E2-A1AZ-10A-01D-A12Q-09	BRCA	WHITE	YES																	
TCGA-EW-A1IW-10A-01D-A13O-09	BRCA	WHITE	YES																	
TCGA-EW-A1J1-10A-01D-A13O-09	BRCA	WHITE	YES																	
TCGA-EW-A1J3-10A-01D-A13O-09	BRCA	WHITE	YES																	
TCGA-EW-A1J6-10A-01D-A13O-09	BRCA	WHITE	YES																	
TCGA-EW-A1OV-10A-01D-A142-09	BRCA	WHITE	YES																	
TCGA-EW-A1OX-10A-01D-A142-09	BRCA	WHITE	YES																	
TCGA-EW-A1P1-10A-01D-A14G-09	BRCA	WHITE	YES																	
TCGA-EW-A1P4-10A-01D-A142-09	BRCA	WHITE	YES																	
TCGA-EW-A1P6-10A-01D-A142-09	BRCA	WHITE	YES																	
TCGA-EW-A1P7-10A-01D-A142-09	BRCA	WHITE	YES																	
TCGA-EW-A1PA-10A-01D-A142-09	BRCA	WHITE	YES																	
TCGA-EW-A1PD-10A-01D-A142-09	BRCA	WHITE	YES																	
TCGA-EW-A1PE-10A-01D-A142-09	BRCA	WHITE	YES																	
TCGA-EW-A1PG-10A-01D-A142-09	BRCA	WHITE	YES																	
TCGA-EW-A1PH-10A-01D-A14K-09	BRCA	WHITE	YES																	
TCGA-EW-A2FV-10A-01D-A17D-09	BRCA	WHITE	YES																	
TCGA-EW-A2FW-10A-01D-A17D-09	BRCA	WHITE	YES																	
TCGA-EW-A3E8-10A-01D-A243-09	BRCA	WHITE	YES																	
TCGA-EW-A423-10A-01D-A243-09	BRCA	WHITE	YES																	
TCGA-GM-A2DM-10C-01D-A17W-09	BRCA	WHITE	YES																	
TCGA-DS-A1OC-10A-01D-A14W-08	CESC	WHITE	YES																	
TCGA-EK-A3GM-10A-01D-A20U-09	CESC	WHITE	YES																	
TCGA-MY-A5BD-10A-01D-A26G-09	CESC	WHITE	YES																	
TCGA-CM-5344-10A-01D-1719-10	COAD	WHITE	YES																	
TCGA-19-4065-10A-01D-2280-08	GBM	WHITE	YES																	
TCGA-28-1753-10B-01D-1494-08	GBM	WHITE	YES																	
TCGA-32-1977-10C-01D-1353-08	GBM	WHITE	YES																	
TCGA-32-2616-10A-01D-1495-08	GBM	WHITE	YES																	
TCGA-32-4209-10A-01D-1353-08	GBM	WHITE	YES																	
TCGA-BA-6873-10A-01D-1870-08	HNSC	WHITE	YES																	
TCGA-BB-7863-10A-01D-2229-08	HNSC	WHITE	YES																	
TCGA-CV-5430-10A-01D-1870-08	HNSC	WHITE	YES																	
TCGA-CV-5970-10A-01D-1870-08	HNSC	WHITE	YES																	
TCGA-CV-6942-10A-01D-2013-08	HNSC	WHITE	YES																	
TCGA-CV-6956-10A-01D-2013-08	HNSC	WHITE	YES																	
TCGA-CV-6962-10A-01D-1912-08	HNSC	WHITE	YES																	
TCGA-CV-7245-10A-01D-2013-08	HNSC	WHITE	YES																	
TCGA-CV-A45R-10A-01D-A24F-08	HNSC	WHITE	YES																	
TCGA-CV-A463-10A-01D-A25Y-08	HNSC	WHITE	YES																	
TCGA-CV-A465-10A-01D-A25Y-08	HNSC	WHITE	YES																	
TCGA-IQ-7630-10A-01D-2078-08	HNSC	WHITE	YES																	
TCGA-IQ-A61G-10A-01D-A30H-08	HNSC	WHITE	YES																	
TCGA-IQ-A61H-10A-01D-A30H-08	HNSC	WHITE	YES																	
TCGA-IQ-A61L-10A-01D-A30H-08	HNSC	WHITE	YES																	
TCGA-IQ-A61O-10A-01D-A30H-08	HNSC	WHITE	YES																	
TCGA-B8-4151-10A-01D-1251-10	KIRC	WHITE	YES																	
TCGA-AT-A5NU-10A-01D-A28G-10	KIRP	WHITE	YES																	
TCGA-MH-A561-10A-01D-A26P-10	KIRP	WHITE	YES																	
TCGA-DH-5141-10A-01D-1468-08	LGG	WHITE	YES																	
TCGA-FG-8186-10A-01D-2253-08	LGG	WHITE	YES																	
TCGA-FG-A4MY-10A-01D-A26K-08	LGG	WHITE	YES																	
TCGA-HT-7473-10A-01D-2024-08	LGG	WHITE	YES																	
TCGA-HT-7476-10A-01D-2024-08	LGG	WHITE	YES																	
TCGA-HT-7680-10A-01D-2253-08	LGG	WHITE	YES																	
TCGA-HT-7882-10A-01D-2396-08	LGG	WHITE	YES																	
TCGA-HT-8010-10A-01D-2396-08	LGG	WHITE	YES																	
TCGA-HT-8109-10A-01D-2396-08	LGG	WHITE	YES																	
TCGA-HT-8564-10A-01D-2396-08	LGG	WHITE	YES																	
TCGA-HT-A5R5-10A-01D-A289-08	LGG	WHITE	YES																	
TCGA-HT-A5RB-10A-01D-A289-08	LGG	WHITE	YES																	
TCGA-IK-7675-10A-01D-2086-08	LGG	WHITE	YES																	
TCGA-R8-A6ML-10A-01D-A329-08	LGG	WHITE	YES																	
TCGA-BW-A5NP-10A-01D-A27I-10	LIHC	WHITE	YES																	
TCGA-DD-A4NQ-10A-01D-A28X-10	LIHC	WHITE	YES																	
TCGA-44-2666-10A-01D-A271-08	LUAD	WHITE	YES																	
TCGA-44-6775-10A-01D-1855-08	LUAD	WHITE	YES																	
TCGA-44-7670-10A-01D-2063-08	LUAD	WHITE	YES																	
TCGA-53-7624-10A-01D-2063-08	LUAD	WHITE	YES																	
TCGA-53-A4EZ-10A-01D-A24P-08	LUAD	WHITE	YES																	
TCGA-69-8255-10A-01D-2284-08	LUAD	WHITE	YES																	
TCGA-86-7711-10A-01D-2063-08	LUAD	WHITE	YES																	
TCGA-52-7622-10A-01D-2122-08	LUSC	WHITE	YES																	
TCGA-52-7811-10A-01D-2122-08	LUSC	WHITE	YES																	
TCGA-52-7812-10A-01D-2122-08	LUSC	WHITE	YES																	
TCGA-68-8251-10A-01D-2293-08	LUSC	WHITE	YES																	
TCGA-13-2066-10A-01D-1526-09	OV	WHITE	YES																	
TCGA-23-1110-10A-01D-0428-01	OV	WHITE	YES																	
TCGA-29-2434-10A-01D-1526-09	OV	WHITE	YES																	
TCGA-BF-A3DN-10A-01D-A20D-08	SKCM	WHITE	YES																	
TCGA-D3-A3BZ-10A-01D-A198-08	SKCM	WHITE	YES																	
TCGA-D3-A51K-10A-01D-A25O-08	SKCM	WHITE	YES																	
TCGA-D3-A5GT-10A-01D-A30X-08	SKCM	WHITE	YES																	
TCGA-FS-A1ZZ-10A-01D-A199-08	SKCM	WHITE	YES																	
TCGA-IH-A3EA-10A-01D-A20D-08	SKCM	WHITE	YES																	
TCGA-F1-A448-10A-01D-A24F-08	STAD	WHITE	YES																	
TCGA-FP-7998-10A-01D-2201-08	STAD	WHITE	YES																	
TCGA-R5-A7O7-10A-01D-A33W-08	STAD	WHITE	YES																	
TCGA-DE-A4MB-10A-01D-A25A-08	THCA	WHITE	YES																	
TCGA-DJ-A13S-10A-01D-A10S-08	THCA	WHITE	YES																	
TCGA-DJ-A2PT-10A-01D-A18F-08	THCA	WHITE	YES																	
TCGA-DJ-A3UT-10A-01D-A22D-08	THCA	WHITE	YES																	
TCGA-DJ-A3VD-10A-01D-A23K-08	THCA	WHITE	YES																	
TCGA-EL-A3CM-10A-01D-A19M-08	THCA	WHITE	YES																	
TCGA-EL-A3CV-10A-01D-A19M-08	THCA	WHITE	YES																	

sample	group	race	hispanic	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
TCGA-EL-A3CX-10A-01D-A19M-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	0	0	0	0	0	1	1	1
TCGA-EL-A3D6-10A-01D-A202-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	1	1	1	0	1	1	0	1
TCGA-EL-A3GO-10A-01D-A202-08	THCA	WHITE	YES	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	1	1
TCGA-EL-A3GS-10A-01D-A20C-08	THCA	WHITE	YES	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	1	1
TCGA-EL-A3GW-10A-01D-A202-08	THCA	WHITE	YES	1	1	1	0	1	1	1	1	1	1	1	0	1	1	0	1	1
TCGA-ET-A39R-10A-01D-A19M-08	THCA	WHITE	YES	1	1	1	1	1	1	1	1	1	1	1	0	1	1	0	1	1
TCGA-ET-A3BP-10A-01D-A19M-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	1	1	0	1	1	0	1	1
TCGA-ET-A3BX-10A-01D-A19M-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	0	0	0	0	0	0	1	1
TCGA-FY-A3ON-10A-01D-A21Z-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	0	0	0	0	0	1	1	1
TCGA-FY-A4B3-10A-01D-A23U-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	1	0	0	0	0	1	1	1
TCGA-H2-A421-10A-01D-A23K-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	0	0	0	0	1	1	1	1
TCGA-IM-A3EB-10A-01D-A202-08	THCA	WHITE	YES	1	1	1	1	1	1	1	1	1	0	1	1	0	0	0	1	1
TCGA-IM-A3ED-10A-01D-A202-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	0	0	0	0	0	1	1	1
TCGA-IM-A3U2-10A-01D-A22D-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	0	0	0	0	0	0	1	1
TCGA-IM-A3U3-10A-01D-A22D-08	THCA	WHITE	YES	1	1	1	1	1	1	1	1	1	0	1	1	0	0	1	1	1
TCGA-IM-A41Y-10A-01D-A23U-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	0	0	0	0	0	0	1	1
TCGA-IM-A41Z-10A-01D-A23K-08	THCA	WHITE	YES	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1
TCGA-IM-A420-10A-01D-A23K-08	THCA	WHITE	YES	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1
TCGA-IM-A4EB-10A-01D-A25A-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	0	0	0	0	0	1	1	1
TCGA-J8-A3O1-10A-01D-A21A-08	THCA	WHITE	YES	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	0	1
TCGA-J8-A4HY-10A-01D-A25A-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1
TCGA-MK-A4N6-10A-01D-A25A-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	1	1	0	1	1	1	0	1
TCGA-MK-A4N7-10A-01D-A25A-08	THCA	WHITE	YES	1	0	0	1	1	1	1	1	1	1	1	0	1	1	1	0	1
TCGA-MK-A4N9-10A-01D-A25A-08	THCA	WHITE	YES	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	0	1
TCGA-A5-A0R6-10A-01D-A10B-09	UCEC	WHITE	YES	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	1	1
TCGA-AJ-A2QK-10A-01D-A18P-09	UCEC	WHITE	YES	1	1	1	0	1	1	1	1	1	1	1	1	0	1	1	0	1
TCGA-AX-A2HG-10A-01D-A17D-09	UCEC	WHITE	YES	1	1	1	0	0	0	1	1	1	0	0	0	0	0	0	1	1
TCGA-D1-A179-10A-01D-A12J-09	UCEC	WHITE	YES	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
TCGA-EO-A3KX-10A-01D-A22A-09	UCEC	WHITE	YES	1	0	0	1	1	1	1	1	1	1	1	0	1	1	0	1	1
TCGA-EY-A1GW-10A-01D-A13O-09	UCEC	WHITE	YES	1	1	1	0	1	1	1	1	1	0	1	1	0	0	0	1	1
TCGA-KJ-A3U4-10A-01D-A22A-09	UCEC	WHITE	YES	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	1	1

Table A10a Unique KIR genotypes for the TCGA samples, European cohort

kirTypeID	count	freq	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
1	689	0.186																	
2	355	0.096																	
3	324	0.088																	
4	258	0.070																	
5	242	0.065																	
6	154	0.042																	
7	136	0.037																	
8	126	0.034																	
9	121	0.033																	
10	112	0.030																	
11	96	0.026																	
12	59	0.016																	
13	50	0.014																	
14	49	0.013																	
15	49	0.013																	
16	47	0.013																	
17	44	0.012																	
18	40	0.011																	
19	40	0.011																	
20	39	0.011																	
21	37	0.010																	
22	37	0.010																	
23	36	0.010																	
24	34	0.009																	
25	28	0.008																	
26	26	0.007																	
27	23	0.006																	
28	23	0.006																	
29	22	0.006																	
30	19	0.005																	
31	19	0.005																	
32	19	0.005																	
33	18	0.005																	
34	18	0.005																	
35	16	0.004																	
36	16	0.004																	
37	15	0.004																	
38	14	0.004																	
39	13	0.004																	
40	10	0.003																	
41	9	0.002																	
42	9	0.002																	
43	8	0.002																	
44	6	0.002																	
45	6	0.002																	
46	6	0.002																	
47	6	0.002																	
48	6	0.002																	
49	6	0.002																	
50	5	0.001																	
51	5	0.001																	
52	5	0.001																	
53	5	0.001																	
54	5	0.001																	
55	4	0.001																	
56	4	0.001																	
57	4	0.001																	
58	4	0.001																	
59	4	0.001																	
60	4	0.001																	
61	4	0.001																	
62	3	0.001																	
63	3	0.001																	
64	3	0.001																	
65	3	0.001																	
66	3	0.001																	
67	3	0.001																	
68	3	0.001																	
69	3	0.001																	
70	3	0.001																	
71	3	0.001																	
72	3	0.001																	
73	3	0.001																	
74	2	0.001																	
75	2	0.001																	
76	2	0.001																	
77	2	0.001																	
78	2	0.001																	

kirTypeID	count	freq	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
79	2	0.001																	
80	2	0.001																	
81	2	0.001																	
82	2	0.001																	
83	2	0.001																	
84	2	0.001																	
85	2	0.001																	
86	2	0.001																	
87	1	0.000																	
88	1	0.000																	
89	1	0.000																	
90	1	0.000																	
91	1	0.000																	
92	1	0.000																	
93	1	0.000																	
94	1	0.000																	
95	1	0.000																	
96	1	0.000																	
97	1	0.000																	
98	1	0.000																	
99	1	0.000																	
100	1	0.000																	
101	1	0.000																	
102	1	0.000																	
103	1	0.000																	
104	1	0.000																	
105	1	0.000																	
106	1	0.000																	
107	1	0.000																	
108	1	0.000																	
109	1	0.000																	
110	1	0.000																	
111	1	0.000																	
112	1	0.000																	
113	1	0.000																	
114	1	0.000																	
115	1	0.000																	
116	1	0.000																	
117	1	0.000																	
118	1	0.000																	
119	1	0.000																	
120	1	0.000																	
121	1	0.000																	
122	1	0.000																	
123	1	0.000																	
124	1	0.000																	
125	1	0.000																	
126	1	0.000																	
127	1	0.000																	
128	1	0.000																	
129	1	0.000																	
130	1	0.000																	
131	1	0.000																	
132	1	0.000																	
133	1	0.000																	
134	1	0.000																	
135	1	0.000																	
136	1	0.000																	
137	1	0.000																	
138	1	0.000																	

Table A10b Unique KIR genotypes for the TCGA samples, African cohort

kirTypeID	count	freq	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
1	66	0.177																	
2	40	0.107																	
3	26	0.070																	
4	25	0.067																	
5	15	0.040																	
6	14	0.038																	
7	11	0.029																	
8	10	0.027																	
9	10	0.027																	
10	10	0.027																	
11	9	0.024																	
12	8	0.021																	
13	8	0.021																	
14	7	0.019																	
15	7	0.019																	
16	6	0.016																	
17	5	0.013																	
18	5	0.013																	
19	4	0.011																	
20	4	0.011																	
21	4	0.011																	
22	3	0.008																	
23	3	0.008																	
24	3	0.008																	
25	3	0.008																	
26	3	0.008																	
27	3	0.008																	
28	3	0.008																	
29	3	0.008																	
30	3	0.008																	
31	3	0.008																	
32	2	0.005																	
33	2	0.005																	
34	2	0.005																	
35	2	0.005																	
36	2	0.005																	
37	2	0.005																	
38	2	0.005																	
39	1	0.003																	
40	1	0.003																	
41	1	0.003																	
42	1	0.003																	
43	1	0.003																	
44	1	0.003																	
45	1	0.003																	
46	1	0.003																	
47	1	0.003																	
48	1	0.003																	
49	1	0.003																	
50	1	0.003																	
51	1	0.003																	
52	1	0.003																	
53	1	0.003																	
54	1	0.003																	
55	1	0.003																	
56	1	0.003																	
57	1	0.003																	
58	1	0.003																	
59	1	0.003																	
60	1	0.003																	
61	1	0.003																	
62	1	0.003																	
63	1	0.003																	
64	1	0.003																	
65	1	0.003																	
66	1	0.003																	
67	1	0.003																	
68	1	0.003																	
69	1	0.003																	
70	1	0.003																	
71	1	0.003																	
72	1	0.003																	
73	1	0.003																	

Table A10c Unique KIR genotypes for the TCGA samples, Asian cohort

kirTypeID	count	freq	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4FUNC	2DS4DEL	3DL2
1	63	0.196																	
2	53	0.165																	
3	24	0.075																	
4	23	0.072																	
5	18	0.056																	
6	15	0.047																	
7	14	0.044																	
8	9	0.028																	
9	6	0.019																	
10	6	0.019																	
11	5	0.016																	
12	5	0.016																	
13	5	0.016																	
14	5	0.016																	
15	4	0.012																	
16	4	0.012																	
17	4	0.012																	
18	3	0.009																	
19	3	0.009																	
20	3	0.009																	
21	2	0.006																	
22	2	0.006																	
23	2	0.006																	
24	2	0.006																	
25	2	0.006																	
26	2	0.006																	
27	2	0.006																	
28	2	0.006																	
29	2	0.006																	
30	1	0.003																	
31	1	0.003																	
32	1	0.003																	
33	1	0.003																	
34	1	0.003																	
35	1	0.003																	
36	1	0.003																	
37	1	0.003																	
38	1	0.003																	
39	1	0.003																	
40	1	0.003																	
41	1	0.003																	
42	1	0.003																	
43	1	0.003																	
44	1	0.003																	
45	1	0.003																	
46	1	0.003																	
47	1	0.003																	
48	1	0.003																	
49	1	0.003																	
50	1	0.003																	
51	1	0.003																	
52	1	0.003																	
53	1	0.003																	
54	1	0.003																	
55	1	0.003																	
56	1	0.003																	
57	1	0.003																	
58	1	0.003																	
59	1	0.003																	
60	1	0.003																	

Table A11a Chi square significance tests for KIR genotypes within the TCGA samples, European cohort

kirTypeID	group1	group2	group1 kirTypeAbsent ObservedCount	group1 kirTypePresent ObservedCount	group2 kirTypeAbsent ObservedCount	group2 kirTypePresent ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
1	OKG	PRAD	334	64	97	35	1.880	1.180	3.010	1.12E-02	5.95E-04	1
4	OKG	PRAD	365	33	129	3	0.257	0.078	0.852	2.91E-02	1.19E-03	2
1	OKG	KIRP	334	64	48	18	1.960	1.070	3.590	4.20E-02	1.79E-03	3
4	OKG	LUSC	365	33	192	7	0.403	0.175	0.928	4.28E-02	2.38E-03	4
4	OKG	STAD	365	33	166	6	0.400	0.164	0.973	5.69E-02	2.98E-03	5
9	OKG	BRCA	388	10	430	24	2.170	1.020	4.600	5.90E-02	3.57E-03	6
4	OKG	COAD	365	33	143	5	0.387	0.148	1.010	6.93E-02	4.17E-03	7
2	OKG	BLCA	352	46	159	11	0.529	0.267	1.050	9.00E-02	4.76E-03	8
6	OKG	STAD	384	14	160	12	2.060	0.932	4.550	1.10E-01	5.36E-03	9
1	OKG	SKCM	334	64	274	72	1.370	0.944	1.990	1.17E-01	5.95E-03	10
5	OKG	COAD	368	30	143	5	0.429	0.163	1.130	1.17E-01	6.55E-03	11
1	OKG	COAD	334	64	115	33	1.500	0.937	2.400	1.18E-01	7.14E-03	12
2	OKG	STAD	352	46	160	12	0.574	0.296	1.110	1.31E-01	7.74E-03	13
8	OKG	BRCA	379	19	442	12	0.542	0.260	1.130	1.41E-01	8.33E-03	14
1	OKG	LGG	334	64	255	66	1.350	0.923	1.980	1.46E-01	8.93E-03	15
2	OKG	LGG	352	46	295	26	0.674	0.407	1.120	1.58E-01	9.52E-03	16
9	OKG	HNSC	388	10	328	16	1.890	0.846	4.220	1.68E-01	1.01E-02	17
8	OKG	SKCM	379	19	337	9	0.533	0.238	1.190	1.74E-01	1.07E-02	18
6	OKG	LUAD	384	14	260	4	0.422	0.137	1.300	1.91E-01	1.13E-02	19
4	OKG	CESC	365	33	82	3	0.405	0.121	1.350	1.97E-01	1.19E-02	20
3	OKG	STAD	358	40	161	11	0.611	0.306	1.220	2.14E-01	1.25E-02	21
13	OKG	BRCA	395	3	445	9	2.660	0.715	9.890	2.20E-01	1.31E-02	22
10	OKG	LGG	385	13	316	5	0.469	0.165	1.330	2.23E-01	1.37E-02	23
3	OKG	COAD	358	40	127	21	1.480	0.841	2.610	2.26E-01	1.43E-02	24
8	OKG	COAD	379	19	145	3	0.413	0.120	1.420	2.28E-01	1.49E-02	25
2	OKG	THCA	352	46	213	19	0.683	0.390	1.200	2.28E-01	1.55E-02	26
7	OKG	BRCA	386	12	432	22	1.640	0.801	3.360	2.35E-01	1.61E-02	27
2	OKG	SKCM	352	46	316	30	0.726	0.447	1.180	2.40E-01	1.67E-02	28
5	OKG	LUAD	368	30	251	13	0.635	0.325	1.240	2.40E-01	1.73E-02	29
8	OKG	LGG	379	19	312	9	0.575	0.257	1.290	2.45E-01	1.79E-02	30
8	OKG	THCA	379	19	226	6	0.530	0.209	1.350	2.52E-01	1.85E-02	31
1	OKG	HNSC	334	64	277	67	1.260	0.864	1.840	2.66E-01	1.91E-02	32
1	OKG	LUSC	334	64	159	40	1.310	0.845	2.030	2.69E-01	1.96E-02	33
9	OKG	STAD	388	10	164	8	1.890	0.733	4.870	2.80E-01	2.02E-02	34
6	OKG	BLCA	384	14	160	10	1.710	0.744	3.930	2.91E-01	2.08E-02	35
4	OKG	GBM	365	33	191	24	1.390	0.799	2.420	3.07E-01	2.14E-02	36
8	OKG	PRAD	379	19	129	3	0.464	0.135	1.590	3.19E-01	2.20E-02	37
3	OKG	CESC	358	40	80	5	0.559	0.214	1.460	3.20E-01	2.26E-02	38
2	OKG	LUSC	352	46	182	17	0.715	0.399	1.280	3.23E-01	2.32E-02	39
6	OKG	HNSC	384	14	326	18	1.510	0.740	3.080	3.34E-01	2.38E-02	40
9	OKG	LUAD	388	10	261	3	0.446	0.122	1.640	3.35E-01	2.44E-02	41
3	OKG	BRCA	358	40	418	36	0.771	0.481	1.240	3.36E-01	2.50E-02	42
1	OKG	SARC	334	64	63	17	1.410	0.775	2.570	3.36E-01	2.56E-02	43
4	OKG	LUAD	365	33	248	16	0.714	0.385	1.330	3.57E-01	2.62E-02	44
4	OKG	SKCM	365	33	324	22	0.751	0.429	1.310	3.87E-01	2.68E-02	45
3	OKG	LUSC	358	40	184	15	0.730	0.393	1.360	3.95E-01	2.74E-02	46
11	OKG	UCEC	387	11	218	3	0.484	0.134	1.750	3.98E-01	2.80E-02	47
11	OKG	LGG	387	11	316	5	0.557	0.192	1.620	4.03E-01	2.86E-02	48
3	OKG	LIHC	358	40	51	3	0.526	0.157	1.760	4.18E-01	2.92E-02	49
10	OKG	PRAD	385	13	125	7	1.660	0.648	4.250	4.23E-01	2.98E-02	50
6	OKG	THCA	384	14	220	12	1.500	0.682	3.300	4.24E-01	3.04E-02	51
8	OKG	STAD	379	19	167	5	0.597	0.219	1.630	4.29E-01	3.10E-02	52
9	OKG	LUSC	388	10	191	8	1.630	0.633	4.200	4.46E-01	3.16E-02	53
8	OKG	LUAD	379	19	247	17	1.370	0.698	2.690	4.53E-01	3.21E-02	54
3	OKG	PRAD	358	40	115	17	1.320	0.721	2.420	4.55E-01	3.27E-02	55
1	OKG	LIHC	334	64	48	6	0.652	0.268	1.590	4.55E-01	3.33E-02	56
2	OKG	HNSC	352	46	311	33	0.812	0.506	1.300	4.56E-01	3.39E-02	57
7	OKG	UCEC	386	12	211	10	1.520	0.646	3.580	4.56E-01	3.45E-02	58
8	OKG	UCEC	379	19	214	7	0.652	0.270	1.580	4.56E-01	3.51E-02	59
3	OKG	GBM	358	40	198	17	0.768	0.424	1.390	4.68E-01	3.57E-02	60
1	OKG	CESC	334	64	68	17	1.300	0.717	2.360	4.73E-01	3.63E-02	61
4	OKG	BRCA	365	33	423	31	0.811	0.487	1.350	4.98E-01	3.69E-02	62
5	OKG	PRAD	368	30	125	7	0.687	0.294	1.600	4.99E-01	3.75E-02	63
19	OKG	LGG	393	5	314	7	1.750	0.550	5.570	5.03E-01	3.81E-02	64
3	OKG	SKCM	358	40	317	29	0.819	0.496	1.350	5.12E-01	3.87E-02	65
3	OKG	HNSC	358	40	315	29	0.824	0.499	1.360	5.28E-01	3.93E-02	66
3	OKG	READ	358	40	57	4	0.628	0.216	1.820	5.29E-01	3.99E-02	67
15	OKG	UCEC	390	8	214	7	1.590	0.569	4.440	5.32E-01	4.05E-02	68
5	OKG	HNSC	368	30	323	21	0.798	0.448	1.420	5.33E-01	4.11E-02	69
6	OKG	SKCM	384	14	330	16	1.330	0.640	2.770	5.63E-01	4.17E-02	70
10	OKG	SKCM	385	13	331	15	1.340	0.629	2.860	5.68E-01	4.23E-02	71
7	OKG	SKCM	386	12	332	14	1.360	0.620	2.980	5.73E-01	4.29E-02	72
1	OKG	UCEC	334	64	190	31	0.851	0.535	1.350	5.74E-01	4.35E-02	73
24	OKG	BRCA	393	5	445	9	1.590	0.528	4.780	5.74E-01	4.41E-02	74
2	OKG	READ	352	46	56	5	0.683	0.260	1.790	5.76E-01	4.46E-02	75
9	OKG	SKCM	388	10	334	12	1.390	0.593	3.260	5.82E-01	4.52E-02	76
4	OKG	THCA	365	33	209	23	1.220	0.698	2.130	5.86E-01	4.58E-02	77
2	OKG	GBM	352	46	194	21	0.828	0.480	1.430	5.88E-01	4.64E-02	78
10	OKG	BRCA	385	13	443	11	0.735	0.326	1.660	5.93E-01	4.70E-02	79
5	OKG	BLCA	368	30	160	10	0.767	0.366	1.610	5.98E-01	4.76E-02	80
17	OKG	BRCA	391	7	449	5	0.622	0.196	1.980	6.02E-01	4.82E-02	81
3	OKG	BLCA	358	40	156	14	0.803	0.425	1.520	6.04E-01	4.88E-02	82
1	OKG	BLCA	334	64	139	31	1.160	0.723	1.860	6.12E-01	4.94E-02	83
9	OKG	LGG	388	10	310	11	1.380	0.579	3.290	6.16E-01	5.00E-02	84
3	OKG	LGG	358	40	293	28	0.855	0.515	1.420	6.34E-01	5.06E-02	85
3	OKG	UCEC	358	40	202	19	0.842	0.475	1.490	6.55E-01	5.12E-02	86

kirTypeID	group1	group2	group1 kirTypeAbsent ObservedCount	group1 kirTypePresent ObservedCount	group2 kirTypeAbsent ObservedCount	group2 kirTypePresent ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
1	OKG	ACC	334	64	27	7	1.350	0.564	3.230	6.60E-01	5.18E-02	87
9	OKG	THCA	388	10	224	8	1.390	0.541	3.570	6.66E-01	5.24E-02	88
1	OKG	BRCA	334	64	375	79	1.100	0.767	1.580	6.73E-01	5.30E-02	89
7	OKG	LUSC	386	12	191	8	1.350	0.543	3.360	6.88E-01	5.36E-02	90
5	OKG	UCEC	368	30	207	14	0.830	0.430	1.600	6.93E-01	5.42E-02	91
4	OKG	SARC	365	33	75	5	0.737	0.279	1.950	6.97E-01	5.48E-02	92
2	OKG	PRAD	352	46	119	13	0.836	0.437	1.600	7.03E-01	5.54E-02	93
2	OKG	KIRP	352	46	60	6	0.765	0.313	1.870	7.06E-01	5.60E-02	94
6	OKG	LUSC	384	14	190	9	1.300	0.553	3.060	7.07E-01	5.66E-02	95
17	OKG	SKCM	391	7	342	4	0.653	0.190	2.250	7.08E-01	5.71E-02	96
2	OKG	KIRC	352	46	48	8	1.280	0.570	2.870	7.11E-01	5.77E-02	97
7	OKG	THCA	386	12	223	9	1.300	0.539	3.130	7.24E-01	5.83E-02	98
7	OKG	HNSC	386	12	336	8	0.766	0.309	1.900	7.26E-01	5.89E-02	99
5	OKG	THCA	368	30	217	15	0.848	0.446	1.610	7.31E-01	5.95E-02	100
10	OKG	BLCA	385	13	166	4	0.714	0.229	2.220	7.52E-01	6.01E-02	101
5	OKG	GBM	368	30	201	14	0.854	0.443	1.650	7.60E-01	6.07E-02	102
10	OKG	HNSC	385	13	335	9	0.796	0.336	1.890	7.61E-01	6.13E-02	103
15	OKG	HNSC	390	8	339	5	0.719	0.233	2.220	7.67E-01	6.19E-02	104
3	OKG	KIRP	358	40	58	8	1.230	0.548	2.760	7.69E-01	6.25E-02	105
5	OKG	LUSC	368	30	186	13	0.857	0.437	1.680	7.80E-01	6.31E-02	106
4	OKG	BLCA	365	33	154	16	1.150	0.615	2.150	7.85E-01	6.37E-02	107
18	OKG	SKCM	392	6	339	7	1.350	0.449	4.060	7.99E-01	6.43E-02	108
11	OKG	THCA	387	11	224	8	1.260	0.499	3.180	8.08E-01	6.49E-02	109
10	OKG	LUSC	385	13	191	8	1.240	0.505	3.040	8.14E-01	6.55E-02	110
10	OKG	STAD	385	13	165	7	1.260	0.494	3.220	8.18E-01	6.61E-02	111
9	OKG	UCEC	388	10	214	7	1.270	0.477	3.380	8.25E-01	6.67E-02	112
8	OKG	LUSC	379	19	191	8	0.835	0.359	1.940	8.35E-01	6.73E-02	113
2	OKG	SARC	352	46	72	8	0.850	0.385	1.880	8.35E-01	6.79E-02	114
7	OKG	LGG	386	12	313	8	0.822	0.332	2.040	8.45E-01	6.85E-02	115
5	OKG	SKCM	368	30	322	24	0.914	0.524	1.600	8.62E-01	6.91E-02	116
6	OKG	BRCA	384	14	440	14	0.873	0.411	1.850	8.71E-01	6.96E-02	117
11	OKG	SKCM	387	11	338	8	0.833	0.331	2.100	8.76E-01	7.02E-02	118
1	OKG	OV	334	64	31	7	1.180	0.498	2.800	8.86E-01	7.08E-02	119
10	OKG	UCEC	385	13	215	6	0.826	0.310	2.200	8.90E-01	7.14E-02	120
6	OKG	UCEC	384	14	212	9	1.160	0.494	2.720	8.98E-01	7.20E-02	121
4	OKG	UCEC	365	33	204	17	0.922	0.501	1.700	9.14E-01	7.26E-02	122
1	OKG	STAD	334	64	143	29	1.060	0.656	1.710	9.14E-01	7.32E-02	123
2	OKG	LUAD	352	46	232	32	1.060	0.655	1.710	9.23E-01	7.38E-02	124
2	OKG	COAD	352	46	132	16	0.928	0.508	1.700	9.26E-01	7.44E-02	125
8	OKG	HNSC	379	19	329	15	0.909	0.455	1.820	9.26E-01	7.50E-02	126
4	OKG	HNSC	365	33	317	27	0.942	0.554	1.600	9.32E-01	7.56E-02	127
1	OKG	LUAD	334	64	223	41	0.960	0.626	1.470	9.35E-01	7.62E-02	128
10	OKG	GBM	385	13	209	6	0.850	0.318	2.270	9.36E-01	7.68E-02	129
1	OKG	READ	334	64	52	9	0.903	0.424	1.920	9.40E-01	7.74E-02	130
4	OKG	LGG	365	33	293	28	1.060	0.626	1.790	9.43E-01	7.80E-02	131
11	OKG	GBM	387	11	210	5	0.838	0.287	2.440	9.53E-01	7.86E-02	132
7	OKG	LUAD	386	12	255	9	1.140	0.474	2.740	9.55E-01	7.92E-02	133
5	OKG	LGG	368	30	298	23	0.947	0.539	1.660	9.63E-01	7.98E-02	134
2	OKG	BRCA	352	46	403	51	0.968	0.634	1.480	9.68E-01	8.04E-02	135
14	OKG	HNSC	391	7	339	5	0.824	0.259	2.620	9.71E-01	8.10E-02	136
7	OKG	STAD	386	12	166	6	1.160	0.428	3.140	9.72E-01	8.16E-02	137
6	OKG	COAD	384	14	143	5	0.959	0.339	2.710	1.00E+00	8.21E-02	138
11	OKG	LUAD	387	11	257	7	0.958	0.367	2.500	1.00E+00	8.27E-02	139
8	OKG	BLCA	379	19	162	8	0.985	0.423	2.300	1.00E+00	8.27E-02	139
11	OKG	LUSC	387	11	194	5	0.907	0.311	2.650	1.00E+00	8.33E-02	140
10	OKG	LUAD	385	13	255	9	1.050	0.442	2.490	1.00E+00	8.33E-02	140
4	OKG	KIRP	365	33	61	5	0.907	0.341	2.410	1.00E+00	8.33E-02	140
11	OKG	HNSC	387	11	334	10	1.050	0.440	2.500	1.00E+00	8.33E-02	140
6	OKG	LGG	384	14	310	11	0.973	0.436	2.170	1.00E+00	8.39E-02	141
10	OKG	THCA	385	13	224	8	1.060	0.433	2.600	1.00E+00	8.45E-02	142
2	OKG	UCEC	352	46	195	26	1.020	0.611	1.700	1.00E+00	8.51E-02	143
5	OKG	STAD	368	30	159	13	1.000	0.508	1.970	1.00E+00	8.51E-02	143
8	OKG	GBM	379	19	204	11	1.080	0.504	2.310	1.00E+00	8.57E-02	144
2	OKG	LIHC	352	46	48	6	0.957	0.388	2.360	1.00E+00	8.63E-02	145
2	OKG	CESC	352	46	75	10	1.020	0.493	2.110	1.00E+00	8.63E-02	145
3	OKG	THCA	358	40	209	23	0.985	0.574	1.690	1.00E+00	8.63E-02	145
5	OKG	SARC	368	30	74	6	0.995	0.400	2.480	1.00E+00	8.63E-02	145
1	OKG	GBM	334	64	180	35	1.010	0.644	1.580	1.00E+00	8.69E-02	146
5	OKG	BRCA	368	30	420	34	0.993	0.596	1.650	1.00E+00	8.69E-02	146
1	OKG	THCA	334	64	194	38	1.020	0.658	1.580	1.00E+00	8.69E-02	146
6	OKG	GBM	384	14	207	8	1.060	0.437	2.570	1.00E+00	8.75E-02	147
7	OKG	GBM	386	12	209	6	0.923	0.341	2.490	1.00E+00	8.75E-02	147
3	OKG	LUAD	358	40	238	26	0.978	0.581	1.650	1.00E+00	8.75E-02	147
15	OKG	LUAD	390	8	258	6	1.130	0.388	3.290	1.00E+00	8.75E-02	147
11	OKG	BRCA	387	11	442	12	0.955	0.417	2.190	1.00E+00	8.75E-02	147
14	OKG	BRCA	391	7	446	8	1.000	0.359	2.780	1.00E+00	8.75E-02	147
15	OKG	BRCA	390	8	445	9	0.986	0.377	2.580	1.00E+00	8.75E-02	147
3	OKG	KIRC	358	40	50	6	1.070	0.432	2.650	1.00E+00	8.75E-02	147
1	OKG	KIRC	334	64	47	9	0.999	0.466	2.140	1.00E+00	8.75E-02	147
14	OKG	SKCM	391	7	340	6	0.986	0.328	2.960	1.00E+00	8.75E-02	147
5	OKG	CESC	368	30	79	6	0.932	0.375	2.310	1.00E+00	8.75E-02	147
3	OKG	SARC	358	40	72	8	0.994	0.447	2.210	1.00E+00	8.75E-02	147

Table A11b Chi square significance tests for KIR genotypes within the TCGA samples, African cohort

kirTypeID	group1	group2	group1 kirTypeAbsent ObservedCount	group1 kirTypePresent ObservedCount	group2 kirTypeAbsent ObservedCount	group2 kirTypePresent ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
1	OKG	UCEC	589	77	35	11	2.400	1.170	4.920	2.57E-02	1.43E-02	1
2	OKG	KIRP	544	122	32	3	0.418	0.126	1.390	2.14E-01	2.86E-02	2
1	OKG	BRCA	589	77	77	15	1.490	0.816	2.720	2.56E-01	4.29E-02	3
2	OKG	BRCA	544	122	80	12	0.669	0.354	1.270	2.72E-01	5.71E-02	4
2	OKG	HNSC	544	122	21	6	1.270	0.502	3.210	7.95E-01	7.14E-02	5
4	OKG	BRCA	628	38	86	6	1.150	0.472	2.800	9.39E-01	8.57E-02	6
2	OKG	UCEC	544	122	38	8	0.939	0.427	2.060	1.00E+00	1.00E-01	7

Table A11c Chi square significance tests for KIR genotypes within the TCGA samples, Asian cohort

kirTypeID	group1	group2	group1 kirTypeAbsent ObservedCount	group1 kirTypePresent ObservedCount	group2 kirTypeAbsent ObservedCount	group2 kirTypePresent ObservedCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
1	OKG	THCA	407	103	40	4	0.395	0.138	1.130	1.12E-01	8.33E-03	1
1	OKG	STAD	407	103	60	20	1.320	0.761	2.290	4.03E-01	1.67E-02	2
2	OKG	LIHC	400	110	25	4	0.582	0.198	1.710	4.45E-01	2.50E-02	3
1	OKG	LIHC	407	103	21	8	1.510	0.650	3.510	4.71E-01	3.33E-02	4
2	OKG	THCA	400	110	37	7	0.688	0.299	1.590	4.90E-01	4.17E-02	5
2	OKG	STAD	400	110	65	15	0.839	0.461	1.530	6.70E-01	5.00E-02	6
2	OKG	BLCA	400	110	21	5	0.866	0.319	2.350	9.69E-01	5.83E-02	7
2	OKG	BRCA	400	110	43	11	0.930	0.464	1.860	9.76E-01	6.67E-02	8
3	OKG	BRCA	458	52	48	6	1.100	0.449	2.690	1.00E+00	7.50E-02	9
3	OKG	STAD	458	52	72	8	0.979	0.447	2.150	1.00E+00	8.33E-02	10
1	OKG	BRCA	407	103	43	11	1.010	0.503	2.030	1.00E+00	9.17E-02	11
1	OKG	BLCA	407	103	21	5	0.941	0.347	2.560	1.00E+00	9.17E-02	11

Table A12a Chi square significance tests for KIR variants within the TCGA samples, European cohort, reference homozygous versus heterozygous

