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## GENOMIC DRIVERS OF CUTANEOUS SQUAMOUS CELL CARCINOMA DEVELOPMENT

Vida Chitsazzadeh

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**GENOMIC DRIVERS OF CUTANEOUS SQUAMOUS CELL CARCINOMA  
DEVELOPMENT**

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**GENOMIC DRIVERS OF CUTANEOUS SQUAMOUS CELL CARCINOMA  
DEVELOPMENT**

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

Vida Chitsazzadeh, B.S.

Houston, Texas

May, 2016



## **DEDICATION**

I dedicate this dissertation to my loving family for all their support throughout the years and also to my husband, William Atabala for his undying kindness and encouragement. I would like to dedicate this work to my uncle, Mahmood Chitsazzadeh, in my home country of Iran, where he continues to fight a life-long battle with psoriasis. Growing up, I witnessed his struggle to cope with this devastating disease. My desire to change the lives of people like my uncle compelled me to dedicate my education to research, volunteer work, and teaching with ultimate goal of becoming a physician-scientist.



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# **GENOMIC DRIVERS OF CUTANEOUS SQUAMOUS CELL CARCINOMA DEVELOPMENT**

By: Vida Chitsazzadeh, B.S.

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Skin cancer is the most common malignancy in humans. Annually, in U.S. there are over 3 million cases with an estimated overall economic impact of \$2 billion. Cutaneous Squamous Cell Carcinoma (cuSCC) comprises 15-20% of all skin cancers. cuSCC has the best-defined progression from a distinct precancerous lesion, the Actinic Keratosis (AK), to invasive cuSCC. Destructive therapies for AK treatment must be used repetitively, causing significant morbidity. There is a tremendous need for targeted diagnostics and therapy for AKs, representing an important opportunity for secondary skin cancer prevention. Our knowledge of the molecular and cellular events that lead to the transformation of normal skin (NS) to AK and subsequently to cuSCC is very limited, thus representing a fundamental gap in our understanding of this progression.

In order to identify novel targets for molecular chemoprevention, we used isogenic human samples throughout cuSCC development and a UV-driven Hairless mouse model of cuSCC to identify genomic drivers of cuSCC by cross-species analysis. RNA-Seq identified 349 transcripts that were differentially expressed across normal skin (NS), AK, and cuSCC. mRNA profiles primarily distinguished NS from other samples, whereas microRNA profiles could segregate the three groups. Using cross-species functional pair analysis (anti-correlated miRNA-mRNA expression) we identified several miRNAs (miR-21,-31,-221) and their targets as major promoters of cuSCC development. TRANSFAC analysis identified ETS2, MAZ, and TCF3 as core transcriptional drivers of progression. Whole exome sequencing demonstrated that UVB signature mutations dominate in AKs and cuSCCs, with frequent mutations in TP53, NOTCH1/2, and CDKN2A, as previously reported. Surprisingly, NS samples adjacent to the cuSCCs had up to 1200 mutations with no significant overlap with cuSCC. Ingenuity Variant Analysis identified NOTCH and its coactivators as the functional modules most perturbed in cuSCCs. Because cuSCC shares commonly mutated genes with lung SCC and head & neck SCC (HNSCC), we assessed the global similarity of gene expression to other cancers. By this measure, cuSCC is most similar to HNSCC and its mRNA signature predicts survival in non-HPV-related HNSCC. cuSCC is also similar to lung SCC as well as basal subtype of breast cancer. Our cross species analysis



has identified key genomic drivers of cuSCC development as potential chemoprevention targets and suggests that our model can serve as the basis for validating chemoprevention targets in cuSCC and molecularly similar cancers such as HNSCC and lung SCC.

Through our initial analysis of 9 sets of matched samples, we identified miR-181a as a potential molecular target; expression of the miR-181a family gradually increases throughout cuSCC progression. Importantly, miR-181a is significantly upregulated in multiple carcinomas. We have focused on the function of TGFBR3, which is downregulated by miR-181a and which has a tumor suppressor role in many contexts. We hypothesize that upregulation of miR-181a promotes initiation and progression of keratinocyte transformation by targeting TGFBR3.

Comparison of miR-181a levels in human cuSCCs to normal skin shows that miR-181a has a significantly higher expression (~8.4 folds) in cuSCCs. Our results show that miR-181a overexpression (OE) and TGFBR3 knockdown (KD) significantly suppresses UV-induced apoptosis in HaCaT keratinocytes and in primary normal human epidermal keratinocytes (NHEKs). In addition, OE of miR-181a or direct KD of TGFBR3 by shRNA is sufficient for enhanced anchorage-independent survival of HaCaTs. Moreover, miR-181a OE or TGFBR3 KD enhances cellular motility through increase of migration and invasion and upregulation of EMT markers, such as *snail*, *slug*, and *vimentin*. Luciferase assay results demonstrate that miR-181a directly and specifically targets the 3'UTR of TGFBR3. Rescue experiments show that miR-181a phenotype can be partially rescued by TGFBR3 overexpression. In summary, we show that miR-181a regulates susceptibility to apoptosis as well as cellular adhesion and motility at least in part through TGFBR3.



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# **Chapter 1**

## **Introduction**



## **1.1 Skin Cancer**

Skin cancer is the most common cancer in human. In USA up to 700,000 cases are diagnosed annually. Cutaneous squamous cell carcinoma (cuSCC) account for 15-20% of all skin cancer, making it the second most common non-melanoma (NMSC) skin cancer worldwide [1]. Annually, in U.S. there are over 250,000 cases of cutaneous squamous cell carcinoma (cuSCC). Due to an aging population and an increase in number of immunocompromised individuals, incidence of cuSCC is on the rise [2]. The precursor to cuSCC is actinic keratosis (AK), which is usually treated with destructive modalities that must be applied repetitively causing significant morbidity. Our understanding of the molecular and genetic events that lead to sequential progression of normal skin (NS) to AK to cuSCC is very poor. This represents a fundamental gap in our knowledge and understanding of this progression sequence is of great importance. Addressing this gap presents an opportunity for secondary skin cancer prevention.

### **1.1.1 Management of cuSCC**

Most cuSCCs can be successfully treated with destructive modalities such as surgical excision, Mohs surgery, electrodesiccation and curettage, topical 5-fluorouracil, and radiation therapy.

### **1.1.2 Classification of cuSCC**

Classification of cutaneous squamous cell carcinoma as high-risk versus low-risk is very important. Early identification and management of cuSCCs that have high rate for recurrence and metastasis can significantly reduce the associated morbidity and mortality [1]. Distinct criteria have been proposed by the National Comprehensive Cancer Network (NCCN) [3] and the American Joint Committee on Cancer (AJCC) [4, 5] for the assessment of the high-risk cuSCCs.



However, no consensus has been reached and the decision is left to the physician based on his/her assessment of the patient's history and clinical features of the lesion [1]. Eyelid carcinomas have a separate AJCC staging system and within NCCN guidelines, tumors with lymph node involvement are evaluated with a different algorithm. Characteristics of high-risk lesions are dependent on tumor as well as host factors.

AJCC and NCCN guidelines are established based on two different methodologies to serve two different purposes. AJCC staging system uses the tumor (T), node (N) and metastases (M) classification. AJCC staging mainly uses the primary tumor anatomic characteristics and does not take into account important clinical and host factors such as immunosuppression or recurrence [3]. AJCC approach has been criticized as being too simplistic and restrictive. On the other hand, NCCN classification has been criticized as being too inclusive. To elaborate, for a tumor to be categorized as high-risk, it has to meet only 1 of 12 high-risk criteria.