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	971	OKG	BRCA	T	C	T/T	T/C	263	49	219	155	3.800	2.630	5.490	3.87E-13	1.14E-04	1
3DL3	971	OKG	HNSC	T	C	T/T	T/C	263	49	309	0	0.000	0.000	NaN	1.16E-12	2.29E-04	2
3DL3	971	OKG	SKCM	T	C	T/T	T/C	263	49	287	0	0.000	0.000	NaN	7.02E-12	3.43E-04	3
3DL3	971	OKG	LGG	T	C	T/T	T/C	263	49	270	0	0.000	0.000	NaN	2.83E-11	4.58E-04	4
3DL3	971	OKG	UCEC	T	C	T/T	T/C	263	49	104	74	3.820	2.490	5.850	4.29E-10	5.72E-04	5
3DL3	971	OKG	LUAD	T	C	T/T	T/C	263	49	224	0	0.000	0.000	NaN	1.27E-09	6.87E-04	6
3DL3	971	OKG	THCA	T	C	T/T	T/C	263	49	199	0	0.000	0.000	NaN	1.03E-08	8.01E-04	7
3DL3	971	OKG	GBM	T	C	T/T	T/C	263	49	195	0	0.000	0.000	NaN	1.44E-08	9.15E-04	8
3DL3	971	OKG	LUSC	T	C	T/T	T/C	263	49	175	0	0.000	0.000	NaN	7.83E-08	1.03E-03	9
3DL3	971	OKG	STAD	T	C	T/T	T/C	263	49	143	0	0.000	0.000	NaN	1.21E-06	1.14E-03	10
3DL3	971	OKG	BLCA	T	C	T/T	T/C	263	49	141	0	0.000	0.000	NaN	1.44E-06	1.26E-03	11
3DL3	971	OKG	PRAD	T	C	T/T	T/C	263	49	117	0	0.000	0.000	NaN	1.16E-05	1.37E-03	12
3DL3	971	OKG	READ	T	C	T/T	T/C	263	49	29	18	3.330	1.720	6.460	4.56E-04	1.49E-03	13
3DL3	971	OKG	SARC	T	C	T/T	T/C	263	49	42	23	2.940	1.630	5.320	4.68E-04	1.60E-03	14
3DL2	394	OKG	UCEC	C	A	C/C	C/A	365	33	216	4	0.205	0.072	0.587	2.14E-03	1.72E-03	15
2DP1	448	OKG	ACC	G	C	G/G	G/C	138	151	19	4	0.192	0.064	0.578	2.69E-03	1.83E-03	16
3DL2	456	OKG	BLCA	C	T	C/C	C/T	348	49	133	37	1.980	1.240	3.170	6.18E-03	1.95E-03	17
3DL2	893	OKG	BLCA	G	A	G/G	G/A	348	49	133	37	1.980	1.240	3.170	6.18E-03	1.95E-03	17
3DL2	456	OKG	LUAD	C	T	C/C	C/T	348	49	209	54	1.830	1.200	2.790	6.36E-03	2.06E-03	18
3DL2	893	OKG	LUAD	G	A	G/G	G/A	348	49	209	54	1.830	1.200	2.790	6.36E-03	2.06E-03	18
3DP1	479	OKG	SKCM	A	C	A/A	A/C	201	176	203	115	0.647	0.477	0.878	6.46E-03	2.17E-03	19
2DL5	583	OKG	KIRC	G	A	G/G	G/A	62	43	17	1	0.085	0.011	0.661	8.57E-03	2.29E-03	20
2DL4	395	OKG	UCEC	C	T	C/C	C/T	355	30	215	5	0.275	0.105	0.719	8.89E-03	2.40E-03	21
2DP1	1313	OKG	GBM	A	C	A/A	A/C	210	112	142	43	0.568	0.377	0.857	8.93E-03	2.52E-03	22
3DL2	456	OKG	COAD	C	T	C/C	C/T	348	49	115	32	1.980	1.210	3.240	9.14E-03	2.63E-03	23
3DL2	893	OKG	COAD	G	A	G/G	G/A	348	49	115	32	1.980	1.210	3.240	9.14E-03	2.63E-03	23
3DL3	408	OKG	LUAD	G	A	G/G	G/A	273	113	153	100	1.580	1.130	2.210	9.25E-03	2.75E-03	24
3DL2	896	OKG	LUAD	C	A	C/C	C/A	392	6	250	14	3.660	1.390	9.650	1.04E-02	2.86E-03	25
3DP1	774	OKG	GBM	G	C	G/G	G/C	234	147	149	57	0.609	0.421	0.880	1.05E-02	2.98E-03	26
3DP1	479	OKG	PRAD	A	C	A/A	A/C	201	176	75	36	0.548	0.351	0.856	1.07E-02	3.09E-03	27
3DL3	869	OKG	UCEC	A	C	A/A	A/C	307	84	148	67	1.650	1.130	2.400	1.12E-02	3.20E-03	28
3DL3	408	OKG	OV	G	A	G/G	G/A	273	113	17	18	2.560	1.270	5.150	1.17E-02	3.32E-03	29
3DL2	394	OKG	COAD	C	A	C/C	C/A	365	33	144	3	0.230	0.069	0.762	1.58E-02	3.43E-03	30
2DP1	471	OKG	STAD	A	G	A/A	A/G	292	64	108	42	1.770	1.130	2.770	1.59E-02	3.55E-03	31
2DL5	517	OKG	COAD	A	G	A/A	A/G	81	44	43	8	0.342	0.148	0.792	1.68E-02	3.66E-03	32
3DL3	971	OKG	CESC	T	C	T/T	T/C	263	49	50	20	2.150	1.180	3.920	1.84E-02	3.78E-03	33
2DL4	395	OKG	LUSC	C	T	C/C	C/T	355	30	193	5	0.307	0.117	0.804	1.87E-02	3.89E-03	34
2DL5	583	OKG	SKCM	G	A	G/G	G/A	62	43	73	24	0.474	0.259	0.867	2.17E-02	4.01E-03	35
3DL2	394	OKG	LUSC	C	A	C/C	C/A	365	33	193	6	0.344	0.142	0.835	2.24E-02	4.12E-03	36
3DL3	455	OKG	THCA	G	A	G/G	G/A	367	31	201	32	1.880	1.110	3.170	2.34E-02	4.23E-03	37
2DP1	448	OKG	THCA	G	C	G/G	G/C	138	151	95	65	0.625	0.423	0.924	2.37E-02	4.35E-03	38
2DL5	517	OKG	KIRC	A	G	A/A	A/G	81	44	17	1	0.108	0.014	0.839	2.38E-02	4.46E-03	39
3DL1	1194	OKG	LUSC	C	T	C/C	C/T	327	22	183	3	0.244	0.072	0.826	2.55E-02	4.58E-03	40
2DP1	1313	OKG	THCA	A	C	A/A	A/C	210	112	154	52	0.633	0.429	0.934	2.68E-02	4.69E-03	41
3DL1	1091	OKG	KIRP	G	A	G/G	G/A	166	53	21	16	2.390	1.160	4.910	2.68E-02	4.81E-03	42
3DL3	971	OKG	LIHC	T	C	T/T	T/C	263	49	23	11	2.570	1.180	5.610	2.81E-02	4.92E-03	43
3DL3	408	OKG	THCA	G	A	G/G	G/A	273	113	137	85	1.500	1.060	2.120	2.83E-02	5.03E-03	44
3DP1	479	OKG	GBM	A	C	A/A	A/C	201	176	127	74	0.665	0.468	0.944	2.83E-02	5.15E-03	45
3DL1	1026	OKG	KIRP	G	C	G/G	G/C	160	52	21	16	2.340	1.140	4.820	3.10E-02	5.26E-03	46
3DL3	408	OKG	LUSC	G	A	G/G	G/A	273	113	113	71	1.520	1.050	2.200	3.34E-02	5.38E-03	47
2DL3	953	OKG	SKCM	G	A	G/G	G/A	144	104	147	69	0.650	0.444	0.952	3.37E-02	5.49E-03	48
2DL5	583	OKG	COAD	G	A	G/G	G/A	62	43	21	4	0.275	0.088	0.858	3.55E-02	5.61E-03	49
3DL2	896	OKG	SKCM	C	A	C/C	C/A	392	6	331	15	2.960	1.140	7.720	3.56E-02	5.72E-03	50
3DL2	893	OKG	SKCM	G	A	G/G	G/A	348	49	281	62	1.570	1.050	2.360	3.80E-02	5.84E-03	51
3DP1	796	OKG	STAD	T	C	T/T	T/C	248	134	122	42	0.637	0.423	0.959	3.84E-02	5.95E-03	52
3DP1	479	OKG	STAD	A	C	A/A	A/C	201	176	105	61	0.663	0.456	0.964	3.97E-02	6.06E-03	53
3DL2	497	OKG	KIRP	G	A	G/G	G/A	327	68	47	19	1.940	1.070	3.510	4.00E-02	6.18E-03	54
3DL3	447	OKG	UCEC	G	T	G/G	G/T	345	50	177	42	1.640	1.050	2.570	4.03E-02	6.29E-03	55
3DL3	961	OKG	READ	C	A	C/C	C/A	118	103	27	10	0.424	0.196	0.918	4.11E-02	6.41E-03	56
2DP1	1062	OKG	UCEC	C	T	C/C	C/T	283	26	195	7	0.391	0.166	0.919	4.12E-02	6.52E-03	57
3DL3	804	OKG	LUAD	G	A	G/G	G/A	228	142	131	116	1.420	1.020	1.970	4.19E-02	6.64E-03	58
2DP1	1313	OKG	COAD	A	C	A/A	A/C	210	112	91	29	0.598	0.371	0.963	4.39E-02	6.75E-03	59
2DL5	583	OKG	SARC	G	A	G/G	G/A	62	43	20	4	0.288	0.092	0.902	4.60E-02	6.87E-03	60
3DP1	479	OKG	READ	A	C	A/A	A/C	201	176	39	18	0.527	0.291	0.955	4.60E-02	6.98E-03	61
3DL2	394	OKG	SARC	C	A	C/C	C/A	365	33	67	13	2.150	1.080	4.300	4.61E-02	7.09E-03	62
3DP1	691	OKG	BLCA	C	T	C/C	C/T	370	24	166	3	0.279	0.083	0.939	4.75E-02	7.21E-03	63
2DL3	953	OKG	STAD	G	A	G/G	G/A	144	104	78	34	0.604	0.376	0.971	4.83E-02	7.32E-03	64
3DL2	456	OKG	SKCM	C	T	C/C	C/T	348	49	282	61	1.540	1.020	2.310	4.87E-02	7.44E-03	65
3DL2	474	OKG	PRAD	G	T	G/G	G/T	258	127	99	30	0.616	0.389	0.976	4.93E-02	7.55E-03	66
2DL3	953	OKG	READ	G	A	G/G	G/A	144	104	29	9	0.430	0.195	0.947	4.94E-02	7.67E-03	67
3DL1	1021	OKG	UCEC	A	G	A/A	A/G	153	14	167	5	0.327	0.115	0.929	5.05E-02	7.78E-03	68
3DL1	1091	OKG	CESC	G	A	G/G	G/A	166	53	40	24	1.880	1.040	3.400	5.20E-02	7.90E-03	69
2DP1	1313	OKG	BRCA	A	C	A/A	A/C	210	112	250	95	0.712	0.512	0.990	5.27E-02	8.01E-03	70
2DP1	1269	OKG	PRAD	A	G	A/A	A/G	350	30	121	3	0.289	0.087	0.964	5.35E-02	8.12E-03	71
2DL4	395	OKG	BRCA	C	T	C/C	C/T	355	30	435	20	0.544	0.304	0.974	5.40E-02	8.24E-03	72
3DL3	971	OKG	COAD	T	C	T/T	T/C	263	49	87	28	1.730	1.020	2.920	5.50E-02	8.35E-03	73
3DL2	394	OKG	LUAD	C	A	C/C	C/A	365	33	252	11	0.483	0.240	0.974	5.55E-02	8.47E-03	74
2DL5	583	OKG	THCA	G	A	G/G	G/A	62	43	61	22	0.520	0.279	0.970	5.57E-02	8.58E-03	75
3DL3	408	OKG	PRAD	G	A	G/G	G/A	273	113	77	49	1.540	1.010	2.340	5.68E-02	8.70E-03	76
3DL1	1021	OKG	BRCA	A	G	A/A	A/G	153	14	342	14	0.447	0.208	0.961	5.75E-02	8.81E-03	77
2DL3	953	OKG	THCA	G	A	G/G	G/A	144	104	97	45	0.642	0.416	0.991	5.80E-02	8.92E-03	78
2DP1	471	OKG	HNSC	A	G	A/A	A/G	292	64	241	77	1.460	1.010	2.120	5.85E-02	9.04E-03	79
3DP1	796	OKG	GBM	T	C	T/T	T/C	248	134	150	56	0.691	0.476	1.000	6.28E-02	9.15E-03	80
3DL3	621	OKG	UCEC	G	A	G/G	G/A	346	49	179	40	1.580	1.000	2.490	6.35E-02	9.27E-03	81
3DP1	479	OKG	HNSC	A	C	A/A	A/C	201	176	189	123	0.743	0.548	1.010	6.62E-02	9.38E-03	82
2DL4	1023	OKG	PRAD	G	A	G/G	G/A	258	128	98	31	0.638	0.404	1.010	6.68E-02	9.50E-03	83
3DL1	1194	OKG	UCEC	C	T	C/C	C/T	327	22	197	5	0.377	0.141	1.010	7.17E-02	9.61E-03	84
2DL4	395	OKG	COAD	C	T	C/C	C/T	355	30	134	4	0.353	0.122	1.020	7.20E-02	9.73E-03	85
3DL2	474	OKG	COAD	G	T	G/G	G/T	258	127	108	35	0.658	0.425	1.020	7.53E-02	9.84E-03	86
3DL1	1021	OKG	LUSC	A	G	A/A	A/G	153	14	93	2	0.235	0.052	1.060	7.64E-02	9.95E-03	87
2DP1	1313	OKG	LUAD	A	C	A/A	A/C	210	112	170	64	0.706	0.489	1.020	7.71E-02	1.01E-02	88
3DL3	777	OKG	LUAD	A	G	A/A	A/G	229	141	135	113	1.360	0.981	1.880	7.79E-02	1.02E-02	89
3DP1	796	OKG	COAD	T	C	T/T	T/C	248	134	79	62	1.450	0.978	2.150	7.80E-02	1.03E-02	90
2DP1	1269	OKG	UCEC	A	G	A/A	A/G	350	30	202	8	0.462	0.208	1.030	7.84E-02	1.04E-02	91
2DP1	448	OKG	BRCA	G	C	G/G	G/C	138	151	175	142	0.742	0.539	1.020	7.97E-02	1.05E-02	92
3DL3	408	OKG	ACC	G	A	G/G	G/A	273	113	18	15	2.010	0.979	4.130	8.19E-02	1.06E-02	93
2DL4	762	OKG	ACC	C	T	C/C	C/T	89	202	12	12	0.441	0.191	1.020	8.34E-02	1.08E-02	94
2DL3	953	OKG	PRAD	G	A	G/G	G/A	144	104	59	26	0.610	0.361	1.030	8.51E-02	1.09E-02	95
2DP1	1313	OKG	LGG	A	C	A/A	A/C	210	112	199	77	0.726	0.512	1.030	8.60E-02	1.10E-02	96
3DP1	774	OKG	STAD	G	C	G/G	G/C	234	147	114	50	0.698	0.472	1.030	8.78E-02	1.11E-02	97
2DL4	395	OKG	LUAD	C	T	C/C	C/T	355	30	252	11	0.517	0.254	1.050	9.12E-02	1.12E-02	98
3DL2	497	OKG	KIRC	G	A	G/G	G/A	327	68	51	4	0.377	0.132	1.080	9.14E-02	1.13E-02	99
3DL3	906	OKG	LUAD	C	T	C/C	C/T	226	143	133	113	1.340	0.967	1.860	9.17E-02	1.14E-02	100
3DL3	777	OKG	OV	A	G	A/A	A/G	229	141	15	18	1.950	0.952	3.990	9.58E-02	1.16E-02	101
3DL1	1194	OKG	BRCA	C	T	C/C	C/T	327	22	414	15	0.539	0.275	1.060	9.68E-02	1.17E-02	102
2DL4	1023	OKG	COAD	G	A	G/G	G/A	258	128	107	36	0.678	0.440	1.050	9.73E-02	1.18E-02	103
2DL5	517	OKG	SKCM	A	G	A/A	A/G	81	44	73	23	0.580	0.320	1.050	9.80E-02	1.19E-02	104
2DP1	1313	OKG	PRAD	A	C	A/A	A/C	210	112	86	30	0.654	0.407	1.050	1.00E-01	1.20E-02	105

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	804	OKG	OV	G	A	G/G	G/A	228	142	15	18	1.930	0.943	3.950	1.02E-01	1.21E-02	106
3DL2	394	OKG	BRCA	C	A	C/C	C/A	365	33	432	24	0.614	0.356	1.060	1.03E-01	1.22E-02	107
3DL1	1026	OKG	COAD	G	C	G/G	G/C	160	52	33	4	0.373	0.126	1.100	1.03E-01	1.24E-02	108
2DP1	448	OKG	OV	G	C	G/G	G/C	138	151	19	10	0.481	0.216	1.070	1.03E-01	1.25E-02	109
3DP1	479	OKG	LGG	A	C	A/A	A/C	201	176	179	120	0.766	0.563	1.040	1.04E-01	1.26E-02	110
2DP1	1313	OKG	KIRC	A	C	A/A	A/C	210	112	39	11	0.529	0.261	1.070	1.04E-01	1.27E-02	111
2DP1	1313	OKG	HNSC	A	C	A/A	A/C	210	112	223	89	0.748	0.534	1.050	1.08E-01	1.28E-02	112
2DP1	1062	OKG	PRAD	C	T	C/C	C/T	283	26	114	4	0.382	0.130	1.120	1.09E-01	1.29E-02	113
3DL3	1042	OKG	UCEC	G	C	G/G	G/C	235	26	191	11	0.521	0.251	1.080	1.09E-01	1.30E-02	114
2DP1	500	OKG	BRCA	C	A	C/C	C/A	386	2	434	9	4.000	0.859	18.600	1.09E-01	1.32E-02	115
3DL2	497	OKG	READ	G	A	G/G	G/A	327	68	56	5	0.429	0.166	1.110	1.10E-01	1.33E-02	116
3DL3	971	OKG	KIRC	T	C	T/T	T/C	263	49	47	3	0.343	0.103	1.150	1.10E-01	1.34E-02	117
3DL1	1091	OKG	COAD	G	A	G/G	G/A	166	53	33	4	0.380	0.129	1.120	1.10E-01	1.35E-02	118
3DL3	906	OKG	OV	C	T	C/C	C/T	226	143	15	18	1.900	0.928	3.890	1.12E-01	1.36E-02	119
2DL4	412	OKG	LUAD	G	A	G/G	G/A	229	142	137	112	1.320	0.953	1.830	1.14E-01	1.37E-02	120
3DP1	479	OKG	ACC	A	C	A/A	A/C	201	176	21	9	0.489	0.218	1.100	1.15E-01	1.38E-02	121
3DL2	497	OKG	OV	G	A	G/G	G/A	327	68	27	11	1.960	0.928	4.140	1.17E-01	1.40E-02	122
2DP1	471	OKG	LUSC	A	G	A/A	A/G	292	64	135	43	1.450	0.937	2.240	1.17E-01	1.41E-02	123
3DL1	1194	OKG	SARC	C	T	C/C	C/T	327	22	64	9	2.090	0.920	4.750	1.22E-01	1.42E-02	124
2DP1	471	OKG	SKCM	A	G	A/A	A/G	292	64	236	71	1.370	0.938	2.000	1.22E-01	1.43E-02	125
2DL5	517	OKG	SARC	A	G	A/A	A/G	81	44	20	4	0.368	0.118	1.140	1.23E-01	1.44E-02	126
2DP1	766	OKG	KIRP	G	C	G/G	G/C	174	54	47	7	0.480	0.205	1.120	1.24E-01	1.45E-02	127
2DL4	395	OKG	SARC	C	T	C/C	C/T	355	30	68	11	1.910	0.913	4.000	1.26E-01	1.47E-02	128
3DP1	479	OKG	LUAD	A	C	A/A	A/C	201	176	145	97	0.764	0.551	1.060	1.26E-01	1.48E-02	129
2DP1	471	OKG	BLCA	A	G	A/A	A/G	292	64	108	35	1.480	0.927	2.360	1.28E-01	1.49E-02	130
3DL1	1180	OKG	LGG	G	C	G/G	G/C	177	86	191	68	0.733	0.502	1.070	1.29E-01	1.50E-02	131
2DP1	471	OKG	READ	A	G	A/A	A/G	292	64	39	15	1.750	0.910	3.370	1.29E-01	1.51E-02	132
2DL3	953	OKG	GBM	G	A	G/G	G/A	144	104	91	46	0.700	0.453	1.080	1.33E-01	1.52E-02	133
3DL2	394	OKG	SKCM	C	A	C/C	C/A	365	33	326	18	0.611	0.338	1.110	1.34E-01	1.53E-02	134
3DL2	497	OKG	LUSC	G	A	G/G	G/A	327	68	174	24	0.663	0.402	1.090	1.35E-01	1.55E-02	135
2DP1	448	OKG	GBM	G	C	G/G	G/C	138	151	81	64	0.722	0.484	1.080	1.36E-01	1.56E-02	136
2DP1	766	OKG	SARC	G	C	G/G	G/C	174	54	64	11	0.554	0.273	1.130	1.37E-01	1.57E-02	137
3DL1	607	OKG	KIRP	C	T	C/C	C/T	151	116	20	26	1.690	0.899	3.180	1.38E-01	1.58E-02	138
3DL3	906	OKG	UCEC	C	T	C/C	C/T	226	143	143	68	0.752	0.526	1.070	1.38E-01	1.59E-02	139
2DP1	471	OKG	BRCA	A	G	A/A	A/G	292	64	316	92	1.330	0.931	1.900	1.41E-01	1.60E-02	140
3DP1	479	OKG	LUSC	A	C	A/A	A/C	201	176	112	74	0.755	0.529	1.080	1.44E-01	1.61E-02	141
3DP1	479	OKG	THCA	A	C	A/A	A/C	201	176	127	85	0.764	0.543	1.070	1.45E-01	1.63E-02	142
2DL4	412	OKG	GBM	G	A	G/G	G/A	229	142	105	86	1.320	0.927	1.880	1.46E-01	1.64E-02	143
3DL1	1180	OKG	GBM	G	C	G/G	G/C	177	86	135	47	0.717	0.471	1.090	1.46E-01	1.65E-02	144
2DP1	1313	OKG	SKCM	A	C	A/A	A/C	210	112	215	88	0.767	0.547	1.080	1.47E-01	1.66E-02	145
3DP1	796	OKG	LGG	T	C	T/T	T/C	248	134	212	89	0.777	0.562	1.080	1.49E-01	1.67E-02	146
2DP1	522	OKG	COAD	T	C	T/T	T/C	280	86	108	22	0.663	0.395	1.110	1.51E-01	1.68E-02	147
3DL3	961	OKG	KIRP	C	A	C/C	C/A	118	103	14	22	1.800	0.876	3.700	1.51E-01	1.69E-02	148
3DL1	1194	OKG	COAD	C	T	C/C	C/T	327	22	121	3	0.369	0.108	1.260	1.54E-01	1.71E-02	149
3DL3	961	OKG	GBM	C	A	C/C	C/A	118	103	78	48	0.705	0.451	1.100	1.54E-01	1.72E-02	150
2DL4	1023	OKG	HNSC	G	A	G/G	G/A	258	128	242	94	0.783	0.569	1.080	1.54E-01	1.73E-02	151
3DL3	455	OKG	HNSC	G	A	G/G	G/A	367	31	327	17	0.615	0.334	1.130	1.55E-01	1.74E-02	152
3DL1	1026	OKG	CESC	G	C	G/G	G/C	160	52	44	23	1.610	0.889	2.910	1.56E-01	1.75E-02	153
3DL3	516	OKG	HNSC	C	T	C/C	C/T	388	10	341	3	0.341	0.093	1.250	1.56E-01	1.76E-02	154
3DL3	502	OKG	CESC	G	A	G/G	G/A	101	187	16	48	1.620	0.876	3.000	1.61E-01	1.77E-02	155
3DL3	804	OKG	UCEC	G	A	G/G	G/A	228	142	143	68	0.764	0.535	1.090	1.63E-01	1.79E-02	156
2DP1	471	OKG	UCEC	A	G	A/A	A/G	292	64	155	47	1.380	0.903	2.110	1.63E-01	1.80E-02	157
2DL4	625	OKG	LUAD	C	G	C/C	C/G	191	121	137	112	1.290	0.920	1.810	1.63E-01	1.81E-02	158
2DP1	522	OKG	KIRC	T	C	T/T	T/C	280	86	44	7	0.518	0.225	1.190	1.64E-01	1.82E-02	159
2DL5	583	OKG	KIRP	G	A	G/G	G/A	62	43	15	4	0.384	0.119	1.240	1.65E-01	1.83E-02	160
3DP1	691	OKG	UCEC	C	T	C/C	C/T	370	24	213	7	0.507	0.215	1.200	1.66E-01	1.84E-02	161
3DP1	479	OKG	BLCA	A	C	A/A	A/C	201	176	97	64	0.754	0.518	1.100	1.66E-01	1.85E-02	162
3DL3	408	OKG	LIHC	G	A	G/G	G/A	273	113	30	20	1.610	0.878	2.950	1.66E-01	1.87E-02	163
2DL5	583	OKG	LUSC	G	A	G/G	G/A	62	43	48	20	0.601	0.314	1.150	1.68E-01	1.88E-02	164
3DP1	774	OKG	LUSC	G	C	G/G	G/C	234	147	126	60	0.758	0.523	1.100	1.69E-01	1.89E-02	165
2DL4	762	OKG	LGG	C	T	C/C	C/T	89	202	84	145	0.761	0.527	1.100	1.70E-01	1.90E-02	166
3DP1	774	OKG	SKCM	G	C	G/G	G/C	234	147	218	109	0.796	0.584	1.080	1.70E-01	1.91E-02	167
3DL2	497	OKG	LGG	G	A	G/G	G/A	327	68	276	42	0.732	0.483	1.110	1.71E-01	1.92E-02	168
2DL3	953	OKG	LUSC	G	A	G/G	G/A	144	104	85	44	0.717	0.460	1.120	1.72E-01	1.93E-02	169
3DL1	732	OKG	CESC	T	C	T/T	T/C	55	46	18	7	0.465	0.179	1.210	1.72E-01	1.95E-02	170
3DP1	774	OKG	HNSC	G	C	G/G	G/C	234	147	214	107	0.796	0.584	1.090	1.73E-01	1.96E-02	171
3DP1	774	OKG	LGG	G	C	G/G	G/C	234	147	199	99	0.792	0.577	1.090	1.73E-01	1.97E-02	172
3DP1	691	OKG	STAD	C	T	C/C	C/T	370	24	166	5	0.464	0.174	1.240	1.74E-01	1.98E-02	173
2DP1	448	OKG	KIRP	G	C	G/G	G/C	138	151	28	19	0.620	0.331	1.160	1.78E-01	1.99E-02	174
2DL3	953	OKG	LUAD	G	A	G/G	G/A	144	104	105	56	0.738	0.489	1.110	1.79E-01	2.00E-02	175
3DL1	1180	OKG	LUAD	G	C	G/G	G/C	177	86	157	57	0.747	0.502	1.110	1.81E-01	2.01E-02	176
3DL2	394	OKG	BLCA	C	A	C/C	C/A	365	33	162	8	0.546	0.247	1.210	1.82E-01	2.03E-02	177
3DL1	1180	OKG	KIRC	G	C	G/G	G/C	177	86	39	11	0.581	0.284	1.190	1.83E-01	2.04E-02	178
3DL1	1161	OKG	LUSC	C	T	C/C	C/T	196	6	144	10	2.270	0.807	6.390	1.83E-01	2.05E-02	179
2DL4	1023	OKG	KIRP	G	A	G/G	G/A	258	128	48	15	0.630	0.340	1.170	1.83E-01	2.06E-02	180
3DL3	777	OKG	UCEC	A	G	A/A	A/G	229	141	143	68	0.772	0.540	1.100	1.83E-01	2.07E-02	181
3DL3	408	OKG	SARC	G	A	G/G	G/A	273	113	46	28	1.470	0.875	2.470	1.85E-01	2.08E-02	182
2DL4	480	OKG	KIRP	G	A	G/G	G/A	265	113	39	25	1.500	0.867	2.600	1.88E-01	2.09E-02	183
3DL3	971	OKG	KIRP	T	C	T/T	T/C	263	49	48	4	0.447	0.154	1.300	1.92E-01	2.11E-02	184
2DL5	583	OKG	PRAD	G	A	G/G	G/A	62	43	31	12	0.558	0.258	1.210	1.92E-01	2.12E-02	185
2DL4	625	OKG	GBM	C	G	C/C	C/G	191	121	105	86	1.290	0.896	1.860	1.98E-01	2.13E-02	186
2DL4	412	OKG	ACC	G	A	G/G	G/A	229	142	15	16	1.720	0.825	3.590	2.04E-01	2.14E-02	187
2DL5	583	OKG	BRCA	G	A	G/G	G/A	62	43	81	38	0.676	0.391	1.170	2.07E-01	2.15E-02	188
2DL3	953	OKG	HNSC	G	A	G/G	G/A	144	104	143	80	0.775	0.534	1.120	2.11E-01	2.16E-02	189
2DL4	395	OKG	SKCM	C	T	C/C	C/T	355	30	326	18	0.653	0.357	1.190	2.14E-01	2.17E-02	190
3DP1	479	OKG	COAD	A	C	A/A	A/C	201	176	81	54	0.761	0.510	1.130	2.15E-01	2.19E-02	191
2DL4	1023	OKG	SARC	G	A	G/G	G/A	258	128	59	20	0.683	0.394	1.180	2.18E-01	2.20E-02	192
2DL4	1023	OKG	KIRC	G	A	G/G	G/A	258	128	39	12	0.620	0.314	1.220	2.20E-01	2.21E-02	193
3DL2	474	OKG	HNSC	G	T	G/G	G/T	258	127	241	96	0.809	0.589	1.110	2.21E-01	2.22E-02	194
2DP1	448	OKG	LUAD	G	C	G/G	G/C	138	151	92	78	0.775	0.530	1.130	2.22E-01	2.23E-02	195
2DP1	522	OKG	SARC	T	C	T/T	T/C	280	86	62	12	0.630	0.324	1.220	2.23E-01	2.24E-02	196
3DL1	1194	OKG	SKCM	C	T	C/C	C/T	327	22	317	13	0.610	0.302	1.230	2.23E-01	2.25E-02	197
3DP1	479	OKG	BRCA	A	C	A/A	A/C	201	176	243	177	0.832	0.629	1.100	2.24E-01	2.27E-02	198
3DL3	961	OKG	LUAD	C	A	C/C	C/A	118	103	87	57	0.751	0.491	1.150	2.25E-01	2.28E-02	199
2DL4	1023	OKG	LUSC	G	A	G/G	G/A	258	128	140	54	0.777	0.532	1.130	2.27E-01	2.29E-02	200
2DL5	517	OKG	KIRP	A	G	A/A	A/G	81	44	17	4	0.433	0.137	1.370	2.27E-01	2.30E-02	201
2DL4	762	OKG	UCEC	C	T	C/C	C/T	89	202	61	106	0.766	0.513	1.140	2.30E-01	2.31E-02	202
3DL1	1180	OKG	READ	G	C	G/G	G/C	177	86	32	9	0.579	0.265	1.270	2.30E-01	2.32E-02	203
2DL4	625	OKG	ACC	C	G	C/C	C/G	191	121	15	16	1.680	0.801	3.520	2.31E-01	2.33E-02	204
2DL2	497	OKG	LIHC	G	A	G/G	G/A	327	68	47	5	0.512	0.196	1.330	2.32E-01	2.35E-02	205
3DL3	777	OKG	PRAD	A	G	A/A	A/G	229	141	68	55	1.310	0.867	1.980	2.34E-01	2.36E-02	206
3DP1	774	OKG	THCA	G	C	G/G	G/C	234	147	144	72	0.796	0.561	1.130	2.34E-01	2.37E-02	207
2DL4	762	OKG	THCA	C	T	C/C	C/T	89	202	65	114	0.773	0.521	1.150	2.37E-01	2.38E-02	208
2DL3	953	OKG	UCEC	G	A	G/G	G/A	144	104	90	49	0.754	0.491	1.160	2.37E-01	2.39E-02	209
2DP1	1313	OKG	OV	A	C	A/A	A/C	210	112	24	7	0.547	0.229	1.310	2.41E-01	2.40E-02	210
3DL3	408	OKG	GBM	G	A	G/G	G/A	273	113	136	71	1.260	0.878	1.810	2.43E-01	2.41E-02	211
3DL3	777	OKG	THCA	A	G	A/A	A/G	229	141	120	92	1.250	0.887	1.760	2.44E-01	2.43E-02	212
3DL2	456	OKG	HNSC	C	T	C/C	C/T	348	49	287	53	1.310	0.862	1.990	2.44E-01	2.44E-02	213
3DL2	893	OKG	HNSC	G	A	G/G	G/A	348	49	287	53	1.310	0.862	1.990	2.44E-01	2.44E-02	213
3DL2	497	OKG	THCA	G	A	G/G	G/A	327	68	201	31	0.742	0.469	1.170	2.44E-01	2.45E-02	214

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DL4	625	OKG	LIHC	C	G	C/C	C/G	191	121	19	19	1.580	0.804	3.100	2.47E-01	2.46E-02	215
2DP1	766	OKG	HNSC	G	C	G/G	G/C	174	54	189	76	1.300	0.867	1.950	2.49E-01	2.47E-02	216
3DL3	455	OKG	LGG	G	A	G/G	G/A	367	31	301	17	0.669	0.363	1.230	2.51E-01	2.48E-02	217
2DL4	480	OKG	LGG	G	A	G/G	G/A	265	113	229	79	0.809	0.577	1.130	2.52E-01	2.49E-02	218
3DL3	455	OKG	READ	G	A	G/G	G/A	367	31	53	8	1.790	0.781	4.100	2.53E-01	2.51E-02	219
3DL1	1161	OKG	LGG	C	T	C/C	C/T	196	6	234	14	1.950	0.736	5.170	2.54E-01	2.52E-02	220
3DL1	1180	OKG	CESC	G	C	G/G	G/C	177	86	37	26	1.450	0.825	2.550	2.55E-01	2.53E-02	221
3DL1	496	OKG	COAD	C	A	C/C	C/A	362	14	128	9	1.820	0.769	4.310	2.56E-01	2.54E-02	222
3DL3	804	OKG	PRAD	G	A	G/G	G/A	228	142	68	55	1.300	0.861	1.960	2.56E-01	2.55E-02	223
3DP1	691	OKG	LUSC	C	T	C/C	C/T	370	24	192	7	0.562	0.238	1.330	2.57E-01	2.56E-02	224
2DL4	1018	OKG	HNSC	G	C	G/G	G/C	394	4	336	8	2.350	0.701	7.870	2.58E-01	2.57E-02	225
3DL3	906	OKG	PRAD	C	T	C/C	C/T	226	143	67	55	1.300	0.860	1.970	2.59E-01	2.59E-02	226
2DP1	766	OKG	COAD	G	C	G/G	G/C	174	54	73	15	0.662	0.351	1.250	2.59E-01	2.60E-02	227
2DL4	762	OKG	KIRP	C	T	C/C	C/T	89	202	10	37	1.630	0.776	3.420	2.59E-01	2.61E-02	228
3DL3	961	OKG	HNSC	C	A	C/C	C/A	118	103	110	75	0.781	0.526	1.160	2.60E-01	2.62E-02	229
3DL2	474	OKG	LUAD	G	T	G/G	G/T	258	127	181	72	0.808	0.572	1.140	2.63E-01	2.63E-02	230
2DL4	412	OKG	THCA	G	A	G/G	G/A	229	142	123	94	1.230	0.875	1.730	2.64E-01	2.64E-02	231
2DL3	953	OKG	LGG	G	A	G/G	G/A	144	104	128	73	0.790	0.539	1.160	2.65E-01	2.65E-02	232
2DL4	762	OKG	GBM	C	T	C/C	C/T	89	202	61	108	0.780	0.522	1.160	2.66E-01	2.67E-02	233
3DL2	497	OKG	STAD	G	A	G/G	G/A	327	68	146	22	0.725	0.432	1.220	2.74E-01	2.68E-02	234
2DP1	766	OKG	READ	G	C	G/G	G/C	174	54	21	11	1.690	0.766	3.730	2.76E-01	2.69E-02	235
3DL3	516	OKG	SKCM	C	T	C/C	C/T	388	10	342	4	0.454	0.141	1.460	2.77E-01	2.70E-02	236
3DL2	497	OKG	LUAD	G	A	G/G	G/A	327	68	226	36	0.766	0.494	1.190	2.78E-01	2.71E-02	237
3DP1	691	OKG	SKCM	C	T	C/C	C/T	370	24	331	14	0.652	0.332	1.280	2.79E-01	2.72E-02	238
3DL2	474	OKG	KIRC	G	T	G/G	G/T	258	127	40	13	0.660	0.341	1.280	2.80E-01	2.74E-02	239
2DL5	583	OKG	HNSC	G	A	G/G	G/A	62	43	66	32	0.699	0.394	1.240	2.81E-01	2.75E-02	240
2DP1	766	OKG	BRCA	G	C	G/G	G/C	174	54	330	81	0.791	0.535	1.170	2.81E-01	2.76E-02	241
2DP1	522	OKG	STAD	T	C	T/T	T/C	280	86	108	43	1.300	0.847	1.990	2.81E-01	2.77E-02	242
3DL2	474	OKG	LUSC	G	T	G/G	G/T	258	127	140	55	0.798	0.547	1.160	2.81E-01	2.78E-02	243
2DL4	395	OKG	GBM	C	T	C/C	C/T	355	30	204	11	0.638	0.313	1.300	2.82E-01	2.79E-02	244
2DL4	480	OKG	KIRC	G	A	G/G	G/A	265	113	43	12	0.654	0.332	1.290	2.82E-01	2.80E-02	245
2DL3	953	OKG	ACC	G	A	G/G	G/A	144	104	12	4	0.462	0.145	1.470	2.83E-01	2.82E-02	246
3DL3	502	OKG	KIRP	G	A	G/G	G/A	101	187	14	39	1.500	0.778	2.890	2.86E-01	2.83E-02	247
3DL3	408	OKG	LGG	G	A	G/G	G/A	273	113	206	103	1.210	0.876	1.670	2.86E-01	2.84E-02	248
2DP1	766	OKG	KIRC	G	C	G/G	G/C	174	54	39	7	0.578	0.244	1.370	2.87E-01	2.85E-02	249
2DL5	583	OKG	LGG	G	A	G/G	G/A	62	43	62	30	0.698	0.389	1.250	2.88E-01	2.86E-02	250
2DL4	1023	OKG	LUAD	G	A	G/G	G/A	258	128	180	73	0.817	0.579	1.150	2.89E-01	2.87E-02	251
3DL1	1091	OKG	LUSC	G	A	G/G	G/A	166	53	104	44	1.330	0.832	2.130	2.90E-01	2.88E-02	252
3DP1	691	OKG	LGG	C	T	C/C	C/T	370	24	308	13	0.651	0.326	1.300	2.91E-01	2.90E-02	253
2DL5	583	OKG	STAD	G	A	G/G	G/A	62	43	34	15	0.636	0.309	1.310	2.91E-01	2.91E-02	254
3DL2	474	OKG	KIRP	G	T	G/G	G/T	258	127	47	16	0.692	0.378	1.270	2.93E-01	2.92E-02	255
2DP1	1062	OKG	BRCA	C	T	C/C	C/T	283	26	399	26	0.709	0.403	1.250	2.93E-01	2.93E-02	256
3DP1	774	OKG	READ	G	C	G/G	G/C	234	147	41	18	0.699	0.387	1.260	2.95E-01	2.94E-02	257
3DL1	607	OKG	PRAD	C	T	C/C	C/T	151	116	56	32	0.744	0.453	1.220	2.97E-01	2.95E-02	258
3DL1	607	OKG	ACC	C	T	C/C	C/T	151	116	18	8	0.579	0.243	1.380	2.98E-01	2.96E-02	259
3DP1	691	OKG	GBM	C	T	C/C	C/T	370	24	205	8	0.602	0.266	1.360	2.99E-01	2.98E-02	260
3DP1	796	OKG	THCA	T	C	T/T	T/C	248	134	150	66	0.814	0.569	1.160	3.00E-01	2.99E-02	261
2DL3	953	OKG	BRCA	G	A	G/G	G/A	144	104	176	104	0.818	0.577	1.160	3.00E-01	3.00E-02	262
2DL4	1023	OKG	READ	G	A	G/G	G/A	258	128	44	15	0.687	0.368	1.280	3.00E-01	3.01E-02	263
3DL3	516	OKG	BRCA	C	T	C/C	C/T	388	10	450	6	0.517	0.186	1.440	3.01E-01	3.02E-02	264
3DL2	456	OKG	STAD	C	T	C/C	C/T	348	49	142	27	1.350	0.812	2.250	3.05E-01	3.03E-02	265
3DL2	893	OKG	STAD	G	A	G/G	G/A	348	49	142	27	1.350	0.812	2.250	3.05E-01	3.03E-02	265
2DL4	412	OKG	SKCM	G	A	G/G	G/A	229	142	185	136	1.190	0.877	1.610	3.09E-01	3.04E-02	266
3DP1	796	OKG	HNSC	T	C	T/T	T/C	248	134	223	101	0.838	0.611	1.150	3.09E-01	3.06E-02	267
3DL2	474	OKG	READ	G	T	G/G	G/T	258	127	44	15	0.693	0.372	1.290	3.12E-01	3.07E-02	268
2DP1	1062	OKG	HNSC	C	T	C/C	C/T	283	26	297	19	0.696	0.377	1.290	3.14E-01	3.08E-02	269
2DL4	480	OKG	PRAD	G	A	G/G	G/A	265	113	83	45	1.270	0.831	1.940	3.17E-01	3.09E-02	270
2DP1	1313	OKG	ACC	A	C	A/A	A/C	210	112	20	6	0.562	0.219	1.440	3.19E-01	3.10E-02	271
2DL3	953	OKG	CESC	G	A	G/G	G/A	144	104	23	24	1.440	0.771	2.690	3.19E-01	3.11E-02	272
3DL3	502	OKG	SKCM	G	A	G/G	G/A	101	187	83	187	1.220	0.856	1.740	3.19E-01	3.12E-02	273
3DP1	796	OKG	SARC	T	C	T/T	T/C	248	134	51	20	0.726	0.415	1.270	3.21E-01	3.14E-02	274
3DL3	777	OKG	LUSC	A	G	A/A	A/G	229	141	101	76	1.220	0.848	1.760	3.24E-01	3.15E-02	275
2DL4	480	OKG	CESC	G	A	G/G	G/A	265	113	51	29	1.330	0.802	2.210	3.25E-01	3.16E-02	276
3DP1	774	OKG	ACC	G	C	G/G	G/C	234	147	23	9	0.623	0.281	1.380	3.26E-01	3.17E-02	277
3DL2	474	OKG	SARC	G	T	G/G	G/T	258	127	58	21	0.736	0.428	1.270	3.27E-01	3.18E-02	278
3DL3	447	OKG	LIHC	G	T	G/G	G/T	345	50	44	10	1.570	0.743	3.320	3.30E-01	3.19E-02	279
3DL2	474	OKG	SKCM	G	T	G/G	G/T	258	127	236	98	0.844	0.615	1.160	3.32E-01	3.20E-02	280
3DL3	804	OKG	THCA	G	A	G/G	G/A	228	142	120	90	1.200	0.850	1.690	3.32E-01	3.22E-02	281
2DP1	1269	OKG	BRCA	A	G	A/A	A/G	350	30	412	26	0.736	0.427	1.270	3.33E-01	3.23E-02	282
3DP1	691	OKG	BRCA	C	T	C/C	C/T	370	24	436	20	0.707	0.384	1.300	3.35E-01	3.24E-02	283
3DL2	456	OKG	UCEC	C	T	C/C	C/T	348	49	186	34	1.300	0.811	2.080	3.36E-01	3.25E-02	284
3DL2	893	OKG	UCEC	G	A	G/G	G/A	348	49	186	34	1.300	0.811	2.080	3.36E-01	3.25E-02	284
3DP1	796	OKG	ACC	T	C	T/T	T/C	248	134	24	8	0.617	0.270	1.410	3.37E-01	3.26E-02	285
3DL1	1180	OKG	LUSC	G	C	G/G	G/C	177	86	117	45	0.792	0.515	1.220	3.38E-01	3.27E-02	286
3DL1	1021	OKG	GBM	A	G	A/A	A/G	153	14	134	7	0.571	0.224	1.460	3.38E-01	3.28E-02	287
2DP1	1269	OKG	LUAD	A	G	A/A	A/G	350	30	237	14	0.689	0.358	1.330	3.38E-01	3.30E-02	288
2DL4	480	OKG	READ	G	A	G/G	G/A	265	113	47	14	0.699	0.370	1.320	3.38E-01	3.31E-02	289
2DL4	625	OKG	THCA	C	G	C/C	C/G	191	121	123	94	1.210	0.851	1.720	3.40E-01	3.32E-02	290
3DL1	607	OKG	GBM	C	T	C/C	C/T	151	116	100	62	0.807	0.542	1.200	3.40E-01	3.33E-02	291
3DL3	869	OKG	ACC	A	C	A/A	A/C	307	84	23	10	1.590	0.728	3.470	3.41E-01	3.34E-02	292
2DL4	625	OKG	PRAD	C	G	C/C	C/G	191	121	82	41	0.789	0.509	1.220	3.43E-01	3.35E-02	293
3DL1	1180	OKG	HNSC	G	C	G/G	G/C	177	86	207	83	0.825	0.574	1.190	3.43E-01	3.36E-02	294
3DL3	408	OKG	BLCA	G	A	G/G	G/A	273	113	110	56	1.230	0.833	1.820	3.46E-01	3.38E-02	295
2DL4	412	OKG	LIHC	G	A	G/G	G/A	229	142	28	24	1.380	0.770	2.470	3.48E-01	3.39E-02	296
2DL4	480	OKG	UCEC	G	A	G/G	G/A	265	113	160	56	0.821	0.564	1.200	3.49E-01	3.40E-02	297
3DL3	455	OKG	KIRP	G	A	G/G	G/A	367	31	58	8	1.630	0.714	3.720	3.50E-01	3.41E-02	298
3DP1	774	OKG	SARC	G	C	G/G	G/C	234	147	49	23	0.747	0.437	1.280	3.50E-01	3.42E-02	299
3DL3	804	OKG	LUSC	G	A	G/G	G/A	228	142	101	76	1.210	0.841	1.740	3.55E-01	3.43E-02	300
3DL3	447	OKG	KIRC	G	T	G/G	G/T	345	50	45	10	1.530	0.725	3.230	3.59E-01	3.44E-02	301
3DL1	1180	OKG	BLCA	G	C	G/G	G/C	177	86	104	40	0.792	0.507	1.240	3.60E-01	3.46E-02	302
2DP1	471	OKG	SARC	A	G	A/A	A/G	292	64	62	9	0.662	0.313	1.400	3.62E-01	3.47E-02	303
3DL1	1091	OKG	OV	G	A	G/G	G/A	166	53	22	11	1.570	0.715	3.450	3.63E-01	3.48E-02	304
3DP1	774	OKG	COAD	G	C	G/G	G/C	234	147	78	60	1.220	0.822	1.810	3.66E-01	3.49E-02	305
2DL4	412	OKG	BLCA	G	A	G/G	G/A	229	142	89	67	1.210	0.828	1.770	3.66E-01	3.50E-02	306
3DL2	394	OKG	CESC	C	A	C/C	C/A	365	33	81	4	0.546	0.188	1.580	3.66E-01	3.51E-02	307
2DL4	762	OKG	READ	C	T	C/C	C/T	89	202	17	27	0.700	0.363	1.350	3.70E-01	3.52E-02	308
3DL2	497	OKG	UCEC	G	A	G/G	G/A	327	68	189	31	0.789	0.498	1.250	3.70E-01	3.54E-02	309
2DP1	1062	OKG	LUAD	C	T	C/C	C/T	283	26	219	14	0.696	0.355	1.360	3.71E-01	3.55E-02	310
2DP1	448	OKG	LUSC	G	C	G/G	G/C	138	151	73	65	0.814	0.542	1.220	3.73E-01	3.56E-02	311
3DP1	796	OKG	UCEC	T	C	T/T	T/C	248	134	144	65	0.835	0.582	1.200	3.75E-01	3.57E-02	312
3DP1	774	OKG	UCEC	G	C	G/G	G/C	234	147	133	70	0.838	0.587	1.200	3.75E-01	3.58E-02	313
3DP1	774	OKG	LUAD	G	C	G/G	G/C	234	147	165	88	0.849	0.610	1.180	3.76E-01	3.59E-02	314
2DP1	766	OKG	STAD	G	C	G/G	G/C	174	54	90	36	1.290	0.788	2.110	3.77E-01	3.60E-02	315
3DL1	1180	OKG	SARC	G	C	G/G	G/C	177	86	33	22	1.370	0.754	2.490	3.77E-01	3.62E-02	316
3DL3	906	OKG	THCA	C	T	C/C	C/T	226	143	120	90	1.190	0.843	1.680	3.79E-01	3.63E-02	317
3DL3	777	OKG	BLCA	A	G	A/A	A/G	229	141	93	69	1.200	0.824	1.750	3.80E-01	3.64E-02	318
2DL4	480	OKG	HNSC	G	A	G/G	G/A	265	113	245	89	0.852	0.614	1.180	3.81E-01	3.65E-02	319
2DL4	412	OKG	PRAD	G	A	G/G	G/A	229	142	82	41	0.806	0.525	1.240	3.81E-01	3.66E-02	320
2DP1	448	OKG	KIRC	G	C	G/G	G/C	138	151	13	21	1.480	0.714	3.070	3.84E-01	3.67E-02	321
3DL3	408	OKG	HNSC	G	A	G/G	G/A	273	113	241	85	0.852	0.612	1.190	3.87E-01	3.68E-02	322

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DL4	762	OKG	STAD	C	T	C/C	C/T	89	202	44	80	0.801	0.514	1.250	3.88E-01	3.70E-02	323
2DP1	471	OKG	LUAD	A	G	A/A	A/G	292	64	182	49	1.230	0.812	1.860	3.88E-01	3.71E-02	324
3DL1	1026	OKG	OV	G	C	G/G	G/C	160	52	22	11	1.540	0.700	3.390	3.88E-01	3.72E-02	325
3DL2	394	OKG	STAD	C	A	C/C	C/A	365	33	162	10	0.683	0.329	1.420	3.92E-01	3.73E-02	326
2DL5	517	OKG	THCA	A	G	A/A	A/G	81	44	60	24	0.736	0.404	1.340	3.94E-01	3.74E-02	327
2DP1	1269	OKG	HNSC	A	G	A/A	A/G	350	30	314	20	0.743	0.414	1.330	3.96E-01	3.75E-02	328
3DP1	796	OKG	LIHC	T	C	T/T	T/C	248	134	34	13	0.708	0.361	1.390	3.96E-01	3.76E-02	329
3DL2	394	OKG	GBM	C	A	C/C	C/A	365	33	202	13	0.712	0.366	1.380	3.97E-01	3.78E-02	330
2DP1	471	OKG	THCA	A	G	A/A	A/G	292	64	167	45	1.230	0.803	1.880	4.00E-01	3.79E-02	331
3DL3	961	OKG	BRCA	C	A	C/C	C/A	118	103	147	108	0.842	0.586	1.210	4.01E-01	3.80E-02	332
3DL1	607	OKG	THCA	C	T	C/C	C/T	151	116	111	71	0.833	0.568	1.220	4.02E-01	3.81E-02	333
2DL4	625	OKG	SKCM	C	G	C/C	C/G	191	121	185	136	1.160	0.844	1.590	4.02E-01	3.82E-02	334
3DL1	1021	OKG	SKCM	A	G	A/A	A/G	153	14	159	21	1.440	0.707	2.930	4.03E-01	3.83E-02	335
2DL4	762	OKG	LIHC	C	T	C/C	C/T	89	202	13	20	0.678	0.323	1.420	4.04E-01	3.84E-02	336
3DL3	516	OKG	UCEC	C	T	C/C	C/T	388	10	212	9	1.650	0.660	4.120	4.04E-01	3.86E-02	337
3DL3	969	OKG	SKCM	C	T	C/C	C/T	329	20	267	11	0.678	0.319	1.440	4.05E-01	3.87E-02	338
2DP1	1062	OKG	LUSC	C	T	C/C	C/T	283	26	174	11	0.688	0.332	1.430	4.05E-01	3.88E-02	339
3DL3	969	OKG	LGG	C	T	C/C	C/T	329	20	246	10	0.669	0.308	1.450	4.06E-01	3.89E-02	340
3DL1	1194	OKG	LUAD	C	T	C/C	C/T	327	22	239	11	0.684	0.325	1.440	4.09E-01	3.90E-02	341
3DL1	1091	OKG	PRAD	G	A	G/G	G/A	166	53	70	29	1.300	0.764	2.210	4.11E-01	3.91E-02	342
3DL2	456	OKG	BRCA	C	T	C/C	C/T	348	49	389	66	1.200	0.807	1.780	4.12E-01	3.92E-02	343
3DL2	893	OKG	BRCA	G	A	G/G	G/A	348	49	389	66	1.200	0.807	1.780	4.12E-01	3.92E-02	343
3DL1	1180	OKG	THCA	G	C	G/G	G/C	177	86	144	58	0.829	0.556	1.240	4.12E-01	3.94E-02	344
2DL5	583	OKG	GBM	G	A	G/G	G/A	62	43	42	21	0.721	0.375	1.380	4.12E-01	3.95E-02	345
2DP1	766	OKG	LUSC	G	C	G/G	G/C	174	54	100	39	1.260	0.780	2.040	4.18E-01	3.96E-02	346
3DL3	969	OKG	LUSC	C	T	C/C	C/T	329	20	160	6	0.617	0.243	1.570	4.18E-01	3.97E-02	347
3DL3	969	OKG	GBM	C	T	C/C	C/T	329	20	181	7	0.636	0.264	1.530	4.19E-01	3.98E-02	348
3DL3	502	OKG	GBM	G	A	G/G	G/A	101	187	49	110	1.210	0.799	1.830	4.20E-01	3.99E-02	349
2DL4	762	OKG	KIRC	C	T	C/C	C/T	89	202	16	26	0.716	0.366	1.400	4.23E-01	4.01E-02	350
2DL5	583	OKG	UCEC	G	A	G/G	G/A	62	43	47	24	0.736	0.393	1.380	4.24E-01	4.02E-02	351
2DP1	471	OKG	PRAD	A	G	A/A	A/G	292	64	93	26	1.280	0.767	2.140	4.25E-01	4.03E-02	352
2DP1	522	OKG	OV	T	C	T/T	T/C	280	86	27	5	0.603	0.225	1.610	4.25E-01	4.04E-02	353
3DL1	1026	OKG	KIRC	G	C	G/G	G/C	160	52	41	9	0.675	0.307	1.480	4.26E-01	4.05E-02	354
3DP1	796	OKG	READ	T	C	T/T	T/C	248	134	42	17	0.749	0.411	1.370	4.26E-01	4.06E-02	355
3DL3	447	OKG	SARC	G	T	G/G	G/T	345	50	73	7	0.662	0.289	1.520	4.28E-01	4.07E-02	356
2DL4	480	OKG	LUAD	G	A	G/G	G/A	265	113	187	68	0.853	0.599	1.220	4.29E-01	4.09E-02	357
2DL4	1023	OKG	SKCM	G	A	G/G	G/A	258	128	234	101	0.870	0.635	1.190	4.32E-01	4.10E-02	358
3DL1	1026	OKG	PRAD	G	C	G/G	G/C	160	52	72	30	1.280	0.755	2.170	4.32E-01	4.11E-02	359
3DP1	796	OKG	SKCM	T	C	T/T	T/C	248	134	223	105	0.871	0.637	1.190	4.34E-01	4.12E-02	360
3DL3	502	OKG	OV	G	A	G/G	G/A	101	187	14	18	0.694	0.331	1.450	4.37E-01	4.13E-02	361
3DL3	961	OKG	COAD	C	A	C/C	C/A	118	103	41	45	1.260	0.765	2.080	4.39E-01	4.14E-02	362
3DP1	774	OKG	OV	G	C	G/G	G/C	234	147	25	11	0.700	0.334	1.470	4.42E-01	4.15E-02	363
2DP1	1062	OKG	LGG	C	T	C/C	C/T	283	26	276	19	0.749	0.405	1.380	4.42E-01	4.17E-02	364
3DL1	1180	OKG	STAD	G	C	G/G	G/C	177	86	103	41	0.819	0.525	1.280	4.42E-01	4.18E-02	365
2DL4	480	OKG	GBM	G	A	G/G	G/A	265	113	155	56	0.847	0.581	1.230	4.43E-01	4.19E-02	366
3DL1	1180	OKG	BRCA	G	C	G/G	G/C	177	86	258	108	0.862	0.612	1.210	4.43E-01	4.20E-02	367
2DL4	625	OKG	BLCA	C	G	C/C	C/G	191	121	89	67	1.190	0.805	1.760	4.43E-01	4.21E-02	368
3DL3	906	OKG	LUSC	C	T	C/C	C/T	226	143	101	75	1.170	0.812	1.690	4.43E-01	4.22E-02	369
3DL1	607	OKG	CESC	C	T	C/C	C/T	151	116	29	29	1.300	0.736	2.300	4.45E-01	4.23E-02	370
2DL4	395	OKG	CESC	C	T	C/C	C/T	355	30	81	4	0.584	0.200	1.700	4.46E-01	4.25E-02	371
3DL1	1026	OKG	LUSC	G	C	G/G	G/C	160	52	107	43	1.240	0.773	1.990	4.47E-01	4.26E-02	372
3DL3	1042	OKG	BRCA	G	C	G/G	G/C	235	26	371	32	0.780	0.453	1.340	4.47E-01	4.27E-02	373
3DL1	1194	OKG	GBM	C	T	C/C	C/T	327	22	196	9	0.683	0.308	1.510	4.50E-01	4.28E-02	374
3DL1	1091	OKG	KIRC	G	A	G/G	G/A	166	53	41	9	0.688	0.314	1.510	4.51E-01	4.29E-02	375
3DP1	796	OKG	LUAD	T	C	T/T	T/C	248	134	171	80	0.866	0.617	1.210	4.54E-01	4.30E-02	376
2DP1	471	OKG	LGG	A	G	A/A	A/G	292	64	223	58	1.190	0.801	1.770	4.55E-01	4.31E-02	377
3DL2	456	OKG	PRAD	C	T	C/C	C/T	348	49	110	20	1.290	0.735	2.260	4.58E-01	4.33E-02	378
3DL2	893	OKG	PRAD	G	A	G/G	G/A	348	49	110	20	1.290	0.735	2.260	4.58E-01	4.33E-02	378
3DP1	796	OKG	LUSC	T	C	T/T	T/C	248	134	128	59	0.853	0.587	1.240	4.59E-01	4.34E-02	379
3DP1	479	OKG	LIHC	A	C	A/A	A/C	201	176	30	20	0.761	0.417	1.390	4.59E-01	4.35E-02	380
3DL3	961	OKG	PRAD	C	A	C/C	C/A	118	103	41	28	0.782	0.452	1.350	4.60E-01	4.36E-02	381
2DP1	1313	OKG	UCEC	A	C	A/A	A/C	210	112	99	44	0.833	0.546	1.270	4.60E-01	4.37E-02	382
3DL3	502	OKG	BRCA	G	A	G/G	G/A	101	187	109	232	1.150	0.825	1.600	4.61E-01	4.38E-02	383
2DP1	1313	OKG	LUSC	A	C	A/A	A/C	210	112	124	56	0.847	0.573	1.250	4.61E-01	4.39E-02	384
3DL3	906	OKG	BLCA	C	T	C/C	C/T	226	143	93	69	1.170	0.804	1.700	4.62E-01	4.41E-02	385
3DL3	621	OKG	SARC	G	A	G/G	G/A	346	49	73	7	0.677	0.295	1.550	4.63E-01	4.42E-02	386
2DP1	804	OKG	SKCM	C	A	C/C	C/A	352	8	328	4	0.537	0.160	1.800	4.64E-01	4.43E-02	387
3DP1	774	OKG	LIHC	G	C	G/G	G/C	234	147	32	15	0.746	0.391	1.420	4.65E-01	4.44E-02	388
3DL3	804	OKG	GBM	G	A	G/G	G/A	228	142	118	85	1.160	0.818	1.640	4.66E-01	4.45E-02	389
3DP1	691	OKG	COAD	C	T	C/C	C/T	370	24	132	12	1.400	0.681	2.880	4.68E-01	4.46E-02	390
3DL3	408	OKG	SKCM	G	A	G/G	G/A	273	113	229	108	1.140	0.830	1.570	4.68E-01	4.47E-02	391
2DL3	953	OKG	BLCA	G	A	G/G	G/A	144	104	66	39	0.818	0.512	1.310	4.72E-01	4.49E-02	392
3DL1	1026	OKG	SKCM	G	C	G/G	G/C	160	52	205	79	1.190	0.793	1.790	4.72E-01	4.50E-02	393
2DP1	522	OKG	KIRP	T	C	T/T	T/C	280	86	49	11	0.731	0.364	1.470	4.73E-01	4.51E-02	394
2DP1	448	OKG	SKCM	G	C	G/G	G/C	138	151	121	115	0.869	0.616	1.230	4.75E-01	4.52E-02	395
3DL3	455	OKG	GBM	G	A	G/G	G/A	367	31	193	21	1.290	0.722	2.310	4.81E-01	4.53E-02	396
3DL3	777	OKG	COAD	A	G	A/A	A/G	229	141	80	58	1.180	0.793	1.760	4.82E-01	4.54E-02	397
3DL3	961	OKG	STAD	C	A	C/C	C/A	118	103	51	36	0.809	0.490	1.340	4.82E-01	4.55E-02	398
3DP1	691	OKG	HNSC	C	T	C/C	C/T	370	24	328	16	0.752	0.393	1.440	4.85E-01	4.57E-02	399
3DL2	497	OKG	SARC	G	A	G/G	G/A	327	68	63	17	1.300	0.716	2.360	4.85E-01	4.58E-02	400
3DP1	774	OKG	BRCA	G	C	G/G	G/C	234	147	276	155	0.894	0.672	1.190	4.85E-01	4.59E-02	401
3DL3	777	OKG	HNSC	A	G	A/A	A/G	229	141	204	111	0.884	0.647	1.210	4.86E-01	4.60E-02	402
3DL3	502	OKG	LGG	G	A	G/G	G/A	101	187	78	167	1.160	0.808	1.670	4.87E-01	4.61E-02	403
3DL3	447	OKG	BRCA	G	T	G/G	G/T	345	50	388	66	1.170	0.788	1.740	4.87E-01	4.62E-02	404
2DP1	1313	OKG	READ	A	C	A/A	A/C	210	112	35	14	0.750	0.387	1.450	4.88E-01	4.63E-02	405
2DP1	522	OKG	BLCA	T	C	T/T	T/C	280	86	106	39	1.200	0.773	1.860	4.89E-01	4.65E-02	406
3DL2	497	OKG	ACC	G	A	G/G	G/A	327	68	26	8	1.480	0.643	3.410	4.89E-01	4.66E-02	407
2DL4	480	OKG	COAD	G	A	G/G	G/A	265	113	101	36	0.836	0.539	1.300	4.90E-01	4.67E-02	408
2DL5	517	OKG	PRAD	A	G	A/A	A/G	81	44	31	12	0.713	0.333	1.530	4.92E-01	4.68E-02	409
3DL3	969	OKG	PRAD	C	T	C/C	C/T	329	20	110	4	0.598	0.200	1.790	4.93E-01	4.69E-02	410
3DL1	1194	OKG	STAD	C	T	C/C	C/T	327	22	154	7	0.676	0.283	1.620	4.96E-01	4.70E-02	411
3DL3	777	OKG	GBM	A	G	A/A	A/G	229	141	119	84	1.150	0.811	1.630	4.98E-01	4.71E-02	412
3DL1	1091	OKG	SKCM	G	A	G/G	G/A	166	53	197	74	1.180	0.784	1.780	4.99E-01	4.73E-02	413
3DL3	906	OKG	HNSC	C	T	C/C	C/T	226	143	203	114	0.888	0.651	1.210	5.00E-01	4.74E-02	414
3DP1	774	OKG	CESC	G	C	G/G	G/C	234	147	43	33	1.220	0.741	2.010	5.09E-01	4.75E-02	415
2DP1	1313	OKG	KIRP	A	C	A/A	A/C	210	112	41	17	0.777	0.422	1.430	5.10E-01	4.76E-02	416
3DL3	804	OKG	BLCA	G	A	G/G	G/A	228	142	93	67	1.160	0.795	1.690	5.10E-01	4.77E-02	417
3DL3	869	OKG	THCA	A	C	A/A	A/C	307	84	173	55	1.160	0.787	1.710	5.10E-01	4.78E-02	418
2DL4	762	OKG	LUSC	C	T	C/C	C/T	89	202	46	88	0.843	0.546	1.300	5.10E-01	4.79E-02	419
2DL4	395	OKG	STAD	C	T	C/C	C/T	355	30	162	10	0.730	0.348	1.530	5.11E-01	4.81E-02	420
2DL5	517	OKG	LUSC	A	G	A/A	A/G	81	44	48	20	0.767	0.405	1.450	5.12E-01	4.82E-02	421
3DL2	497	OKG	HNSC	G	A	G/G	G/A	327	68	291	52	0.859	0.579	1.270	5.13E-01	4.83E-02	422
3DL1	1180	OKG	SKCM	G	C	G/G	G/C	177	86	212	90	0.874	0.612	1.250	5.15E-01	4.84E-02	423
3DL2	474	OKG	STAD	G	T	G/G	G/T	258	127	118	50	0.861	0.581	1.280	5.17E-01	4.85E-02	424
3DL3	621	OKG	THCA	G	A	G/G	G/A	346	49	208	24	0.815	0.486	1.370	5.17E-01	4.86E-02	425
3DL3	804	OKG	COAD	G	A	G/G	G/A	228	142	80	58	1.160	0.779	1.730	5.18E-01	4.87E-02	426
3DL3	408	OKG	BRCA	G	A	G/G	G/A	273	113	301	139	1.120	0.832	1.510	5.19E-01	4.89E-02	427
2DL4	1023	OKG	STAD	G	A	G/G	G/A	258	128	117	50	0.861	0.581	1.280	5.19E-01	4.90E-02	428
3DL3	502	OKG	KIRC	G	A	G/G	G/A	101	187	13	32	1.330	0.668	2.650	5.20E-01	4.91E-02	429
2DL5	583	OKG	LUAD	G	A	G/G	G/A	62	43	60	33	0.793	0.446	1.410	5.20E-01	4.92E-02	430

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL1	607	OKG	OV	C	T	C/C	C/T	151	116	13	14	1.400	0.634	3.090	5.26E-01	4.93E-02	431
3DL1	607	OKG	BLCA	C	T	C/C	C/T	151	116	78	51	0.851	0.555	1.310	5.29E-01	4.94E-02	432
2DP1	766	OKG	OV	G	C	G/G	G/C	174	54	25	5	0.644	0.235	1.760	5.29E-01	4.95E-02	433
2DL3	953	OKG	LIHC	G	A	G/G	G/A	144	104	21	11	0.725	0.335	1.570	5.30E-01	4.97E-02	434
3DL3	408	OKG	UCEC	G	A	G/G	G/A	273	113	158	57	0.872	0.600	1.270	5.31E-01	4.98E-02	435
3DL2	456	OKG	GBM	C	T	C/C	C/T	348	49	183	31	1.200	0.740	1.950	5.33E-01	4.99E-02	436
3DL2	893	OKG	GBM	G	A	G/G	G/A	348	49	183	31	1.200	0.740	1.950	5.33E-01	4.99E-02	436
3DL2	456	OKG	KIRC	C	T	C/C	C/T	348	49	46	9	1.390	0.641	3.020	5.35E-01	5.00E-02	437
3DL2	893	OKG	KIRC	G	A	G/G	G/A	348	49	46	9	1.390	0.641	3.020	5.35E-01	5.00E-02	437
2DL4	480	OKG	STAD	G	A	G/G	G/A	265	113	120	44	0.860	0.571	1.300	5.36E-01	5.01E-02	438
3DP1	479	OKG	UCEC	A	C	A/A	A/C	201	176	115	89	0.884	0.627	1.250	5.36E-01	5.02E-02	439
3DL3	455	OKG	LUAD	G	A	G/G	G/A	367	31	239	25	1.240	0.714	2.150	5.36E-01	5.03E-02	440
2DL4	480	OKG	SARC	G	A	G/G	G/A	265	113	52	27	1.220	0.729	2.040	5.37E-01	5.05E-02	441
3DL2	497	OKG	BRCA	G	A	G/G	G/A	327	68	384	70	0.877	0.609	1.260	5.39E-01	5.06E-02	442
3DL3	502	OKG	LUAD	G	A	G/G	G/A	101	187	63	134	1.150	0.783	1.690	5.43E-01	5.07E-02	443
2DL4	395	OKG	BLCA	C	T	C/C	C/T	355	30	159	10	0.744	0.355	1.560	5.44E-01	5.08E-02	444
2DL4	625	OKG	SARC	C	G	C/C	C/G	191	121	50	26	0.821	0.485	1.390	5.45E-01	5.09E-02	445
3DL2	497	OKG	GBM	G	A	G/G	G/A	327	68	182	32	0.846	0.535	1.340	5.45E-01	5.10E-02	446
2DP1	522	OKG	LUAD	T	C	T/T	T/C	280	86	184	49	0.867	0.583	1.290	5.46E-01	5.11E-02	447
2DP1	804	OKG	LGG	C	A	C/C	C/A	352	8	304	4	0.579	0.173	1.940	5.46E-01	5.13E-02	448
3DP1	796	OKG	CESC	T	C	T/T	T/C	248	134	46	30	1.210	0.730	2.010	5.49E-01	5.14E-02	449
2DP1	1062	OKG	STAD	C	T	C/C	C/T	283	26	147	10	0.740	0.347	1.580	5.50E-01	5.15E-02	450
3DL3	516	OKG	LUAD	C	T	C/C	C/T	388	10	260	4	0.597	0.185	1.920	5.50E-01	5.16E-02	451
3DL3	804	OKG	HNSC	G	A	G/G	G/A	228	142	202	113	0.898	0.658	1.230	5.51E-01	5.17E-02	452
2DP1	1062	OKG	THCA	C	T	C/C	C/T	283	26	198	14	0.770	0.392	1.510	5.52E-01	5.18E-02	453
2DP1	471	OKG	KIRP	A	G	A/A	A/G	292	64	50	8	0.730	0.330	1.610	5.53E-01	5.20E-02	454
3DL2	474	OKG	CESC	G	T	G/G	G/T	258	127	59	24	0.826	0.491	1.390	5.55E-01	5.21E-02	455
3DL3	777	OKG	STAD	A	G	A/A	A/G	229	141	94	66	1.140	0.781	1.660	5.59E-01	5.22E-02	456
3DL3	869	OKG	READ	A	C	A/A	A/C	307	84	43	15	1.270	0.673	2.400	5.61E-01	5.23E-02	457
2DL4	480	OKG	BLCA	G	A	G/G	G/A	265	113	119	44	0.867	0.575	1.310	5.63E-01	5.24E-02	458
3DL3	447	OKG	LGG	G	T	G/G	G/T	345	50	273	46	1.160	0.754	1.780	5.65E-01	5.25E-02	459
3DL3	906	OKG	COAD	C	T	C/C	C/T	226	143	77	56	1.150	0.769	1.720	5.66E-01	5.26E-02	460
2DP1	1269	OKG	KIRP	A	G	A/A	A/G	350	30	57	7	1.430	0.600	3.410	5.68E-01	5.28E-02	461
3DL3	447	OKG	HNSC	G	T	G/G	G/T	345	50	292	49	1.160	0.759	1.770	5.69E-01	5.29E-02	462
3DL1	1091	OKG	THCA	G	A	G/G	G/A	166	53	134	50	1.170	0.747	1.830	5.71E-01	5.30E-02	463
3DP1	796	OKG	BRCA	T	C	T/T	T/C	248	134	291	143	0.909	0.680	1.220	5.71E-01	5.31E-02	464
2DL5	583	OKG	BLCA	G	A	G/G	G/A	62	43	37	20	0.779	0.399	1.520	5.74E-01	5.32E-02	465
2DP1	1269	OKG	LUSC	A	G	A/A	A/G	350	30	181	12	0.773	0.387	1.550	5.77E-01	5.33E-02	466
3DL3	869	OKG	BRCA	A	C	A/A	A/C	307	84	345	105	1.110	0.802	1.540	5.77E-01	5.34E-02	467
3DL3	969	OKG	THCA	C	T	C/C	C/T	329	20	182	8	0.723	0.312	1.670	5.78E-01	5.36E-02	468
3DL3	621	OKG	CESC	G	A	G/G	G/A	346	49	76	8	0.743	0.338	1.630	5.79E-01	5.37E-02	469
3DL3	621	OKG	KIRC	G	A	G/G	G/A	346	49	47	9	1.350	0.623	2.930	5.80E-01	5.38E-02	470
2DP1	766	OKG	SKCM	G	C	G/G	G/C	174	54	156	56	1.160	0.753	1.790	5.82E-01	5.39E-02	471
3DL2	497	OKG	PRAD	G	A	G/G	G/A	327	68	105	26	1.190	0.720	1.970	5.82E-01	5.40E-02	472
3DL3	447	OKG	BLCA	G	T	G/G	G/T	345	50	144	25	1.200	0.715	2.010	5.83E-01	5.41E-02	473
3DL3	869	OKG	LUSC	A	C	A/A	A/C	307	84	150	47	1.150	0.766	1.730	5.84E-01	5.42E-02	474
2DL4	412	OKG	UCEC	G	A	G/G	G/A	229	142	118	82	1.120	0.788	1.590	5.85E-01	5.44E-02	475
3DL3	621	OKG	HNSC	G	A	G/G	G/A	346	49	294	48	1.150	0.750	1.760	5.87E-01	5.45E-02	476
2DL3	953	OKG	KIRP	G	A	G/G	G/A	144	104	25	14	0.775	0.384	1.560	5.91E-01	5.46E-02	477
2DL4	412	OKG	SARC	G	A	G/G	G/A	229	142	50	26	0.839	0.500	1.410	5.92E-01	5.47E-02	478
2DL4	1023	OKG	ACC	G	A	G/G	G/A	258	128	20	13	1.310	0.631	2.720	5.92E-01	5.48E-02	479
2DL4	1023	OKG	LGG	G	A	G/G	G/A	258	128	214	96	0.904	0.656	1.250	5.93E-01	5.49E-02	480
3DP1	479	OKG	SARC	A	C	A/A	A/C	201	176	42	31	0.843	0.508	1.400	5.94E-01	5.50E-02	481
3DL1	607	OKG	STAD	C	T	C/C	C/T	151	116	68	60	1.150	0.753	1.760	5.94E-01	5.52E-02	482
3DL1	607	OKG	LUSC	C	T	C/C	C/T	151	116	74	65	1.140	0.755	1.720	5.94E-01	5.53E-02	483
3DL2	394	OKG	HNSC	C	A	C/C	C/A	365	33	320	24	0.830	0.480	1.430	5.94E-01	5.54E-02	484
3DL3	869	OKG	BLCA	A	C	A/A	A/C	307	84	127	40	1.150	0.748	1.770	5.95E-01	5.55E-02	485
2DP1	522	OKG	THCA	T	C	T/T	T/C	280	86	167	45	0.877	0.583	1.320	5.99E-01	5.56E-02	486
3DL3	804	OKG	STAD	G	A	G/G	G/A	228	142	94	66	1.130	0.774	1.650	6.00E-01	5.57E-02	487
2DP1	471	OKG	GBM	A	G	A/A	A/G	292	64	154	39	1.160	0.745	1.810	6.00E-01	5.58E-02	488
2DP1	766	OKG	UCEC	G	C	G/G	G/C	174	54	157	42	0.862	0.546	1.360	6.03E-01	5.60E-02	489
2DP1	522	OKG	READ	T	C	T/T	T/C	280	86	39	15	1.250	0.657	2.380	6.05E-01	5.61E-02	490
3DL3	621	OKG	STAD	G	A	G/G	G/A	346	49	154	18	0.825	0.465	1.460	6.06E-01	5.62E-02	491
2DP1	471	OKG	CESC	A	G	A/A	A/G	292	64	59	16	1.240	0.670	2.290	6.06E-01	5.63E-02	492
3DL2	474	OKG	LGG	G	T	G/G	G/T	258	127	215	96	0.907	0.658	1.250	6.07E-01	5.64E-02	493
3DL1	1091	OKG	GBM	G	A	G/G	G/A	166	53	142	39	0.860	0.537	1.380	6.11E-01	5.65E-02	494
3DL1	1091	OKG	STAD	G	A	G/G	G/A	166	53	99	37	1.170	0.718	1.910	6.12E-01	5.66E-02	495
3DL3	455	OKG	UCEC	G	A	G/G	G/A	367	31	207	14	0.801	0.417	1.540	6.13E-01	5.68E-02	496
3DL1	607	OKG	SARC	C	T	C/C	C/T	151	116	29	27	1.210	0.679	2.160	6.13E-01	5.69E-02	497
3DL3	408	OKG	KIRP	G	A	G/G	G/A	273	113	42	21	1.210	0.686	2.140	6.14E-01	5.70E-02	498
2DP1	766	OKG	CESC	G	C	G/G	G/C	174	54	60	15	0.806	0.424	1.530	6.16E-01	5.71E-02	499
2DL4	762	OKG	BLCA	C	T	C/C	C/T	89	202	43	85	0.871	0.559	1.360	6.19E-01	5.72E-02	500
3DL1	1180	OKG	UCEC	G	C	G/G	G/C	177	86	126	54	0.882	0.585	1.330	6.20E-01	5.73E-02	501
3DL3	961	OKG	BLCA	C	A	C/C	C/A	118	103	41	42	1.170	0.706	1.940	6.22E-01	5.74E-02	502
3DL2	456	OKG	LUSC	C	T	C/C	C/T	348	49	170	28	1.170	0.710	1.930	6.27E-01	5.76E-02	503
3DL2	893	OKG	LUSC	G	A	G/G	G/A	348	49	170	28	1.170	0.710	1.930	6.27E-01	5.76E-02	503
3DL1	607	OKG	HNSC	C	T	C/C	C/T	151	116	147	102	0.903	0.636	1.280	6.30E-01	5.77E-02	504
3DL1	496	OKG	BLCA	C	A	C/C	C/A	362	14	158	4	0.655	0.212	2.020	6.31E-01	5.78E-02	505
3DL1	1026	OKG	GBM	G	C	G/G	G/C	160	52	142	40	0.867	0.542	1.390	6.33E-01	5.79E-02	506
3DL3	455	OKG	BLCA	G	A	G/G	G/A	367	31	154	16	1.230	0.654	2.310	6.34E-01	5.80E-02	507
3DL3	906	OKG	SKCM	C	T	C/C	C/T	226	143	193	133	1.090	0.804	1.480	6.37E-01	5.81E-02	508
2DP1	448	OKG	LGG	G	C	G/G	G/C	138	151	115	114	0.906	0.640	1.280	6.39E-01	5.82E-02	509
2DP1	1062	OKG	BLCA	C	T	C/C	C/T	283	26	140	10	0.777	0.365	1.660	6.40E-01	5.84E-02	510
3DL1	1021	OKG	LGG	A	G	A/A	A/G	153	14	146	10	0.749	0.323	1.740	6.43E-01	5.85E-02	511
2DL4	1023	OKG	BLCA	G	A	G/G	G/A	258	128	115	51	0.894	0.604	1.320	6.44E-01	5.86E-02	512
3DL3	906	OKG	BRCA	C	T	C/C	C/T	226	143	256	175	1.080	0.813	1.440	6.45E-01	5.87E-02	513
2DL4	762	OKG	HNSC	C	T	C/C	C/T	89	202	82	168	0.903	0.628	1.300	6.46E-01	5.88E-02	514
3DL3	906	OKG	GBM	C	T	C/C	C/T	226	143	119	83	1.100	0.775	1.560	6.48E-01	5.89E-02	515
3DL3	408	OKG	CESC	G	A	G/G	G/A	273	113	56	27	1.160	0.697	1.930	6.49E-01	5.90E-02	516
2DL4	625	OKG	UCEC	C	G	C/C	C/G	191	121	117	82	1.110	0.772	1.600	6.50E-01	5.92E-02	517
2DL4	480	OKG	THCA	G	A	G/G	G/A	265	113	166	64	0.904	0.629	1.300	6.51E-01	5.93E-02	518
2DL5	517	OKG	BRCA	A	G	A/A	A/G	81	44	82	38	0.853	0.501	1.450	6.52E-01	5.94E-02	519
2DP1	1313	OKG	BLCA	A	C	A/A	A/C	210	112	97	46	0.889	0.585	1.350	6.58E-01	5.95E-02	520
3DL3	455	OKG	SKCM	G	A	G/G	G/A	367	31	315	31	1.170	0.696	1.970	6.58E-01	5.96E-02	521
3DL3	906	OKG	STAD	C	T	C/C	C/T	226	143	94	66	1.110	0.761	1.620	6.58E-01	5.97E-02	522
3DL1	607	OKG	SKCM	C	T	C/C	C/T	151	116	140	118	1.100	0.780	1.550	6.60E-01	5.98E-02	523
2DP1	1269	OKG	THCA	A	G	A/A	A/G	350	30	213	15	0.822	0.432	1.560	6.60E-01	6.00E-02	524
2DP1	471	OKG	KIRC	A	G	A/A	A/G	292	64	42	7	0.760	0.327	1.770	6.62E-01	6.01E-02	525
2DL4	480	OKG	LIHC	G	A	G/G	G/A	265	113	33	17	1.210	0.648	2.260	6.67E-01	6.02E-02	526
2DP1	1313	OKG	LIHC	A	C	A/A	A/C	210	112	28	12	0.804	0.394	1.640	6.71E-01	6.03E-02	527
3DL2	474	OKG	BLCA	G	T	G/G	G/T	258	127	115	51	0.901	0.609	1.330	6.73E-01	6.04E-02	528
3DL3	969	OKG	STAD	C	T	C/C	C/T	329	20	134	6	0.737	0.290	1.880	6.74E-01	6.05E-02	529
3DL3	804	OKG	LGG	G	A	G/G	G/A	228	142	178	120	1.080	0.790	1.480	6.76E-01	6.06E-02	530
3DL1	1026	OKG	BRCA	G	C	G/G	G/C	160	52	280	82	0.901	0.605	1.340	6.81E-01	6.08E-02	531
2DP1	1313	OKG	CESC	A	C	A/A	A/C	210	112	36	16	0.833	0.443	1.570	6.83E-01	6.09E-02	532
2DL4	1023	OKG	CESC	G	A	G/G	G/A	258	128	58	25	0.869	0.519	1.450	6.84E-01	6.10E-02	533
2DL4	762	OKG	LUAD	C	T	C/C	C/T	89	202	69	142	0.907	0.620	1.330	6.84E-01	6.11E-02	534
3DL3	961	OKG	CESC	C	A	C/C	C/A	118	103	25	18	0.825	0.426	1.600	6.86E-01	6.12E-02	535
3DL1	1180	OKG	PRAD	G	C	G/G	G/C	177	86	67	37	1.140	0.708	1.840	6.87E-01	6.13E-02	536
3DL3	869	OKG	KIRP	A	C	A/A	A/C	307	84	49	16	1.190	0.644	2.200	6.87E-01	6.14E-02	537

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL1	1091	OKG	UCEC	G	A	G/G	G/A	166	53	135	38	0.882	0.549	1.420	6.89E-01	6.16E-02	538
3DL3	447	OKG	STAD	G	T	G/G	G/T	345	50	153	19	0.857	0.489	1.500	6.89E-01	6.17E-02	539
3DL3	777	OKG	SKCM	A	G	A/A	A/G	229	141	196	130	1.080	0.796	1.470	6.89E-01	6.18E-02	540
2DL5	517	OKG	STAD	A	G	A/A	A/G	81	44	34	15	0.812	0.399	1.650	6.91E-01	6.19E-02	541
3DL3	869	OKG	SARC	A	C	A/A	A/C	307	84	65	15	0.843	0.458	1.550	6.92E-01	6.20E-02	542
3DP1	774	OKG	PRAD	G	C	G/G	G/C	234	147	73	41	0.894	0.579	1.380	6.93E-01	6.21E-02	543
3DP1	479	OKG	CESC	A	C	A/A	A/C	201	176	43	33	0.876	0.533	1.440	6.93E-01	6.22E-02	544
2DL4	625	OKG	KIRC	C	G	C/C	C/G	191	121	32	17	0.839	0.446	1.580	6.97E-01	6.24E-02	545
3DL3	455	OKG	LUSC	G	A	G/G	G/A	367	31	180	18	1.180	0.643	2.170	6.99E-01	6.25E-02	546
2DL4	412	OKG	STAD	G	A	G/G	G/A	229	142	94	64	1.100	0.752	1.610	7.01E-01	6.26E-02	547
3DL1	607	OKG	UCEC	C	T	C/C	C/T	151	116	92	64	0.906	0.607	1.350	7.01E-01	6.27E-02	548
2DL4	625	OKG	KIRP	C	G	C/C	C/G	191	121	37	20	0.853	0.473	1.540	7.04E-01	6.28E-02	549
2DL4	412	OKG	LGG	G	A	G/G	G/A	229	142	183	122	1.080	0.792	1.470	7.05E-01	6.29E-02	550
3DL3	516	OKG	THCA	C	T	C/C	C/T	388	10	229	4	0.678	0.210	2.190	7.08E-01	6.30E-02	551
3DL2	394	OKG	KIRP	C	A	C/C	C/A	365	33	62	4	0.714	0.244	2.090	7.08E-01	6.32E-02	552
3DL1	607	OKG	LGG	C	T	C/C	C/T	151	116	140	99	0.921	0.647	1.310	7.12E-01	6.33E-02	553
2DP1	522	OKG	HNSC	T	C	T/T	T/C	280	86	240	80	1.090	0.768	1.550	7.12E-01	6.34E-02	554
3DL2	456	OKG	READ	C	T	C/C	C/T	348	49	51	9	1.250	0.579	2.700	7.13E-01	6.35E-02	555
3DL2	893	OKG	READ	G	A	G/G	G/A	348	49	51	9	1.250	0.579	2.700	7.13E-01	6.35E-02	555
3DL3	1042	OKG	COAD	G	C	G/G	G/C	235	26	112	10	0.807	0.376	1.730	7.16E-01	6.36E-02	556
2DL4	625	OKG	CESC	C	G	C/C	C/G	191	121	52	29	0.880	0.529	1.460	7.16E-01	6.37E-02	557
2DL5	517	OKG	HNSC	A	G	A/A	A/G	81	44	66	31	0.865	0.493	1.520	7.16E-01	6.38E-02	558
2DL4	762	OKG	SKCM	C	T	C/C	C/T	89	202	81	169	0.919	0.639	1.320	7.18E-01	6.40E-02	559
3DL3	961	OKG	SKCM	C	A	C/C	C/A	118	103	103	82	0.912	0.616	1.350	7.19E-01	6.41E-02	560
3DP1	796	OKG	PRAD	T	C	T/T	T/C	248	134	77	46	1.110	0.728	1.690	7.20E-01	6.42E-02	561
2DP1	1269	OKG	STAD	A	G	A/A	A/G	350	30	156	11	0.823	0.402	1.680	7.20E-01	6.43E-02	562
2DL4	1023	OKG	GBM	G	A	G/G	G/A	258	128	136	62	0.919	0.636	1.330	7.20E-01	6.44E-02	563
3DL1	496	OKG	BRCA	C	A	C/C	C/A	362	14	416	13	0.808	0.375	1.740	7.27E-01	6.45E-02	564
3DL1	1180	OKG	OV	G	C	G/G	G/C	177	86	20	12	1.230	0.575	2.630	7.30E-01	6.47E-02	565
3DL1	1091	OKG	BRCA	G	A	G/G	G/A	166	53	281	82	0.914	0.616	1.360	7.30E-01	6.48E-02	566
3DL3	906	OKG	LIHC	C	T	C/C	C/T	226	143	27	20	1.170	0.633	2.160	7.31E-01	6.49E-02	567
3DL1	496	OKG	SKCM	C	A	C/C	C/A	362	14	317	15	1.220	0.580	2.570	7.32E-01	6.50E-02	568
2DL4	480	OKG	SKCM	G	A	G/G	G/A	265	113	239	95	0.932	0.674	1.290	7.32E-01	6.51E-02	569
2DP1	1269	OKG	LGG	A	G	A/A	A/G	350	30	283	21	0.866	0.485	1.550	7.33E-01	6.52E-02	570
3DL3	502	OKG	COAD	G	A	G/G	G/A	101	187	42	70	0.900	0.572	1.420	7.34E-01	6.53E-02	571
3DL3	969	OKG	LUAD	C	T	C/C	C/T	329	20	203	10	0.810	0.372	1.770	7.36E-01	6.55E-02	572
3DL3	502	OKG	ACC	G	A	G/G	G/A	101	187	12	18	0.810	0.375	1.750	7.36E-01	6.56E-02	573
3DL1	1026	OKG	UCEC	G	C	G/G	G/C	160	52	134	39	0.896	0.558	1.440	7.37E-01	6.57E-02	574
2DL4	762	OKG	BRCA	C	T	C/C	C/T	89	202	107	226	0.931	0.663	1.310	7.42E-01	6.58E-02	575
2DL4	412	OKG	KIRC	G	A	G/G	G/A	229	142	32	17	0.857	0.459	1.600	7.42E-01	6.59E-02	576
3DL3	777	OKG	BRCA	A	G	A/A	A/G	229	141	262	171	1.060	0.797	1.410	7.43E-01	6.60E-02	577
3DP1	479	OKG	KIRC	A	C	A/A	A/C	201	176	29	22	0.866	0.480	1.560	7.44E-01	6.61E-02	578
3DL3	516	OKG	LGG	C	T	C/C	C/T	388	10	315	6	0.739	0.266	2.060	7.44E-01	6.63E-02	579
3DL3	804	OKG	SKCM	G	A	G/G	G/A	228	142	196	130	1.060	0.781	1.440	7.44E-01	6.64E-02	580
3DL3	869	OKG	LIHC	A	C	A/A	A/C	307	84	40	13	1.190	0.609	2.330	7.44E-01	6.65E-02	581
3DL3	408	OKG	COAD	G	A	G/G	G/A	273	113	97	44	1.100	0.724	1.670	7.48E-01	6.66E-02	582
2DP1	1062	OKG	CESC	C	T	C/C	C/T	283	26	72	5	0.756	0.281	2.040	7.49E-01	6.67E-02	583
2DP1	1313	OKG	SARC	A	C	A/A	A/C	210	112	27	12	0.833	0.406	1.710	7.49E-01	6.68E-02	584
3DL3	777	OKG	LIHC	A	G	A/A	A/G	229	141	28	20	1.160	0.630	2.140	7.50E-01	6.69E-02	585
3DL3	804	OKG	BRCA	G	A	G/G	G/A	228	142	261	172	1.060	0.798	1.410	7.52E-01	6.71E-02	586
3DL3	621	OKG	LGG	G	A	G/G	G/A	346	49	276	43	1.100	0.709	1.710	7.54E-01	6.72E-02	587
3DP1	774	OKG	KIRP	G	C	G/G	G/C	234	147	35	25	1.140	0.656	1.980	7.54E-01	6.73E-02	588
2DP1	522	OKG	CESC	T	C	T/T	T/C	280	86	60	16	0.868	0.475	1.580	7.56E-01	6.74E-02	589
2DP1	522	OKG	ACC	T	C	T/T	T/C	280	86	25	6	0.781	0.310	1.970	7.62E-01	6.75E-02	590
2DP1	1313	OKG	STAD	A	C	A/A	A/C	210	112	100	49	0.919	0.609	1.390	7.65E-01	6.76E-02	591
3DP1	796	OKG	KIRC	T	C	T/T	T/C	248	134	34	21	1.140	0.636	2.040	7.65E-01	6.77E-02	592
2DL4	762	OKG	SARC	C	T	C/C	C/T	89	202	16	42	1.160	0.619	2.170	7.66E-01	6.79E-02	593
3DL3	961	OKG	KIRC	C	A	C/C	C/A	118	103	18	13	0.827	0.386	1.770	7.67E-01	6.80E-02	594
2DL4	1023	OKG	BRCA	G	A	G/G	G/A	258	128	296	139	0.947	0.707	1.270	7.69E-01	6.81E-02	595
2DL4	412	OKG	CESC	G	A	G/G	G/A	229	142	52	29	0.899	0.545	1.480	7.72E-01	6.82E-02	596
2DL4	625	OKG	STAD	C	G	C/C	C/G	191	121	95	65	1.080	0.732	1.590	7.73E-01	6.83E-02	597
3DL3	961	OKG	LGG	C	A	C/C	C/A	118	103	90	85	1.080	0.726	1.610	7.74E-01	6.84E-02	598
3DL1	1021	OKG	THCA	A	G	A/A	A/G	153	14	123	9	0.800	0.335	1.910	7.75E-01	6.85E-02	599
2DP1	766	OKG	GBM	G	C	G/G	G/C	174	54	135	38	0.907	0.566	1.450	7.75E-01	6.87E-02	600
2DL4	412	OKG	LUSC	G	A	G/G	G/A	229	142	121	70	0.933	0.650	1.340	7.76E-01	6.88E-02	601
3DL3	804	OKG	LIHC	G	A	G/G	G/A	228	142	28	20	1.150	0.624	2.120	7.78E-01	6.89E-02	602
2DP1	471	OKG	LIHC	A	G	A/A	A/G	292	64	38	10	1.200	0.568	2.530	7.78E-01	6.90E-02	603
3DL3	621	OKG	LIHC	G	A	G/G	G/A	346	49	46	8	1.230	0.548	2.760	7.79E-01	6.91E-02	604
2DP1	522	OKG	LUSC	T	C	T/T	T/C	280	86	135	45	1.090	0.720	1.650	7.80E-01	6.92E-02	605
2DL4	395	OKG	HNSC	C	T	C/C	C/T	355	30	320	24	0.888	0.508	1.550	7.81E-01	6.93E-02	606
2DL4	412	OKG	KIRP	G	A	G/G	G/A	229	142	40	22	0.887	0.506	1.550	7.81E-01	6.95E-02	607
3DL3	621	OKG	READ	G	A	G/G	G/A	346	49	53	6	0.799	0.326	1.960	7.82E-01	6.96E-02	608
3DL1	1026	OKG	STAD	G	C	G/G	G/C	160	52	103	37	1.110	0.681	1.810	7.82E-01	6.97E-02	609
3DP1	796	OKG	OV	T	C	T/T	T/C	248	134	22	14	1.180	0.585	2.380	7.84E-01	6.98E-02	610
2DP1	522	OKG	BRCA	T	C	T/T	T/C	280	86	315	91	0.941	0.673	1.320	7.86E-01	6.99E-02	611
2DL4	412	OKG	BRCA	G	A	G/G	G/A	229	142	253	165	1.050	0.788	1.400	7.86E-01	7.00E-02	612
3DP1	691	OKG	THCA	C	T	C/C	C/T	370	24	213	16	1.160	0.603	2.230	7.87E-01	7.01E-02	613
3DL3	869	OKG	GBM	A	C	A/A	A/C	307	84	170	43	0.924	0.612	1.400	7.88E-01	7.03E-02	614
2DP1	1269	OKG	BLCA	A	G	A/A	A/G	350	30	151	11	0.850	0.415	1.740	7.89E-01	7.04E-02	615
3DL2	456	OKG	CESC	C	T	C/C	C/T	348	49	76	9	0.841	0.396	1.790	7.89E-01	7.05E-02	616
3DL2	893	OKG	CESC	G	A	G/G	G/A	348	49	76	9	0.841	0.396	1.790	7.89E-01	7.05E-02	616
3DL3	447	OKG	KIRP	G	T	G/G	G/T	345	50	59	7	0.819	0.354	1.890	7.90E-01	7.06E-02	617
2DL4	625	OKG	LUSC	C	G	C/C	C/G	191	121	120	71	0.934	0.644	1.350	7.90E-01	7.07E-02	618
3DL1	732	OKG	BRCA	T	C	T/T	T/C	55	46	60	56	1.120	0.656	1.910	7.90E-01	7.08E-02	619
3DL3	408	OKG	READ	G	A	G/G	G/A	273	113	44	16	0.879	0.476	1.620	7.94E-01	7.09E-02	620
3DL3	869	OKG	KIRC	A	C	A/A	A/C	307	84	41	13	1.160	0.594	2.260	7.98E-01	7.11E-02	621
3DL1	496	OKG	LUAD	C	A	C/C	C/A	362	14	235	11	1.210	0.540	2.710	7.98E-01	7.12E-02	622
2DP1	448	OKG	STAD	G	C	G/G	G/C	138	151	54	64	1.080	0.703	1.660	7.99E-01	7.13E-02	623
3DP1	691	OKG	LUAD	C	T	C/C	C/T	370	24	250	14	0.863	0.438	1.700	7.99E-01	7.14E-02	624
2DP1	448	OKG	READ	G	C	G/G	G/C	138	151	22	21	0.872	0.459	1.660	7.99E-01	7.15E-02	625
2DL5	517	OKG	LGG	A	G	A/A	A/G	81	44	62	30	0.891	0.504	1.580	8.00E-01	7.16E-02	626
3DL2	394	OKG	LGG	C	A	C/C	C/A	365	33	296	24	0.897	0.519	1.550	8.02E-01	7.17E-02	627
3DL3	961	OKG	THCA	C	A	C/C	C/A	118	103	66	53	0.920	0.588	1.440	8.02E-01	7.19E-02	628
3DL3	1042	OKG	SARC	G	C	G/G	G/C	235	26	59	8	1.230	0.530	2.860	8.03E-01	7.20E-02	629
2DP1	522	OKG	PRAD	T	C	T/T	T/C	280	86	93	26	0.910	0.553	1.500	8.06E-01	7.21E-02	630
3DL1	496	OKG	UCEC	C	A	C/C	C/A	362	14	197	6	0.788	0.298	2.080	8.07E-01	7.22E-02	631
2DP1	1269	OKG	CESC	A	G	A/A	A/G	350	30	74	5	0.788	0.296	2.100	8.07E-01	7.23E-02	632
2DP1	522	OKG	LGG	T	C	T/T	T/C	280	86	222	64	0.939	0.650	1.360	8.08E-01	7.24E-02	633
3DL2	497	OKG	CESC	G	A	G/G	G/A	327	68	68	16	1.130	0.618	2.070	8.08E-01	7.25E-02	634
2DL4	395	OKG	KIRP	C	T	C/C	C/T	355	30	62	4	0.763	0.260	2.240	8.10E-01	7.27E-02	635
2DL4	480	OKG	OV	G	A	G/G	G/A	265	113	24	12	1.170	0.565	2.420	8.11E-01	7.28E-02	636
3DL1	1091	OKG	BLCA	G	A	G/G	G/A	166	53	97	34	1.100	0.668	1.810	8.11E-01	7.29E-02	637
3DL2	497	OKG	BLCA	G	A	G/G	G/A	327	68	142	27	0.914	0.561	1.490	8.12E-01	7.30E-02	638
3DP1	479	OKG	KIRP	A	C	A/A	A/C	201	176	33	26	0.900	0.518	1.560	8.15E-01	7.31E-02	639
3DL3	502	OKG	THCA	G	A	G/G	G/A	101	187	68	118	0.937	0.638	1.380	8.16E-01	7.32E-02	640
3DL1	1180	OKG	ACC	G	C	G/G	G/C	177	86	20	8	0.823	0.348	1.940	8.17E-01	7.33E-02	641
3DL3	906	OKG	SARC	C	T	C/C	C/T	226	143	42	24	0.903	0.524	1.550	8.18E-01	7.35E-02	642
3DL3	777	OKG	ACC	A	G	A/A	A/G	229	141	18	13	1.170	0.556	2.460	8.19E-01	7.36E-02	643
2DL4	625	OKG	LGG	C	G	C/C	C/G	191	121	183	122	1.050	0.760	1.450	8.20E-01	7.37E-02	644
2DP1	766	OKG	BLCA	G	C	G/G	G/C	174	54	88	30	1.100	0.657	1.840	8.22E-01	7.38E-02	645