A recent study has evaluated the concordance of the AJCC and NCCN definitions of the high-risk cuSCCs [3]. They demonstrate that there is a significant discordance between the 2 definitions and based on AJCC criteria majority of tumors (82.1%) were stage 1 and conversely based on NCCN criteria majority of tumors (87%) were classified as high-risk [3]. Outcome of this study further highlights the need for a unified definition of high-risk tumors for improving patient outcomes. In recent years, Brigham and Women's Hospital (BWH) system was proposed as an alternative guideline to improve T-stage stratification [6].

## **1.2 Hairless mice in skin cancer**

The *hairless* locus is located on mouse chromosome 14. In mice, *Hr* gene encodes a ~130kDa protein that is a transcriptional co-repressor for family of receptors such as thyroid hormone, vitamin D and retinoic acids [7]. Embryonically, *Hr* is expressed in various tissues and



highly expressed in both hair follicle and interfollicular keratinocytes of epidermis by birth. There are various strains of hairless mice (18 murine *Hr* alleles are known) and outbred albino SKH1 (Charles River Laboratories, Wilmington, MA) is the most widely used strain. The mutant allele that is carried by SKH1 mice is autosomal recessive, *hr*, which has an aberrant splicing due to stable integration of a retrovirus into the 6<sup>th</sup> intron of the gene[7]. In human, two autosomal recessive diseases are associated with *Hr* mutations. Various studies have shown that for normal hair growth *Hr* is necessary and sufficient. Hair growth in hairless mice is normal during the first coat; however, mice rapidly lose hair starting cephalically and proceeding caudally. During consecutive hair cycles, follicles develop abnormally with characteristic histological findings of utriculus, deep dermal cysts, and sebaceous gland hyperplasia [7].

Hairless mice have been extensively used as a model in the field of dermatology for many years and processes such as wound healing, tumorigenesis, and inflammation are well characterized in these mice [7]. We chose this model to avoid chronic irritation as a confounding variable in our studies that is due to depilation of mice. In addition, with this model we can eliminate the effects of hair cycle on skin carcinogenesis.

Each mice can produce multiple skin tumors, independent of one another, and this feature can be used to discern the rate of development and individual aggressiveness of each tumor [7]. Tumor progression starts from epithelial hyperplasia which then progresses to papilloma and eventually into carcinoma. From this progression sequence, we can identify markers for tumor initiation, promotion and progression [7]. Hairless mice have been shown to be sensitive to development of UV-induced carcinoma that have similar pattern of mutations as human cuSCC. Of important note, haired mice are less susceptible to UVR immunosuppressive effects than hairless mice. In the SKH-1 Hairless mouse model of UV-induced cuSCC, *p53*, *RAS*, and *CDKN2A* are similarly affected as seen in human cuSCC [7-16]. For this reason, we believe that



this model faithfully recapitulates human disease both clinically and molecularly.

### **1.3 UV spectrum of solar radiation (UVR)**

Ultraviolet (UV) rays are a form of invisible energy given off by the sun. Based on wavelength solar UV radiation (UVR) is divided into three categories, UVA (320-400nm), UVB (280-320nm) and UVC (100-280nm). Minute amount of UVC reaches the earth surface by penetrating the ozone layer of atmosphere and for this reason UVC is not physiologically relevant for studies of human skin cancer. On the other hand, UVA rays account for the majority (95%) of the UV radiation reaching the earth's surface; terrestrial radiation from the midday sun comprises about 95% UVA and 5% UVB [17]. UVA is mainly responsible in the aging of the cells and some DNA damage. On the other hand, UVB rays cause direct DNA damage and responsible for sunburns. UVA rays can penetrate deeply into the skin and mainly cause dermal compartment damage. Whereas, UVB damage is mainly in the epidermal compartment.

UV radiation can cause an increase in collagen breakdown and abnormal deposition of elastin [18, 19]. This process and its pathological manifestation is referred to as solar elastosis. In addition, UV radiation can cause an increase in free radicals resulting in damage of cellular functions and DNA damage. Moreover, UV radiation can suppress the immune system by inducing release of certain cytokines, inhibiting antigen presentation, and enhancing leukocytes apoptosis [20].