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	777	OKG	LGG	A	G	A/A	A/G	229	141	181	117	1.050	0.768	1.440	8.22E-01	7.39E-02	646
2DL4	412	OKG	HNSC	G	A	G/G	G/A	229	142	197	128	1.050	0.774	1.430	8.24E-01	7.40E-02	647
2DL4	412	OKG	READ	G	A	G/G	G/A	229	142	36	20	0.896	0.499	1.610	8.26E-01	7.41E-02	648
2DL4	412	OKG	OV	G	A	G/G	G/A	229	142	21	15	1.150	0.574	2.300	8.26E-01	7.43E-02	649
2DP1	1062	OKG	GBM	C	T	C/C	C/T	283	26	186	15	0.878	0.453	1.700	8.26E-01	7.44E-02	650
3DL1	607	OKG	LUAD	C	T	C/C	C/T	151	116	116	84	0.943	0.651	1.370	8.27E-01	7.45E-02	651
3DL3	969	OKG	HNSC	C	T	C/C	C/T	329	20	283	15	0.872	0.438	1.740	8.29E-01	7.46E-02	652
3DL2	893	OKG	LGG	G	A	G/G	G/A	348	49	277	42	1.080	0.695	1.680	8.29E-01	7.47E-02	653
2DP1	448	OKG	BLCA	G	C	G/G	G/C	138	151	58	68	1.070	0.703	1.630	8.29E-01	7.48E-02	654
3DL3	502	OKG	LUSC	G	A	G/G	G/A	101	187	56	97	0.936	0.622	1.410	8.30E-01	7.49E-02	655
3DL1	1026	OKG	HNSC	G	C	G/G	G/C	160	52	213	74	1.070	0.710	1.610	8.30E-01	7.51E-02	656
3DL3	621	OKG	KIRP	G	A	G/G	G/A	346	49	59	7	0.838	0.362	1.940	8.33E-01	7.52E-02	657
3DL1	1021	OKG	PRAD	A	G	A/A	A/G	153	14	71	8	1.230	0.494	3.070	8.35E-01	7.53E-02	658
3DL3	961	OKG	LIHC	C	A	C/C	C/A	118	103	15	11	0.840	0.369	1.910	8.35E-01	7.54E-02	659
3DL3	455	OKG	STAD	G	A	G/G	G/A	367	31	157	15	1.130	0.593	2.150	8.36E-01	7.55E-02	660
2DP1	522	OKG	GBM	T	C	T/T	T/C	280	86	153	44	0.936	0.619	1.420	8.36E-01	7.56E-02	661
2DL5	517	OKG	READ	A	G	A/A	A/G	81	44	16	7	0.805	0.308	2.100	8.39E-01	7.57E-02	662
3DL2	474	OKG	ACC	G	T	G/G	G/T	258	127	21	12	1.160	0.553	2.430	8.39E-01	7.59E-02	663
3DL2	893	OKG	SARC	G	A	G/G	G/A	348	49	68	11	1.150	0.569	2.320	8.41E-01	7.60E-02	664
3DL3	804	OKG	ACC	G	A	G/G	G/A	228	142	18	13	1.160	0.552	2.440	8.43E-01	7.61E-02	665
3DL3	961	OKG	UCEC	C	A	C/C	C/A	118	103	63	59	1.070	0.687	1.670	8.43E-01	7.62E-02	666
3DL1	1180	OKG	KIRP	G	C	G/G	G/C	177	86	33	18	1.120	0.597	2.100	8.43E-01	7.63E-02	667
3DL3	408	OKG	STAD	G	A	G/G	G/A	273	113	116	51	1.060	0.714	1.570	8.43E-01	7.64E-02	668
3DL1	1161	OKG	BRCA	C	T	C/C	C/T	196	6	222	5	0.736	0.221	2.450	8.45E-01	7.65E-02	669
3DL1	1091	OKG	HNSC	G	A	G/G	G/A	166	53	206	70	1.060	0.703	1.600	8.48E-01	7.67E-02	670
3DL2	474	OKG	GBM	G	T	G/G	G/T	258	127	137	64	0.949	0.659	1.370	8.51E-01	7.68E-02	671
3DL2	474	OKG	UCEC	G	T	G/G	G/T	258	127	143	67	0.952	0.664	1.360	8.59E-01	7.69E-02	672
2DL4	395	OKG	PRAD	C	T	C/C	C/T	355	30	123	9	0.866	0.400	1.880	8.61E-01	7.70E-02	673
2DL4	395	OKG	LGG	C	T	C/C	C/T	355	30	298	23	0.913	0.519	1.610	8.64E-01	7.71E-02	674
2DL4	625	OKG	COAD	C	G	C/C	C/G	191	121	59	40	1.070	0.674	1.700	8.65E-01	7.72E-02	675
3DL2	394	OKG	THCA	C	A	C/C	C/A	365	33	212	21	1.100	0.620	1.950	8.69E-01	7.74E-02	676
3DP1	796	OKG	KIRP	T	C	T/T	T/C	248	134	39	23	1.090	0.625	1.900	8.69E-01	7.75E-02	677
3DL3	621	OKG	PRAD	G	A	G/G	G/A	346	49	117	15	0.905	0.489	1.670	8.70E-01	7.76E-02	678
3DL3	969	OKG	COAD	C	T	C/C	C/T	329	20	119	6	0.829	0.325	2.110	8.70E-01	7.77E-02	679
3DL2	456	OKG	SARC	C	T	C/C	C/T	348	49	69	11	1.130	0.559	2.280	8.72E-01	7.78E-02	680
2DP1	1269	OKG	SKCM	A	G	A/A	A/G	350	30	305	24	0.918	0.525	1.600	8.74E-01	7.79E-02	681
3DL1	607	OKG	COAD	C	T	C/C	C/T	151	116	53	38	0.933	0.576	1.510	8.74E-01	7.80E-02	682
3DL1	1194	OKG	PRAD	C	T	C/C	C/T	327	22	115	9	1.160	0.519	2.590	8.75E-01	7.82E-02	683
3DL1	607	OKG	LIHC	C	T	C/C	C/T	151	116	22	15	0.888	0.441	1.790	8.75E-01	7.83E-02	684
3DL3	906	OKG	ACC	C	T	C/C	C/T	226	143	18	13	1.140	0.542	2.400	8.75E-01	7.84E-02	685
2DL4	625	OKG	OV	C	G	C/C	C/G	191	121	21	15	1.130	0.561	2.280	8.76E-01	7.85E-02	686
3DL3	969	OKG	UCEC	C	T	C/C	C/T	329	20	189	10	0.870	0.399	1.900	8.78E-01	7.86E-02	687
3DL3	502	OKG	LIHC	G	A	G/G	G/A	101	187	14	23	0.887	0.437	1.800	8.82E-01	7.87E-02	688
3DL3	502	OKG	HNSC	G	A	G/G	G/A	101	187	89	172	1.040	0.731	1.480	8.82E-01	7.88E-02	689
3DL1	732	OKG	SARC	T	C	T/T	T/C	55	46	18	13	0.864	0.383	1.950	8.83E-01	7.90E-02	690
3DL1	1194	OKG	BLCA	C	T	C/C	C/T	327	22	154	9	0.869	0.391	1.930	8.83E-01	7.91E-02	691
3DL1	607	OKG	BRCA	C	T	C/C	C/T	151	116	192	142	0.963	0.696	1.330	8.84E-01	7.92E-02	692
3DL1	607	OKG	READ	C	T	C/C	C/T	151	116	21	18	1.120	0.571	2.200	8.84E-01	7.93E-02	693
2DP1	804	OKG	HNSC	C	A	C/C	C/A	352	8	331	6	0.798	0.274	2.320	8.84E-01	7.94E-02	694
3DL3	502	OKG	UCEC	G	A	G/G	G/A	101	187	57	111	1.050	0.703	1.570	8.85E-01	7.95E-02	695
3DL3	621	OKG	LUSC	G	A	G/G	G/A	346	49	175	23	0.928	0.547	1.570	8.85E-01	7.96E-02	696
2DL4	625	OKG	READ	C	G	C/C	C/G	191	121	28	16	0.902	0.468	1.740	8.86E-01	7.98E-02	697
3DP1	796	OKG	BLCA	T	C	T/T	T/C	248	134	106	60	1.050	0.718	1.540	8.87E-01	7.99E-02	698
3DL3	906	OKG	LGG	C	T	C/C	C/T	226	143	180	118	1.040	0.761	1.420	8.87E-01	8.00E-02	699
2DP1	1062	OKG	SARC	C	T	C/C	C/T	283	26	66	5	0.825	0.305	2.230	8.88E-01	8.01E-02	700
3DL3	869	OKG	SKCM	A	C	A/A	A/C	307	84	263	75	1.040	0.731	1.480	8.88E-01	8.02E-02	701
2DL5	583	OKG	READ	G	A	G/G	G/A	62	43	8	7	1.260	0.425	3.730	8.89E-01	8.03E-02	702
2DP1	766	OKG	LIHC	G	C	G/G	G/C	174	54	25	9	1.160	0.510	2.640	8.89E-01	8.04E-02	703
3DL2	456	OKG	KIRP	C	T	C/C	C/T	348	49	56	9	1.140	0.531	2.450	8.91E-01	8.06E-02	704
3DL2	893	OKG	KIRP	G	A	G/G	G/A	348	49	56	9	1.140	0.531	2.450	8.91E-01	8.06E-02	704
3DL1	496	OKG	THCA	C	A	C/C	C/A	362	14	215	7	0.842	0.335	2.120	8.92E-01	8.07E-02	705
3DL1	1161	OKG	SKCM	C	T	C/C	C/T	196	6	266	10	1.230	0.440	3.440	8.93E-01	8.08E-02	706
3DL1	1026	OKG	LUAD	G	C	G/G	G/C	160	52	150	46	0.944	0.599	1.490	8.93E-01	8.09E-02	707
2DL4	1023	OKG	OV	G	A	G/G	G/A	258	128	25	11	0.887	0.423	1.860	8.94E-01	8.10E-02	708
2DP1	766	OKG	THCA	G	C	G/G	G/C	174	54	140	41	0.944	0.594	1.500	8.98E-01	8.11E-02	709
3DL3	447	OKG	LUAD	G	T	G/G	G/T	345	50	228	35	1.060	0.667	1.680	9.01E-01	8.12E-02	710
3DL2	474	OKG	BRCA	G	T	G/G	G/T	258	127	295	141	0.971	0.725	1.300	9.02E-01	8.14E-02	711
2DL4	625	OKG	HNSC	C	G	C/C	C/G	191	121	197	129	1.030	0.749	1.420	9.02E-01	8.15E-02	712
2DP1	522	OKG	SKCM	T	C	T/T	T/C	280	86	235	75	1.040	0.729	1.480	9.04E-01	8.16E-02	713
3DP1	691	OKG	PRAD	C	T	C/C	C/T	370	24	125	7	0.863	0.363	2.050	9.05E-01	8.17E-02	714
2DL4	480	OKG	ACC	G	A	G/G	G/A	265	113	24	9	0.879	0.396	1.950	9.07E-01	8.18E-02	715
3DL3	804	OKG	SARC	G	A	G/G	G/A	228	142	43	25	0.934	0.547	1.600	9.08E-01	8.19E-02	716
3DL1	1026	OKG	LGG	G	C	G/G	G/C	160	52	197	61	0.953	0.623	1.460	9.09E-01	8.20E-02	717
3DL2	474	OKG	OV	G	T	G/G	G/T	258	127	25	11	0.894	0.426	1.870	9.11E-01	8.22E-02	718
3DL2	456	OKG	THCA	C	T	C/C	C/T	348	49	201	30	1.060	0.652	1.720	9.12E-01	8.23E-02	719
3DL2	893	OKG	THCA	G	A	G/G	G/A	348	49	201	30	1.060	0.652	1.720	9.12E-01	8.23E-02	719
2DL3	953	OKG	KIRC	G	A	G/G	G/A	144	104	23	15	0.903	0.449	1.810	9.12E-01	8.24E-02	720
3DL1	1180	OKG	LIHC	G	C	G/G	G/C	177	86	20	11	1.130	0.518	2.460	9.12E-01	8.25E-02	721
2DP1	766	OKG	LUAD	G	C	G/G	G/C	174	54	146	43	0.949	0.601	1.500	9.14E-01	8.26E-02	722
3DL3	869	OKG	CESC	A	C	A/A	A/C	307	84	67	17	0.927	0.517	1.660	9.15E-01	8.27E-02	723
2DP1	1269	OKG	GBM	A	G	A/A	A/G	350	30	191	15	0.916	0.481	1.740	9.17E-01	8.28E-02	724
3DL1	1021	OKG	STAD	A	G	A/A	A/G	153	14	90	7	0.850	0.331	2.180	9.19E-01	8.30E-02	725
3DL1	496	OKG	STAD	C	A	C/C	C/A	362	14	156	5	0.829	0.294	2.340	9.20E-01	8.31E-02	726
2DP1	1269	OKG	COAD	A	G	A/A	A/G	350	30	130	10	0.897	0.426	1.890	9.20E-01	8.32E-02	727
2DP1	448	OKG	UCEC	G	C	G/G	G/C	138	151	76	80	0.962	0.652	1.420	9.24E-01	8.33E-02	728
2DP1	471	OKG	OV	A	G	A/A	A/G	292	64	27	5	0.845	0.313	2.280	9.27E-01	8.34E-02	729
2DL5	517	OKG	GBM	A	G	A/A	A/G	81	44	42	21	0.920	0.485	1.740	9.27E-01	8.35E-02	730
3DL2	456	OKG	LGG	C	T	C/C	C/T	348	49	278	41	1.050	0.674	1.640	9.27E-01	8.36E-02	731
2DL4	762	OKG	CESC	C	T	C/C	C/T	89	202	19	40	0.928	0.509	1.690	9.28E-01	8.38E-02	732
2DL5	517	OKG	CESC	A	G	A/A	A/G	81	44	16	10	1.150	0.481	2.750	9.28E-01	8.39E-02	733
2DL3	953	OKG	COAD	G	A	G/G	G/A	144	104	58	44	1.050	0.659	1.670	9.30E-01	8.40E-02	734
3DL1	1026	OKG	THCA	G	C	G/G	G/C	160	52	144	49	1.050	0.669	1.650	9.32E-01	8.41E-02	735
3DL2	896	OKG	LGG	C	A	C/C	C/A	392	6	315	6	1.240	0.396	3.880	9.33E-01	8.42E-02	736
3DP1	479	OKG	OV	A	C	A/A	A/C	201	176	20	16	0.914	0.459	1.820	9.34E-01	8.43E-02	737
3DL1	651	OKG	BRCA	CA	C	CA/CA	CA/C	13	7	58	26	0.833	0.298	2.330	9.34E-01	8.44E-02	738
2DL4	480	OKG	BRCA	G	A	G/G	G/A	265	113	310	129	0.976	0.722	1.320	9.35E-01	8.46E-02	739
3DL1	496	OKG	LGG	C	A	C/C	C/A	362	14	292	10	0.886	0.388	2.020	9.37E-01	8.47E-02	740
3DL1	1021	OKG	LUAD	A	G	A/A	A/G	153	14	124	10	0.881	0.378	2.050	9.37E-01	8.48E-02	741
2DP1	448	OKG	CESC	G	C	G/G	G/C	138	151	32	33	0.942	0.550	1.610	9.38E-01	8.49E-02	742
3DL3	869	OKG	LGG	A	C	A/A	A/C	307	84	248	70	1.030	0.720	1.470	9.38E-01	8.50E-02	743
3DL2	474	OKG	LIHC	G	T	G/G	G/T	258	127	34	18	1.080	0.587	1.990	9.38E-01	8.51E-02	744
3DL2	394	OKG	PRAD	C	A	C/C	C/A	365	33	122	10	0.907	0.434	1.890	9.39E-01	8.52E-02	745
3DL3	447	OKG	LUSC	G	T	G/G	G/T	345	50	175	24	0.946	0.563	1.590	9.39E-01	8.54E-02	746
3DL3	777	OKG	SARC	A	G	A/A	A/G	229	141	43	25	0.944	0.552	1.610	9.41E-01	8.55E-02	747
2DL4	412	OKG	COAD	G	A	G/G	G/A	229	142	84	54	1.040	0.697	1.550	9.41E-01	8.56E-02	748
2DP1	766	OKG	LGG	G	C	G/G	G/C	174	54	164	53	1.040	0.673	1.610	9.43E-01	8.57E-02	749
3DL1	496	OKG	LUSC	C	A	C/C	C/A	362	14	181	6	0.857	0.324	2.270	9.45E-01	8.58E-02	750
3DL1	1091	OKG	LGG	G	A	G/G	G/A	166	53	190	63	1.040	0.683	1.580	9.45E-01	8.59E-02	751
3DL1	1194	OKG	HNSC	C	T	C/C	C/T	327	22	304	19	0.929	0.493	1.750	9.47E-01	8.60E-02	752
2DP1	471	OKG	COAD	A	G	A/A	A/G	292	64	106	22	0.947	0.556	1.610	9.48E-01	8.62E-02	753

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	455	OKG	SARC	G	A	G/G	G/A	367	31	73	7	1.140	0.483	2.690	9.49E-01	8.63E-02	754
3DL3	804	OKG	CESC	G	A	G/G	G/A	228	142	49	32	1.050	0.642	1.720	9.50E-01	8.64E-02	755
3DL3	621	OKG	BLCA	G	A	G/G	G/A	346	49	147	22	1.060	0.618	1.820	9.50E-01	8.65E-02	756
3DL3	455	OKG	BRCA	G	A	G/G	G/A	367	31	418	37	1.050	0.639	1.730	9.54E-01	8.66E-02	757
3DL3	502	OKG	PRAD	G	A	G/G	G/A	101	187	32	62	1.050	0.643	1.710	9.55E-01	8.67E-02	758
2DL4	395	OKG	THCA	C	T	C/C	C/T	355	30	215	17	0.936	0.504	1.740	9.57E-01	8.68E-02	759
3DL2	497	OKG	COAD	G	A	G/G	G/A	327	68	121	24	0.954	0.573	1.590	9.58E-01	8.70E-02	760
3DL3	1042	OKG	CESC	G	C	G/G	G/C	235	26	47	6	1.150	0.449	2.950	9.61E-01	8.71E-02	761
3DL2	497	OKG	SKCM	G	A	G/G	G/A	327	68	287	58	0.972	0.662	1.430	9.62E-01	8.72E-02	762
3DL3	502	OKG	READ	G	A	G/G	G/A	101	187	14	28	1.080	0.544	2.140	9.62E-01	8.73E-02	763
2DL5	517	OKG	UCEC	A	G	A/A	A/G	81	44	47	24	0.940	0.509	1.740	9.67E-01	8.74E-02	764
3DL1	1194	OKG	THCA	C	T	C/C	C/T	327	22	207	15	1.080	0.548	2.130	9.68E-01	8.75E-02	765
2DL4	480	OKG	LUSC	G	A	G/G	G/A	265	113	135	59	1.020	0.700	1.490	9.75E-01	8.76E-02	766
3DL1	607	OKG	KIRC	C	T	C/C	C/T	151	116	25	18	0.937	0.488	1.800	9.77E-01	8.78E-02	767
3DL3	869	OKG	COAD	A	C	A/A	A/C	307	84	113	32	1.030	0.650	1.630	9.78E-01	8.79E-02	768
3DL1	732	OKG	UCEC	T	C	T/T	T/C	55	46	42	37	1.050	0.582	1.900	9.83E-01	8.80E-02	769
3DL1	496	OKG	HNSC	C	A	C/C	C/A	362	14	309	13	1.090	0.505	2.350	9.86E-01	8.81E-02	770
3DL3	455	OKG	PRAD	G	A	G/G	G/A	367	31	121	11	1.080	0.527	2.210	9.88E-01	8.82E-02	771
3DL3	906	OKG	KIRP	C	T	C/C	C/T	226	143	38	23	0.957	0.547	1.670	9.89E-01	8.83E-02	772
2DL4	762	OKG	PRAD	C	T	C/C	C/T	89	202	31	68	0.966	0.590	1.580	9.92E-01	8.84E-02	773
3DL3	447	OKG	PRAD	G	T	G/G	G/T	345	50	116	16	0.952	0.522	1.740	9.92E-01	8.86E-02	774
2DL5	583	OKG	CESC	G	A	G/G	G/A	62	43	16	10	0.901	0.373	2.170	9.93E-01	8.87E-02	775
3DL3	447	OKG	CESC	G	T	G/G	G/T	345	50	74	10	0.932	0.452	1.920	9.94E-01	8.88E-02	776
3DL3	455	OKG	CESC	G	A	G/G	G/A	367	31	79	6	0.899	0.363	2.230	9.96E-01	8.89E-02	777
3DL1	651	OKG	UCEC	CA	C	CA/CA	CA/C	13	7	39	18	0.857	0.292	2.510	9.97E-01	8.90E-02	778
3DL3	869	OKG	LUAD	A	C	A/A	A/C	307	84	205	55	0.981	0.669	1.440	9.98E-01	8.91E-02	779
3DL3	447	OKG	GBM	G	T	G/G	G/T	345	50	187	28	1.030	0.627	1.690	9.98E-01	8.92E-02	780
3DL3	804	OKG	KIRP	G	A	G/G	G/A	228	142	37	24	1.040	0.597	1.810	9.99E-01	8.94E-02	781
3DP1	774	OKG	BLCA	G	C	G/G	G/C	234	147	100	64	1.020	0.701	1.480	9.99E-01	8.95E-02	782
3DL3	502	OKG	SARC	G	A	G/G	G/A	101	187	22	39	0.957	0.538	1.700	1.00E+00	8.96E-02	783
3DL2	896	OKG	BRCA	C	A	C/C	C/A	392	6	449	7	1.020	0.340	3.060	1.00E+00	8.97E-02	784
3DL3	869	OKG	OV	A	C	A/A	A/C	307	84	30	8	0.975	0.431	2.210	1.00E+00	8.98E-02	785
2DP1	794	OKG	BRCA	C	T	C/C	C/T	347	6	433	7	0.935	0.311	2.810	1.00E+00	8.99E-02	786
3DL3	455	OKG	COAD	G	A	G/G	G/A	367	31	137	11	0.951	0.465	1.940	1.00E+00	8.99E-02	786
3DL1	1161	OKG	THCA	C	T	C/C	C/T	196	6	184	6	1.070	0.339	3.380	1.00E+00	9.01E-02	787
3DL1	496	OKG	GBM	C	A	C/C	C/A	362	14	198	7	0.914	0.363	2.300	1.00E+00	9.02E-02	788
3DL3	621	OKG	COAD	G	A	G/G	G/A	346	49	129	18	0.985	0.553	1.750	1.00E+00	9.02E-02	788
3DL3	869	OKG	PRAD	A	C	A/A	A/C	307	84	103	29	1.030	0.639	1.660	1.00E+00	9.02E-02	788
2DP1	1062	OKG	SKCM	C	T	C/C	C/T	283	26	269	24	0.971	0.544	1.730	1.00E+00	9.03E-02	789
3DL1	1021	OKG	HNSC	A	G	A/A	A/G	153	14	179	17	1.040	0.496	2.180	1.00E+00	9.03E-02	789
3DL3	447	OKG	THCA	G	T	G/G	G/T	345	50	201	30	1.030	0.634	1.670	1.00E+00	9.03E-02	789
3DL3	621	OKG	GBM	G	A	G/G	G/A	346	49	189	26	0.971	0.585	1.610	1.00E+00	9.03E-02	789
2DL4	762	OKG	COAD	C	T	C/C	C/T	89	202	32	72	0.991	0.610	1.610	1.00E+00	9.04E-02	790
2DL4	1023	OKG	LIHC	G	A	G/G	G/A	258	128	34	17	1.010	0.544	1.880	1.00E+00	9.04E-02	790
2DP1	522	OKG	LIHC	T	C	T/T	T/C	280	86	38	11	0.942	0.462	1.920	1.00E+00	9.04E-02	790
2DP1	766	OKG	ACC	G	C	G/G	G/C	174	54	21	6	0.921	0.354	2.400	1.00E+00	9.04E-02	790
3DL1	1180	OKG	COAD	G	C	G/G	G/C	177	86	56	28	1.030	0.611	1.740	1.00E+00	9.04E-02	790
3DL2	456	OKG	LIHC	C	T	C/C	C/T	348	49	46	7	1.080	0.462	2.530	1.00E+00	9.04E-02	790
3DL2	893	OKG	LIHC	G	A	G/G	G/A	348	49	46	7	1.080	0.462	2.530	1.00E+00	9.04E-02	790
3DL3	447	OKG	COAD	G	T	G/G	G/T	345	50	129	18	0.963	0.542	1.710	1.00E+00	9.04E-02	790
3DL3	447	OKG	READ	G	T	G/G	G/T	345	50	52	7	0.929	0.400	2.160	1.00E+00	9.04E-02	790
3DL3	777	OKG	CESC	A	G	A/A	A/G	229	141	50	31	1.010	0.616	1.660	1.00E+00	9.04E-02	790
3DL3	804	OKG	KIRC	G	A	G/G	G/A	228	142	32	20	1.000	0.551	1.820	1.00E+00	9.04E-02	790
2DL4	762	OKG	OV	C	T	C/C	C/T	89	202	8	19	1.050	0.443	2.490	1.00E+00	9.05E-02	791
2DL5	517	OKG	BLCA	A	G	A/A	A/G	81	44	36	20	1.020	0.528	1.970	1.00E+00	9.05E-02	791
2DP1	448	OKG	COAD	G	C	G/G	G/C	138	151	44	49	1.020	0.639	1.630	1.00E+00	9.05E-02	791
2DP1	448	OKG	PRAD	G	C	G/G	G/C	138	151	43	46	0.978	0.608	1.570	1.00E+00	9.05E-02	791
2DP1	471	OKG	ACC	A	G	A/A	A/G	292	64	25	6	1.100	0.434	2.790	1.00E+00	9.05E-02	791
2DP1	1062	OKG	COAD	C	T	C/C	C/T	283	26	91	9	1.080	0.488	2.390	1.00E+00	9.05E-02	791
3DL1	1021	OKG	BLCA	A	G	A/A	A/G	153	14	89	8	0.982	0.396	2.430	1.00E+00	9.05E-02	791
3DL1	1194	OKG	LGG	C	T	C/C	C/T	327	22	282	18	0.949	0.499	1.810	1.00E+00	9.05E-02	791
3DL3	502	OKG	STAD	G	A	G/G	G/A	101	187	44	82	1.010	0.651	1.570	1.00E+00	9.05E-02	791
3DL3	869	OKG	HNSC	A	C	A/A	A/C	307	84	263	73	1.010	0.709	1.440	1.00E+00	9.05E-02	791
3DL3	869	OKG	STAD	A	C	A/A	A/C	307	84	133	36	0.989	0.637	1.540	1.00E+00	9.05E-02	791
3DL3	906	OKG	KIRC	C	T	C/C	C/T	226	143	32	20	0.988	0.544	1.790	1.00E+00	9.05E-02	791
3DL3	961	OKG	OV	C	A	C/C	C/A	118	103	11	9	0.937	0.374	2.350	1.00E+00	9.05E-02	791
2DL3	953	OKG	OV	G	A	G/G	G/A	144	104	12	8	0.923	0.364	2.340	1.00E+00	9.06E-02	792
2DL3	953	OKG	SARC	G	A	G/G	G/A	144	104	28	21	1.040	0.560	1.930	1.00E+00	9.06E-02	792
2DP1	448	OKG	HNSC	G	C	G/G	G/C	138	151	118	130	1.010	0.719	1.420	1.00E+00	9.06E-02	792
2DP1	448	OKG	LIHC	G	C	G/G	G/C	138	151	18	19	0.965	0.487	1.910	1.00E+00	9.06E-02	792
2DP1	448	OKG	SARC	G	C	G/G	G/C	138	151	29	33	1.040	0.600	1.800	1.00E+00	9.06E-02	792
2DP1	522	OKG	UCEC	T	C	T/T	T/C	280	86	154	47	0.994	0.662	1.490	1.00E+00	9.06E-02	792
2DP1	804	OKG	BRCA	C	A	C/C	C/A	352	8	430	10	1.020	0.398	2.610	1.00E+00	9.06E-02	792
2DP1	1269	OKG	SARC	A	G	A/A	A/G	350	30	69	6	1.010	0.405	2.520	1.00E+00	9.06E-02	792
3DL1	732	OKG	OV	T	C	T/T	T/C	55	46	9	8	1.060	0.379	2.970	1.00E+00	9.06E-02	792
3DL1	1026	OKG	SARC	G	C	G/G	G/C	160	52	42	14	1.030	0.521	2.040	1.00E+00	9.06E-02	792
3DL1	1091	OKG	LUAD	G	A	G/G	G/A	166	53	140	44	0.984	0.622	1.560	1.00E+00	9.06E-02	792
3DL1	1091	OKG	SARC	G	A	G/G	G/A	166	53	43	14	1.020	0.518	2.010	1.00E+00	9.06E-02	792
3DL3	447	OKG	SKCM	G	T	G/G	G/T	345	50	302	43	0.982	0.635	1.520	1.00E+00	9.06E-02	792
3DL3	621	OKG	BRCA	G	A	G/G	G/A	346	49	395	56	1.000	0.664	1.510	1.00E+00	9.06E-02	792
3DL3	777	OKG	KIRC	A	G	A/A	A/G	229	141	32	20	1.020	0.562	1.850	1.00E+00	9.06E-02	792
3DL3	777	OKG	KIRP	A	G	A/A	A/G	229	141	38	23	0.983	0.562	1.720	1.00E+00	9.06E-02	792
3DL3	777	OKG	READ	A	G	A/A	A/G	229	141	37	23	1.010	0.576	1.770	1.00E+00	9.06E-02	792
3DL3	804	OKG	READ	G	A	G/G	G/A	228	142	37	23	0.998	0.569	1.750	1.00E+00	9.06E-02	792
3DL3	906	OKG	READ	C	T	C/C	C/T	226	143	37	23	0.982	0.560	1.720	1.00E+00	9.06E-02	792
3DL3	961	OKG	ACC	C	A	C/C	C/A	118	103	8	7	1.000	0.351	2.850	1.00E+00	9.06E-02	792
3DL3	961	OKG	LUSC	C	A	C/C	C/A	118	103	57	51	1.030	0.650	1.630	1.00E+00	9.06E-02	792
3DP1	774	OKG	KIRC	G	C	G/G	G/C	234	147	33	21	1.010	0.563	1.810	1.00E+00	9.06E-02	792
2DL4	625	OKG	BRCA	C	G	C/C	C/G	191	121	255	163	1.010	0.748	1.360	1.00E+00	9.07E-02	793
2DL4	1023	OKG	THCA	G	A	G/G	G/A	258	128	151	75	1.000	0.706	1.420	1.00E+00	9.07E-02	793
2DL4	1023	OKG	UCEC	G	A	G/G	G/A	258	128	140	70	1.010	0.707	1.440	1.00E+00	9.07E-02	793
2DL5	517	OKG	LIHC	A	G	A/A	A/G	81	44	11	6	1.000	0.346	2.890	1.00E+00	9.07E-02	793
2DL5	517	OKG	LUAD	A	G	A/A	A/G	81	44	60	33	1.010	0.576	1.770	1.00E+00	9.07E-02	793
2DL5	583	OKG	LIHC	G	A	G/G	G/A	62	43	9	6	0.961	0.319	2.900	1.00E+00	9.07E-02	793
2DP1	766	OKG	PRAD	G	C	G/G	G/C	174	54	76	24	1.020	0.588	1.770	1.00E+00	9.07E-02	793
3DL1	1026	OKG	BLCA	G	C	G/G	G/C	160	52	103	34	1.020	0.620	1.680	1.00E+00	9.07E-02	793
3DL2	474	OKG	THCA	G	T	G/G	G/T	258	127	154	75	0.989	0.698	1.400	1.00E+00	9.07E-02	793
3DL3	408	OKG	KIRC	G	A	G/G	G/A	273	113	37	16	1.040	0.556	1.950	1.00E+00	9.07E-02	793
3DL3	502	OKG	BLCA	G	A	G/G	G/A	101	187	44	83	1.020	0.658	1.580	1.00E+00	9.07E-02	793
3DL3	516	OKG	LUSC	C	T	C/C	C/T	388	10	194	5	1.000	0.337	2.970	1.00E+00	9.07E-02	793
3DL3	621	OKG	LUAD	G	A	G/G	G/A	346	49	230	33	1.010	0.630	1.620	1.00E+00	9.07E-02	793
3DL3	621	OKG	SKCM	G	A	G/G	G/A	346	49	303	42	0.979	0.630	1.520	1.00E+00	9.07E-02	793
3DL3	906	OKG	CESC	C	T	C/C	C/T	226	143	49	32	1.030	0.630	1.690	1.00E+00	9.07E-02	793
3DL3	961	OKG	SARC	C	A	C/C	C/A	118	103	25	22	1.010	0.537	1.900	1.00E+00	9.07E-02	793
3DL3	969	OKG	BLCA	C	T	C/C	C/T	329	20	127	7	0.907	0.374	2.200	1.00E+00	9.07E-02	793
3DL3	969	OKG	BRCA	C	T	C/C	C/T	329	20	383	24	1.030	0.559	1.900	1.00E+00	9.07E-02	793

Table A12b Chi square significance tests for KIR variants within the TCGA samples, European cohort, heterozygous versus alternate homozygous

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DP1	479	OKG	PRAD	A	C	A/C	C/C	176	21	36	21	4.890	2.420	9.880	7.34E-06	2.39E-04	1
3DP1	774	OKG	PRAD	G	C	G/C	C/C	147	16	41	18	4.030	1.890	8.590	3.56E-04	4.79E-04	2
3DL3	961	OKG	SKCM	C	A	C/A	A/A	103	102	82	33	0.406	0.249	0.661	3.97E-04	7.18E-04	3
2DL4	762	OKG	LUSC	C	T	C/T	T/T	202	72	88	64	2.040	1.340	3.100	1.16E-03	9.57E-04	4
2DP1	1313	OKG	GBM	A	C	A/C	C/C	112	22	43	26	3.080	1.580	6.010	1.36E-03	1.20E-03	5
3DL3	961	OKG	LGG	C	A	C/A	A/A	103	102	85	40	0.475	0.298	0.756	2.32E-03	1.44E-03	6
2DL4	762	OKG	LGG	C	T	C/T	T/T	202	72	145	92	1.780	1.220	2.590	3.35E-03	1.68E-03	7
2DL5	583	OKG	SKCM	G	A	G/A	A/A	43	54	24	74	2.460	1.340	4.530	5.67E-03	1.91E-03	8
3DL1	1180	OKG	UCEC	G	C	G/C	C/C	86	51	54	11	0.344	0.165	0.717	5.79E-03	2.15E-03	9
2DL5	517	OKG	SKCM	A	G	A/G	G/G	44	63	23	75	2.280	1.240	4.180	1.10E-02	2.39E-03	10
2DL5	583	OKG	STAD	G	A	G/A	A/A	43	54	15	49	2.600	1.290	5.250	1.13E-02	2.63E-03	11
2DL5	583	OKG	BRCA	G	A	G/A	A/A	43	54	38	100	2.100	1.210	3.630	1.15E-02	2.87E-03	12
3DP1	479	OKG	HNSC	A	C	A/C	C/C	176	21	123	32	2.180	1.200	3.960	1.43E-02	3.11E-03	13
3DL3	961	OKG	LUSC	C	A	C/A	A/A	103	102	51	25	0.495	0.285	0.859	1.70E-02	3.35E-03	14
3DL3	906	OKG	SARC	C	T	C/T	T/T	143	28	24	13	2.770	1.260	6.090	1.76E-02	3.59E-03	15
2DL4	1023	OKG	GBM	G	A	G/A	A/A	128	12	62	16	2.750	1.230	6.170	2.06E-02	3.83E-03	16
2DP1	448	OKG	ACC	G	C	G/C	C/C	151	89	4	10	4.240	1.290	13.900	2.26E-02	4.07E-03	17
2DL4	762	OKG	SKCM	C	T	C/T	T/T	202	72	169	94	1.560	1.080	2.260	2.27E-02	4.31E-03	18
3DL3	961	OKG	BLCA	C	A	C/A	A/A	103	102	42	20	0.481	0.264	0.875	2.27E-02	4.55E-03	19
2DL4	762	OKG	HNSC	C	T	C/T	T/T	202	72	168	93	1.550	1.070	2.240	2.46E-02	4.79E-03	20
2DL5	583	OKG	HNSC	G	A	G/A	A/A	43	54	32	79	1.970	1.110	3.500	2.94E-02	5.02E-03	21
2DL4	762	OKG	STAD	C	T	C/T	T/T	202	72	80	48	1.680	1.070	2.630	2.97E-02	5.26E-03	22
2DP1	448	OKG	THCA	G	C	G/C	C/C	151	89	65	63	1.640	1.060	2.530	3.23E-02	5.50E-03	23
2DP1	448	OKG	GBM	G	C	G/C	C/C	151	89	64	62	1.640	1.060	2.540	3.34E-02	5.74E-03	24
2DL5	517	OKG	BRCA	A	G	A/G	G/G	44	63	38	100	1.840	1.080	3.150	3.59E-02	5.98E-03	25
3DL3	777	OKG	SARC	A	G	A/G	G/G	141	27	25	12	2.510	1.130	5.600	3.90E-02	6.22E-03	26
2DP1	1313	OKG	BRCA	A	C	A/C	C/C	112	22	95	36	1.930	1.060	3.510	4.25E-02	6.46E-03	27
2DP1	448	OKG	LUAD	G	C	G/C	C/C	151	89	78	72	1.570	1.040	2.370	4.29E-02	6.70E-03	28
3DP1	479	OKG	THCA	A	C	A/C	C/C	176	21	85	21	2.070	1.070	4.000	4.29E-02	6.94E-03	29
3DP1	774	OKG	LGG	G	C	G/C	C/C	147	16	99	23	2.130	1.070	4.230	4.32E-02	7.18E-03	30
2DP1	1313	OKG	LGG	A	C	A/C	C/C	112	22	77	30	1.980	1.060	3.690	4.33E-02	7.42E-03	31
3DP1	479	OKG	SKCM	A	C	A/C	C/C	176	21	115	27	1.970	1.060	3.650	4.35E-02	7.66E-03	32
3DP1	796	OKG	THCA	T	C	T/C	C/C	134	15	66	17	2.300	1.080	4.890	4.48E-02	7.90E-03	33
3DL3	804	OKG	SARC	G	A	G/A	A/A	142	28	25	12	2.430	1.090	5.400	4.56E-02	8.13E-03	34
2DL5	517	OKG	STAD	A	G	A/G	G/G	44	63	15	46	2.140	1.060	4.300	4.65E-02	8.37E-03	35
3DP1	774	OKG	UCEC	G	C	G/C	C/C	147	16	70	17	2.230	1.060	4.670	4.91E-02	8.61E-03	36
3DL1	607	OKG	LUAD	C	T	C/T	T/T	116	96	84	43	0.619	0.392	0.977	5.05E-02	8.85E-03	37
3DL3	502	OKG	SKCM	G	A	G/A	A/A	187	110	187	76	0.691	0.484	0.986	5.10E-02	9.09E-03	38
3DP1	796	OKG	CESC	T	C	T/C	C/C	134	15	30	9	2.680	1.070	6.700	5.77E-02	9.33E-03	39
3DP1	774	OKG	THCA	G	C	G/C	C/C	147	16	72	17	2.170	1.040	4.540	5.84E-02	9.57E-03	40
2DL3	953	OKG	COAD	G	A	G/A	A/A	104	112	44	27	0.570	0.329	0.986	5.94E-02	9.81E-03	41
2DL3	953	OKG	ACC	G	A	G/A	A/A	104	112	4	14	3.250	1.040	10.200	6.10E-02	1.01E-02	42
2DL5	517	OKG	HNSC	A	G	A/G	G/G	44	63	31	79	1.780	1.010	3.140	6.27E-02	1.03E-02	43
3DL3	961	OKG	THCA	C	A	C/A	A/A	103	102	53	31	0.591	0.351	0.995	6.28E-02	1.05E-02	44
2DL4	480	OKG	COAD	G	A	G/A	A/A	113	14	36	11	2.470	1.030	5.920	6.82E-02	1.08E-02	45
3DP1	479	OKG	LUAD	A	C	A/C	C/C	176	21	97	22	1.900	0.995	3.630	7.23E-02	1.10E-02	46
2DP1	448	OKG	BRCA	G	C	G/C	C/C	151	89	142	118	1.410	0.986	2.020	7.31E-02	1.12E-02	47
3DP1	774	OKG	CESC	G	C	G/C	C/C	147	16	33	9	2.510	1.020	6.170	7.40E-02	1.15E-02	48
3DL1	607	OKG	THCA	C	T	C/T	T/T	116	96	71	37	0.630	0.390	1.020	7.64E-02	1.17E-02	49
3DL1	1180	OKG	SKCM	G	C	G/C	C/C	86	51	90	32	0.600	0.353	1.020	7.85E-02	1.20E-02	50
3DL3	502	OKG	THCA	G	A	G/A	A/A	187	110	118	47	0.677	0.448	1.020	7.89E-02	1.22E-02	51
3DP1	796	OKG	LGG	T	C	T/C	C/C	134	15	89	20	2.010	0.977	4.130	8.28E-02	1.24E-02	52
2DP1	1313	OKG	BLCA	A	C	A/C	C/C	112	22	46	18	1.990	0.977	4.050	8.37E-02	1.27E-02	53
2DL5	583	OKG	LGG	G	A	G/A	A/A	43	54	30	66	1.750	0.971	3.150	8.45E-02	1.29E-02	54
3DP1	479	OKG	BRCA	A	C	A/C	C/C	176	21	177	36	1.700	0.954	3.030	9.25E-02	1.32E-02	55
3DP1	479	OKG	CESC	A	C	A/C	C/C	176	21	33	9	2.290	0.964	5.440	9.77E-02	1.34E-02	56
3DP1	774	OKG	HNSC	G	C	G/C	C/C	147	16	107	22	1.890	0.948	3.770	9.88E-02	1.36E-02	57
3DL2	474	OKG	GBM	G	T	G/T	T/T	127	13	64	14	2.140	0.950	4.820	9.96E-02	1.39E-02	58
3DP1	479	OKG	COAD	A	C	A/C	C/C	176	21	54	13	2.020	0.949	4.300	1.02E-01	1.41E-02	59
3DL3	961	OKG	KIRP	C	A	C/A	A/A	103	102	22	11	0.505	0.233	1.090	1.17E-01	1.44E-02	60
3DL3	408	OKG	HNSC	G	A	G/A	A/A	113	12	85	18	1.990	0.910	4.350	1.20E-01	1.46E-02	61
2DP1	471	OKG	BLCA	A	G	A/G	G/G	64	14	35	16	2.090	0.914	4.780	1.21E-01	1.48E-02	62
3DL3	502	OKG	ACC	G	A	G/A	A/A	187	110	18	4	0.378	0.125	1.150	1.21E-01	1.51E-02	63
2DL4	625	OKG	GBM	C	G	C/G	G/G	121	17	86	22	1.820	0.912	3.630	1.24E-01	1.53E-02	64
3DL3	502	OKG	KIRP	G	A	G/A	A/A	187	110	39	13	0.567	0.290	1.110	1.29E-01	1.56E-02	65
3DP1	774	OKG	LUSC	G	C	G/C	C/C	147	16	60	13	1.990	0.902	4.390	1.30E-01	1.58E-02	66
2DL5	583	OKG	SARC	G	A	G/A	A/A	43	54	4	14	2.790	0.856	9.090	1.36E-01	1.60E-02	67
3DL3	408	OKG	LUSC	G	A	G/A	A/A	113	12	71	15	1.990	0.881	4.500	1.43E-01	1.63E-02	68
2DP1	766	OKG	BRCA	G	C	G/C	C/C	54	9	81	27	2.000	0.873	4.580	1.43E-01	1.65E-02	69
2DP1	522	OKG	BLCA	T	C	T/C	C/C	86	20	39	17	1.870	0.884	3.960	1.44E-01	1.68E-02	70
2DL5	517	OKG	SARC	A	G	A/G	G/G	44	63	4	15	2.620	0.815	8.430	1.60E-01	1.70E-02	71
2DP1	1313	OKG	THCA	A	C	A/C	C/C	112	22	52	18	1.760	0.870	3.560	1.61E-01	1.72E-02	72
3DP1	796	OKG	HNSC	T	C	T/C	C/C	134	15	101	20	1.770	0.864	3.630	1.65E-01	1.75E-02	73
2DL4	762	OKG	BRCA	C	T	C/T	T/T	202	72	226	105	1.300	0.912	1.850	1.69E-01	1.77E-02	74
2DP1	448	OKG	SKCM	G	C	G/C	C/C	151	89	115	90	1.330	0.909	1.950	1.72E-01	1.79E-02	75
2DP1	766	OKG	HNSC	G	C	G/C	C/C	54	9	76	5	0.395	0.125	1.240	1.78E-01	1.82E-02	76
2DP1	522	OKG	BRCA	T	C	T/C	C/C	86	20	91	34	1.610	0.861	3.010	1.82E-01	1.84E-02	77
3DL1	1180	OKG	THCA	G	C	G/C	C/C	86	51	58	22	0.640	0.351	1.170	1.89E-01	1.87E-02	78
2DL5	517	OKG	LGG	A	G	A/G	G/G	44	63	30	66	1.540	0.864	2.750	1.89E-01	1.89E-02	79
3DL3	502	OKG	LGG	G	A	G/A	A/A	187	110	167	76	0.774	0.540	1.110	1.90E-01	1.91E-02	80
2DL4	762	OKG	READ	C	T	C/T	T/T	202	72	27	16	1.660	0.846	3.260	1.92E-01	1.94E-02	81
2DL4	412	OKG	GBM	G	A	G/A	A/A	142	25	86	24	1.590	0.855	2.960	1.93E-01	1.96E-02	82
3DL3	502	OKG	KIRC	G	A	G/A	A/A	187	110	32	11	0.584	0.283	1.210	1.95E-01	1.99E-02	83
3DL3	906	OKG	BLCA	C	T	C/T	T/T	143	28	69	7	0.518	0.216	1.240	1.96E-01	2.01E-02	84
2DP1	471	OKG	COAD	A	G	A/G	G/G	64	14	22	10	2.080	0.808	5.350	2.01E-01	2.03E-02	85
2DL4	480	OKG	THCA	G	A	G/A	A/A	113	14	64	3	0.378	0.105	1.370	2.05E-01	2.06E-02	86
3DL3	961	OKG	LUAD	C	A	C/A	A/A	103	102	57	40	0.709	0.435	1.160	2.07E-01	2.08E-02	87
2DL3	953	OKG	THCA	G	A	G/A	A/A	104	112	45	67	1.380	0.869	2.190	2.08E-01	2.11E-02	88
2DL5	583	OKG	THCA	G	A	G/A	A/A	43	54	22	44	1.590	0.830	3.050	2.13E-01	2.13E-02	89
2DP1	522	OKG	COAD	T	C	T/C	C/C	86	20	22	10	1.950	0.799	4.760	2.14E-01	2.15E-02	90
3DL1	1091	OKG	THCA	G	A	G/A	A/A	53	9	50	3	0.353	0.090	1.380	2.14E-01	2.18E-02	91
2DP1	471	OKG	LGG	A	G	A/G	G/G	64	14	58	22	1.730	0.810	3.690	2.14E-01	2.20E-02	92
3DL1	1026	OKG	THCA	G	C	G/C	C/C	52	9	49	3	0.354	0.091	1.380	2.15E-01	2.23E-02	93
3DL1	1026	OKG	SKCM	G	C	G/C	C/C	52	9	79	6	0.439	0.147	1.310	2.17E-01	2.25E-02	94
2DL5	517	OKG	COAD	A	G	A/G	G/G	44	63	8	22	1.920	0.784	4.700	2.19E-01	2.27E-02	95
3DP1	796	OKG	LUSC	T	C	T/C	C/C	134	15	59	12	1.820	0.803	4.130	2.21E-01	2.30E-02	96
2DL5	583	OKG	GBM	G	A	G/A	A/A	43	54	21	42	1.590	0.822	3.070	2.22E-01	2.32E-02	97
2DP1	522	OKG	LGG	T	C	T/C	C/C	86	20	64	24	1.610	0.819	3.160	2.23E-01	2.34E-02	98
3DL2	474	OKG	THCA	G	T	G/T	T/T	127	13	75	3	0.391	0.108	1.420	2.28E-01	2.37E-02	99
2DL4	625	OKG	UCEC	C	G	C/G	G/G	121	17	82	19	1.650	0.810	3.360	2.29E-01	2.39E-02	100
2DP1	1313	OKG	STAD	A	C	A/C	C/C	112	22	49	16	1.660	0.803	3.430	2.35E-01	2.42E-02	101
2DL4	625	OKG	BRCA	C	G	C/G	G/G	121	17	163	35	1.530	0.819	2.860	2.37E-01	2.44E-02	102
3DL3	961	OKG	BRCA	C	A	C/A	A/A	103	102	108	136	1.270	0.875	1.840	2.42E-01	2.46E-02	103
3DL1	607	OKG	STAD	C	T	C/T	T/T	116	96	60	36	0.725	0.442	1.190	2.48E-01	2.49E-02	104
3DP1	479	OKG	LGG	A	C	A/C	C/C	176	21	120	22	1.540	0.811	2.920	2.49E-01	2.51E-02	105
3DL1	1180	OKG	HNSC	G	C	G/C	C/C	86	51	83	35	0.711	0.420	1.200	2.54E-01	2.54E-02	106
3DL3	804	OKG	BRCA	G	A	G/A	A/A	142	28	172	23	0.678	0.374	1.230	2.57E-01	2.56E-02	107
3DL3	777	OKG	LUSC	A	G	A/G	G/G	141	27	76	22	1.510	0.806	2.830	2.58E-01	2.58E-02	108

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DL5	583	OKG	LUSC	G	A	G/A	A/A	43	54	20	39	1.550	0.792	3.030	2.63E-01	2.61E-02	109
3DL3	906	OKG	LUSC	C	T	C/T	T/T	143	28	75	22	1.500	0.803	2.800	2.67E-01	2.63E-02	110
2DP1	1313	OKG	SKCM	A	C	A/C	C/C	112	22	88	26	1.500	0.797	2.820	2.68E-01	2.66E-02	111
2DL4	762	OKG	PRAD	C	T	C/T	T/T	202	72	68	33	1.360	0.829	2.230	2.74E-01	2.68E-02	112
3DL1	607	OKG	GBM	C	T	C/T	T/T	116	96	62	38	0.741	0.456	1.200	2.76E-01	2.70E-02	113
3DL3	961	OKG	READ	C	A	C/A	A/A	103	102	10	17	1.720	0.752	3.940	2.78E-01	2.73E-02	114
3DL1	607	OKG	SKCM	C	T	C/T	T/T	116	96	118	77	0.788	0.531	1.170	2.80E-01	2.75E-02	115
2DP1	766	OKG	SKCM	G	C	G/C	C/C	54	9	56	4	0.429	0.125	1.480	2.80E-01	2.78E-02	116
3DL1	1180	OKG	CESC	G	C	G/C	C/C	86	51	26	9	0.584	0.254	1.340	2.82E-01	2.80E-02	117
3DL1	1091	OKG	SKCM	G	A	G/A	A/A	53	9	74	6	0.477	0.160	1.420	2.83E-01	2.82E-02	118
3DL1	1026	OKG	BRCA	G	C	G/C	C/C	52	9	82	7	0.493	0.173	1.400	2.83E-01	2.85E-02	119
3DL1	607	OKG	LGG	C	T	C/T	T/T	116	96	99	64	0.781	0.516	1.180	2.88E-01	2.87E-02	120
2DP1	448	OKG	COAD	G	C	G/C	C/C	151	89	49	39	1.350	0.823	2.220	2.88E-01	2.90E-02	121
2DL4	762	OKG	BLCA	C	T	C/T	T/T	202	72	85	40	1.320	0.831	2.100	2.89E-01	2.92E-02	122
3DP1	479	OKG	GBM	A	C	A/C	C/C	176	21	74	14	1.590	0.767	3.300	2.93E-01	2.94E-02	123
2DP1	522	OKG	LUAD	T	C	T/C	C/C	86	20	49	18	1.580	0.764	3.270	2.94E-01	2.97E-02	124
3DL3	804	OKG	LUSC	G	A	G/A	A/A	142	28	76	22	1.470	0.788	2.740	2.95E-01	2.99E-02	125
3DL3	906	OKG	BRCA	C	T	C/T	T/T	143	28	175	24	0.700	0.389	1.260	2.98E-01	3.01E-02	126
3DL3	502	OKG	HNSC	G	A	G/A	A/A	187	110	172	83	0.820	0.577	1.170	3.11E-01	3.04E-02	127
2DL5	583	OKG	COAD	G	A	G/A	A/A	43	54	4	11	2.190	0.651	7.360	3.13E-01	3.06E-02	128
3DL3	777	OKG	BRCA	A	G	A/G	G/G	141	27	171	23	0.702	0.386	1.280	3.14E-01	3.09E-02	129
3DL3	502	OKG	BRCA	G	A	G/A	A/A	187	110	232	114	0.835	0.603	1.160	3.16E-01	3.11E-02	130
3DP1	796	OKG	BLCA	T	C	T/C	C/C	134	15	60	3	0.447	0.125	1.600	3.19E-01	3.13E-02	131
2DL4	762	OKG	OV	C	T	C/T	T/T	202	72	19	11	1.620	0.735	3.570	3.19E-01	3.16E-02	132
3DP1	796	OKG	UCEC	T	C	T/C	C/C	134	15	65	12	1.650	0.730	3.730	3.19E-01	3.18E-02	133
3DP1	774	OKG	BRCA	G	C	G/C	C/C	147	16	155	25	1.480	0.760	2.880	3.20E-01	3.21E-02	134
3DP1	796	OKG	PRAD	T	C	T/C	C/C	134	15	46	9	1.750	0.717	4.270	3.20E-01	3.23E-02	135
3DL3	777	OKG	BLCA	A	G	A/G	G/G	141	27	69	8	0.605	0.261	1.400	3.26E-01	3.25E-02	136
2DP1	448	OKG	KIRP	G	C	G/C	C/C	151	89	19	17	1.520	0.751	3.080	3.26E-01	3.28E-02	137
3DP1	479	OKG	UCEC	A	C	A/C	C/C	176	21	89	16	1.510	0.751	3.040	3.31E-01	3.30E-02	138
3DL1	1026	OKG	LUAD	G	C	G/C	C/C	52	9	46	14	1.760	0.697	4.450	3.32E-01	3.33E-02	139
2DL4	762	OKG	KIRC	C	T	C/T	T/T	202	72	26	14	1.510	0.747	3.050	3.34E-01	3.35E-02	140
3DL1	1180	OKG	BRCA	G	C	G/C	C/C	86	51	108	49	0.765	0.472	1.240	3.36E-01	3.37E-02	141
3DP1	774	OKG	SKCM	G	C	G/C	C/C	147	16	109	18	1.520	0.742	3.120	3.37E-01	3.40E-02	142
3DL3	502	OKG	OV	G	A	G/A	A/A	187	110	18	6	0.567	0.219	1.470	3.37E-01	3.42E-02	143
2DL5	517	OKG	KIRP	A	G	A/G	G/G	44	63	4	12	2.100	0.635	6.940	3.38E-01	3.45E-02	144
2DP1	471	OKG	STAD	A	G	A/G	G/G	64	14	42	15	1.630	0.714	3.720	3.39E-01	3.47E-02	145
2DP1	448	OKG	LUSC	G	C	G/C	C/C	151	89	65	49	1.280	0.813	2.020	3.44E-01	3.49E-02	146
2DL4	1023	OKG	UCEC	G	A	G/A	A/A	128	12	70	11	1.680	0.705	4.000	3.44E-01	3.52E-02	147
2DL5	583	OKG	PRAD	G	A	G/A	A/A	43	54	12	24	1.590	0.714	3.540	3.44E-01	3.54E-02	148
2DP1	471	OKG	GBM	A	G	A/G	G/G	64	14	39	14	1.640	0.707	3.800	3.46E-01	3.57E-02	149
2DL4	762	OKG	THCA	C	T	C/T	T/T	202	72	114	51	1.260	0.823	1.930	3.49E-01	3.59E-02	150
2DP1	471	OKG	LUAD	A	G	A/G	G/G	64	14	49	17	1.590	0.715	3.540	3.51E-01	3.61E-02	151
2DL4	1023	OKG	BRCA	G	A	G/A	A/A	128	12	139	20	1.530	0.719	3.250	3.52E-01	3.64E-02	152
3DL1	1091	OKG	LUAD	G	A	G/A	A/A	53	9	44	13	1.740	0.680	4.450	3.54E-01	3.66E-02	153
3DL3	502	OKG	UCEC	G	A	G/A	A/A	187	110	111	53	0.812	0.543	1.220	3.61E-01	3.68E-02	154
3DL3	777	OKG	HNSC	A	G	A/G	G/G	141	27	111	29	1.360	0.761	2.430	3.66E-01	3.71E-02	155
3DL3	502	OKG	LUSC	G	A	G/A	A/A	187	110	97	46	0.806	0.528	1.230	3.72E-01	3.73E-02	156
3DL3	502	OKG	CESC	G	A	G/A	A/A	187	110	48	21	0.744	0.423	1.310	3.73E-01	3.76E-02	157
3DL1	1180	OKG	SARC	G	C	G/C	C/C	86	51	22	8	0.613	0.254	1.480	3.76E-01	3.78E-02	158
3DP1	796	OKG	STAD	T	C	T/C	C/C	134	15	42	8	1.700	0.674	4.290	3.79E-01	3.80E-02	159
2DL4	762	OKG	COAD	C	T	C/T	T/T	202	72	72	33	1.290	0.789	2.110	3.82E-01	3.83E-02	160
2DP1	766	OKG	UCEC	G	C	G/C	C/C	54	9	42	12	1.710	0.659	4.440	3.82E-01	3.85E-02	161
3DL2	474	OKG	UCEC	G	T	G/T	T/T	127	13	67	11	1.600	0.680	3.770	3.88E-01	3.88E-02	162
2DL3	953	OKG	SKCM	G	A	G/A	A/A	104	112	69	91	1.220	0.809	1.840	3.89E-01	3.90E-02	163
2DL5	583	OKG	UCEC	G	A	G/A	A/A	43	54	24	42	1.390	0.732	2.640	3.94E-01	3.92E-02	164
2DL4	1023	OKG	LUAD	G	A	G/A	A/A	128	12	73	11	1.610	0.676	3.830	3.94E-01	3.95E-02	165
2DP1	522	OKG	STAD	T	C	T/C	C/C	86	20	43	15	1.500	0.699	3.220	3.98E-01	3.97E-02	166
2DL5	517	OKG	GBM	A	G	A/G	G/G	44	63	21	42	1.400	0.731	2.680	3.98E-01	4.00E-02	167
3DP1	479	OKG	LUSC	A	C	A/C	C/C	176	21	74	13	1.470	0.699	3.090	4.08E-01	4.02E-02	168
2DL5	583	OKG	KIRP	G	A	G/A	A/A	43	54	4	10	1.990	0.584	6.790	4.09E-01	4.04E-02	169
2DL4	412	OKG	UCEC	G	A	G/A	A/A	142	25	82	20	1.390	0.727	2.660	4.12E-01	4.07E-02	170
3DL1	1091	OKG	BRCA	G	A	G/A	A/A	53	9	82	8	0.575	0.209	1.580	4.12E-01	4.09E-02	171
3DL1	1180	OKG	BLCA	G	C	G/C	C/C	86	51	40	17	0.717	0.369	1.390	4.13E-01	4.12E-02	172
3DL1	607	OKG	BRCA	C	T	C/T	T/T	116	96	142	99	0.842	0.580	1.220	4.20E-01	4.14E-02	173
2DL4	412	OKG	LUSC	G	A	G/A	A/A	142	25	70	8	0.649	0.278	1.510	4.20E-01	4.16E-02	174
3DP1	796	OKG	SKCM	T	C	T/C	C/C	134	15	105	17	1.450	0.692	3.040	4.28E-01	4.19E-02	175
2DP1	448	OKG	CESC	G	C	G/C	C/C	151	89	33	14	0.720	0.366	1.420	4.31E-01	4.21E-02	176
3DL3	804	OKG	UCEC	G	A	G/A	A/A	142	28	68	9	0.671	0.300	1.500	4.34E-01	4.23E-02	177
3DL3	961	OKG	HNSC	C	A	C/A	A/A	103	102	75	61	0.821	0.531	1.270	4.37E-01	4.26E-02	178
2DL3	953	OKG	READ	G	A	G/A	A/A	104	112	9	15	1.550	0.650	3.690	4.38E-01	4.28E-02	179
3DL1	607	OKG	COAD	C	T	C/T	T/T	116	96	38	40	1.270	0.755	2.140	4.38E-01	4.31E-02	180
2DL4	480	OKG	LUSC	G	A	G/A	A/A	113	14	59	4	0.547	0.172	1.740	4.40E-01	4.33E-02	181
2DL4	625	OKG	PRAD	C	G	C/G	G/G	121	17	41	9	1.560	0.646	3.770	4.48E-01	4.35E-02	182
3DL1	607	OKG	KIRC	C	T	C/T	T/T	116	96	18	10	0.671	0.296	1.520	4.50E-01	4.38E-02	183
3DL3	502	OKG	LUAD	G	A	G/A	A/A	187	110	134	67	0.850	0.584	1.240	4.52E-01	4.40E-02	184
2DL5	517	OKG	LUSC	A	G	A/G	G/G	44	63	20	39	1.360	0.701	2.640	4.54E-01	4.43E-02	185
3DL3	804	OKG	BLCA	G	A	G/A	A/A	142	28	67	9	0.681	0.304	1.520	4.56E-01	4.45E-02	186
3DL3	804	OKG	LUAD	G	A	G/A	A/A	142	28	116	17	0.743	0.388	1.420	4.63E-01	4.47E-02	187
2DP1	448	OKG	PRAD	G	C	G/C	C/C	151	89	46	34	1.250	0.747	2.090	4.65E-01	4.50E-02	188
2DP1	471	OKG	BRCA	A	G	A/G	G/G	64	14	92	28	1.390	0.679	2.850	4.67E-01	4.52E-02	189
3DL3	804	OKG	GBM	G	A	G/A	A/A	142	28	85	12	0.716	0.346	1.480	4.69E-01	4.55E-02	190
3DL3	777	OKG	LUAD	A	G	A/G	G/G	141	27	113	16	0.739	0.380	1.440	4.69E-01	4.57E-02	191
2DP1	471	OKG	SKCM	A	G	A/G	G/G	64	14	71	22	1.420	0.670	3.010	4.69E-01	4.59E-02	192
3DL1	607	OKG	LUSC	C	T	C/T	T/T	116	96	65	44	0.818	0.512	1.310	4.70E-01	4.62E-02	193
3DP1	796	OKG	BRCA	T	C	T/C	C/C	134	15	143	22	1.370	0.682	2.750	4.71E-01	4.64E-02	194
3DL2	474	OKG	LUAD	G	T	G/T	T/T	127	13	72	11	1.490	0.635	3.500	4.84E-01	4.67E-02	195
3DL1	607	OKG	BLCA	C	T	C/T	T/T	116	96	51	34	0.806	0.483	1.340	4.84E-01	4.69E-02	196
2DL5	583	OKG	BLCA	G	A	G/A	A/A	43	54	20	34	1.350	0.682	2.670	4.85E-01	4.71E-02	197
2DL4	412	OKG	LGG	G	A	G/A	A/A	142	25	122	16	0.745	0.380	1.460	4.89E-01	4.74E-02	198
3DL1	1180	OKG	OV	G	C	G/C	C/C	86	51	12	4	0.562	0.172	1.840	4.91E-01	4.76E-02	199
2DL4	762	OKG	GBM	C	T	C/T	T/T	202	72	108	46	1.190	0.768	1.840	4.93E-01	4.79E-02	200
3DL2	474	OKG	BRCA	G	T	G/T	T/T	127	13	141	20	1.390	0.664	2.910	4.94E-01	4.81E-02	201
3DL3	906	OKG	SKCM	C	T	C/T	T/T	143	28	133	20	0.768	0.413	1.430	4.97E-01	4.83E-02	202
3DL3	961	OKG	COAD	C	A	C/A	A/A	103	102	45	36	0.808	0.482	1.350	4.97E-01	4.86E-02	203
2DL4	480	OKG	GBM	G	A	G/A	A/A	113	14	56	4	0.577	0.182	1.830	4.98E-01	4.88E-02	204
2DL4	762	OKG	SARC	C	T	C/T	T/T	202	72	42	11	0.735	0.359	1.500	5.01E-01	4.90E-02	205
3DL3	961	OKG	GBM	C	A	C/A	A/A	103	102	48	39	0.820	0.496	1.360	5.20E-01	4.93E-02	206
3DL1	607	OKG	PRAD	C	T	C/T	T/T	116	96	32	33	1.250	0.717	2.180	5.26E-01	4.95E-02	207
2DP1	522	OKG	SKCM	T	C	T/C	C/C	86	20	75	23	1.320	0.672	2.590	5.27E-01	4.98E-02	208
3DL3	906	OKG	LUAD	C	T	C/T	T/T	143	28	113	17	0.768	0.400	1.470	5.28E-01	5.00E-02	209
2DL5	517	OKG	PRAD	A	G	A/G	G/G	44	63	12	24	1.400	0.634	3.090	5.28E-01	5.02E-02	210
2DP1	766	OKG	LUAD	G	C	G/C	C/C	54	9	43	4	0.558	0.161	1.940	5.29E-01	5.05E-02	211
2DP1	522	OKG	PRAD	T	C	T/C	C/C	86	20	26	9	1.490	0.605	3.670	5.30E-01	5.07E-02	212
3DL3	804	OKG	SKCM	G	A	G/A	A/A	142	28	130	20	0.780	0.419	1.450	5.30E-01	5.10E-02	213
3DL3	804	OKG	HNSC	G	A	G/A	A/A	142	28	113	28	1.260	0.706	2.250	5.31E-01	5.12E-02	214
2DL4	412	OKG	BRCA	G	A	G/A	A/A	142	25	165	36	1.240	0.710	2.170	5.39E-01	5.14E-02	215
2DL4	412	OKG	LUAD	G	A	G/A	A/A	142	25	112	15	0.761	0.383	1.510	5.41E-01	5.17E-02	216
3DL3	502	OKG	GBM	G	A	G/A	A/A	187	110	110	56	0.865	0.581	1.290	5.42E-01	5.19E-02	217
2DL4	625	OKG	BLCA	C	G	C/G	G/G	121	17	67	13	1.380	0.632	3.010	5.43E-01	5.22E-02	218

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	777	OKG	GBM	A	G	A/G	G/G	141	27	84	12	0.746	0.359	1.550	5.44E-01	5.24E-02	219
3DP1	774	OKG	GBM	G	C	G/C	C/C	147	16	57	9	1.450	0.606	3.470	5.45E-01	5.26E-02	220
2DP1	522	OKG	GBM	T	C	T/C	C/C	86	20	44	14	1.370	0.632	2.970	5.52E-01	5.29E-02	221
3DP1	774	OKG	STAD	G	C	G/C	C/C	147	16	50	8	1.470	0.593	3.640	5.55E-01	5.31E-02	222
3DL3	961	OKG	STAD	C	A	C/A	A/A	103	102	36	29	0.813	0.464	1.420	5.62E-01	5.34E-02	223
3DL1	1180	OKG	PRAD	G	C	G/C	C/C	86	51	37	17	0.775	0.396	1.520	5.63E-01	5.36E-02	224
2DL4	762	OKG	CESC	C	T	C/T	T/T	202	72	40	18	1.260	0.679	2.340	5.63E-01	5.38E-02	225
2DL5	517	OKG	READ	A	G	A/G	G/G	44	63	7	15	1.500	0.565	3.980	5.66E-01	5.41E-02	226
2DL3	953	OKG	KIRP	G	A	G/A	A/A	104	112	14	20	1.330	0.639	2.770	5.67E-01	5.43E-02	227
3DP1	796	OKG	GBM	T	C	T/C	C/C	134	15	56	9	1.440	0.595	3.480	5.69E-01	5.46E-02	228
2DL4	762	OKG	UCEC	C	T	C/T	T/T	202	72	106	44	1.160	0.745	1.810	5.75E-01	5.48E-02	229
2DL4	480	OKG	STAD	G	A	G/A	A/A	113	14	44	8	1.470	0.577	3.750	5.78E-01	5.50E-02	230
3DL3	804	OKG	CESC	G	A	G/A	A/A	142	28	32	4	0.634	0.208	1.930	5.80E-01	5.53E-02	231
3DL3	906	OKG	THCA	C	T	C/T	T/T	143	28	90	22	1.250	0.674	2.320	5.85E-01	5.55E-02	232
3DL3	906	OKG	CESC	C	T	C/T	T/T	143	28	32	4	0.638	0.209	1.950	5.89E-01	5.57E-02	233
2DP1	522	OKG	THCA	T	C	T/C	C/C	86	20	45	14	1.340	0.619	2.900	5.90E-01	5.60E-02	234
2DL5	517	OKG	THCA	A	G	A/G	G/G	44	63	24	43	1.250	0.665	2.350	5.91E-01	5.62E-02	235
3DL3	906	OKG	UCEC	C	T	C/T	T/T	143	28	68	10	0.751	0.345	1.630	5.94E-01	5.65E-02	236
3DL3	408	OKG	COAD	G	A	G/A	A/A	113	12	44	7	1.500	0.555	4.060	5.94E-01	5.67E-02	237
2DP1	471	OKG	LUSC	A	G	A/G	G/G	64	14	43	13	1.380	0.591	3.220	5.95E-01	5.69E-02	238
2DP1	448	OKG	STAD	G	C	G/C	C/C	151	89	64	44	1.170	0.735	1.860	5.96E-01	5.72E-02	239
3DL3	777	OKG	SKCM	A	G	A/G	G/G	141	27	130	20	0.803	0.430	1.500	5.97E-01	5.74E-02	240
3DL1	1180	OKG	KIRC	G	C	G/C	C/C	86	51	11	4	0.613	0.185	2.030	6.00E-01	5.77E-02	241
3DL1	607	OKG	KIRP	C	T	C/T	T/T	116	96	26	17	0.790	0.405	1.540	6.01E-01	5.79E-02	242
3DL3	804	OKG	THCA	G	A	G/A	A/A	142	28	90	22	1.240	0.669	2.300	6.01E-01	5.81E-02	243
2DL4	625	OKG	COAD	C	G	C/G	G/G	121	17	40	8	1.420	0.570	3.540	6.07E-01	5.84E-02	244
3DL3	961	OKG	KIRC	C	A	C/A	A/A	103	102	13	17	1.320	0.610	2.860	6.09E-01	5.86E-02	245
3DL3	804	OKG	PRAD	G	A	G/A	A/A	142	28	55	8	0.738	0.317	1.720	6.15E-01	5.89E-02	246
2DP1	448	OKG	UCEC	G	C	G/C	C/C	151	89	80	54	1.150	0.746	1.770	6.15E-01	5.91E-02	247
3DP1	796	OKG	LUAD	T	C	T/C	C/C	134	15	80	12	1.340	0.597	3.010	6.16E-01	5.93E-02	248
2DL4	625	OKG	SKCM	C	G	C/G	G/G	121	17	136	24	1.260	0.646	2.460	6.16E-01	5.96E-02	249
3DP1	774	OKG	COAD	G	C	G/C	C/C	147	16	60	9	1.380	0.578	3.290	6.22E-01	5.98E-02	250
2DP1	1313	OKG	COAD	A	C	A/C	C/C	112	22	29	8	1.400	0.566	3.470	6.22E-01	6.01E-02	251
3DL1	607	OKG	SARC	C	T	C/T	T/T	116	96	27	18	0.806	0.419	1.550	6.29E-01	6.03E-02	252
2DL4	480	OKG	LGG	G	A	G/A	A/A	113	14	79	13	1.330	0.593	2.980	6.30E-01	6.05E-02	253
3DL1	607	OKG	HNSC	C	T	C/T	T/T	116	96	102	75	0.888	0.594	1.330	6.36E-01	6.08E-02	254
3DL3	777	OKG	UCEC	A	G	A/G	G/G	141	27	68	10	0.768	0.352	1.680	6.37E-01	6.10E-02	255
3DL3	502	OKG	SARC	G	A	G/A	A/A	187	110	39	19	0.828	0.456	1.500	6.38E-01	6.12E-02	256
3DL1	1180	OKG	GBM	G	C	G/C	C/C	86	51	47	23	0.825	0.450	1.510	6.40E-01	6.15E-02	257
2DP1	766	OKG	LUSC	G	C	G/C	C/C	54	9	39	4	0.615	0.177	2.140	6.41E-01	6.17E-02	258
2DL3	953	OKG	OV	G	A	G/A	A/A	104	112	8	12	1.390	0.546	3.540	6.43E-01	6.20E-02	259
2DL4	625	OKG	STAD	C	G	C/G	G/G	121	17	65	12	1.310	0.590	2.910	6.43E-01	6.22E-02	260
2DL3	953	OKG	GBM	G	A	G/A	A/A	104	112	46	57	1.150	0.718	1.840	6.43E-01	6.24E-02	261
2DL5	517	OKG	UCEC	A	G	A/G	G/G	44	63	24	42	1.220	0.648	2.300	6.44E-01	6.27E-02	262
3DL2	474	OKG	HNSC	G	T	G/T	T/T	127	13	96	7	0.712	0.274	1.850	6.44E-01	6.29E-02	263
3DL3	502	OKG	BLCA	G	A	G/A	A/A	187	110	83	43	0.881	0.569	1.360	6.46E-01	6.32E-02	264
3DL3	502	OKG	COAD	G	A	G/A	A/A	187	110	70	36	0.874	0.549	1.390	6.54E-01	6.34E-02	265
3DL1	1180	OKG	STAD	G	C	G/C	C/C	86	51	41	20	0.823	0.435	1.560	6.59E-01	6.36E-02	266
3DL3	906	OKG	GBM	C	T	C/T	T/T	143	28	83	13	0.800	0.393	1.630	6.61E-01	6.39E-02	267
3DL3	777	OKG	CESC	A	G	A/G	G/G	141	27	31	4	0.674	0.220	2.070	6.63E-01	6.41E-02	268
3DL1	1091	OKG	STAD	G	A	G/A	A/A	53	9	37	9	1.430	0.518	3.950	6.63E-01	6.44E-02	269
3DL3	961	OKG	CESC	C	A	C/A	A/A	103	102	18	22	1.230	0.623	2.430	6.64E-01	6.46E-02	270
2DP1	471	OKG	THCA	A	G	A/G	G/G	64	14	45	13	1.320	0.567	3.080	6.68E-01	6.48E-02	271
2DP1	448	OKG	BLCA	G	C	G/C	C/C	151	89	68	35	0.873	0.538	1.420	6.70E-01	6.51E-02	272
2DP1	471	OKG	PRAD	A	G	A/G	G/G	64	14	26	8	1.410	0.529	3.760	6.71E-01	6.53E-02	273
2DP1	448	OKG	SARC	G	C	G/C	C/C	151	89	33	16	0.823	0.429	1.580	6.71E-01	6.56E-02	274
2DP1	1313	OKG	PRAD	A	C	A/C	C/C	112	22	30	8	1.360	0.551	3.360	6.73E-01	6.58E-02	275
3DL3	961	OKG	OV	C	A	C/A	A/A	103	102	9	12	1.350	0.545	3.340	6.78E-01	6.60E-02	276
3DL1	1180	OKG	KIRP	G	C	G/C	C/C	86	51	18	8	0.749	0.304	1.850	6.85E-01	6.63E-02	277
3DL3	961	OKG	LIHC	C	A	C/A	A/A	103	102	11	8	0.734	0.284	1.900	6.90E-01	6.65E-02	278
3DL1	1026	OKG	STAD	G	C	G/C	C/C	52	9	37	9	1.410	0.511	3.890	6.91E-01	6.68E-02	279
3DL1	1091	OKG	LUSC	G	A	G/A	A/A	53	9	44	5	0.669	0.209	2.140	6.95E-01	6.70E-02	280
3DL3	777	OKG	THCA	A	G	A/G	G/G	141	27	92	21	1.190	0.635	2.230	6.99E-01	6.72E-02	281
3DL3	408	OKG	BLCA	G	A	G/A	A/A	113	12	56	4	0.673	0.208	2.180	7.00E-01	6.75E-02	282
2DP1	448	OKG	LGG	G	C	G/C	C/C	151	89	114	74	1.100	0.743	1.630	7.03E-01	6.77E-02	283
2DP1	1313	OKG	HNSC	A	C	A/C	C/C	112	22	89	21	1.200	0.621	2.320	7.07E-01	6.79E-02	284
3DP1	774	OKG	BLCA	G	C	G/C	C/C	147	16	64	5	0.718	0.252	2.040	7.09E-01	6.82E-02	285
3DL3	869	OKG	BRCA	A	C	A/C	C/C	84	7	105	6	0.686	0.222	2.120	7.11E-01	6.84E-02	286
2DL4	412	OKG	HNSC	G	A	G/A	A/A	142	25	128	19	0.843	0.443	1.600	7.20E-01	6.87E-02	287
2DL3	953	OKG	LIHC	G	A	G/A	A/A	104	112	11	15	1.270	0.558	2.890	7.22E-01	6.89E-02	288
3DL3	961	OKG	UCEC	C	A	C/A	A/A	103	102	59	65	1.110	0.710	1.730	7.23E-01	6.91E-02	289
3DL1	1091	OKG	PRAD	G	A	G/A	A/A	53	9	29	7	1.420	0.479	4.210	7.24E-01	6.94E-02	290
2DL5	583	OKG	READ	G	A	G/A	A/A	43	54	7	6	0.683	0.214	2.180	7.26E-01	6.96E-02	291
2DP1	448	OKG	KIRC	G	C	G/C	C/C	151	89	21	15	1.210	0.593	2.470	7.30E-01	6.99E-02	292
2DP1	448	OKG	READ	G	C	G/C	C/C	151	89	21	15	1.210	0.593	2.470	7.30E-01	6.99E-02	292
2DL4	480	OKG	UCEC	G	A	G/A	A/A	113	14	56	5	0.721	0.247	2.100	7.31E-01	7.01E-02	293
3DL1	607	OKG	OV	C	T	C/T	T/T	116	96	14	9	0.777	0.322	1.870	7.32E-01	7.03E-02	294
2DL3	953	OKG	KIRC	G	A	G/A	A/A	104	112	15	13	0.805	0.366	1.770	7.34E-01	7.06E-02	295
2DP1	522	OKG	LUSC	T	C	T/C	C/C	86	20	45	13	1.240	0.565	2.720	7.35E-01	7.08E-02	296
2DL3	953	OKG	CESC	G	A	G/A	A/A	104	112	24	22	0.851	0.450	1.610	7.39E-01	7.11E-02	297
2DL5	517	OKG	BLCA	A	G	A/G	G/G	44	63	20	34	1.190	0.607	2.330	7.42E-01	7.13E-02	298
2DL4	625	OKG	THCA	C	G	C/G	G/G	121	17	94	16	1.210	0.581	2.520	7.45E-01	7.15E-02	299
3DL1	1180	OKG	LUSC	G	C	G/C	C/C	86	51	45	23	0.862	0.468	1.590	7.47E-01	7.18E-02	300
3DL3	502	OKG	LIHC	G	A	G/A	A/A	187	110	23	16	1.180	0.598	2.330	7.58E-01	7.20E-02	301
2DL3	953	OKG	PRAD	G	A	G/A	A/A	104	112	26	32	1.140	0.637	2.040	7.63E-01	7.23E-02	302
3DL3	408	OKG	SKCM	G	A	G/A	A/A	113	12	108	9	0.785	0.318	1.940	7.65E-01	7.25E-02	303
2DL4	412	OKG	PRAD	G	A	G/A	A/A	142	25	41	9	1.250	0.541	2.890	7.68E-01	7.27E-02	304
2DP1	1313	OKG	LUAD	A	C	A/C	C/C	112	22	64	15	1.190	0.577	2.460	7.71E-01	7.30E-02	305
3DL1	607	OKG	LIHC	C	T	C/T	T/T	116	96	15	10	0.806	0.346	1.880	7.72E-01	7.32E-02	306
2DL4	480	OKG	PRAD	G	A	G/A	A/A	113	14	45	4	0.717	0.224	2.300	7.77E-01	7.34E-02	307
3DL3	502	OKG	READ	G	A	G/A	A/A	187	110	28	19	1.150	0.613	2.160	7.77E-01	7.37E-02	308
2DP1	471	OKG	UCEC	A	G	A/G	G/G	64	14	47	8	0.778	0.302	2.010	7.77E-01	7.39E-02	309
2DL4	625	OKG	LUSC	C	G	C/G	G/G	121	17	71	8	0.802	0.329	1.950	7.90E-01	7.42E-02	310
2DL3	953	OKG	BRCA	G	A	G/A	A/A	104	112	104	120	1.070	0.736	1.560	7.90E-01	7.44E-02	311
3DL1	1026	OKG	GBM	G	C	G/C	C/C	52	9	40	5	0.722	0.224	2.320	7.97E-01	7.46E-02	312
3DL3	961	OKG	ACC	C	A	C/A	A/A	103	102	7	5	0.721	0.222	2.350	8.04E-01	7.49E-02	313
2DL3	953	OKG	BLCA	G	A	G/A	A/A	104	112	39	38	0.905	0.538	1.520	8.07E-01	7.51E-02	314
2DL4	1023	OKG	LGG	G	A	G/A	A/A	128	12	96	11	1.220	0.516	2.880	8.13E-01	7.54E-02	315
2DP1	1313	OKG	LUSC	A	C	A/C	C/C	112	22	56	13	1.180	0.554	2.520	8.13E-01	7.56E-02	316
3DL3	869	OKG	HNSC	A	C	A/C	C/C	84	7	73	8	1.320	0.457	3.820	8.13E-01	7.58E-02	317
3DL1	1194	OKG	SKCM	C	T	C/T	T/T	22	7	13	6	1.450	0.400	5.260	8.14E-01	7.61E-02	318
3DL3	961	OKG	SARC	C	A	C/A	A/A	103	102	22	19	0.872	0.445	1.710	8.20E-01	7.63E-02	319
3DL3	408	OKG	THCA	G	A	G/A	A/A	113	12	85	11	1.220	0.514	2.900	8.21E-01	7.66E-02	320
3DL3	906	OKG	HNSC	C	T	C/T	T/T	143	28	114	25	1.120	0.619	2.030	8.23E-01	7.68E-02	321
2DL3	953	OKG	LUAD	G	A	G/A	A/A	104	112	56	65	1.080	0.691	1.690	8.29E-01	7.70E-02	322
3DL1	607	OKG	UCEC	C	T	C/T	T/T	116	96	64	49	0.925	0.584	1.470	8.30E-01	7.73E-02	323
3DL2	474	OKG	SKCM	G	T	G/T	T/T	127	13	98	12	1.200	0.524	2.750	8.32E-01	7.75E-02	324
2DP1	448	OKG	LIHC	G	C	G/C	C/C	151	89	19	13	1.160	0.547	2.460	8.46E-01	7.78E-02	325
2DL4	412	OKG	STAD	G	A	G/A	A/A	142	25	64	13	1.150	0.553	2.390	8.47E-01	7.80E-02	326
2DL3	953	OKG	SARC	G	A	G/A	A/A	104	112	21	20	0.884	0.453	1.720	8.49E-01	7.82E-02	327

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DL5	517	OKG	LIHC	A	G	A/G	G/G	44	63	6	11	1.280	0.441	3.720	8.50E-01	7.85E-02	328
3DL3	869	OKG	SKCM	A	C	A/C	C/C	84	7	75	8	1.280	0.443	3.700	8.52E-01	7.87E-02	329
3DL3	961	OKG	PRAD	C	A	C/A	A/A	103	102	28	25	0.902	0.493	1.650	8.56E-01	7.90E-02	330
3DL1	1091	OKG	GBM	G	A	G/A	A/A	53	9	39	5	0.755	0.235	2.430	8.56E-01	7.92E-02	331
3DL1	607	OKG	READ	C	T	C/T	T/T	116	96	18	17	1.140	0.557	2.330	8.58E-01	7.94E-02	332
3DL3	777	OKG	PRAD	A	G	A/G	G/G	141	27	55	9	0.855	0.378	1.930	8.61E-01	7.97E-02	333
2DL4	625	OKG	LGG	C	G	C/G	G/G	121	17	122	15	0.875	0.418	1.830	8.68E-01	7.99E-02	334
3DP1	479	OKG	STAD	A	C	A/C	C/C	176	21	61	6	0.824	0.318	2.140	8.69E-01	8.01E-02	335
3DL1	1180	OKG	LUAD	G	C	G/C	C/C	86	51	57	31	0.917	0.525	1.600	8.71E-01	8.04E-02	336
2DL3	953	OKG	LGG	G	A	G/A	A/A	104	112	73	83	1.060	0.702	1.600	8.79E-01	8.06E-02	337
3DL3	804	OKG	COAD	G	A	G/A	A/A	142	28	58	10	0.874	0.399	1.910	8.89E-01	8.09E-02	338
3DP1	774	OKG	LUAD	G	C	G/C	C/C	147	16	88	11	1.150	0.511	2.590	9.01E-01	8.11E-02	339
3DL1	607	OKG	CESC	C	T	C/T	T/T	116	96	29	22	0.917	0.495	1.700	9.05E-01	8.13E-02	340
3DL3	502	OKG	STAD	G	A	G/A	A/A	187	110	82	46	0.954	0.620	1.470	9.16E-01	8.16E-02	341
2DL4	412	OKG	THCA	G	A	G/A	A/A	142	25	94	15	0.906	0.454	1.810	9.17E-01	8.18E-02	342
3DL1	1026	OKG	LUSC	G	C	G/C	C/C	52	9	43	6	0.806	0.266	2.440	9.19E-01	8.21E-02	343
2DL5	517	OKG	LUAD	A	G	A/G	G/G	44	63	33	44	0.931	0.514	1.690	9.33E-01	8.23E-02	344
2DP1	448	OKG	OV	G	C	G/C	C/C	151	89	10	7	1.190	0.437	3.240	9.38E-01	8.25E-02	345
2DL4	412	OKG	BLCA	G	A	G/A	A/A	142	25	67	13	1.100	0.530	2.280	9.42E-01	8.28E-02	346
2DP1	522	OKG	HNSC	T	C	T/C	C/C	86	20	80	17	0.914	0.447	1.870	9.48E-01	8.30E-02	347
2DL5	583	OKG	LIHC	G	A	G/A	A/A	43	54	6	6	0.796	0.240	2.640	9.48E-01	8.33E-02	348
3DL3	777	OKG	COAD	A	G	A/G	G/G	141	27	58	10	0.900	0.410	1.980	9.49E-01	8.35E-02	349
2DP1	448	OKG	HNSC	G	C	G/C	C/C	151	89	130	79	1.030	0.702	1.510	9.53E-01	8.37E-02	350
2DL3	953	OKG	UCEC	G	A	G/A	A/A	104	112	49	55	1.040	0.651	1.660	9.57E-01	8.40E-02	351
3DL3	502	OKG	PRAD	G	A	G/A	A/A	187	110	62	38	1.040	0.652	1.660	9.58E-01	8.42E-02	352
2DL4	762	OKG	LUAD	C	T	C/T	T/T	202	72	142	49	0.968	0.635	1.480	9.66E-01	8.45E-02	353
3DL3	906	OKG	COAD	C	T	C/T	T/T	143	28	56	10	0.912	0.416	2.000	9.74E-01	8.47E-02	354
3DL3	804	OKG	STAD	G	A	G/A	A/A	142	28	66	12	0.922	0.441	1.930	9.76E-01	8.49E-02	355
3DL1	1194	OKG	BRCA	C	T	C/T	T/T	22	7	15	6	1.260	0.353	4.500	9.79E-01	8.52E-02	356
2DL3	953	OKG	STAD	G	A	G/A	A/A	104	112	34	35	0.956	0.556	1.640	9.80E-01	8.54E-02	357
2DP1	522	OKG	UCEC	T	C	T/C	C/C	86	20	47	12	1.100	0.495	2.450	9.81E-01	8.57E-02	358
3DL3	906	OKG	STAD	C	T	C/T	T/T	143	28	66	12	0.929	0.445	1.940	9.91E-01	8.59E-02	359
2DL4	480	OKG	HNSC	G	A	G/A	A/A	113	14	89	10	0.907	0.385	2.140	9.95E-01	8.61E-02	360
2DL5	583	OKG	CESC	G	A	G/A	A/A	43	54	10	14	1.110	0.449	2.740	9.95E-01	8.64E-02	361
2DL4	762	OKG	KIRP	C	T	C/T	T/T	202	72	37	14	1.060	0.542	2.070	9.99E-01	8.66E-02	362
3DL1	1091	OKG	HNSC	G	A	G/A	A/A	53	9	70	13	1.090	0.434	2.740	1.00E+00	8.68E-02	363
2DL4	480	OKG	BRCA	G	A	G/A	A/A	113	14	129	16	1.000	0.467	2.140	1.00E+00	8.71E-02	364
2DL4	480	OKG	LUAD	G	A	G/A	A/A	113	14	68	9	1.070	0.439	2.610	1.00E+00	8.71E-02	364
2DL4	762	OKG	LIHC	C	T	C/T	T/T	202	72	20	7	0.982	0.399	2.420	1.00E+00	8.71E-02	364
2DL4	1023	OKG	HNSC	G	A	G/A	A/A	128	12	94	8	0.908	0.357	2.310	1.00E+00	8.71E-02	364
2DL4	1023	OKG	THCA	G	A	G/A	A/A	128	12	75	7	0.996	0.376	2.640	1.00E+00	8.71E-02	364
3DL3	408	OKG	GBM	G	A	G/A	A/A	113	12	71	8	1.060	0.413	2.720	1.00E+00	8.71E-02	364
3DL3	777	OKG	LGG	A	G	A/G	G/G	141	27	117	23	1.030	0.561	1.890	1.00E+00	8.71E-02	364
3DL3	777	OKG	STAD	A	G	A/G	G/G	141	27	66	12	0.949	0.453	1.990	1.00E+00	8.71E-02	364
3DP1	479	OKG	BLCA	A	C	A/C	C/C	176	21	64	8	1.050	0.443	2.490	1.00E+00	8.71E-02	364
2DL4	412	OKG	COAD	G	A	G/A	A/A	142	25	54	9	0.947	0.415	2.160	1.00E+00	8.73E-02	365
2DL4	412	OKG	SKCM	G	A	G/A	A/A	142	25	136	24	1.000	0.545	1.840	1.00E+00	8.73E-02	365
2DL4	480	OKG	BLCA	G	A	G/A	A/A	113	14	44	6	1.100	0.398	3.040	1.00E+00	8.73E-02	365
2DL4	1023	OKG	SKCM	G	A	G/A	A/A	128	12	101	10	1.060	0.440	2.550	1.00E+00	8.73E-02	365
2DP1	471	OKG	HNSC	A	G	A/G	G/G	64	14	77	16	0.950	0.431	2.090	1.00E+00	8.73E-02	365
2DP1	766	OKG	LGG	G	C	G/C	C/C	54	9	53	8	0.906	0.325	2.530	1.00E+00	8.73E-02	365
2DP1	1313	OKG	UCEC	A	C	A/C	C/C	112	22	44	9	1.040	0.444	2.430	1.00E+00	8.73E-02	365
3DL1	732	OKG	BRCA	T	C	T/C	C/C	46	9	56	10	0.913	0.342	2.440	1.00E+00	8.73E-02	365
3DL1	732	OKG	UCEC	T	C	T/C	C/C	46	9	37	7	0.967	0.329	2.840	1.00E+00	8.73E-02	365
3DL1	1026	OKG	HNSC	G	C	G/C	C/C	52	9	74	12	0.937	0.368	2.380	1.00E+00	8.73E-02	365
3DL1	1026	OKG	PRAD	G	C	G/C	C/C	52	9	30	5	0.963	0.295	3.140	1.00E+00	8.73E-02	365
3DL1	1091	OKG	LGG	G	A	G/A	A/A	53	9	63	10	0.935	0.354	2.470	1.00E+00	8.73E-02	365
3DL1	1180	OKG	COAD	G	C	G/C	C/C	86	51	28	17	1.020	0.509	2.040	1.00E+00	8.73E-02	365
3DL1	1180	OKG	LGG	G	C	G/C	C/C	86	51	68	39	0.967	0.572	1.630	1.00E+00	8.73E-02	365
3DL3	408	OKG	LUAD	G	A	G/A	A/A	113	12	100	11	1.040	0.440	2.460	1.00E+00	8.73E-02	365
3DL3	408	OKG	UCEC	G	A	G/A	A/A	113	12	57	6	0.991	0.354	2.780	1.00E+00	8.73E-02	365
3DL3	804	OKG	LGG	G	A	G/A	A/A	142	28	120	23	0.972	0.532	1.780	1.00E+00	8.73E-02	365
3DL3	869	OKG	UCEC	A	C	A/C	C/C	84	7	67	6	1.070	0.343	3.330	1.00E+00	8.73E-02	365
3DL3	906	OKG	LGG	C	T	C/T	T/T	143	28	118	23	0.995	0.544	1.820	1.00E+00	8.73E-02	365
3DL3	906	OKG	PRAD	C	T	C/T	T/T	143	28	55	10	0.929	0.423	2.040	1.00E+00	8.73E-02	365
3DP1	796	OKG	COAD	T	C	T/C	C/C	134	15	62	7	1.010	0.392	2.600	1.00E+00	8.73E-02	365
2DL3	953	OKG	HNSC	G	A	G/A	A/A	104	112	80	88	1.020	0.681	1.530	1.00E+00	8.76E-02	366
2DL3	953	OKG	LUSC	G	A	G/A	A/A	104	112	44	46	0.971	0.594	1.590	1.00E+00	8.76E-02	366
2DL4	480	OKG	SKCM	G	A	G/A	A/A	113	14	95	11	0.935	0.405	2.160	1.00E+00	8.76E-02	366
2DL4	625	OKG	HNSC	C	G	C/G	G/G	121	17	129	18	0.993	0.489	2.020	1.00E+00	8.76E-02	366
2DL4	625	OKG	LUAD	C	G	C/G	G/G	121	17	112	15	0.953	0.455	2.000	1.00E+00	8.76E-02	366
2DL4	1023	OKG	LUSC	G	A	G/A	A/A	128	12	54	5	0.988	0.332	2.940	1.00E+00	8.76E-02	366
2DL5	517	OKG	CESC	A	G	A/G	G/G	44	63	10	14	0.978	0.398	2.400	1.00E+00	8.76E-02	366
2DL5	583	OKG	LUAD	G	A	G/A	A/A	43	54	33	43	1.040	0.568	1.900	1.00E+00	8.76E-02	366
2DP1	766	OKG	BLCA	G	C	G/C	C/C	54	9	30	5	1.000	0.307	3.260	1.00E+00	8.76E-02	366
2DP1	766	OKG	GBM	G	C	G/C	C/C	54	9	38	6	0.947	0.311	2.880	1.00E+00	8.76E-02	366
2DP1	766	OKG	STAD	G	C	G/C	C/C	54	9	36	6	1.000	0.328	3.050	1.00E+00	8.76E-02	366
2DP1	1269	OKG	BRCA	A	G	A/G	G/G	30	6	26	6	1.150	0.330	4.000	1.00E+00	8.76E-02	366
3DL1	607	OKG	ACC	C	T	C/T	T/T	116	96	8	6	0.906	0.304	2.700	1.00E+00	8.76E-02	366
3DL1	1021	OKG	BRCA	A	G	A/G	G/G	14	7	14	6	0.857	0.229	3.200	1.00E+00	8.76E-02	366
3DL1	1026	OKG	BLCA	G	C	G/C	C/C	52	9	34	5	0.850	0.262	2.750	1.00E+00	8.76E-02	366
3DL1	1026	OKG	LGG	G	C	G/C	C/C	52	9	61	10	0.947	0.358	2.510	1.00E+00	8.76E-02	366
3DL1	1091	OKG	BLCA	G	A	G/A	A/A	53	9	34	6	1.040	0.340	3.180	1.00E+00	8.76E-02	366
3DL1	1180	OKG	LIHC	G	C	G/C	C/C	86	51	11	7	1.070	0.390	2.930	1.00E+00	8.76E-02	366
3DL1	1194	OKG	HNSC	C	T	C/T	T/T	22	7	19	5	0.827	0.225	3.040	1.00E+00	8.76E-02	366
3DL1	1194	OKG	LGG	C	T	C/T	T/T	22	7	18	5	0.873	0.237	3.220	1.00E+00	8.76E-02	366
3DL2	474	OKG	LGG	G	T	G/T	T/T	127	13	96	10	1.020	0.429	2.420	1.00E+00	8.76E-02	366
3DL3	408	OKG	BRCA	G	A	G/A	A/A	113	12	139	16	1.080	0.491	2.380	1.00E+00	8.76E-02	366
3DL3	408	OKG	LGG	G	A	G/A	A/A	113	12	103	12	1.100	0.473	2.560	1.00E+00	8.76E-02	366
3DL3	408	OKG	PRAD	G	A	G/A	A/A	113	12	49	6	1.150	0.408	3.240	1.00E+00	8.76E-02	366

Table A12c Chi square significance tests for KIR variants within the TCGA samples, European cohort, reference homozygous versus alternate homozygous

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	961	OKG	SKCM	C	A	C/C	A/A	118	102	103	33	0.371	0.231	0.596	4.84E-05	2.36E-04	1
3DP1	774	OKG	PRAD	G	C	G/G	C/C	234	16	73	18	3.610	1.750	7.440	5.74E-04	4.72E-04	2
3DL1	1180	OKG	UCEC	G	C	G/G	C/C	177	51	126	11	0.303	0.152	0.604	7.03E-04	7.08E-04	3
2DP1	471	OKG	BLCA	A	G	A/A	G/G	292	14	108	16	3.090	1.460	6.540	4.21E-03	9.43E-04	4
3DP1	479	OKG	PRAD	A	C	A/A	C/C	201	21	75	21	2.680	1.380	5.190	4.78E-03	1.18E-03	5
3DL3	961	OKG	LGG	C	A	C/C	A/A	118	102	90	40	0.514	0.325	0.812	5.81E-03	1.42E-03	6
3DL1	607	OKG	THCA	C	T	C/C	T/T	151	96	111	37	0.524	0.334	0.823	6.67E-03	1.65E-03	7
3DL3	408	OKG	LUSC	G	A	G/G	A/A	273	12	113	15	3.020	1.370	6.660	8.30E-03	1.89E-03	8
2DP1	471	OKG	STAD	A	G	A/A	G/G	292	14	108	15	2.900	1.350	6.210	8.53E-03	2.12E-03	9
3DL3	961	OKG	LUAD	C	A	C/C	A/A	118	102	87	40	0.532	0.336	0.842	9.32E-03	2.36E-03	10
3DL1	1180	OKG	SKCM	G	C	G/G	C/C	177	51	212	32	0.524	0.323	0.851	1.18E-02	2.59E-03	11
2DL4	625	OKG	GBM	C	G	C/C	G/G	191	17	105	22	2.350	1.200	4.620	1.84E-02	2.83E-03	12
3DL3	961	OKG	LUSC	C	A	C/C	A/A	118	102	57	25	0.507	0.296	0.870	1.85E-02	3.07E-03	13
3DL1	607	OKG	LUAD	C	T	C/C	T/T	151	96	116	43	0.583	0.378	0.899	1.91E-02	3.30E-03	14
3DL3	906	OKG	SARC	C	T	C/C	T/T	226	28	42	13	2.500	1.200	5.220	2.26E-02	3.54E-03	15
3DL3	961	OKG	THCA	C	A	C/C	A/A	118	102	66	31	0.543	0.329	0.897	2.31E-02	3.77E-03	16
2DL4	412	OKG	GBM	G	A	G/G	A/A	229	25	105	24	2.090	1.140	3.830	2.35E-02	4.01E-03	17
2DL4	1023	OKG	GBM	G	A	G/G	A/A	258	12	136	16	2.530	1.160	5.500	2.74E-02	4.25E-03	18
2DL3	953	OKG	STAD	G	A	G/G	A/A	144	112	78	35	0.577	0.361	0.922	2.81E-02	4.48E-03	19
3DL3	961	OKG	GBM	C	A	C/C	A/A	118	102	78	39	0.578	0.362	0.922	2.83E-02	4.72E-03	20
2DP1	522	OKG	BLCA	T	C	T/T	C/C	280	20	106	17	2.250	1.140	4.460	2.96E-02	4.95E-03	21
3DL1	1180	OKG	THCA	G	C	G/G	C/C	177	51	144	22	0.530	0.307	0.915	3.01E-02	5.19E-03	22
3DL1	607	OKG	GBM	C	T	C/C	T/T	151	96	100	38	0.598	0.380	0.940	3.35E-02	5.43E-03	23
3DL1	1180	OKG	HNSC	G	C	G/G	C/C	177	51	207	35	0.587	0.365	0.944	3.61E-02	5.66E-03	24
3DL3	777	OKG	SARC	A	G	A/A	G/G	229	27	43	12	2.370	1.120	5.040	3.89E-02	5.90E-03	25
2DL4	762	OKG	LUSC	C	T	C/C	T/T	89	72	46	64	1.720	1.050	2.810	4.01E-02	6.13E-03	26
3DL3	961	OKG	HNSC	C	A	C/C	A/A	118	102	110	61	0.642	0.426	0.967	4.30E-02	6.37E-03	27
3DL3	804	OKG	SARC	G	A	G/G	A/A	228	28	43	12	2.270	1.070	4.810	4.94E-02	6.60E-03	28
2DP1	471	OKG	LGG	A	G	A/A	G/G	292	14	223	22	2.060	1.030	4.120	5.67E-02	6.84E-03	29
2DL5	517	OKG	BRCA	A	G	A/A	G/G	81	63	82	100	1.570	1.010	2.440	5.80E-02	7.08E-03	30
3DL3	502	OKG	ACC	G	A	G/G	A/A	101	110	12	4	0.306	0.096	0.979	6.67E-02	7.31E-03	31
2DL5	517	OKG	STAD	A	G	A/A	G/G	81	63	34	46	1.740	1.000	3.020	6.68E-02	7.55E-03	32
3DL3	777	OKG	LUSC	A	G	A/A	G/G	229	27	101	22	1.850	1.010	3.400	6.72E-02	7.78E-03	33
3DL3	502	OKG	THCA	G	A	G/G	A/A	101	110	68	47	0.635	0.401	1.010	6.74E-02	8.02E-03	34
2DL3	953	OKG	COAD	G	A	G/G	A/A	144	112	58	27	0.599	0.356	1.010	6.86E-02	8.26E-03	35
3DL1	1180	OKG	GBM	G	C	G/G	C/C	177	51	135	23	0.591	0.344	1.020	7.42E-02	8.49E-03	36
3DL1	1180	OKG	BRCA	G	C	G/G	C/C	177	51	258	49	0.659	0.426	1.020	7.71E-02	8.73E-03	37
3DL1	1180	OKG	KIRC	G	C	G/G	C/C	177	51	39	4	0.356	0.121	1.040	8.06E-02	8.96E-03	38
3DL3	961	OKG	BLCA	C	A	C/C	A/A	118	102	41	20	0.564	0.311	1.020	8.06E-02	9.20E-03	39
2DP1	471	OKG	SKCM	A	G	A/A	G/G	292	14	236	22	1.940	0.971	3.870	8.19E-02	9.43E-03	40
3DL1	1180	OKG	BLCA	G	C	G/G	C/C	177	51	104	17	0.567	0.311	1.030	8.45E-02	9.67E-03	41
3DL3	804	OKG	LUSC	G	A	G/G	A/A	228	28	101	22	1.770	0.966	3.240	8.74E-02	9.91E-03	42
2DL5	517	OKG	HNSC	A	G	A/A	G/G	81	63	66	79	1.540	0.968	2.450	8.78E-02	1.01E-02	43
2DP1	471	OKG	BRCA	A	G	A/A	G/G	292	14	316	28	1.850	0.955	3.580	9.19E-02	1.04E-02	44
2DP1	522	OKG	STAD	T	C	T/T	C/C	280	20	108	15	1.940	0.958	3.930	9.30E-02	1.06E-02	45
3DL3	906	OKG	LUSC	C	T	C/C	T/T	226	28	101	22	1.760	0.960	3.230	9.30E-02	1.09E-02	46
2DP1	1313	OKG	GBM	A	C	A/A	C/C	210	22	142	26	1.750	0.954	3.210	9.60E-02	1.11E-02	47
3DL3	502	OKG	OV	G	A	G/G	A/A	101	110	14	6	0.394	0.146	1.060	9.73E-02	1.13E-02	48
2DP1	471	OKG	LUAD	A	G	A/A	G/G	292	14	182	17	1.950	0.939	4.050	1.04E-01	1.16E-02	49
2DL5	583	OKG	STAD	G	A	G/G	A/A	62	54	34	49	1.650	0.933	2.920	1.11E-01	1.18E-02	50
3DL2	474	OKG	GBM	G	T	G/G	T/T	258	13	137	14	2.030	0.928	4.440	1.11E-01	1.20E-02	51
2DP1	471	OKG	LUSC	A	G	A/A	G/G	292	14	135	13	2.010	0.920	4.390	1.17E-01	1.23E-02	52
3DL1	607	OKG	LGG	C	T	C/C	T/T	151	96	140	64	0.719	0.486	1.060	1.20E-01	1.25E-02	53
3DP1	774	OKG	UCEC	G	C	G/G	C/C	234	16	133	17	1.870	0.915	3.820	1.22E-01	1.27E-02	54
2DL4	762	OKG	SKCM	C	T	C/C	T/T	89	72	81	94	1.430	0.930	2.200	1.24E-01	1.30E-02	55
2DL4	625	OKG	UCEC	C	G	C/C	G/G	191	17	117	19	1.820	0.910	3.640	1.24E-01	1.32E-02	56
3DP1	796	OKG	THCA	T	C	T/T	C/C	248	15	150	17	1.870	0.907	3.850	1.25E-01	1.34E-02	57
3DL3	804	OKG	UCEC	G	A	G/G	A/A	228	28	143	9	0.512	0.235	1.120	1.27E-01	1.37E-02	58
2DL4	480	OKG	COAD	G	A	G/G	A/A	265	14	101	11	2.060	0.905	4.690	1.27E-01	1.39E-02	59
2DL3	953	OKG	LUSC	G	A	G/G	A/A	144	112	85	46	0.696	0.450	1.080	1.27E-01	1.42E-02	60
2DP1	1313	OKG	BLCA	A	C	A/A	C/C	210	22	97	18	1.770	0.908	3.450	1.30E-01	1.44E-02	61
2DL4	480	OKG	THCA	G	A	G/G	A/A	265	14	166	3	0.342	0.097	1.210	1.37E-01	1.46E-02	62
3DP1	479	OKG	HNSC	A	C	A/A	C/C	201	21	189	32	1.620	0.902	2.910	1.38E-01	1.49E-02	63
2DP1	471	OKG	GBM	A	G	A/A	G/G	292	14	154	14	1.900	0.883	4.090	1.45E-01	1.51E-02	64
3DL1	607	OKG	BLCA	C	T	C/C	T/T	151	96	78	34	0.686	0.426	1.110	1.51E-01	1.53E-02	65
2DL4	762	OKG	HNSC	C	T	C/C	T/T	89	72	82	93	1.400	0.911	2.150	1.52E-01	1.56E-02	66
3DL3	961	OKG	STAD	C	A	C/C	A/A	118	102	51	29	0.658	0.388	1.110	1.53E-01	1.58E-02	67
3DP1	774	OKG	LGG	G	C	G/G	C/C	234	16	199	23	1.690	0.869	3.290	1.64E-01	1.60E-02	68
3DP1	479	OKG	CESC	A	C	A/A	C/C	201	21	43	9	2.000	0.857	4.670	1.66E-01	1.63E-02	69
3DL1	1180	OKG	LUAD	G	C	G/G	C/C	177	51	157	31	0.685	0.417	1.120	1.69E-01	1.65E-02	70
2DP1	471	OKG	COAD	A	G	A/A	G/G	292	14	106	10	1.970	0.849	4.570	1.72E-01	1.68E-02	71
3DL1	1026	OKG	BRCA	G	C	G/G	C/C	160	9	280	7	0.444	0.162	1.210	1.76E-01	1.70E-02	72
2DL5	583	OKG	BRCA	G	A	G/G	A/A	62	54	81	100	1.420	0.889	2.270	1.79E-01	1.72E-02	73
3DL1	1180	OKG	LGG	G	C	G/G	C/C	177	51	191	39	0.709	0.446	1.130	1.80E-01	1.75E-02	74
3DL3	906	OKG	UCEC	C	T	C/C	T/T	226	28	143	10	0.564	0.266	1.200	1.83E-01	1.77E-02	75
3DP1	774	OKG	THCA	G	C	G/G	C/C	234	16	144	17	1.730	0.848	3.530	1.84E-01	1.79E-02	76
3DL1	1180	OKG	READ	G	C	G/G	C/C	177	51	32	4	0.434	0.147	1.280	1.85E-01	1.82E-02	77
2DL3	953	OKG	PRAD	G	A	G/G	A/A	144	112	59	32	0.697	0.424	1.140	1.92E-01	1.84E-02	78
2DL4	762	OKG	LGG	C	T	C/C	T/T	89	72	84	92	1.350	0.879	2.070	2.02E-01	1.86E-02	79
2DP1	522	OKG	BRCA	T	C	T/T	C/C	280	20	315	34	1.510	0.849	2.680	2.03E-01	1.89E-02	80
3DP1	796	OKG	PRAD	T	C	T/T	C/C	248	15	77	9	1.930	0.813	4.580	2.04E-01	1.91E-02	81
2DP1	448	OKG	KIRC	G	C	G/G	C/C	138	89	13	15	1.790	0.813	3.940	2.09E-01	1.93E-02	82
2DL4	625	OKG	BRCA	C	G	C/C	G/G	191	17	255	35	1.540	0.838	2.830	2.10E-01	1.96E-02	83
3DL2	474	OKG	THCA	G	T	G/G	T/T	258	13	154	3	0.387	0.109	1.380	2.10E-01	1.98E-02	84
3DL1	1180	OKG	LUSC	G	C	G/G	C/C	177	51	117	23	0.682	0.396	1.180	2.13E-01	2.01E-02	85
3DP1	479	OKG	THCA	A	C	A/A	C/C	201	21	127	21	1.580	0.829	3.010	2.16E-01	2.03E-02	86
3DL1	1026	OKG	THCA	G	C	G/G	C/C	160	9	144	3	0.370	0.098	1.390	2.19E-01	2.05E-02	87
3DL1	1180	OKG	STAD	G	C	G/G	C/C	177	51	103	20	0.674	0.381	1.190	2.22E-01	2.08E-02	88
2DL4	412	OKG	UCEC	G	A	G/G	A/A	229	25	118	20	1.550	0.827	2.910	2.25E-01	2.10E-02	89
3DL3	408	OKG	HNSC	G	A	G/G	A/A	273	12	241	18	1.700	0.802	3.600	2.26E-01	2.12E-02	90
2DL5	517	OKG	COAD	A	G	A/A	G/G	81	63	43	22	0.658	0.357	1.210	2.31E-01	2.15E-02	91
3DL3	408	OKG	THCA	G	A	G/G	A/A	273	12	137	11	1.830	0.787	4.250	2.33E-01	2.17E-02	92
3DL3	777	OKG	UCEC	A	G	A/A	G/G	229	27	143	10	0.593	0.279	1.260	2.34E-01	2.19E-02	93
2DL3	953	OKG	HNSC	G	A	G/G	A/A	144	112	143	88	0.791	0.550	1.140	2.40E-01	2.22E-02	94
2DL5	517	OKG	LGG	A	G	A/A	G/G	81	63	62	66	1.370	0.849	2.210	2.43E-01	2.24E-02	95
2DP1	522	OKG	LGG	T	C	T/T	C/C	280	20	222	24	1.510	0.813	2.800	2.45E-01	2.26E-02	96
3DL3	804	OKG	THCA	G	A	G/G	A/A	228	28	120	22	1.490	0.817	2.720	2.48E-01	2.29E-02	97
2DL3	953	OKG	SKCM	G	A	G/G	A/A	144	112	147	91	0.796	0.556	1.140	2.49E-01	2.31E-02	98
2DL5	583	OKG	HNSC	G	A	G/G	A/A	62	54	66	79	1.370	0.839	2.240	2.51E-01	2.34E-02	99
2DL3	953	OKG	BLCA	G	A	G/G	A/A	144	112	66	38	0.740	0.463	1.180	2.54E-01	2.36E-02	100
3DL3	906	OKG	THCA	C	T	C/C	T/T	226	28	120	22	1.480	0.812	2.700	2.60E-01	2.38E-02	101
3DL1	607	OKG	ACC	C	T	C/C	T/T	151	96	18	6	0.524	0.201	1.370	2.64E-01	2.41E-02	102
3DL3	777	OKG	THCA	A	G	A/A	G/G	229	27	120	21	1.480	0.803	2.730	2.67E-01	2.43E-02	103
2DL5	583	OKG	KIRC	G	A	G/G	A/A	62	54	17	8	0.540	0.216	1.350	2.68E-01	2.45E-02	104
2DP1	448	OKG	COAD	G	C	G/G	C/C	138	89	44	39	1.370	0.825	2.270	2.71E-01	2.48E-02	105
3DP1	796	OKG	LGG	T	C	T/T	C/C	248	15	212	20	1.560	0.779	3.120	2.77E-01	2.50E-02	106
3DL2	474	OKG	LUSC	G	T	G/G	T/T	258	13	140	3	0.425	0.119	1.520	2.77E-01	2.52E-02	107
2DP1	1313	OKG	LGG	A	C	A/A	C/C	210	22	199	30	1.440	0.804	2.580	2.80E-01	2.55E-02	108

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	961	OKG	PRAD	C	A	C/C	A/A	118	102	41	25	0.705	0.401	1.240	2.82E-01	2.57E-02	109
3DL1	607	OKG	BRCA	C	T	C/C	T/T	151	96	192	99	0.811	0.570	1.150	2.82E-01	2.59E-02	110
2DL4	625	OKG	BLCA	C	G	C/C	G/G	191	17	89	13	1.640	0.763	3.520	2.82E-01	2.62E-02	111
2DL5	517	OKG	SKCM	A	G	A/A	G/G	81	63	73	75	1.320	0.833	2.090	2.86E-01	2.64E-02	112
3DL1	1091	OKG	BRCA	G	A	G/G	A/A	166	9	281	8	0.525	0.199	1.390	2.87E-01	2.67E-02	113
3DP1	479	OKG	STAD	A	C	A/A	C/C	201	21	105	6	0.547	0.214	1.400	2.87E-01	2.69E-02	114
3DP1	479	OKG	BRCA	A	C	A/A	C/C	201	21	243	36	1.420	0.803	2.510	2.87E-01	2.71E-02	115
3DL1	1091	OKG	THCA	G	A	G/G	A/A	166	9	134	3	0.413	0.110	1.560	2.94E-01	2.74E-02	116
3DL3	502	OKG	LUSC	G	A	G/G	A/A	101	110	56	46	0.754	0.469	1.210	2.96E-01	2.76E-02	117
3DL1	607	OKG	HNSC	C	T	C/C	T/T	151	96	147	75	0.803	0.550	1.170	2.96E-01	2.78E-02	118
2DP1	471	OKG	PRAD	A	G	A/A	G/G	292	14	93	8	1.790	0.728	4.400	3.00E-01	2.81E-02	119
2DP1	1313	OKG	STAD	A	C	A/A	C/C	210	22	100	16	1.530	0.770	3.040	3.02E-01	2.83E-02	120
2DL3	953	OKG	READ	G	A	G/G	A/A	144	112	29	15	0.665	0.340	1.300	3.02E-01	2.85E-02	121
2DL3	953	OKG	LUAD	G	A	G/G	A/A	144	112	105	65	0.796	0.536	1.180	3.03E-01	2.88E-02	122
2DL3	953	OKG	UCEC	G	A	G/G	A/A	144	112	90	55	0.786	0.518	1.190	3.03E-01	2.90E-02	123
3DP1	774	OKG	HNSC	G	C	G/G	C/C	234	16	214	22	1.500	0.767	2.930	3.03E-01	2.93E-02	124
2DL4	762	OKG	KIRP	C	T	C/C	T/T	89	72	10	14	1.730	0.726	4.120	3.04E-01	2.95E-02	125
2DL5	583	OKG	COAD	G	A	G/G	A/A	62	54	21	11	0.601	0.266	1.360	3.04E-01	2.97E-02	126
2DP1	471	OKG	THCA	A	G	A/A	G/G	292	14	167	13	1.620	0.744	3.530	3.05E-01	3.00E-02	127
2DL4	480	OKG	GBM	G	A	G/G	A/A	265	14	155	4	0.488	0.158	1.510	3.09E-01	3.02E-02	128
2DL4	762	OKG	STAD	C	T	C/C	T/T	89	72	44	48	1.350	0.808	2.260	3.12E-01	3.04E-02	129
2DP1	448	OKG	OV	G	C	G/G	C/C	138	89	19	7	0.571	0.231	1.410	3.13E-01	3.07E-02	130
2DL4	412	OKG	LUSC	G	A	G/G	A/A	229	25	121	8	0.606	0.265	1.380	3.14E-01	3.09E-02	131
2DL4	1023	OKG	UCEC	G	A	G/G	A/A	258	12	140	11	1.690	0.727	3.930	3.14E-01	3.11E-02	132
3DP1	479	OKG	LUAD	A	C	A/A	C/C	201	21	145	22	1.450	0.768	2.740	3.21E-01	3.14E-02	133
3DL1	607	OKG	KIRC	C	T	C/C	T/T	151	96	25	10	0.629	0.289	1.370	3.22E-01	3.16E-02	134
3DL1	1091	OKG	LUAD	G	A	G/G	A/A	166	9	140	13	1.710	0.710	4.120	3.22E-01	3.18E-02	135
2DP1	766	OKG	BRCA	G	C	G/G	C/C	174	9	330	27	1.580	0.727	3.430	3.25E-01	3.21E-02	136
3DL1	1021	OKG	SKCM	A	G	A/A	G/G	153	7	159	3	0.412	0.105	1.620	3.25E-01	3.23E-02	137
3DL3	804	OKG	BRCA	G	A	G/G	A/A	228	28	261	23	0.718	0.402	1.280	3.28E-01	3.26E-02	138
2DP1	1313	OKG	BRCA	A	C	A/A	C/C	210	22	250	36	1.370	0.782	2.400	3.30E-01	3.28E-02	139
3DP1	774	OKG	COAD	G	C	G/G	C/C	234	16	78	9	1.690	0.718	3.980	3.31E-01	3.30E-02	140
2DL4	625	OKG	SKCM	C	G	C/C	G/G	191	17	185	24	1.460	0.760	2.810	3.32E-01	3.33E-02	141
3DL1	1026	OKG	SKCM	G	C	G/G	C/C	160	9	205	6	0.520	0.181	1.490	3.32E-01	3.35E-02	142
2DL4	762	OKG	ACC	C	T	C/C	T/T	89	72	12	5	0.515	0.173	1.530	3.40E-01	3.37E-02	143
2DP1	448	OKG	CESC	G	C	G/G	C/C	138	89	32	14	0.678	0.343	1.340	3.41E-01	3.40E-02	144
3DP1	479	OKG	COAD	A	C	A/A	C/C	201	21	81	13	1.540	0.736	3.220	3.43E-01	3.42E-02	145
3DL3	906	OKG	BLCA	C	T	C/C	T/T	226	28	93	7	0.608	0.257	1.440	3.45E-01	3.44E-02	146
3DP1	796	OKG	HNSC	T	C	T/T	C/C	248	15	223	20	1.480	0.740	2.960	3.45E-01	3.47E-02	147
3DP1	796	OKG	BLCA	T	C	T/T	C/C	248	15	106	3	0.468	0.133	1.650	3.46E-01	3.49E-02	148
3DL1	1026	OKG	LUAD	G	C	G/G	C/C	160	9	150	14	1.660	0.698	3.950	3.48E-01	3.51E-02	149
3DL2	474	OKG	HNSC	G	T	G/G	T/T	258	13	241	7	0.576	0.226	1.470	3.48E-01	3.54E-02	150
3DL3	408	OKG	LUAD	G	A	G/G	A/A	273	12	153	11	1.640	0.707	3.810	3.51E-01	3.56E-02	151
2DP1	766	OKG	HNSC	G	C	G/G	C/C	174	9	189	5	0.511	0.168	1.550	3.53E-01	3.59E-02	152
2DL3	953	OKG	GBM	G	A	G/G	A/A	144	112	91	57	0.805	0.533	1.220	3.56E-01	3.61E-02	153
3DP1	796	OKG	LUSC	T	C	T/T	C/C	248	15	128	12	1.550	0.705	3.410	3.75E-01	3.63E-02	154
2DP1	766	OKG	SKCM	G	C	G/G	C/C	174	9	156	4	0.496	0.150	1.640	3.75E-01	3.66E-02	155
2DL5	517	OKG	KIRC	A	G	A/A	G/G	81	63	17	8	0.605	0.245	1.490	3.79E-01	3.68E-02	156
2DL3	953	OKG	LGG	G	A	G/G	A/A	144	112	128	83	0.834	0.576	1.210	3.85E-01	3.70E-02	157
3DP1	774	OKG	LUSC	G	C	G/G	C/C	234	16	126	13	1.510	0.704	3.240	3.89E-01	3.73E-02	158
2DL4	625	OKG	THCA	C	G	C/C	G/G	191	17	123	16	1.460	0.711	3.000	3.94E-01	3.75E-02	159
2DL4	762	OKG	OV	C	T	C/C	T/T	89	72	8	11	1.700	0.649	4.450	3.97E-01	3.77E-02	160
3DL3	777	OKG	BRCA	A	G	A/A	G/G	229	27	262	23	0.745	0.416	1.340	3.98E-01	3.80E-02	161
3DL3	961	OKG	LIHC	C	A	C/C	A/A	118	102	15	8	0.617	0.251	1.510	4.00E-01	3.82E-02	162
2DP1	448	OKG	STAD	G	C	G/G	C/C	138	89	54	44	1.260	0.780	2.030	4.04E-01	3.84E-02	163
2DP1	522	OKG	SKCM	T	C	T/T	C/C	280	20	235	23	1.370	0.734	2.560	4.05E-01	3.87E-02	164
2DP1	448	OKG	LUAD	G	C	G/G	C/C	138	89	92	72	1.210	0.805	1.820	4.08E-01	3.89E-02	165
2DL4	412	OKG	BRCA	G	A	G/G	A/A	229	25	253	36	1.300	0.757	2.230	4.09E-01	3.92E-02	166
3DL1	1091	OKG	SKCM	G	A	G/G	A/A	166	9	197	6	0.562	0.196	1.610	4.11E-01	3.94E-02	167
2DL4	1023	OKG	BRCA	G	A	G/G	A/A	258	12	296	20	1.450	0.695	3.020	4.13E-01	3.96E-02	168
3DL1	1091	OKG	STAD	G	A	G/G	A/A	166	9	99	9	1.680	0.645	4.370	4.14E-01	3.99E-02	169
2DL4	762	OKG	BRCA	C	T	C/C	T/T	89	72	107	105	1.210	0.802	1.830	4.14E-01	4.01E-02	170
3DL3	906	OKG	BRCA	C	T	C/C	T/T	226	28	256	24	0.757	0.426	1.340	4.19E-01	4.03E-02	171
3DL2	474	OKG	UCEC	G	T	G/G	T/T	258	13	143	11	1.530	0.668	3.500	4.30E-01	4.06E-02	172
2DL4	762	OKG	PRAD	C	T	C/C	T/T	89	72	31	33	1.320	0.739	2.360	4.35E-01	4.08E-02	173
2DL3	953	OKG	ACC	G	A	G/G	A/A	144	112	12	14	1.500	0.668	3.370	4.36E-01	4.10E-02	174
2DL5	517	OKG	GBM	A	G	A/A	G/G	81	63	42	42	1.290	0.752	2.210	4.38E-01	4.13E-02	175
3DL3	961	OKG	READ	C	A	C/C	A/A	118	102	27	17	0.728	0.375	1.410	4.39E-01	4.15E-02	176
2DP1	766	OKG	LUAD	G	C	G/G	C/C	174	9	146	4	0.530	0.160	1.760	4.41E-01	4.18E-02	177
3DL3	502	OKG	COAD	G	A	G/G	A/A	101	110	42	36	0.787	0.468	1.320	4.41E-01	4.20E-02	178
2DP1	522	OKG	LUAD	T	C	T/T	C/C	280	20	184	18	1.370	0.706	2.660	4.47E-01	4.22E-02	179
2DL4	480	OKG	LUSC	G	A	G/G	A/A	265	14	135	4	0.561	0.181	1.740	4.47E-01	4.25E-02	180
2DL4	480	OKG	UCEC	G	A	G/G	A/A	265	14	160	5	0.592	0.209	1.670	4.49E-01	4.27E-02	181
3DL3	408	OKG	COAD	G	A	G/G	A/A	273	12	97	7	1.640	0.628	4.290	4.50E-01	4.29E-02	182
3DL3	502	OKG	SKCM	G	A	G/G	A/A	101	110	83	76	0.841	0.557	1.270	4.71E-01	4.32E-02	183
3DL1	607	OKG	UCEC	C	T	C/C	T/T	151	96	92	49	0.838	0.545	1.290	4.86E-01	4.34E-02	184
2DL4	625	OKG	COAD	C	G	C/C	G/G	191	17	59	8	1.520	0.624	3.700	4.91E-01	4.36E-02	185
2DL3	953	OKG	KIRC	G	A	G/G	A/A	144	112	23	13	0.727	0.353	1.500	4.92E-01	4.39E-02	186
3DP1	774	OKG	BRCA	G	C	G/G	C/C	234	16	276	25	1.320	0.688	2.530	4.93E-01	4.41E-02	187
3DL3	961	OKG	UCEC	C	A	C/C	A/A	118	102	63	65	1.190	0.769	1.840	4.94E-01	4.43E-02	188
2DP1	448	OKG	GBM	G	C	G/G	C/C	138	89	81	62	1.190	0.778	1.820	4.95E-01	4.46E-02	189
2DP1	471	OKG	HNSC	A	G	A/A	G/G	292	14	241	16	1.380	0.660	2.880	4.96E-01	4.48E-02	190
2DL4	625	OKG	STAD	C	G	C/C	G/G	191	17	95	12	1.420	0.652	3.090	4.97E-01	4.51E-02	191
2DL4	762	OKG	COAD	C	T	C/C	T/T	89	72	32	33	1.270	0.713	2.260	4.98E-01	4.53E-02	192
2DL3	953	OKG	BRCA	G	A	G/G	A/A	144	112	176	120	0.877	0.625	1.230	4.99E-01	4.55E-02	193
3DL1	1026	OKG	STAD	G	C	G/G	C/C	160	9	103	9	1.550	0.596	4.030	5.09E-01	4.58E-02	194
3DL1	607	OKG	SKCM	C	T	C/C	T/T	151	96	140	77	0.865	0.593	1.260	5.12E-01	4.60E-02	195
2DL5	583	OKG	LGG	G	A	G/G	A/A	62	54	62	66	1.220	0.738	2.020	5.13E-01	4.62E-02	196
3DL3	502	OKG	HNSC	G	A	G/G	A/A	101	110	89	83	0.856	0.572	1.280	5.14E-01	4.65E-02	197
3DL1	607	OKG	LIHC	C	T	C/C	T/T	151	96	22	10	0.715	0.324	1.580	5.21E-01	4.67E-02	198
3DL1	607	OKG	KIRP	C	T	C/C	T/T	151	96	20	17	1.340	0.669	2.690	5.22E-01	4.69E-02	199
2DP1	766	OKG	UCEC	G	C	G/G	C/C	174	9	157	12	1.480	0.607	3.610	5.23E-01	4.72E-02	200
3DP1	479	OKG	UCEC	A	C	A/A	C/C	201	21	115	16	1.330	0.667	2.650	5.25E-01	4.74E-02	201
2DP1	448	OKG	SKCM	G	C	G/G	C/C	138	89	121	90	1.150	0.785	1.680	5.25E-01	4.76E-02	202
3DP1	479	OKG	SKCM	A	C	A/A	C/C	201	21	203	27	1.270	0.695	2.320	5.26E-01	4.79E-02	203
3DL2	474	OKG	BRCA	G	T	G/G	T/T	258	13	295	20	1.350	0.658	2.770	5.27E-01	4.81E-02	204
2DP1	448	OKG	PRAD	G	C	G/G	C/C	138	89	43	34	1.230	0.729	2.070	5.29E-01	4.84E-02	205
3DL1	607	OKG	STAD	C	T	C/C	T/T	151	96	68	36	0.833	0.516	1.340	5.29E-01	4.86E-02	206
2DP1	522	OKG	LUSC	T	C	T/T	C/C	280	20	135	13	1.350	0.652	2.800	5.39E-01	4.88E-02	207
2DL4	412	OKG	BLCA	G	A	G/G	A/A	229	25	89	13	1.340	0.656	2.740	5.40E-01	4.91E-02	208
3DP1	796	OKG	UCEC	T	C	T/T	C/C	248	15	144	12	1.380	0.629	3.030	5.51E-01	4.93E-02	209
2DL4	762	OKG	LIHC	C	T	C/C	T/T	89	72	13	7	0.666	0.252	1.760	5.57E-01	4.95E-02	210
2DL5	583	OKG	LUAD	G	A	G/G	A/A	62	54	60	43	0.823	0.482	1.410	5.63E-01	4.98E-02	211
3DL1	607	OKG	COAD	C	T	C/C	T/T	151	96	53	40	1.190	0.734	1.930	5.68E-01	5.00E-02	212
2DL5	583	OKG	THCA	G	A	G/G	A/A	62	54	61	44	0.828	0.486	1.410	5.76E-01	5.02E-02	213
3DL1	1026	OKG	GBM	G	C	G/G	C/C	160	9	142	5	0.626	0.205	1.910	5.79E-01	5.05E-02	214
3DL3	502	OKG	UCEC	G	A	G/G	A/A	101	110	57	53	0.854	0.538	1.350	5.79E-01	5.07E-02	215
3DL3	777	OKG	BLCA	A	G	A/A	G/G	229	27	93	8	0.730	0.320	1.670	5.80E-01	5.09E-02	216
3DP1	796	OKG	COAD	T	C	T/T	C/C	248	15	79	7	1.460	0.575	3.710	5.81E-01	5.12E-02	217
2DL5	517	OKG	BLCA	A	G	A/A	G/G	81	63	36	34	1.210	0.682	2.150	6.04E-01	5.14E-02	218

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	777	OKG	HNSC	A	G	A/A	G/G	229	27	204	29	1.210	0.693	2.110	6.05E-01	5.17E-02	219
3DL1	607	OKG	READ	C	T	C/C	T/T	151	96	21	17	1.270	0.638	2.530	6.10E-01	5.19E-02	220
2DL4	1023	OKG	HNSC	G	A	G/G	A/A	258	12	242	8	0.711	0.286	1.770	6.11E-01	5.21E-02	221
3DL3	502	OKG	SARC	G	A	G/G	A/A	101	110	22	19	0.793	0.406	1.550	6.11E-01	5.24E-02	222
3DL3	906	OKG	CESC	C	T	C/C	T/T	226	28	49	4	0.659	0.221	1.960	6.13E-01	5.26E-02	223
2DP1	522	OKG	PRAD	T	C	T/T	C/C	280	20	93	9	1.350	0.594	3.070	6.13E-01	5.28E-02	224
2DL4	412	OKG	LGG	G	A	G/G	A/A	229	25	183	16	0.801	0.415	1.540	6.18E-01	5.31E-02	225
2DP1	522	OKG	GBM	T	C	T/T	C/C	280	20	153	14	1.280	0.629	2.610	6.18E-01	5.33E-02	226
3DL3	804	OKG	CESC	G	A	G/G	A/A	228	28	49	4	0.665	0.223	1.980	6.24E-01	5.35E-02	227
3DL1	1091	OKG	GBM	G	A	G/G	A/A	166	9	142	5	0.649	0.213	1.980	6.25E-01	5.38E-02	228
2DL5	583	OKG	SKCM	G	A	G/G	A/A	62	54	73	74	1.160	0.712	1.890	6.27E-01	5.40E-02	229
2DL5	583	OKG	ACC	G	A	G/G	A/A	62	54	9	5	0.638	0.202	2.020	6.28E-01	5.43E-02	230
2DL3	953	OKG	THCA	G	A	G/G	A/A	144	112	97	67	0.888	0.597	1.320	6.28E-01	5.45E-02	231
2DL3	953	OKG	CESC	G	A	G/G	A/A	144	112	23	22	1.230	0.652	2.320	6.33E-01	5.47E-02	232
3DP1	796	OKG	BRCA	T	C	T/T	C/C	248	15	291	22	1.250	0.635	2.460	6.34E-01	5.50E-02	233
2DL4	412	OKG	STAD	G	A	G/G	A/A	229	25	94	13	1.270	0.623	2.590	6.42E-01	5.52E-02	234
3DL3	408	OKG	LGG	G	A	G/G	A/A	273	12	206	12	1.330	0.586	3.020	6.43E-01	5.54E-02	235
3DP1	796	OKG	SKCM	T	C	T/T	C/C	248	15	223	17	1.260	0.615	2.580	6.52E-01	5.57E-02	236
3DL3	777	OKG	CESC	A	G	A/A	G/G	229	27	50	4	0.679	0.227	2.030	6.53E-01	5.59E-02	237
3DL3	804	OKG	SKCM	G	A	G/G	A/A	228	28	196	20	0.831	0.454	1.520	6.54E-01	5.61E-02	238
2DL4	625	OKG	LUSC	C	G	C/C	G/G	191	17	120	8	0.749	0.314	1.790	6.61E-01	5.64E-02	239
2DL5	517	OKG	OV	A	G	A/A	G/G	81	63	7	8	1.470	0.506	4.270	6.62E-01	5.66E-02	240
2DP1	522	OKG	COAD	T	C	T/T	C/C	280	20	108	10	1.300	0.589	2.870	6.64E-01	5.68E-02	241
3DL3	906	OKG	SKCM	C	T	C/C	T/T	226	28	193	20	0.836	0.456	1.530	6.70E-01	5.71E-02	242
2DL4	1023	OKG	LUAD	G	A	G/G	A/A	258	12	180	11	1.310	0.566	3.030	6.73E-01	5.73E-02	243
2DL4	412	OKG	SKCM	G	A	G/G	A/A	229	25	185	24	1.190	0.658	2.150	6.75E-01	5.76E-02	244
3DL3	502	OKG	LGG	G	A	G/G	A/A	101	110	78	76	0.895	0.591	1.360	6.75E-01	5.78E-02	245
3DL1	1194	OKG	BRCA	C	T	C/C	T/T	327	7	414	6	0.677	0.225	2.030	6.76E-01	5.80E-02	246
3DL2	474	OKG	STAD	G	T	G/G	T/T	258	13	118	4	0.673	0.215	2.110	6.77E-01	5.83E-02	247
3DL1	607	OKG	CESC	C	T	C/C	T/T	151	96	29	22	1.190	0.646	2.190	6.81E-01	5.85E-02	248
2DL4	762	OKG	LUAD	C	T	C/C	T/T	89	72	69	49	0.878	0.543	1.420	6.82E-01	5.87E-02	249
2DL4	480	OKG	HNSC	G	A	G/G	A/A	265	14	245	10	0.773	0.337	1.770	6.88E-01	5.90E-02	250
3DL3	804	OKG	BLCA	G	A	G/G	A/A	228	28	93	9	0.788	0.358	1.730	6.89E-01	5.92E-02	251
3DL3	502	OKG	READ	G	A	G/G	A/A	101	110	14	19	1.250	0.596	2.620	6.93E-01	5.94E-02	252
3DL1	1180	OKG	OV	G	C	G/G	C/C	177	51	20	4	0.694	0.227	2.120	7.01E-01	5.97E-02	253
3DL3	408	OKG	GBM	G	A	G/G	A/A	273	12	136	8	1.340	0.535	3.360	7.03E-01	5.99E-02	254
2DL4	762	OKG	BLCA	C	T	C/C	T/T	89	72	43	40	1.150	0.676	1.960	7.04E-01	6.01E-02	255
2DL5	517	OKG	UCEC	A	G	A/A	G/G	81	63	47	42	1.150	0.676	1.960	7.06E-01	6.04E-02	256
2DL5	583	OKG	KIRP	G	A	G/G	A/A	62	54	15	10	0.765	0.318	1.840	7.07E-01	6.06E-02	257
2DL3	953	OKG	OV	G	A	G/G	A/A	144	112	12	12	1.290	0.558	2.980	7.08E-01	6.09E-02	258
2DL4	412	OKG	CESC	G	A	G/G	A/A	229	25	52	4	0.705	0.235	2.110	7.08E-01	6.11E-02	259
2DL4	625	OKG	LUAD	C	G	C/C	G/G	191	17	137	15	1.230	0.594	2.550	7.11E-01	6.13E-02	260
3DL2	474	OKG	BLCA	G	T	G/G	T/T	258	13	115	4	0.690	0.220	2.160	7.11E-01	6.16E-02	261
3DL3	502	OKG	KIRC	G	A	G/G	A/A	101	110	13	11	0.777	0.333	1.810	7.12E-01	6.18E-02	262
2DL5	583	OKG	SARC	G	A	G/G	A/A	62	54	20	14	0.804	0.371	1.740	7.20E-01	6.20E-02	263
3DP1	774	OKG	SKCM	G	C	G/G	C/C	234	16	218	18	1.210	0.602	2.430	7.25E-01	6.23E-02	264
3DP1	774	OKG	BLCA	G	C	G/G	C/C	234	16	100	5	0.731	0.261	2.050	7.26E-01	6.25E-02	265
3DP1	479	OKG	LGG	A	C	A/A	C/C	201	21	179	22	1.180	0.628	2.220	7.31E-01	6.27E-02	266
3DL3	804	OKG	GBM	G	A	G/G	A/A	228	28	118	12	0.828	0.406	1.690	7.31E-01	6.30E-02	267
3DL3	502	OKG	CESC	G	A	G/G	A/A	101	110	16	21	1.210	0.598	2.450	7.33E-01	6.32E-02	268
2DL5	583	OKG	GBM	G	A	G/G	A/A	62	54	42	42	1.150	0.655	2.020	7.35E-01	6.34E-02	269
3DP1	479	OKG	BLCA	A	C	A/A	C/C	201	21	97	8	0.789	0.337	1.850	7.35E-01	6.37E-02	270
2DL4	762	OKG	UCEC	C	T	C/C	T/T	89	72	61	44	0.892	0.543	1.470	7.44E-01	6.39E-02	271
2DP1	448	OKG	UCEC	G	C	G/G	C/C	138	89	76	54	1.100	0.709	1.710	7.49E-01	6.42E-02	272
2DL5	517	OKG	LIHC	A	G	A/A	G/G	81	63	11	11	1.290	0.525	3.170	7.50E-01	6.44E-02	273
2DP1	1313	OKG	SKCM	A	C	A/A	C/C	210	22	215	26	1.150	0.632	2.090	7.51E-01	6.46E-02	274
2DP1	1313	OKG	LUAD	A	C	A/A	C/C	210	22	170	15	0.842	0.424	1.670	7.51E-01	6.49E-02	275
3DL3	961	OKG	OV	C	A	C/C	A/A	118	102	11	12	1.260	0.533	2.980	7.55E-01	6.51E-02	276
3DL3	777	OKG	SKCM	A	G	A/A	G/G	229	27	196	20	0.865	0.471	1.590	7.56E-01	6.53E-02	277
2DL4	412	OKG	SARC	G	A	G/G	A/A	229	25	50	4	0.733	0.244	2.200	7.64E-01	6.56E-02	278
3DL3	502	OKG	BLCA	G	A	G/G	A/A	101	110	44	43	0.897	0.544	1.480	7.66E-01	6.58E-02	279
2DL5	517	OKG	ACC	A	G	A/A	G/G	81	63	9	5	0.714	0.228	2.240	7.66E-01	6.60E-02	280
3DL3	408	OKG	BRCA	G	A	G/G	A/A	273	12	301	16	1.210	0.562	2.600	7.70E-01	6.63E-02	281
2DP1	448	OKG	SARC	G	C	G/G	C/C	138	89	29	16	0.855	0.439	1.660	7.70E-01	6.65E-02	282
2DP1	448	OKG	ACC	G	C	G/G	C/C	138	89	19	10	0.816	0.363	1.840	7.72E-01	6.68E-02	283
3DL3	869	OKG	HNSC	A	C	A/A	C/C	307	7	263	8	1.330	0.476	3.720	7.72E-01	6.70E-02	284
3DL3	869	OKG	SKCM	A	C	A/A	C/C	307	7	263	8	1.330	0.476	3.720	7.72E-01	6.70E-02	284
3DL3	961	OKG	BRCA	C	A	C/C	A/A	118	102	147	136	1.070	0.752	1.520	7.74E-01	6.72E-02	285
3DL3	804	OKG	HNSC	G	A	G/G	A/A	228	28	202	28	1.130	0.647	1.970	7.76E-01	6.75E-02	286
2DL4	480	OKG	STAD	G	A	G/G	A/A	265	14	120	8	1.260	0.515	3.080	7.84E-01	6.77E-02	287
2DL5	517	OKG	READ	A	G	A/A	G/G	81	63	16	15	1.210	0.556	2.630	7.86E-01	6.79E-02	288
3DL3	906	OKG	PRAD	C	T	C/C	T/T	226	28	67	10	1.200	0.555	2.600	7.88E-01	6.82E-02	289
3DL3	961	OKG	ACC	C	A	C/C	A/A	118	102	8	5	0.723	0.229	2.280	7.88E-01	6.84E-02	290
2DL4	625	OKG	PRAD	C	G	C/C	G/G	191	17	82	9	1.230	0.527	2.870	7.93E-01	6.86E-02	291
2DP1	522	OKG	THCA	T	C	T/T	C/C	280	20	167	14	1.170	0.576	2.380	7.95E-01	6.89E-02	292
3DL3	777	OKG	GBM	A	G	A/A	G/G	229	27	119	12	0.855	0.418	1.750	8.02E-01	6.91E-02	293
3DL1	1180	OKG	PRAD	G	C	G/G	C/C	177	51	67	17	0.881	0.475	1.630	8.03E-01	6.93E-02	294
2DL4	762	OKG	CESC	C	T	C/C	T/T	89	72	19	18	1.170	0.572	2.390	8.03E-01	6.96E-02	295
3DL2	474	OKG	LUAD	G	T	G/G	T/T	258	13	181	11	1.210	0.530	2.760	8.16E-01	6.98E-02	296
2DL4	412	OKG	HNSC	G	A	G/G	A/A	229	25	197	19	0.883	0.472	1.650	8.19E-01	7.01E-02	297
2DL4	1023	OKG	LUSC	G	A	G/G	A/A	258	12	140	5	0.768	0.265	2.220	8.19E-01	7.03E-02	298
3DL1	1180	OKG	CESC	G	C	G/G	C/C	177	51	37	9	0.844	0.382	1.860	8.23E-01	7.05E-02	299
3DL3	961	OKG	SARC	C	A	C/C	A/A	118	102	25	19	0.879	0.458	1.690	8.25E-01	7.08E-02	300
2DL5	583	OKG	OV	G	A	G/G	A/A	62	54	7	8	1.310	0.446	3.850	8.26E-01	7.10E-02	301
2DL5	583	OKG	LIHC	G	A	G/G	A/A	62	54	9	6	0.765	0.256	2.290	8.38E-01	7.12E-02	302
2DL4	762	OKG	READ	C	T	C/C	T/T	89	72	17	16	1.160	0.548	2.460	8.39E-01	7.15E-02	303
3DL3	869	OKG	BRCA	A	C	A/A	C/C	307	7	345	6	0.763	0.254	2.290	8.39E-01	7.17E-02	304
3DL1	1180	OKG	KIRP	G	C	G/G	C/C	177	51	33	8	0.841	0.366	1.930	8.40E-01	7.19E-02	305
3DL1	1180	OKG	SARC	G	C	G/G	C/C	177	51	33	8	0.841	0.366	1.930	8.40E-01	7.19E-02	305
2DP1	1313	OKG	COAD	A	C	A/A	C/C	210	22	91	8	0.839	0.360	1.950	8.43E-01	7.22E-02	306
2DL5	583	OKG	PRAD	G	A	G/G	A/A	62	54	31	24	0.889	0.466	1.700	8.47E-01	7.24E-02	307
2DP1	766	OKG	STAD	G	C	G/G	C/C	174	9	90	6	1.290	0.445	3.740	8.50E-01	7.26E-02	308
3DL3	502	OKG	KIRP	G	A	G/G	A/A	101	110	14	13	0.853	0.383	1.900	8.53E-01	7.29E-02	309
2DL5	517	OKG	THCA	A	G	A/A	G/G	81	63	60	43	0.921	0.552	1.540	8.55E-01	7.31E-02	310
3DL3	906	OKG	GBM	C	T	C/C	T/T	226	28	119	13	0.882	0.441	1.770	8.56E-01	7.34E-02	311
2DL4	762	OKG	SARC	C	T	C/C	T/T	89	72	16	11	0.850	0.371	1.950	8.60E-01	7.36E-02	312
3DL1	607	OKG	LUSC	C	T	C/C	T/T	151	96	74	44	0.935	0.595	1.470	8.61E-01	7.38E-02	313
3DL3	502	OKG	PRAD	G	A	G/G	A/A	101	110	32	38	1.090	0.634	1.870	8.61E-01	7.41E-02	314
3DL1	1180	OKG	LIHC	G	C	G/G	C/C	177	51	20	7	1.210	0.484	3.020	8.62E-01	7.43E-02	315
2DP1	1313	OKG	HNSC	A	C	A/A	C/C	210	22	223	21	0.899	0.480	1.680	8.62E-01	7.45E-02	316
3DL1	607	OKG	PRAD	C	T	C/C	T/T	151	96	56	33	0.927	0.562	1.530	8.65E-01	7.48E-02	317
3DP1	796	OKG	LUAD	T	C	T/T	C/C	248	15	171	12	1.160	0.530	2.540	8.65E-01	7.50E-02	318
2DP1	1313	OKG	THCA	A	C	A/A	C/C	210	22	154	18	1.120	0.581	2.160	8.74E-01	7.52E-02	319
2DP1	448	OKG	BRCA	G	C	G/G	C/C	138	89	175	118	1.050	0.737	1.500	8.76E-01	7.55E-02	320
3DL1	1194	OKG	HNSC	C	T	C/C	T/T	327	7	304	5	0.768	0.241	2.450	8.76E-01	7.57E-02	321
2DL4	762	OKG	GBM	C	T	C/C	T/T	89	72	61	46	0.932	0.569	1.530	8.78E-01	7.59E-02	322
2DL4	412	OKG	THCA	G	A	G/G	A/A	229	25	123	15	1.120	0.569	2.200	8.84E-01	7.62E-02	323
2DP1	1313	OKG	UCEC	A	C	A/A	C/C	210	22	99	9	0.868	0.386	1.950	8.88E-01	7.64E-02	324
2DP1	448	OKG	BLCA	G	C	G/G	C/C	138	89	58	35	0.936	0.569	1.540	8.92E-01	7.67E-02	325
2DL4	480	OKG	SKCM	G	A	G/G	A/A	265	14	239	11	0.871	0.388	1.960	8.97E-01	7.69E-02	326

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL1	1091	OKG	HNSC	G	A	G/G	A/A	166	9	206	13	1.160	0.484	2.780	9.05E-01	7.71E-02	327
3DL3	502	OKG	BRCA	G	A	G/G	A/A	101	110	109	114	0.960	0.659	1.400	9.09E-01	7.74E-02	328
2DL3	953	OKG	SARC	G	A	G/G	A/A	144	112	28	20	0.918	0.492	1.710	9.14E-01	7.76E-02	329
2DL5	583	OKG	LUSC	G	A	G/G	A/A	62	54	48	39	0.933	0.534	1.630	9.19E-01	7.78E-02	330
3DL3	777	OKG	LGG	A	G	A/A	G/G	229	27	181	23	1.080	0.599	1.950	9.22E-01	7.81E-02	331
2DL5	517	OKG	LUAD	A	G	A/A	G/G	81	63	60	44	0.943	0.566	1.570	9.23E-01	7.83E-02	332
2DP1	448	OKG	LIHC	G	C	G/G	C/C	138	89	18	13	1.120	0.523	2.400	9.24E-01	7.85E-02	333
3DP1	479	OKG	LUSC	A	C	A/A	C/C	201	21	112	13	1.110	0.535	2.300	9.24E-01	7.88E-02	334
2DL5	517	OKG	CESC	A	G	A/A	G/G	81	63	16	14	1.130	0.513	2.490	9.28E-01	7.90E-02	335
2DP1	448	OKG	HNSC	G	C	G/G	C/C	138	89	118	79	1.040	0.704	1.540	9.30E-01	7.93E-02	336
3DL3	502	OKG	GBM	G	A	G/G	A/A	101	110	49	56	1.050	0.657	1.680	9.35E-01	7.95E-02	337
3DP1	774	OKG	GBM	G	C	G/G	C/C	234	16	149	9	0.883	0.380	2.050	9.39E-01	7.97E-02	338
3DL3	777	OKG	PRAD	A	G	A/A	G/G	229	27	68	9	1.120	0.503	2.500	9.41E-01	8.00E-02	339
2DP1	1313	OKG	PRAD	A	C	A/A	C/C	210	22	86	8	0.888	0.381	2.070	9.49E-01	8.02E-02	340
3DL3	961	OKG	KIRC	C	A	C/C	A/A	118	102	18	17	1.090	0.534	2.230	9.52E-01	8.04E-02	341
2DP1	448	OKG	LUSC	G	C	G/G	C/C	138	89	73	49	1.040	0.663	1.630	9.53E-01	8.07E-02	342
2DL3	953	OKG	LIHC	G	A	G/G	A/A	144	112	21	15	0.918	0.453	1.860	9.55E-01	8.09E-02	343
2DL4	625	OKG	LGG	C	G	C/C	G/G	191	17	183	15	0.921	0.447	1.900	9.69E-01	8.11E-02	344
2DP1	522	OKG	UCEC	T	C	T/T	C/C	280	20	154	12	1.090	0.519	2.290	9.69E-01	8.14E-02	345
3DL3	408	OKG	UCEC	G	A	G/G	A/A	273	12	158	6	0.864	0.318	2.350	9.70E-01	8.16E-02	346
3DL3	502	OKG	STAD	G	A	G/G	A/A	101	110	44	46	0.960	0.586	1.570	9.71E-01	8.18E-02	347
3DL3	777	OKG	STAD	A	G	A/A	G/G	229	27	94	12	1.080	0.525	2.220	9.76E-01	8.21E-02	348
2DL5	517	OKG	KIRP	A	G	A/A	G/G	81	63	17	12	0.908	0.404	2.040	9.76E-01	8.23E-02	349
3DL1	1194	OKG	LGG	C	T	C/C	T/T	327	7	282	5	0.828	0.260	2.640	9.79E-01	8.26E-02	350
2DL5	583	OKG	BLCA	G	A	G/G	A/A	62	54	37	34	1.060	0.587	1.920	9.79E-01	8.28E-02	351
2DP1	448	OKG	THCA	G	C	G/G	C/C	138	89	95	63	1.030	0.680	1.560	9.80E-01	8.30E-02	352
3DL3	408	OKG	SKCM	G	A	G/G	A/A	273	12	229	9	0.894	0.370	2.160	9.80E-01	8.33E-02	353
2DL5	517	OKG	LUSC	A	G	A/A	G/G	81	63	48	39	1.040	0.609	1.780	9.82E-01	8.35E-02	354
3DL3	804	OKG	LGG	G	A	G/G	A/A	228	28	178	23	1.050	0.585	1.890	9.84E-01	8.37E-02	355
2DL4	1023	OKG	LGG	G	A	G/G	A/A	258	12	214	11	1.110	0.480	2.570	9.84E-01	8.40E-02	356
2DP1	766	OKG	GBM	G	C	G/G	C/C	174	9	135	6	0.859	0.298	2.470	9.88E-01	8.42E-02	357
3DL3	961	OKG	KIRP	C	A	C/C	A/A	118	102	14	11	0.909	0.395	2.090	9.90E-01	8.44E-02	358
2DP1	448	OKG	KIRP	G	C	G/G	C/C	138	89	28	17	0.941	0.487	1.820	9.90E-01	8.47E-02	359
3DL3	804	OKG	LUAD	G	A	G/G	A/A	228	28	131	17	1.060	0.559	2.010	9.96E-01	8.49E-02	360
3DL1	1180	OKG	COAD	G	C	G/G	C/C	177	51	56	17	1.050	0.562	1.960	9.98E-01	8.51E-02	361
2DL4	762	OKG	THCA	C	T	C/C	T/T	89	72	65	51	0.970	0.600	1.570	9.98E-01	8.54E-02	362
2DL4	480	OKG	BLCA	G	A	G/G	A/A	265	14	119	6	0.954	0.358	2.540	1.00E+00	8.56E-02	363
2DL4	480	OKG	BRCA	G	A	G/G	A/A	265	14	310	16	0.977	0.468	2.040	1.00E+00	8.56E-02	363
2DL4	480	OKG	LUAD	G	A	G/G	A/A	265	14	187	9	0.911	0.386	2.150	1.00E+00	8.59E-02	364
2DL4	1023	OKG	COAD	G	A	G/G	A/A	258	12	107	5	1.000	0.344	2.910	1.00E+00	8.61E-02	365
2DL4	1023	OKG	STAD	G	A	G/G	A/A	258	12	117	5	0.919	0.317	2.670	1.00E+00	8.63E-02	366
2DL4	1023	OKG	THCA	G	A	G/G	A/A	258	12	151	7	0.997	0.384	2.590	1.00E+00	8.63E-02	366
3DL1	1026	OKG	BLCA	G	C	G/G	C/C	160	9	103	5	0.863	0.281	2.650	1.00E+00	8.63E-02	366
3DL1	1194	OKG	SKCM	C	T	C/C	T/T	327	7	317	6	0.884	0.294	2.660	1.00E+00	8.63E-02	366
3DL3	906	OKG	LUAD	C	T	C/C	T/T	226	28	133	17	1.030	0.543	1.950	1.00E+00	8.63E-02	366
2DL4	480	OKG	LGG	G	A	G/G	A/A	265	14	229	13	1.070	0.493	2.320	1.00E+00	8.66E-02	367
3DL1	1026	OKG	LUSC	G	C	G/G	C/C	160	9	107	6	0.997	0.345	2.880	1.00E+00	8.66E-02	367
3DL1	1091	OKG	BLCA	G	A	G/G	A/A	166	9	97	6	1.140	0.394	3.300	1.00E+00	8.66E-02	367
3DL1	1091	OKG	LGG	G	A	G/G	A/A	166	9	190	10	0.971	0.385	2.450	1.00E+00	8.66E-02	367
3DL2	474	OKG	SKCM	G	T	G/G	T/T	258	13	236	12	1.010	0.452	2.260	1.00E+00	8.66E-02	367
2DL4	412	OKG	LUAD	G	A	G/G	A/A	229	25	137	15	1.000	0.510	1.960	1.00E+00	8.68E-02	368
2DL4	762	OKG	KIRC	C	T	C/C	T/T	89	72	16	14	1.080	0.494	2.360	1.00E+00	8.68E-02	368
2DP1	448	OKG	LGG	G	C	G/G	C/C	138	89	115	74	0.998	0.672	1.480	1.00E+00	8.68E-02	368
2DP1	471	OKG	UCEC	A	G	A/A	G/G	292	14	155	8	1.080	0.443	2.630	1.00E+00	8.68E-02	368
2DP1	522	OKG	HNSC	T	C	T/T	C/C	280	20	240	17	0.992	0.508	1.940	1.00E+00	8.68E-02	368
3DL1	1091	OKG	LUSC	G	A	G/G	A/A	166	9	104	5	0.887	0.289	2.720	1.00E+00	8.68E-02	368
3DL3	777	OKG	COAD	A	G	A/A	G/G	229	27	80	10	1.060	0.491	2.290	1.00E+00	8.68E-02	368
3DP1	796	OKG	STAD	T	C	T/T	C/C	248	15	122	8	1.080	0.446	2.620	1.00E+00	8.68E-02	368
2DL3	953	OKG	KIRP	G	A	G/G	A/A	144	112	25	20	1.030	0.544	1.950	1.00E+00	8.70E-02	369
2DL4	412	OKG	COAD	G	A	G/G	A/A	229	25	84	9	0.981	0.440	2.190	1.00E+00	8.70E-02	369
2DL4	412	OKG	PRAD	G	A	G/G	A/A	229	25	82	9	1.010	0.453	2.250	1.00E+00	8.70E-02	369
2DL5	517	OKG	PRAD	A	G	A/A	G/G	81	63	31	24	0.995	0.532	1.860	1.00E+00	8.70E-02	369
2DL5	517	OKG	SARC	A	G	A/A	G/G	81	63	20	15	0.964	0.457	2.030	1.00E+00	8.70E-02	369
2DL5	583	OKG	READ	G	A	G/G	A/A	62	54	8	6	0.861	0.281	2.640	1.00E+00	8.70E-02	369
2DP1	448	OKG	READ	G	C	G/G	C/C	138	89	22	15	1.060	0.522	2.150	1.00E+00	8.70E-02	369
2DP1	766	OKG	LGG	G	C	G/G	C/C	174	9	164	8	0.943	0.355	2.500	1.00E+00	8.70E-02	369
2DP1	1313	OKG	LUSC	A	C	A/A	C/C	210	22	124	13	1.000	0.486	2.060	1.00E+00	8.70E-02	369
3DL1	607	OKG	OV	C	T	C/C	T/T	151	96	13	9	1.090	0.449	2.650	1.00E+00	8.70E-02	369
3DL1	607	OKG	SARC	C	T	C/C	T/T	151	96	29	18	0.976	0.514	1.850	1.00E+00	8.70E-02	369
3DL1	732	OKG	BRCA	T	C	T/T	C/C	55	9	60	10	1.020	0.386	2.700	1.00E+00	8.70E-02	369
3DL1	1026	OKG	HNSC	G	C	G/G	C/C	160	9	213	12	1.000	0.411	2.430	1.00E+00	8.70E-02	369
3DL1	1026	OKG	LGG	G	C	G/G	C/C	160	9	197	10	0.902	0.358	2.270	1.00E+00	8.70E-02	369
3DL3	502	OKG	LIHC	G	A	G/G	A/A	101	110	14	16	1.050	0.488	2.260	1.00E+00	8.70E-02	369
3DL3	502	OKG	LUAD	G	A	G/G	A/A	101	110	63	67	0.976	0.630	1.510	1.00E+00	8.70E-02	369
3DL3	777	OKG	LUAD	A	G	A/A	G/G	229	27	135	16	1.010	0.525	1.940	1.00E+00	8.70E-02	369
3DL3	804	OKG	PRAD	G	A	G/G	A/A	228	28	68	8	0.958	0.417	2.200	1.00E+00	8.70E-02	369
3DL3	804	OKG	STAD	G	A	G/G	A/A	228	28	94	12	1.040	0.507	2.130	1.00E+00	8.70E-02	369
3DL3	906	OKG	COAD	C	T	C/C	T/T	226	28	77	10	1.050	0.488	2.260	1.00E+00	8.70E-02	369
3DL3	906	OKG	LGG	C	T	C/C	T/T	226	28	180	23	1.030	0.574	1.850	1.00E+00	8.70E-02	369
3DL3	906	OKG	STAD	C	T	C/C	T/T	226	28	94	12	1.030	0.502	2.110	1.00E+00	8.70E-02	369
3DL3	961	OKG	COAD	C	A	C/C	A/A	118	102	41	36	1.020	0.606	1.720	1.00E+00	8.70E-02	369
3DP1	774	OKG	LUAD	G	C	G/G	C/C	234	16	165	11	0.975	0.441	2.150	1.00E+00	8.70E-02	369
3DP1	774	OKG	STAD	G	C	G/G	C/C	234	16	114	8	1.030	0.428	2.480	1.00E+00	8.70E-02	369
3DP1	796	OKG	GBM	T	C	T/T	C/C	248	15	150	9	0.992	0.424	2.320	1.00E+00	8.70E-02	369
2DL4	625	OKG	HNSC	C	G	C/C	G/G	191	17	197	18	1.030	0.516	2.060	1.00E+00	8.73E-02	370
2DL4	1023	OKG	SKCM	G	A	G/G	A/A	258	12	234	10	0.919	0.390	2.170	1.00E+00	8.73E-02	370
2DL5	583	OKG	CESC	G	A	G/G	A/A	62	54	16	14	1.000	0.447	2.240	1.00E+00	8.73E-02	370
2DL5	583	OKG	UCEC	G	A	G/G	A/A	62	54	47	42	1.030	0.592	1.790	1.00E+00	8.73E-02	370
2DP1	1269	OKG	BRCA	A	G	A/A	G/G	350	6	412	6	0.850	0.272	2.660	1.00E+00	8.73E-02	370
3DL1	732	OKG	UCEC	T	C	T/T	C/C	55	9	42	7	1.020	0.351	2.960	1.00E+00	8.73E-02	370
3DL2	474	OKG	COAD	G	T	G/G	T/T	258	13	108	5	0.919	0.320	2.640	1.00E+00	8.73E-02	370
3DL2	474	OKG	LGG	G	T	G/G	T/T	258	13	215	10	0.923	0.397	2.150	1.00E+00	8.73E-02	370
3DL3	804	OKG	COAD	G	A	G/G	A/A	228	28	80	10	1.020	0.474	2.190	1.00E+00	8.73E-02	370
3DL3	906	OKG	HNSC	C	T	C/C	T/T	226	28	203	25	0.994	0.561	1.760	1.00E+00	8.73E-02	370
3DL3	961	OKG	CESC	C	A	C/C	A/A	118	102	25	22	1.020	0.543	1.920	1.00E+00	8.73E-02	370
3DP1	479	OKG	GBM	A	C	A/A	C/C	201	21	127	14	1.060	0.520	2.160	1.00E+00	8.73E-02	370

Table A12d Chi square significance tests for KIR variants within the TCGA samples, African cohort, reference homozygous versus heterozygous

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DL1	549	OKG	BRCA	T	C	T/T	T/C	137	9	71	7	1.500	0.536	4.200	6.13E-01	4.64E-02	97
2DL1	358	OKG	BRCA	A	G	A/A	A/G	50	5	67	9	1.340	0.423	4.240	8.29E-01	6.51E-02	136
2DL3	953	OKG	BRCA	G	A	G/G	G/A	84	36	41	27	1.540	0.826	2.870	2.33E-01	1.82E-02	38
2DL3	953	OKG	LUAD	G	A	G/G	G/A	84	36	9	7	1.810	0.626	5.240	4.09E-01	3.01E-02	63
2DL3	953	OKG	HNSC	G	A	G/G	G/A	84	36	13	9	1.620	0.636	4.130	4.46E-01	3.21E-02	67
2DL3	953	OKG	KIRP	G	A	G/G	G/A	84	36	17	10	1.370	0.572	3.280	6.29E-01	4.93E-02	103
2DL3	240	OKG	BRCA	C	T	C/C	C/T	68	6	62	8	1.460	0.480	4.440	6.96E-01	5.26E-02	110
2DL3	953	OKG	COAD	G	A	G/G	G/A	84	36	15	6	0.933	0.335	2.600	1.00E+00	8.04E-02	168
2DL3	953	OKG	UCEC	G	A	G/G	G/A	84	36	19	9	1.110	0.459	2.690	1.00E+00	8.09E-02	169
2DL4	480	OKG	LUAD	G	A	G/G	G/A	128	30	15	9	2.560	1.020	6.400	7.31E-02	6.22E-03	13
2DL4	625	OKG	UCEC	C	G	C/C	C/G	36	60	8	26	1.950	0.798	4.770	2.05E-01	1.58E-02	33
2DL4	412	OKG	UCEC	G	A	G/G	G/A	41	72	8	26	1.850	0.767	4.460	2.40E-01	1.96E-02	41
2DL4	762	OKG	LUAD	C	T	C/C	C/T	77	55	10	12	1.680	0.678	4.160	3.70E-01	2.68E-02	56
2DL4	412	OKG	KIRP	G	A	G/G	G/A	41	72	5	16	1.820	0.621	5.330	3.92E-01	2.82E-02	59
2DL4	480	OKG	BRCA	G	A	G/G	G/A	128	30	68	22	1.380	0.740	2.580	3.94E-01	2.87E-02	60
2DL4	625	OKG	KIRP	C	G	C/C	C/G	36	60	5	15	1.800	0.603	5.370	4.20E-01	3.11E-02	65
2DL4	762	OKG	UCEC	C	T	C/C	C/T	77	55	20	20	1.400	0.688	2.850	4.54E-01	3.25E-02	68
2DL4	762	OKG	COAD	C	T	C/C	C/T	77	55	14	6	0.600	0.217	1.660	4.55E-01	3.30E-02	69
2DL4	625	OKG	LUAD	C	G	C/C	C/G	36	60	5	14	1.680	0.558	5.050	5.04E-01	3.64E-02	76
2DL4	762	OKG	KIRC	C	T	C/C	C/T	77	55	8	9	1.580	0.574	4.350	5.33E-01	3.88E-02	81
2DL4	412	OKG	LUAD	G	A	G/G	G/A	41	72	5	14	1.590	0.534	4.730	5.60E-01	4.02E-02	84
2DL4	625	OKG	BRCA	C	G	C/C	C/G	36	60	22	47	1.280	0.666	2.460	5.62E-01	4.16E-02	87
2DL4	412	OKG	BRCA	G	A	G/G	G/A	41	72	21	46	1.250	0.657	2.380	6.09E-01	4.55E-02	95
2DL4	762	OKG	GBM	C	T	C/C	C/T	77	55	11	11	1.400	0.567	3.460	6.18E-01	4.69E-02	98
2DL4	625	OKG	GBM	C	G	C/C	C/G	36	60	6	14	1.400	0.494	3.970	7.05E-01	5.31E-02	111
2DL4	1023	OKG	BRCA	G	A	G/G	G/A	146	16	85	7	0.751	0.297	1.900	7.06E-01	5.36E-02	112
2DL4	625	OKG	HNSC	C	G	C/C	C/G	36	60	5	12	1.440	0.469	4.420	7.15E-01	5.55E-02	116
2DL4	412	OKG	GBM	G	A	G/G	G/A	41	72	6	14	1.330	0.475	3.730	7.73E-01	6.08E-02	127
2DL4	412	OKG	HNSC	G	A	G/G	G/A	41	72	5	12	1.370	0.451	4.160	7.79E-01	6.17E-02	129
2DL4	480	OKG	UCEC	G	A	G/G	G/A	128	30	35	10	1.220	0.544	2.740	7.88E-01	6.27E-02	131
2DL4	886	OKG	BRCA	C	G	C/C	C/G	142	11	82	8	1.260	0.487	3.260	8.19E-01	6.41E-02	134
2DL4	762	OKG	HNSC	C	T	C/C	C/T	77	55	14	12	1.200	0.515	2.790	8.37E-01	6.65E-02	139
2DL4	762	OKG	BRCA	C	T	C/C	C/T	77	55	44	34	1.080	0.613	1.900	8.98E-01	7.03E-02	147
2DL4	762	OKG	KIRP	C	T	C/C	C/T	77	55	19	12	0.884	0.397	1.970	9.22E-01	7.27E-02	152
2DL4	1019	OKG	BRCA	C	T	C/C	C/T	148	14	83	9	1.150	0.477	2.770	9.39E-01	7.51E-02	157
2DL4	480	OKG	HNSC	G	A	G/G	G/A	128	30	22	5	0.970	0.340	2.770	1.00E+00	7.94E-02	166
2DL4	412	OKG	COAD	G	A	G/G	G/A	41	72	5	9	1.020	0.320	3.250	1.00E+00	8.09E-02	169
2DL4	395	OKG	BRCA	C	T	C/C	C/T	139	16	84	9	0.931	0.394	2.200	1.00E+00	8.13E-02	170
2DL4	480	OKG	KIRP	G	A	G/G	G/A	128	30	28	6	0.914	0.347	2.400	1.00E+00	8.13E-02	170
2DL5	583	OKG	BRCA	G	A	G/G	G/A	39	14	27	4	0.413	0.123	1.390	2.38E-01	1.87E-02	39
2DL5	517	OKG	BRCA	A	G	A/A	A/G	42	14	27	4	0.444	0.132	1.490	2.90E-01	2.34E-02	49
2DP1	1313	OKG	BRCA	A	C	A/A	A/C	71	50	13	33	3.600	1.720	7.520	8.41E-04	9.57E-04	2
2DP1	471	OKG	BRCA	A	G	A/A	A/G	101	34	46	33	2.130	1.180	3.850	1.77E-02	2.87E-03	6
2DP1	522	OKG	LUAD	T	C	T/T	T/C	85	59	17	2	0.169	0.038	0.759	2.00E-02	3.35E-03	7
2DP1	471	OKG	KIRP	A	G	A/A	A/G	101	34	16	14	2.600	1.150	5.880	3.39E-02	4.31E-03	9
2DP1	522	OKG	UCEC	T	C	T/T	T/C	85	59	28	10	0.515	0.233	1.140	1.42E-01	1.15E-02	24
2DP1	1313	OKG	LUAD	A	C	A/A	A/C	71	50	15	4	0.379	0.119	1.210	1.52E-01	1.24E-02	26
2DP1	1313	OKG	KIRC	A	C	A/A	A/C	71	50	12	3	0.355	0.095	1.320	1.88E-01	1.48E-02	31
2DP1	522	OKG	KIRC	T	C	T/T	T/C	85	59	12	3	0.360	0.097	1.330	1.91E-01	1.53E-02	32
2DP1	899	OKG	BRCA	C	A	C/C	C/A	72	10	79	5	0.456	0.149	1.400	2.58E-01	2.11E-02	44
2DP1	522	OKG	COAD	T	C	T/T	T/C	85	59	17	6	0.508	0.189	1.360	2.59E-01	2.15E-02	45
2DP1	448	OKG	GBM	G	C	G/G	G/C	43	67	11	9	0.525	0.201	1.370	2.80E-01	2.25E-02	47
2DP1	816	OKG	BRCA	G	A	G/G	G/A	141	10	80	10	1.760	0.702	4.410	3.27E-01	2.39E-02	50
2DP1	448	OKG	UCEC	G	C	G/G	G/C	43	67	16	16	0.642	0.291	1.420	3.69E-01	2.63E-02	55
2DP1	1313	OKG	COAD	A	C	A/A	A/C	71	50	15	6	0.568	0.206	1.570	3.89E-01	2.78E-02	58
2DP1	448	OKG	LUAD	G	C	G/G	G/C	43	67	9	8	0.570	0.204	1.590	4.15E-01	3.06E-02	64
2DP1	522	OKG	HNSC	T	C	T/T	T/C	85	59	16	7	0.630	0.244	1.630	4.65E-01	3.40E-02	71
2DP1	1313	OKG	KIRP	A	C	A/A	A/C	71	50	14	14	1.420	0.623	3.240	5.33E-01	3.83E-02	80
2DP1	471	OKG	HNSC	A	G	A/A	A/G	101	34	16	8	1.490	0.586	3.790	5.60E-01	4.07E-02	85
2DP1	1313	OKG	GBM	A	C	A/A	A/C	71	50	13	6	0.655	0.233	1.840	5.80E-01	4.31E-02	90
2DP1	766	OKG	BRCA	G	C	G/G	G/C	83	25	69	16	0.770	0.381	1.560	5.81E-01	4.35E-02	91
2DP1	522	OKG	GBM	T	C	T/T	T/C	85	59	13	6	0.665	0.239	1.850	5.91E-01	4.40E-02	92
2DP1	448	OKG	BRCA	G	C	G/G	G/C	43	67	32	41	0.822	0.451	1.500	6.27E-01	4.88E-02	102
2DP1	522	OKG	KIRP	T	C	T/T	T/C	85	59	16	14	1.260	0.572	2.780	7.10E-01	5.46E-02	114
2DP1	1313	OKG	HNSC	A	C	A/A	A/C	71	50	15	8	0.757	0.298	1.920	7.23E-01	5.69E-02	119
2DP1	766	OKG	UCEC	G	C	G/G	G/C	83	25	34	8	0.781	0.321	1.900	7.45E-01	5.93E-02	124
2DP1	448	OKG	HNSC	G	C	G/G	G/C	43	67	7	14	1.280	0.478	3.430	8.01E-01	6.36E-02	133
2DP1	448	OKG	THCA	G	C	G/G	G/C	43	67	6	7	0.749	0.236	2.380	8.47E-01	6.75E-02	141
2DP1	522	OKG	BRCA	T	C	T/T	T/C	85	59	46	35	1.100	0.634	1.910	8.53E-01	6.79E-02	142
2DP1	448	OKG	COAD	G	C	G/G	G/C	43	67	7	9	0.825	0.286	2.380	9.34E-01	7.46E-02	156
2DP1	448	OKG	KIRP	G	C	G/G	G/C	43	67	9	16	1.140	0.463	2.810	9.53E-01	7.61E-02	159
2DP1	899	OKG	UCEC	C	A	C/C	C/A	72	10	36	6	1.200	0.404	3.560	9.64E-01	7.70E-02	161
2DP1	1248	OKG	BRCA	C	T	C/C	C/T	148	10	84	5	0.881	0.291	2.660	1.00E+00	7.94E-02	166
2DP1	471	OKG	COAD	A	G	A/A	A/G	101	34	17	6	1.050	0.383	2.880	1.00E+00	8.09E-02	169
2DP1	471	OKG	UCEC	A	G	A/A	A/G	101	34	28	10	1.060	0.467	2.410	1.00E+00	8.09E-02	169
2DP1	1313	OKG	UCEC	A	C	A/A	A/C	71	50	14	9	0.913	0.367	2.270	1.00E+00	8.09E-02	169
2DP1	766	OKG	KIRP	G	C	G/G	G/C	83	25	19	6	1.050	0.378	2.910	1.00E+00	8.13E-02	170
3DL1	607	OKG	LUAD	C	T	C/C	C/T	113	37	12	12	3.050	1.260	7.370	2.05E-02	3.83E-03	8
3DL1	1180	OKG	LUAD	G	C	G/G	G/C	102	32	12	10	2.660	1.050	6.730	6.36E-02	5.74E-03	12
3DL1	607	OKG	HNSC	C	T	C/C	C/T	113	37	24	2	0.255	0.058	1.130	9.53E-02	8.13E-03	17
3DL1	1180	OKG	HNSC	G	C	G/G	G/C	102	32	23	2	0.277	0.062	1.240	1.30E-01	1.10E-02	23
3DL1	607	OKG	COAD	C	T	C/C	C/T	113	37	20	2	0.305	0.068	1.370	1.75E-01	1.34E-02	28
3DL1	1180	OKG	BRCA	G	C	G/G	G/C	102	32	57	25	1.400	0.757	2.590	3.63E-01	2.54E-02	53
3DL1	496	OKG	BRCA	C	A	C/C	C/A	141	15	79	13	1.550	0.702	3.420	3.80E-01	2.73E-02	57
3DL1	607	OKG	BRCA	C	T	C/C	C/T	113	37	62	26	1.280	0.710	2.310	5.02E-01	3.59E-02	75
3DL1	607	OKG	GBM	C	T	C/C	C/T	113	37	14	7	1.530	0.574	4.080	5.59E-01	3.97E-02	83
3DL1	1303	OKG	BRCA	A	G	A/A	A/G	119	28	68	12	0.750	0.358	1.570	5.60E-01	4.12E-02	86
3DL1	1026	OKG	BRCA	G	C	G/G	G/C	93	12	68	12	1.370	0.580	3.230	6.20E-01	4.79E-02	100
3DL1	1021	OKG	BRCA	A	G	A/A	A/G	81	7	69	8	1.340	0.462	3.880	7.86E-01	6.22E-02	130
3DL1	1180	OKG	UCEC	G	C	G/G	G/C	102	32	30	11	1.170	0.527	2.600	8.60E-01	6.84E-02	143
3DL1	1303	OKG	UCEC	A	G	A/A	A/G	119	28	33	9	1.160	0.499	2.700	9.03E-01	7.13E-02	149
3DL1	732	OKG	BRCA	T	C	T/T	T/C	35	16	25	10	0.875	0.341	2.240	9.69E-01	7.75E-02	162
3DL1	1194	OKG	BRCA	C	T	C/C	C/T	132	15	81	9	0.978	0.409	2.340	1.00E+00	7.99E-02	167
3DL1	607	OKG	KIRP	C	T	C/C	C/T	113	37	25	8	0.977	0.406	2.350	1.00E+00	8.04E-02	168
3DL1	1091	OKG	UCEC	G	A	G/G	G/A	97	18	36	6	0.898	0.330	2.440	1.00E+00	8.04E-02	168
3DL1	607	OKG	UCEC	C	T	C/C	C/T	113	37	32	11	1.050	0.482	2.290	1.00E+00	8.09E-02	169
3DL1	732	OKG	UCEC	T	C	T/T	T/C	35	16	22	10	0.994	0.383	2.580	1.00E+00	8.09E-02	169
3DL1	1180	OKG	KIRP	G	C	G/G	G/C	102	32	24	8	1.060	0.434	2.590	1.00E+00	8.09E-02	169
3DL1	1091	OKG	BRCA	G	A	G/G	G/A	97	18	68	13	1.030	0.473	2.240	1.00E+00	8.13E-02	170
3DL1	1303	OKG	KIRP	A	G	A/A	A/G	119	28	28	7	1.060	0.420	2.670	1.00E+00	8.13E-02	170
3DL2	474	OKG	UCEC	G	T	G/G	G/T	136	24	34	11	1.830	0.817	4.100	2.06E-01	1.63E-02	34
3DL2	456	OKG	UCEC	C	T	C/C	C/T	139	23	41	4	0.590	0.193	1.800	4.93E-01	3.49E-02	73
3DL2	893	OKG	UCEC	G	A	G/G	G/A	139	23	41	4	0.590	0.193	1.800	4.93E-01	3.49E-02	73
3DL2	474	OKG	BRCA	G	T	G/G	G/T	136	24	79	12	0.861	0.408	1.820	8.36E-01	6.60E-02	138
3DL2	456	OKG	BRCA	C	T	C/C	C/T	139	23	81	12	0.895	0.423	1.890	9.20E-01	7.23E-02	151
3DL2	893	OKG	BRCA	G	A	G/G	G/A	139	23	81	12	0.895	0.423	1.890	9.20E-01	7.23E-02	151
3DL2	497	OKG	BRCA	G	A	G/G	G/A	150	12	87	6	0.862	0.312	2.380	9.74E-01	7.80E-02	163
3DL2	394	OKG	BRCA	C	A	C/C	C/A	148	14	85	8	0.995	0.401	2.470	1.00E+00	8.09E-02	169

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL2	474	OKG	KIRP	G	T	G/G	G/T	136	24	30	5	0.944	0.333	2.670	1.00E+00	8.13E-02	170
3DL3	971	OKG	BRCA	T	C	T/T	T/C	112	21	51	31	3.240	1.700	6.180	4.69E-04	4.79E-04	1
3DL3	971	OKG	UCEC	T	C	T/T	T/C	112	21	24	16	3.560	1.620	7.810	2.26E-03	1.44E-03	3
3DL3	961	OKG	HNSC	C	T	C/C	C/T	95	34	24	0	0.000	0.000	NaN	9.75E-03	2.39E-03	5
3DL3	961	OKG	BRCA	C	T	C/C	C/T	95	34	47	32	1.900	1.050	3.450	4.83E-02	4.79E-03	10
3DL3	408	OKG	HNSC	G	A	G/G	G/A	83	66	21	6	0.359	0.137	0.941	5.32E-02	5.26E-03	11
3DL3	804	OKG	KIRP	G	A	G/G	G/A	81	67	24	9	0.453	0.197	1.040	8.93E-02	7.66E-03	16
3DL3	804	OKG	HNSC	G	A	G/G	G/A	81	67	20	7	0.423	0.169	1.060	9.70E-02	8.61E-03	18
3DL3	408	OKG	KIRP	G	A	G/G	G/A	83	66	24	9	0.472	0.206	1.080	1.09E-01	9.09E-03	19
3DL3	869	OKG	UCEC	A	C	A/A	A/C	115	41	27	18	1.870	0.933	3.750	1.11E-01	9.57E-03	20
3DL3	961	OKG	KIRP	C	T	C/C	C/T	95	34	21	2	0.266	0.059	1.190	1.17E-01	1.01E-02	21
3DL3	502	OKG	GBM	G	A	G/G	G/A	67	73	5	14	2.570	0.878	7.520	1.27E-01	1.05E-02	22
3DL3	738	OKG	KIRP	C	T	C/C	C/T	113	45	29	5	0.433	0.158	1.190	1.48E-01	1.20E-02	25
3DL3	692	OKG	KIRP	G	A	G/G	G/A	111	44	28	5	0.450	0.163	1.240	1.76E-01	1.39E-02	29
3DL3	502	OKG	KIRP	G	A	G/G	G/A	67	73	9	19	1.940	0.821	4.580	1.88E-01	1.44E-02	30
3DL3	738	OKG	HNSC	C	T	C/C	C/T	113	45	23	4	0.437	0.143	1.330	2.11E-01	1.68E-02	35
3DL3	692	OKG	HNSC	G	A	G/G	G/A	111	44	23	4	0.439	0.144	1.340	2.15E-01	1.72E-02	36
3DL3	869	OKG	COAD	A	C	A/A	A/C	115	41	15	10	1.870	0.779	4.490	2.40E-01	1.91E-02	40
3DL3	1042	OKG	BRCA	G	C	G/G	G/C	71	19	56	24	1.600	0.797	3.210	2.48E-01	2.01E-02	42
3DL3	961	OKG	UCEC	C	T	C/C	C/T	95	34	23	14	1.700	0.786	3.680	2.49E-01	2.06E-02	43
3DL3	502	OKG	UCEC	G	A	G/G	G/A	67	73	22	15	0.626	0.300	1.310	2.84E-01	2.30E-02	48
3DL3	777	OKG	HNSC	A	G	A/A	A/G	125	33	24	3	0.473	0.134	1.670	3.56E-01	2.49E-02	52
3DL3	804	OKG	THCA	G	A	G/G	G/A	81	67	5	8	1.930	0.603	6.180	4.02E-01	2.97E-02	62
3DL3	869	OKG	BRCA	A	C	A/A	A/C	115	41	63	29	1.290	0.732	2.270	4.60E-01	3.35E-02	70
3DL3	906	OKG	UCEC	C	T	C/C	C/T	133	26	41	5	0.624	0.225	1.730	4.96E-01	3.54E-02	74
3DL3	777	OKG	LUAD	A	G	A/A	A/G	125	33	17	7	1.560	0.597	4.070	5.17E-01	3.68E-02	77
3DL3	777	OKG	UCEC	A	G	A/A	A/G	125	33	39	7	0.680	0.279	1.660	5.21E-01	3.73E-02	78
3DL3	804	OKG	KIRC	G	A	G/G	G/A	81	67	8	10	1.510	0.564	4.040	5.65E-01	4.21E-02	88
3DL3	447	OKG	BRCA	G	T	G/G	G/T	143	19	85	8	0.708	0.297	1.690	5.69E-01	4.26E-02	89
3DL3	738	OKG	LUAD	C	T	C/C	C/T	113	45	19	5	0.661	0.233	1.880	5.92E-01	4.45E-02	93
3DL3	692	OKG	LUAD	G	A	G/G	G/A	111	44	19	5	0.664	0.233	1.890	5.99E-01	4.50E-02	94
3DL3	869	OKG	KIRP	A	C	A/A	A/C	115	41	23	11	1.340	0.601	2.990	6.12E-01	4.59E-02	96
3DL3	804	OKG	COAD	G	A	G/G	G/A	81	67	15	9	0.725	0.298	1.760	6.24E-01	4.83E-02	101
3DL3	777	OKG	BRCA	A	G	A/A	A/G	125	33	69	22	1.210	0.655	2.240	6.57E-01	5.02E-02	105
3DL3	738	OKG	GBM	C	T	C/C	C/T	113	45	18	5	0.698	0.244	1.990	6.70E-01	5.07E-02	106
3DL3	692	OKG	COAD	G	A	G/G	G/A	111	44	18	5	0.701	0.245	2.000	6.77E-01	5.12E-02	107
3DL3	692	OKG	GBM	G	A	G/G	G/A	111	44	18	5	0.701	0.245	2.000	6.77E-01	5.12E-02	107
3DL3	906	OKG	KIRP	C	T	C/C	C/T	133	26	30	4	0.682	0.221	2.100	6.82E-01	5.17E-02	108
3DL3	502	OKG	BLCA	G	A	G/G	G/A	67	73	7	5	0.656	0.199	2.170	6.92E-01	5.22E-02	109
3DL3	408	OKG	THCA	G	A	G/G	G/A	83	66	6	7	1.470	0.471	4.580	7.09E-01	5.41E-02	113
3DL3	692	OKG	UCEC	G	A	G/G	G/A	111	44	31	15	1.220	0.601	2.480	7.13E-01	5.50E-02	115
3DL3	738	OKG	UCEC	C	T	C/C	C/T	113	45	31	15	1.220	0.602	2.470	7.21E-01	5.60E-02	117
3DL3	869	OKG	HNSC	A	C	A/A	A/C	115	41	17	8	1.320	0.530	3.290	7.23E-01	5.65E-02	118
3DL3	502	OKG	HNSC	G	A	G/G	G/A	67	73	13	11	0.777	0.326	1.850	7.26E-01	5.79E-02	121
3DL3	804	OKG	UCEC	G	A	G/G	G/A	81	67	26	18	0.837	0.423	1.660	7.35E-01	5.89E-02	123
3DL3	804	OKG	LUSC	G	A	G/G	G/A	81	67	5	6	1.450	0.424	4.960	7.78E-01	6.12E-02	128
3DL3	777	OKG	KIRP	A	G	A/A	A/G	125	33	29	6	0.784	0.300	2.050	7.90E-01	6.32E-02	132
3DL3	408	OKG	UCEC	G	A	G/G	G/A	83	66	26	18	0.871	0.440	1.720	8.22E-01	6.46E-02	135
3DL3	738	OKG	BRCA	C	T	C/C	C/T	113	45	67	24	0.900	0.504	1.610	8.33E-01	6.56E-02	137
3DL3	692	OKG	BRCA	G	A	G/G	G/A	111	44	67	24	0.904	0.505	1.620	8.47E-01	6.70E-02	140
3DL3	502	OKG	BRCA	G	A	G/G	G/A	67	73	39	39	0.918	0.528	1.600	8.71E-01	6.89E-02	144
3DL3	502	OKG	COAD	G	A	G/G	G/A	67	73	11	14	1.170	0.497	2.760	8.90E-01	6.94E-02	145
3DL3	502	OKG	KIRC	G	A	G/G	G/A	67	73	8	7	0.803	0.276	2.330	8.95E-01	6.99E-02	146
3DL3	408	OKG	BRCA	G	A	G/G	G/A	83	66	50	37	0.931	0.546	1.590	8.98E-01	7.08E-02	148
3DL3	738	OKG	COAD	C	T	C/C	C/T	113	45	18	6	0.837	0.312	2.240	9.12E-01	7.18E-02	150
3DL3	869	OKG	GBM	A	C	A/A	A/C	115	41	17	5	0.825	0.286	2.380	9.23E-01	7.32E-02	153
3DL3	906	OKG	BRCA	C	T	C/C	C/T	133	26	75	16	1.090	0.550	2.160	9.41E-01	7.56E-02	158
3DL3	869	OKG	LUAD	A	C	A/A	A/C	115	41	17	7	1.150	0.445	2.970	9.60E-01	7.66E-02	160
3DL3	408	OKG	COAD	G	A	G/G	G/A	83	66	14	10	0.898	0.375	2.150	9.85E-01	7.90E-02	165
3DL3	408	OKG	BLCA	G	A	G/G	G/A	83	66	7	5	0.898	0.273	2.960	1.00E+00	7.99E-02	167
3DL3	699	OKG	BRCA	G	A	G/G	G/A	152	10	87	6	1.050	0.369	2.990	1.00E+00	7.99E-02	167
3DL3	502	OKG	LUAD	G	A	G/G	G/A	67	73	10	12	1.100	0.446	2.710	1.00E+00	8.04E-02	168
3DL3	502	OKG	THCA	G	A	G/G	G/A	67	73	6	7	1.070	0.342	3.340	1.00E+00	8.04E-02	168
3DL3	1042	OKG	UCEC	G	C	G/G	G/C	71	19	33	8	0.906	0.360	2.280	1.00E+00	8.04E-02	168
3DL3	408	OKG	LUAD	G	A	G/G	G/A	83	66	13	10	0.967	0.399	2.340	1.00E+00	8.09E-02	169
3DL3	447	OKG	UCEC	G	T	G/G	G/T	143	19	41	5	0.918	0.323	2.610	1.00E+00	8.09E-02	169
3DL3	502	OKG	LUSC	G	A	G/G	G/A	67	73	6	6	0.918	0.282	2.990	1.00E+00	8.09E-02	169
3DL3	804	OKG	BLCA	G	A	G/G	G/A	81	67	7	5	0.864	0.262	2.850	1.00E+00	8.09E-02	169
3DL3	804	OKG	BRCA	G	A	G/G	G/A	81	67	47	38	0.977	0.571	1.670	1.00E+00	8.09E-02	169
3DL3	804	OKG	LGG	G	A	G/G	G/A	81	67	6	5	1.010	0.295	3.460	1.00E+00	8.09E-02	169
3DL3	804	OKG	LUAD	G	A	G/G	G/A	81	67	13	10	0.930	0.384	2.250	1.00E+00	8.09E-02	169
3DL3	408	OKG	GBM	G	A	G/G	G/A	83	66	12	9	0.943	0.375	2.370	1.00E+00	8.13E-02	170
3DL3	408	OKG	KIRC	G	A	G/G	G/A	83	66	10	8	1.010	0.377	2.700	1.00E+00	8.13E-02	170
3DL3	804	OKG	GBM	G	A	G/G	G/A	81	67	11	10	1.100	0.440	2.750	1.00E+00	8.13E-02	170
3DP1	939	OKG	BRCA	T	G	T/T	T/G	92	16	32	17	3.050	1.380	6.740	8.76E-03	1.91E-03	4
3DP1	796	OKG	LGG	T	C	T/T	T/C	73	71	2	9	4.630	0.967	22.200	7.73E-02	6.70E-03	14
3DP1	774	OKG	KIRC	G	C	G/G	G/C	71	75	4	13	3.080	0.959	9.890	8.76E-02	7.18E-03	15
3DP1	796	OKG	KIRC	T	C	T/T	T/C	73	71	5	12	2.470	0.828	7.370	1.60E-01	1.29E-02	27
3DP1	774	OKG	BLCA	G	C	G/G	G/C	71	75	8	3	0.355	0.091	1.390	2.19E-01	1.77E-02	37
3DP1	774	OKG	LUSC	G	C	G/G	G/C	71	75	8	3	0.355	0.091	1.390	2.19E-01	1.77E-02	37
3DP1	796	OKG	LUSC	T	C	T/T	T/C	73	71	8	3	0.386	0.098	1.510	2.73E-01	2.20E-02	46
3DP1	796	OKG	THCA	T	C	T/T	T/C	73	71	8	3	0.386	0.098	1.510	2.73E-01	2.20E-02	46
3DP1	774	OKG	KIRP	G	C	G/G	G/C	71	75	18	12	0.631	0.284	1.400	3.50E-01	2.44E-02	51
3DP1	774	OKG	THCA	G	C	G/G	G/C	71	75	8	4	0.473	0.136	1.640	3.68E-01	2.58E-02	54
3DP1	774	OKG	BRCA	G	C	G/G	G/C	71	75	46	37	0.761	0.443	1.310	3.95E-01	2.92E-02	61
3DP1	796	OKG	BLCA	T	C	T/T	T/C	73	71	8	4	0.514	0.148	1.780	4.45E-01	3.16E-02	66
3DP1	796	OKG	KIRP	T	C	T/T	T/C	73	71	18	12	0.685	0.308	1.520	4.67E-01	3.45E-02	72
3DP1	796	OKG	GBM	T	C	T/T	T/C	73	71	9	13	1.490	0.599	3.700	5.31E-01	3.78E-02	79
3DP1	774	OKG	GBM	G	C	G/G	G/C	71	75	9	14	1.470	0.599	3.610	5.33E-01	3.92E-02	82
3DP1	774	OKG	HNSC	G	C	G/G	G/C	71	75	12	9	0.710	0.282	1.790	6.20E-01	4.74E-02	99
3DP1	774	OKG	LUAD	G	C	G/G	G/C	71	75	12	9	0.710	0.282	1.790	6.20E-01	4.74E-02	99
3DP1	796	OKG	BRCA	T	C	T/T	T/C	73	71	46	38	0.849	0.495	1.460	6.49E-01	4.98E-02	104
3DP1	410	OKG	BRCA	A	G	A/A	A/G	102	7	89	4	0.655	0.186	2.310	7.26E-01	5.74E-02	120
3DP1	796	OKG	LUAD	T	C	T/T	T/C	73	71	11	8	0.748	0.284	1.970	7.29E-01	5.84E-02	122
3DP1	796	OKG	UCEC	T	C	T/T	T/C	73	71	18	21	1.200	0.590	2.440	7.47E-01	5.98E-02	125
3DP1	796	OKG	HNSC	T	C	T/T	T/C	73	71	12	9	0.771	0.306	1.940	7.50E-01	6.03E-02	126
3DP1	774	OKG	COAD	G	C	G/G	G/C	71	75	11	10	0.861	0.345	2.150	9.30E-01	7.37E-02	154
3DP1	479	OKG	BRCA	A	C	A/A	A/C	140	21	82	11	0.894	0.410	1.950	9.32E-01	7.42E-02	155
3DP1	796	OKG	COAD	T	C	T/T	T/C	73	71	10	11	1.130	0.452	2.830	9.76E-01	7.85E-02	164
3DP1	479	OKG	UCEC	A	C	A/A	A/C	140	21	39	6	1.030	0.389	2.730	1.00E+00	8.09E-02	169
3DP1	774	OKG	UCEC	G	C	G/G	G/C	71	75	20	20	0.947	0.470	1.910	1.00E+00	8.09E-02	169

Table A12e Chi square significance tests for KIR variants within the TCGA samples, African cohort, heterozygous versus alternate homozygous

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DL4	625	OKG	GBM	C	G	C/G	G/G	60	42	14	3	0.306	0.083	1.130	1.14E-01	2.33E-03	1
2DL4	412	OKG	GBM	G	A	G/A	A/A	72	47	14	3	0.328	0.089	1.200	1.39E-01	4.65E-03	2
2DP1	448	OKG	BRCA	G	C	G/C	C/C	67	43	41	16	0.608	0.304	1.220	2.14E-01	6.98E-03	3
2DL4	625	OKG	BRCA	C	G	C/G	G/G	60	42	47	21	0.638	0.334	1.220	2.30E-01	9.30E-03	4
3DL3	502	OKG	UCEC	G	A	G/A	A/A	73	22	15	9	1.990	0.767	5.170	2.42E-01	1.16E-02	5
2DL3	953	OKG	UCEC	G	A	G/A	A/A	36	29	9	14	1.930	0.732	5.090	2.72E-01	1.40E-02	6
2DL4	412	OKG	COAD	G	A	G/A	A/A	72	47	9	11	1.870	0.720	4.860	2.91E-01	1.63E-02	7
2DL4	625	OKG	UCEC	C	G	C/G	G/G	60	42	26	11	0.604	0.269	1.350	3.03E-01	1.86E-02	8
2DL4	625	OKG	LUAD	C	G	C/G	G/G	60	42	14	5	0.510	0.171	1.520	3.35E-01	2.09E-02	9
2DL3	953	OKG	HNSC	G	A	G/A	A/A	36	29	9	3	0.414	0.103	1.670	3.43E-01	2.33E-02	10
2DL5	583	OKG	BRCA	G	A	G/A	A/A	14	24	4	15	2.190	0.606	7.920	3.65E-01	2.56E-02	11
2DL4	412	OKG	UCEC	G	A	G/A	A/A	72	47	26	11	0.648	0.293	1.430	3.79E-01	2.79E-02	12
2DP1	471	OKG	BRCA	A	G	A/G	G/G	34	13	33	7	0.555	0.197	1.560	3.86E-01	3.02E-02	13
2DL4	412	OKG	LUAD	G	A	G/A	A/A	72	47	14	5	0.547	0.185	1.620	3.98E-01	3.26E-02	14
2DL4	625	OKG	COAD	C	G	C/G	G/G	60	42	6	8	1.900	0.614	5.880	3.99E-01	3.49E-02	15
2DL3	953	OKG	KIRP	G	A	G/A	A/A	36	29	10	4	0.497	0.141	1.750	4.21E-01	3.72E-02	16
2DL5	517	OKG	BRCA	A	G	A/G	G/G	14	26	4	15	2.020	0.562	7.270	4.33E-01	3.95E-02	17
2DP1	1313	OKG	BRCA	A	C	A/C	C/C	50	17	33	7	0.624	0.233	1.670	4.81E-01	4.19E-02	18
2DP1	448	OKG	COAD	G	C	G/C	C/C	67	43	9	9	1.560	0.574	4.240	5.39E-01	4.42E-02	19
2DL3	953	OKG	GBM	G	A	G/A	A/A	36	29	5	7	1.740	0.500	6.060	5.75E-01	4.65E-02	20
2DP1	448	OKG	HNSC	G	C	G/C	C/C	67	43	14	6	0.668	0.238	1.870	6.02E-01	4.88E-02	21
2DL4	412	OKG	KIRP	G	A	G/A	A/A	72	47	16	14	1.340	0.599	3.000	6.13E-01	5.12E-02	22
2DL4	412	OKG	BRCA	G	A	G/A	A/A	72	47	46	25	0.833	0.453	1.530	6.64E-01	5.35E-02	23
3DL3	502	OKG	BRCA	G	A	G/A	A/A	73	22	39	15	1.280	0.597	2.740	6.67E-01	5.58E-02	24
3DL1	607	OKG	BRCA	C	T	C/T	T/T	37	9	26	4	0.632	0.176	2.270	6.94E-01	5.81E-02	25
2DL4	762	OKG	BRCA	C	T	C/T	T/T	55	11	34	9	1.320	0.496	3.510	7.57E-01	6.05E-02	26
2DL4	412	OKG	HNSC	G	A	G/A	A/A	72	47	12	10	1.280	0.512	3.200	7.74E-01	6.28E-02	27
2DL3	953	OKG	BRCA	G	A	G/A	A/A	36	29	27	18	0.828	0.383	1.790	7.76E-01	6.51E-02	28
3DL3	502	OKG	KIRP	G	A	G/A	A/A	73	22	19	7	1.220	0.454	3.280	8.89E-01	6.74E-02	29
2DL4	625	OKG	HNSC	C	G	C/G	G/G	60	42	12	10	1.190	0.471	3.010	8.96E-01	6.98E-02	30
2DL4	625	OKG	KIRP	C	G	C/G	G/G	60	42	15	12	1.140	0.485	2.680	9.31E-01	7.21E-02	31
3DP1	774	OKG	BRCA	G	C	G/C	C/C	75	16	37	9	1.140	0.460	2.820	9.60E-01	7.44E-02	32
3DL1	1180	OKG	BRCA	G	C	G/C	C/C	32	8	25	5	0.800	0.233	2.750	9.65E-01	7.67E-02	33
2DL4	625	OKG	KIRC	C	G	C/G	G/G	60	42	7	6	1.220	0.383	3.890	9.65E-01	7.91E-02	34
2DP1	522	OKG	BRCA	T	C	T/C	C/C	59	15	35	10	1.120	0.454	2.760	9.83E-01	8.14E-02	35
3DP1	796	OKG	UCEC	T	C	T/C	C/C	71	18	21	6	1.130	0.398	3.210	1.00E+00	8.37E-02	36
2DP1	448	OKG	KIRP	G	C	G/C	C/C	67	43	16	10	0.974	0.405	2.340	1.00E+00	8.61E-02	37
2DL4	412	OKG	KIRC	G	A	G/A	A/A	72	47	8	6	1.150	0.375	3.530	1.00E+00	8.84E-02	38
2DP1	471	OKG	KIRP	A	G	A/G	G/G	34	13	14	5	0.934	0.280	3.120	1.00E+00	8.84E-02	38
3DL3	804	OKG	BRCA	G	A	G/A	A/A	67	14	38	8	1.010	0.388	2.630	1.00E+00	8.84E-02	38
3DP1	796	OKG	BRCA	T	C	T/C	C/C	71	18	38	9	0.934	0.383	2.280	1.00E+00	8.84E-02	38
2DP1	448	OKG	UCEC	G	C	G/C	C/C	67	43	16	11	1.070	0.454	2.520	1.00E+00	9.07E-02	39
3DL3	408	OKG	BRCA	G	A	G/A	A/A	66	12	37	6	0.892	0.309	2.570	1.00E+00	9.07E-02	39

Table A12f Chi square significance tests for KIR variants within the TCGA samples, African cohort, reference homozygous versus alternate homozygous

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
2DP1	448	OKG	GBM	G	C	G/G	C/C	43	43	11	2	0.182	0.038	0.870	4.16E-02	2.50E-03	1
2DP1	448	OKG	BRCA	G	C	G/G	C/C	43	43	32	16	0.500	0.240	1.040	9.26E-02	5.00E-03	2
2DL3	953	OKG	UCEC	G	A	G/G	A/A	84	29	19	14	2.130	0.948	4.780	1.01E-01	7.50E-03	3
2DL5	517	OKG	KIRP	A	G	A/A	G/G	42	26	5	9	2.910	0.879	9.640	1.34E-01	1.00E-02	4
2DL4	412	OKG	KIRP	G	A	G/G	A/A	41	47	5	14	2.440	0.809	7.360	1.73E-01	1.25E-02	5
2DS5	535	OKG	BRCA	G	A	G/G	A/A	25	26	18	10	0.534	0.207	1.380	2.86E-01	1.50E-02	6
2DP1	448	OKG	LUAD	G	C	G/G	C/C	43	43	9	4	0.444	0.127	1.550	3.19E-01	1.75E-02	7
2DL4	625	OKG	KIRP	C	G	C/C	G/G	36	42	5	12	2.060	0.663	6.400	3.21E-01	2.00E-02	8
2DL5	583	OKG	KIRP	G	A	G/G	A/A	39	24	5	7	2.280	0.650	8.000	3.25E-01	2.25E-02	9
2DL5	517	OKG	COAD	A	G	A/A	G/G	42	26	11	3	0.441	0.112	1.730	3.73E-01	2.50E-02	10
2DL4	412	OKG	COAD	G	A	G/G	A/A	41	47	5	11	1.920	0.616	5.990	3.88E-01	2.75E-02	11
2DL4	412	OKG	HNSC	G	A	G/G	A/A	41	47	5	10	1.740	0.550	5.510	5.00E-01	3.00E-02	12
2DL4	625	OKG	HNSC	C	G	C/C	G/G	36	42	5	10	1.710	0.535	5.470	5.27E-01	3.25E-02	13
2DP1	448	OKG	UCEC	G	C	G/G	C/C	43	43	16	11	0.688	0.286	1.650	5.36E-01	3.50E-02	14
2DL3	953	OKG	BRCA	G	A	G/G	A/A	84	29	41	18	1.270	0.633	2.550	6.19E-01	3.75E-02	15
2DS5	535	OKG	UCEC	G	A	G/G	A/A	25	26	8	5	0.601	0.173	2.090	6.20E-01	4.00E-02	16
2DL4	762	OKG	BRCA	C	T	C/C	T/T	77	11	44	9	1.430	0.550	3.720	6.24E-01	4.25E-02	17
2DL3	953	OKG	KIRP	G	A	G/G	A/A	84	29	17	4	0.682	0.212	2.190	7.11E-01	4.50E-02	18
2DL4	625	OKG	BRCA	C	G	C/C	G/G	36	42	22	21	0.818	0.388	1.720	7.36E-01	4.75E-02	19
3DP1	796	OKG	BRCA	T	C	T/T	C/C	73	18	46	9	0.793	0.329	1.910	7.68E-01	5.00E-02	20
3DP1	796	OKG	UCEC	T	C	T/T	C/C	73	18	18	6	1.350	0.469	3.890	7.81E-01	5.25E-02	21
2DP1	522	OKG	BRCA	T	C	T/T	C/C	85	15	46	10	1.230	0.512	2.960	8.11E-01	5.50E-02	22
3DL3	502	OKG	UCEC	G	A	G/G	A/A	67	22	22	9	1.250	0.502	3.110	8.15E-01	5.75E-02	23
3DL3	502	OKG	BRCA	G	A	G/G	A/A	67	22	39	15	1.170	0.544	2.520	8.35E-01	6.00E-02	24
2DP1	448	OKG	KIRC	G	C	G/G	C/C	43	43	6	8	1.330	0.425	4.160	8.36E-01	6.25E-02	25
2DP1	448	OKG	COAD	G	C	G/G	C/C	43	43	7	9	1.290	0.441	3.780	8.52E-01	6.50E-02	26
2DL4	412	OKG	UCEC	G	A	G/G	A/A	41	47	8	11	1.200	0.440	3.270	9.19E-01	6.75E-02	27
2DP1	522	OKG	UCEC	T	C	T/T	C/C	85	15	28	6	1.210	0.428	3.420	9.25E-01	7.00E-02	28
3DL3	408	OKG	BRCA	G	A	G/G	A/A	83	12	50	6	0.830	0.293	2.350	9.27E-01	7.25E-02	29
3DP1	774	OKG	BRCA	G	C	G/G	C/C	71	16	46	9	0.868	0.354	2.130	9.34E-01	7.50E-02	30
2DP1	471	OKG	BRCA	A	G	A/A	G/G	101	13	46	7	1.180	0.442	3.150	9.38E-01	7.75E-02	31
2DL5	517	OKG	BRCA	A	G	A/A	G/G	42	26	27	15	0.897	0.404	1.990	9.50E-01	8.00E-02	32
2DL4	625	OKG	UCEC	C	G	C/C	G/G	36	42	8	11	1.180	0.428	3.250	9.51E-01	8.25E-02	33
2DL5	583	OKG	BRCA	G	A	G/G	A/A	39	24	27	15	0.903	0.402	2.030	9.67E-01	8.50E-02	34
2DL5	583	OKG	UCEC	G	A	G/G	A/A	39	24	10	6	0.975	0.314	3.030	1.00E+00	8.75E-02	35
3DL3	804	OKG	BRCA	G	A	G/G	A/A	81	14	47	8	0.985	0.385	2.520	1.00E+00	8.75E-02	35
2DP1	448	OKG	HNSC	G	C	G/G	C/C	43	43	7	6	0.857	0.266	2.760	1.00E+00	9.00E-02	36
2DL4	412	OKG	BRCA	G	A	G/G	A/A	41	47	21	25	1.040	0.508	2.130	1.00E+00	9.25E-02	37
2DL5	517	OKG	UCEC	A	G	A/A	G/G	42	26	10	6	0.969	0.315	2.980	1.00E+00	9.25E-02	37
2DP1	448	OKG	KIRP	G	C	G/G	C/C	43	43	9	10	1.110	0.410	3.000	1.00E+00	9.25E-02	37

Table A12g Chi square significance tests for KIR variants within the TCGA samples, Asian cohort, reference homozygous versus heterozygous

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	971	OKG	STAD	T	C	T/T	T/C	151	22	77	0	0.000	0.000	NaN	2.41E-03	9.26E-04	1
2DL4	1023	OKG	STAD	G	A	G/G	G/A	80	85	21	49	2.200	1.210	3.990	1.34E-02	1.85E-03	2
2DL4	412	OKG	STAD	G	A	G/G	G/A	71	89	16	47	2.340	1.220	4.470	1.38E-02	2.78E-03	3
2DL4	625	OKG	STAD	C	G	C/C	C/G	59	81	16	48	2.190	1.130	4.230	2.78E-02	3.70E-03	4
3DL3	969	OKG	THCA	C	T	C/C	C/T	85	78	24	8	0.363	0.154	0.855	2.88E-02	4.63E-03	5
3DL1	1021	OKG	STAD	A	G	A/A	A/G	119	16	45	14	2.310	1.040	5.120	5.89E-02	5.56E-03	6
3DL2	394	OKG	STAD	C	A	C/C	C/A	166	29	61	20	1.880	0.990	3.570	7.66E-02	6.48E-03	7
3DL2	474	OKG	STAD	G	T	G/G	G/T	49	92	14	51	1.940	0.977	3.850	8.01E-02	7.41E-03	8
2DP1	522	OKG	BRCA	T	C	T/T	T/C	174	16	43	9	2.280	0.944	5.510	1.08E-01	8.33E-03	9
2DP1	1313	OKG	BRCA	A	C	A/A	A/C	161	16	40	9	2.260	0.931	5.490	1.13E-01	9.26E-03	10
3DP1	774	OKG	BRCA	G	C	G/G	G/C	146	48	46	8	0.529	0.233	1.200	1.74E-01	1.02E-02	11
3DL1	1180	OKG	STAD	G	C	G/G	G/C	134	19	59	15	1.790	0.851	3.760	1.75E-01	1.11E-02	12
3DP1	774	OKG	THCA	G	C	G/G	G/C	146	48	37	6	0.493	0.196	1.240	1.85E-01	1.20E-02	13
2DL4	395	OKG	BRCA	C	T	C/C	C/T	165	28	41	12	1.720	0.806	3.670	2.26E-01	1.30E-02	14
2DL4	1023	OKG	BRCA	G	A	G/G	G/A	80	85	15	26	1.630	0.805	3.300	2.33E-01	1.39E-02	15
3DP1	796	OKG	BRCA	T	C	T/T	T/C	145	50	45	9	0.580	0.265	1.270	2.33E-01	1.48E-02	16
2DL4	762	OKG	STAD	C	T	C/C	C/T	116	68	55	22	0.682	0.383	1.220	2.47E-01	1.57E-02	17
3DL1	1194	OKG	STAD	C	T	C/C	C/T	144	22	60	15	1.640	0.797	3.380	2.49E-01	1.67E-02	18
2DL4	395	OKG	STAD	C	T	C/C	C/T	165	28	64	17	1.570	0.805	3.060	2.53E-01	1.76E-02	19
3DL3	971	OKG	BRCA	T	C	T/T	T/C	151	22	39	10	1.760	0.770	4.020	2.62E-01	1.85E-02	20
3DL3	969	OKG	BLCA	C	T	C/C	C/T	85	78	13	6	0.503	0.182	1.390	2.70E-01	1.94E-02	21
2DL4	1023	OKG	BLCA	G	A	G/G	G/A	80	85	7	14	1.880	0.722	4.900	2.81E-01	2.04E-02	22
3DL3	621	OKG	STAD	G	A	G/G	G/A	152	41	69	12	0.645	0.319	1.300	2.88E-01	2.13E-02	23
2DP1	471	OKG	BRCA	A	G	A/A	A/G	173	18	43	8	1.790	0.730	4.390	3.04E-01	2.22E-02	24
3DL2	474	OKG	THCA	G	T	G/G	G/T	49	92	16	19	0.632	0.299	1.340	3.14E-01	2.32E-02	25
3DP1	479	OKG	THCA	A	C	A/A	A/C	153	42	38	6	0.575	0.228	1.450	3.30E-01	2.41E-02	26
3DL2	756	OKG	STAD	C	G	C/C	C/G	183	15	78	3	0.469	0.132	1.670	3.54E-01	2.50E-02	27
2DL5	583	OKG	STAD	G	A	G/G	G/A	40	15	18	3	0.444	0.114	1.730	3.74E-01	2.59E-02	28
3DL3	869	OKG	STAD	A	C	A/A	A/C	149	44	67	14	0.708	0.363	1.380	3.91E-01	2.69E-02	29
3DL3	621	OKG	BRCA	G	A	G/G	G/A	152	41	46	8	0.645	0.282	1.470	3.93E-01	2.78E-02	30
2DL4	762	OKG	BRCA	C	T	C/C	C/T	116	68	36	15	0.711	0.363	1.390	4.05E-01	2.87E-02	31
3DL2	394	OKG	BRCA	C	A	C/C	C/A	166	29	42	11	1.500	0.693	3.250	4.11E-01	2.96E-02	32
3DP1	774	OKG	BLCA	G	C	G/G	G/C	146	48	22	4	0.553	0.181	1.680	4.19E-01	3.06E-02	33
3DL2	474	OKG	BLCA	G	T	G/G	G/T	49	92	4	14	1.860	0.581	5.960	4.26E-01	3.15E-02	34
3DL3	502	OKG	STAD	G	A	G/G	G/A	25	88	8	44	1.560	0.651	3.740	4.26E-01	3.24E-02	35
3DL3	869	OKG	BRCA	A	C	A/A	A/C	149	44	45	9	0.677	0.307	1.490	4.34E-01	3.33E-02	36
3DP1	796	OKG	THCA	T	C	T/T	T/C	145	50	35	8	0.663	0.288	1.520	4.37E-01	3.43E-02	37
2DL4	762	OKG	THCA	C	T	C/C	C/T	116	68	22	18	1.400	0.701	2.790	4.42E-01	3.52E-02	38
3DL3	447	OKG	STAD	G	T	G/G	G/T	150	43	67	14	0.729	0.374	1.420	4.43E-01	3.61E-02	39
3DL3	969	OKG	LIHC	C	T	C/C	C/T	85	78	9	13	1.570	0.636	3.880	4.46E-01	3.70E-02	40
2DL4	412	OKG	BLCA	G	A	G/G	G/A	71	89	7	14	1.600	0.613	4.180	4.68E-01	3.80E-02	41
3DL3	447	OKG	BRCA	G	T	G/G	G/T	150	43	45	9	0.698	0.316	1.540	4.80E-01	3.89E-02	42
2DL4	395	OKG	THCA	C	T	C/C	C/T	165	28	40	4	0.589	0.195	1.770	4.81E-01	3.98E-02	43
2DP1	766	OKG	BRCA	G	C	G/G	G/C	145	14	46	7	1.580	0.601	4.150	5.07E-01	4.07E-02	44
2DL4	412	OKG	BRCA	G	A	G/G	G/A	71	89	14	24	1.370	0.661	2.840	5.09E-01	4.17E-02	45
3DP1	774	OKG	LIHC	G	C	G/G	G/C	146	48	24	5	0.634	0.229	1.750	5.15E-01	4.26E-02	46
3DP1	479	OKG	STAD	A	C	A/A	A/C	153	42	67	14	0.761	0.390	1.490	5.25E-01	4.35E-02	47
3DL2	456	OKG	STAD	C	T	C/C	C/T	182	16	75	4	0.607	0.196	1.880	5.36E-01	4.44E-02	48
3DL2	893	OKG	STAD	G	A	G/G	G/A	182	16	75	4	0.607	0.196	1.880	5.36E-01	4.44E-02	48
2DP1	471	OKG	STAD	A	G	A/A	A/G	173	18	74	5	0.649	0.232	1.810	5.56E-01	4.54E-02	49
3DL1	1180	OKG	BRCA	G	C	G/G	G/C	134	19	39	8	1.450	0.590	3.570	5.73E-01	4.63E-02	50
2DL4	762	OKG	LIHC	C	T	C/C	C/T	116	68	15	12	1.360	0.601	3.080	5.92E-01	4.72E-02	51
2DL4	625	OKG	BLCA	C	G	C/C	C/G	59	81	7	14	1.460	0.555	3.840	5.98E-01	4.82E-02	52
3DP1	774	OKG	STAD	G	C	G/G	G/C	146	48	64	17	0.808	0.432	1.510	6.08E-01	4.91E-02	53
2DL3	953	OKG	THCA	G	A	G/G	G/A	143	38	32	6	0.706	0.275	1.810	6.13E-01	5.00E-02	54
2DL4	625	OKG	THCA	C	G	C/C	C/G	59	81	17	18	0.771	0.367	1.620	6.20E-01	5.09E-02	55
2DP1	766	OKG	STAD	G	C	G/G	G/C	145	14	64	4	0.647	0.205	2.040	6.32E-01	5.19E-02	56
3DP1	479	OKG	BLCA	A	C	A/A	A/C	153	42	22	4	0.662	0.216	2.030	6.39E-01	5.28E-02	57
3DP1	796	OKG	BLCA	T	C	T/T	T/C	145	50	21	5	0.690	0.247	1.930	6.39E-01	5.37E-02	58
2DP1	1313	OKG	STAD	A	C	A/A	A/C	161	16	73	5	0.689	0.243	1.950	6.48E-01	5.46E-02	59
3DL2	474	OKG	LIHC	G	T	G/G	G/T	49	92	6	16	1.420	0.522	3.860	6.54E-01	5.56E-02	60
2DL4	412	OKG	UCEC	G	A	G/G	G/A	71	89	4	8	1.600	0.463	5.530	6.58E-01	5.65E-02	61
3DL3	621	OKG	BLCA	G	A	G/G	G/A	152	41	22	4	0.674	0.220	2.070	6.63E-01	5.74E-02	62
2DL4	1023	OKG	THCA	G	A	G/G	G/A	80	85	20	17	0.800	0.391	1.640	6.67E-01	5.83E-02	63
3DL1	1021	OKG	BRCA	A	G	A/A	A/G	119	16	38	7	1.370	0.524	3.580	6.99E-01	5.93E-02	64
3DL3	961	OKG	BRCA	C	A	C/C	C/A	141	36	38	12	1.240	0.589	2.610	7.16E-01	6.02E-02	65
3DL2	394	OKG	THCA	C	A	C/C	C/A	166	29	39	5	0.734	0.267	2.020	7.17E-01	6.11E-02	66
3DL3	961	OKG	THCA	C	A	C/C	C/A	141	36	24	8	1.310	0.543	3.160	7.19E-01	6.20E-02	67
3DP1	796	OKG	LIHC	T	C	T/T	T/C	145	50	23	6	0.757	0.292	1.970	7.30E-01	6.30E-02	68
2DP1	522	OKG	STAD	T	C	T/T	T/C	174	16	74	5	0.735	0.260	2.080	7.39E-01	6.39E-02	69
3DL3	502	OKG	THCA	G	A	G/G	G/A	25	88	5	24	1.360	0.471	3.930	7.49E-01	6.48E-02	70
2DL3	953	OKG	BLCA	G	A	G/G	G/A	143	38	21	4	0.717	0.232	2.210	7.52E-01	6.57E-02	71
3DL3	969	OKG	STAD	C	T	C/C	C/T	85	78	35	28	0.872	0.486	1.560	7.55E-01	6.67E-02	72
2DL4	762	OKG	BLCA	C	T	C/C	C/T	116	68	15	11	1.250	0.543	2.880	7.56E-01	6.76E-02	73
3DL1	1194	OKG	BRCA	C	T	C/C	C/T	144	22	41	8	1.280	0.531	3.090	7.56E-01	6.85E-02	74
2DL4	625	OKG	UCEC	C	G	C/C	C/G	59	81	4	8	1.460	0.420	5.080	7.72E-01	6.94E-02	75
3DP1	479	OKG	LIHC	A	C	A/A	A/C	153	42	24	5	0.759	0.273	2.110	7.75E-01	7.04E-02	76
3DP1	479	OKG	BRCA	A	C	A/A	A/C	153	42	40	13	1.180	0.579	2.410	7.81E-01	7.13E-02	77
3DL2	474	OKG	BRCA	G	T	G/G	G/T	49	92	11	25	1.210	0.550	2.660	7.81E-01	7.22E-02	78
3DL3	621	OKG	LIHC	G	A	G/G	G/A	152	41	24	5	0.772	0.277	2.150	8.02E-01	7.32E-02	79
3DL3	621	OKG	THCA	G	A	G/G	G/A	152	41	36	8	0.824	0.356	1.910	8.05E-01	7.41E-02	80
2DL4	625	OKG	BRCA	C	G	C/C	C/G	59	81	15	24	1.170	0.565	2.420	8.19E-01	7.50E-02	81
3DP1	796	OKG	STAD	T	C	T/T	T/C	145	50	62	19	0.889	0.485	1.630	8.19E-01	7.59E-02	82
2DL3	953	OKG	LIHC	G	A	G/G	G/A	143	38	24	5	0.784	0.281	2.190	8.28E-01	7.69E-02	83
2DL3	953	OKG	STAD	G	A	G/G	G/A	143	38	64	15	0.882	0.453	1.720	8.40E-01	7.78E-02	84
3DL3	869	OKG	BLCA	A	C	A/A	A/C	149	44	21	5	0.806	0.287	2.260	8.74E-01	7.87E-02	85
2DL4	1023	OKG	UCEC	G	A	G/G	G/A	80	85	5	7	1.320	0.403	4.330	8.75E-01	7.96E-02	86
3DL3	869	OKG	THCA	A	C	A/A	A/C	149	44	35	9	0.871	0.389	1.950	8.92E-01	8.06E-02	87
2DL4	412	OKG	LIHC	G	A	G/G	G/A	71	89	8	12	1.200	0.465	3.090	8.94E-01	8.15E-02	88
3DL3	969	OKG	CESC	C	T	C/C	C/T	85	78	6	7	1.270	0.409	3.940	8.98E-01	8.24E-02	89
2DL4	412	OKG	THCA	G	A	G/G	G/A	71	89	17	19	0.892	0.432	1.840	9.01E-01	8.33E-02	90
3DL3	447	OKG	BLCA	G	T	G/G	G/T	150	43	21	5	0.831	0.296	2.330	9.20E-01	8.43E-02	91
3DL3	969	OKG	BRCA	C	T	C/C	C/T	85	78	24	24	1.090	0.573	2.080	9.22E-01	8.52E-02	92
2DL4	625	OKG	LIHC	C	G	C/C	C/G	59	81	6	10	1.210	0.417	3.510	9.29E-01	8.61E-02	93
3DL1	607	OKG	BRCA	C	T	C/C	C/T	123	37	36	12	1.110	0.525	2.350	9.41E-01	8.70E-02	94
3DL3	961	OKG	LIHC	C	A	C/C	C/A	141	36	20	6	1.170	0.438	3.130	9.50E-01	8.80E-02	95
3DL3	447	OKG	THCA	G	T	G/G	G/T	150	43	35	9	0.897	0.400	2.010	9.50E-01	8.89E-02	96
3DL3	961	OKG	STAD	C	A	C/C	C/A	141	36	59	14	0.929	0.467	1.850	9.72E-01	8.98E-02	97
3DL3	869	OKG	LIHC	A	C	A/A	A/C	149	44	23	6	0.883	0.338	2.300	9.88E-01	9.07E-02	98
3DL3	447	OKG	LIHC	G	T	G/G	G/T	150	43	23	6	0.910	0.348	2.380	1.00E+00	9.17E-02	99
2DL3	953	OKG	BRCA	G	A	G/G	G/A	143	38	40	11	1.030	0.483	2.200	1.00E+00	9.26E-02	100
2DL4	1023	OKG	LIHC	G	A	G/G	G/A	80	85	10	11	1.040	0.419	2.580	1.00E+00	9.26E-02	100
3DL3	502	OKG	BRCA	G	A	G/G	G/A	25	88	6	20	0.947	0.343	2.610	1.00E+00	9.26E-02	100
2DL4	762	OKG	CESC	C	T	C/C	C/T	116	68	9	5	0.948	0.305	2.940	1.00E+00	9.35E-02	101
3DL1	607	OKG	BLCA	C	T	C/C	C/T	123	37	19	6	1.050	0.391	2.820	1.00E+00	9.35E-02	101
3DL1	607	OKG	LIHC	C	T	C/C	C/T	123	37	18	6	1.110	0.411	3.000	1.00E+00	9.35E-02	101
3DL1	607	OKG	STAD	C	T	C/C	C/T	123	37	57	17	0.991	0.515	1.910	1.00E+00	9.35E-02	101
3DL1	607	OKG	THCA	C	T	C/C	C/T	123	37	29	8	0.917	0.386	2.180	1.00E+00	9.44E-02	102

Table A12h Chi square significance tests for KIR variants within the TCGA samples, Asian cohort, heterozygous versus alternate homozygous

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL3	502	OKG	CESC	G	A	G/A	A/A	88	85	1	12	12.400	1.580	97.500	6.58E-03	2.78E-03	1
3DL2	474	OKG	STAD	G	T	G/T	T/T	92	57	51	16	0.506	0.264	0.971	5.61E-02	5.56E-03	2
3DL1	607	OKG	STAD	C	T	C/T	T/T	37	20	17	3	0.326	0.085	1.250	1.60E-01	8.33E-03	3
2DP1	448	OKG	THCA	G	C	G/C	C/C	53	125	15	20	0.565	0.269	1.190	1.87E-01	1.11E-02	4
3DL3	969	OKG	STAD	C	T	C/T	T/T	78	21	28	14	1.860	0.834	4.150	1.90E-01	1.39E-02	5
2DL4	1023	OKG	STAD	G	A	G/A	A/A	85	33	49	11	0.578	0.268	1.250	2.21E-01	1.67E-02	6
3DL3	502	OKG	STAD	G	A	G/A	A/A	88	85	44	29	0.682	0.391	1.190	2.26E-01	1.94E-02	7
2DP1	448	OKG	BRCA	G	C	G/C	C/C	53	125	20	31	0.657	0.344	1.260	2.69E-01	2.22E-02	8
2DL4	625	OKG	BRCA	C	G	C/G	G/G	81	31	24	15	1.630	0.757	3.510	2.90E-01	2.50E-02	9
3DL3	502	OKG	THCA	G	A	G/A	A/A	88	85	24	15	0.647	0.318	1.320	3.04E-01	2.78E-02	10
2DL4	412	OKG	LIHC	G	A	G/A	A/A	89	37	12	9	1.800	0.699	4.630	3.27E-01	3.06E-02	11
2DL4	1023	OKG	LIHC	G	A	G/A	A/A	85	33	11	8	1.870	0.691	5.060	3.28E-01	3.33E-02	12
3DL3	969	OKG	BRCA	C	T	C/T	T/T	78	21	24	3	0.464	0.127	1.690	3.64E-01	3.61E-02	13
2DP1	448	OKG	STAD	G	C	G/C	C/C	53	125	18	59	1.390	0.749	2.580	3.71E-01	3.89E-02	14
2DL4	412	OKG	BRCA	G	A	G/A	A/A	89	37	24	15	1.500	0.708	3.180	3.84E-01	4.17E-02	15
3DL3	502	OKG	BRCA	G	A	G/A	A/A	88	85	20	27	1.400	0.730	2.680	3.97E-01	4.44E-02	16
3DL3	502	OKG	BLCA	G	A	G/A	A/A	88	85	14	9	0.666	0.274	1.620	4.97E-01	4.72E-02	17
3DL3	502	OKG	LIHC	G	A	G/A	A/A	88	85	15	10	0.690	0.294	1.620	5.22E-01	5.00E-02	18
3DL2	474	OKG	LIHC	G	T	G/T	T/T	92	57	16	7	0.706	0.274	1.820	6.24E-01	5.28E-02	19
3DL3	502	OKG	UCEC	G	A	G/A	A/A	88	85	8	5	0.647	0.204	2.060	6.49E-01	5.56E-02	20
2DL4	1023	OKG	BRCA	G	A	G/A	A/A	85	33	26	13	1.290	0.593	2.810	6.63E-01	5.83E-02	21
3DL2	474	OKG	THCA	G	T	G/T	T/T	92	57	19	9	0.765	0.324	1.810	6.89E-01	6.11E-02	22
2DL4	625	OKG	STAD	C	G	C/G	G/G	81	31	48	15	0.817	0.401	1.670	7.05E-01	6.39E-02	23
2DP1	448	OKG	LIHC	G	C	G/C	C/C	53	125	7	21	1.270	0.509	3.170	7.69E-01	6.67E-02	24
3DL2	474	OKG	BRCA	G	T	G/T	T/T	92	57	25	18	1.160	0.582	2.310	8.03E-01	6.94E-02	25
2DL4	412	OKG	STAD	G	A	G/A	A/A	89	37	47	17	0.870	0.443	1.710	8.14E-01	7.22E-02	26
2DL4	625	OKG	THCA	C	G	C/G	G/G	81	31	18	8	1.160	0.458	2.940	9.41E-01	7.50E-02	27
2DL4	412	OKG	BLCA	G	A	G/A	A/A	89	37	14	5	0.859	0.289	2.560	9.99E-01	7.78E-02	28
2DL4	1023	OKG	THCA	G	A	G/A	A/A	85	33	17	7	1.060	0.403	2.790	1.00E+00	8.06E-02	29
2DL4	412	OKG	THCA	G	A	G/A	A/A	89	37	19	8	1.010	0.406	2.510	1.00E+00	8.33E-02	30
2DL4	625	OKG	BLCA	C	G	C/G	G/G	81	31	14	5	0.933	0.310	2.810	1.00E+00	8.33E-02	30
2DL4	1023	OKG	BLCA	G	A	G/A	A/A	85	33	14	5	0.920	0.307	2.760	1.00E+00	8.33E-02	30
3DL1	732	OKG	BRCA	T	C	T/C	C/C	27	21	9	8	1.140	0.376	3.460	1.00E+00	8.33E-02	30
3DL2	474	OKG	BLCA	G	T	G/T	T/T	92	57	14	8	0.922	0.364	2.340	1.00E+00	8.33E-02	30
2DP1	448	OKG	BLCA	G	C	G/C	C/C	53	125	7	18	1.090	0.430	2.760	1.00E+00	8.61E-02	31
3DL1	607	OKG	BRCA	C	T	C/T	T/T	37	20	11	5	0.841	0.256	2.760	1.00E+00	8.61E-02	31

Table A12i Chi square significance tests for KIR variants within the TCGA samples, Asian cohort, reference homozygous versus alternate homozygous

gene	pos	group1	group2	ref	alt	genotype1	genotype2	group1 genotype1 observerdCount	group1 genotype2 observerdCount	group2 genotype1 observerdCount	group2 genotype2 observerdCount	chisqOR	chisqORlowCI	chisqORhighCI	chisqPval	(i/m)Q	rankPval
3DL1	607	OKG	STAD	C	T	C/C	T/T	123	20	57	3	0.324	0.093	1.130	1.09E-01	3.23E-03	1
2DL4	1023	OKG	BRCA	G	A	G/G	A/A	80	33	15	13	2.100	0.901	4.890	1.30E-01	6.45E-03	2
2DL4	412	OKG	BRCA	G	A	G/G	A/A	71	37	14	15	2.060	0.899	4.720	1.32E-01	9.68E-03	3
2DL4	412	OKG	STAD	G	A	G/G	A/A	71	37	17	17	1.920	0.879	4.190	1.48E-01	1.29E-02	4
3DL2	474	OKG	THCA	G	T	G/G	T/T	49	57	16	9	0.484	0.196	1.190	1.69E-01	1.61E-02	5
2DL4	625	OKG	BRCA	C	G	C/C	G/G	60	31	15	15	1.940	0.840	4.480	1.79E-01	1.94E-02	6
2DL4	412	OKG	LIHC	G	A	G/G	A/A	71	37	8	9	2.160	0.770	6.060	2.25E-01	2.26E-02	7
2DL4	625	OKG	STAD	C	G	C/C	G/G	60	31	16	15	1.810	0.792	4.140	2.28E-01	2.58E-02	8
3DL1	732	OKG	BRCA	T	C	T/T	C/C	22	21	3	8	2.790	0.651	12.000	2.81E-01	2.90E-02	9
3DL3	969	OKG	STAD	C	T	C/C	T/T	86	21	35	14	1.640	0.750	3.590	3.00E-01	3.23E-02	10
2DL4	1023	OKG	LIHC	G	A	G/G	A/A	80	33	10	8	1.940	0.704	5.350	3.07E-01	3.55E-02	11
2DL5	517	OKG	BRCA	A	G	A/A	G/G	46	30	9	11	1.870	0.692	5.050	3.20E-01	3.87E-02	12
2DL5	583	OKG	BRCA	G	A	G/G	A/A	40	27	9	11	1.810	0.661	4.960	3.65E-01	4.19E-02	13
3DL2	474	OKG	BRCA	G	T	G/G	T/T	49	57	11	18	1.410	0.608	3.270	5.58E-01	4.52E-02	14
2DL5	583	OKG	THCA	G	A	G/G	A/A	40	27	14	6	0.635	0.217	1.860	5.68E-01	4.84E-02	15
3DL2	474	OKG	BLCA	G	T	G/G	T/T	49	57	4	8	1.720	0.488	6.060	5.86E-01	5.16E-02	16
2DL4	1023	OKG	STAD	G	A	G/G	A/A	80	33	21	11	1.270	0.551	2.930	7.31E-01	5.48E-02	17
3DL3	502	OKG	BRCA	G	A	G/G	A/A	25	85	6	27	1.320	0.490	3.550	7.53E-01	5.81E-02	18
2DL5	517	OKG	THCA	A	G	A/A	G/G	46	30	13	7	0.826	0.296	2.310	9.14E-01	6.13E-02	19
2DL4	1023	OKG	THCA	G	A	G/G	A/A	80	33	20	7	0.848	0.327	2.200	9.19E-01	6.45E-02	20
3DL1	607	OKG	BRCA	C	T	C/C	T/T	123	20	36	5	0.854	0.299	2.440	9.71E-01	6.77E-02	21
3DL3	969	OKG	THCA	C	T	C/C	T/T	86	21	24	5	0.853	0.291	2.500	9.81E-01	7.10E-02	22
2DL4	412	OKG	THCA	G	A	G/G	A/A	71	37	17	8	0.903	0.356	2.290	1.00E+00	7.42E-02	23
2DL5	583	OKG	BLCA	G	A	G/G	A/A	40	27	8	5	0.926	0.274	3.130	1.00E+00	7.42E-02	23
3DL2	474	OKG	LIHC	G	T	G/G	T/T	49	57	6	7	1.000	0.315	3.180	1.00E+00	7.42E-02	23
2DL4	625	OKG	THCA	C	G	C/C	G/G	60	31	17	8	0.911	0.354	2.350	1.00E+00	7.74E-02	24
2DL5	517	OKG	BLCA	A	G	A/A	G/G	46	30	8	5	0.958	0.286	3.210	1.00E+00	7.74E-02	24
2DL5	517	OKG	STAD	A	G	A/A	G/G	46	30	19	12	0.968	0.411	2.280	1.00E+00	7.74E-02	24
2DL5	583	OKG	STAD	G	A	G/G	A/A	40	27	18	12	0.988	0.410	2.380	1.00E+00	7.74E-02	24
3DL2	474	OKG	STAD	G	T	G/G	T/T	49	57	14	16	0.982	0.436	2.210	1.00E+00	7.74E-02	24
3DL3	502	OKG	STAD	G	A	G/G	A/A	25	85	8	29	1.070	0.435	2.630	1.00E+00	7.74E-02	24

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Vita

Howard Rosoff was born in Baltimore, Maryland. After high school, he enrolled at the University of Maryland Baltimore County as a biology major but left to pursue opportunities in the IT field. He spent several years in systems administration at a Fortune 500 company and in data acquisition for the motorsports, computer animation, and digital media systems markets. He returned to UMBC in January 2006, graduated *cum laude* with a B.S. in Bioinformatics and Computational Biology in May 2008, and was awarded Outstanding Graduating Senior in Bioinformatics 2008. He then spent a year as a Genome Analyst at a biotech startup near NIH in the metro Washington, DC area while completing graduate coursework at Johns Hopkins University. He enrolled at the University of Texas Graduate School of Biomedical Sciences at Houston in September 2009 with an interdisciplinary focus, completing life sciences training at GSBS and computational training at Rice University. He joined Dean Lee's lab in May 2010 and worked on the development of an NK cell-based cancer immunotherapy product before initiating the invention of the genotyping algorithm that became the subject of his graduate research.