### **1.4 Sunscreens**

Sunscreens are the main protection modality against solar UV radiation. Marketing and labeling of sunscreens are nationally regulated, and for this reason, there is differences between sunscreens in America and European countries [21]. Sun Protection Factor (SPF) is determined



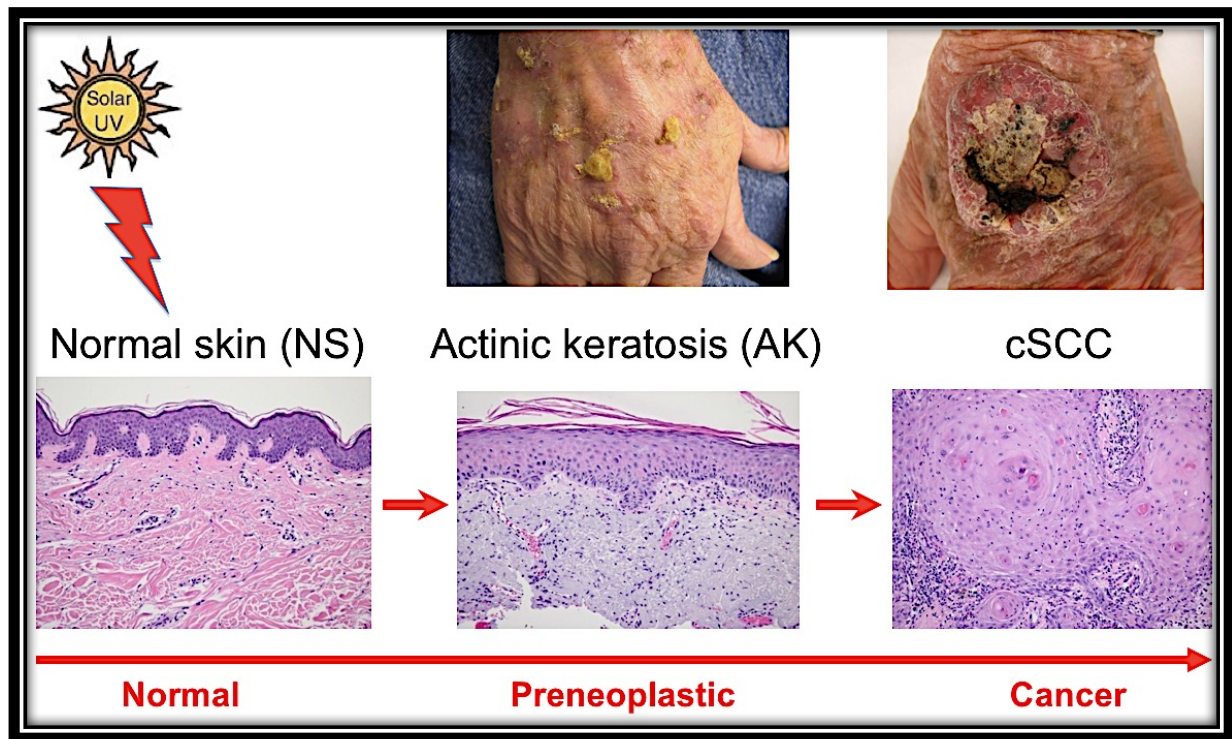
by the amount of light that induces erythema in sunscreen protected skin divided by the amount of light that induces erythema in unprotected skin. SPF ratings vary from 1 to 100 or even higher. For sunscreens to be protective they must be applied regularly and in sufficient amounts (recommended amount of 2 mg/cm<sup>2</sup>).

Most sunscreens fully protect against UVB, but only few ingredients protect against UVA. There are 2 types of UV filters: Physical filters (inorganic) and chemical filters (organic). Currently 16 filters are proved in USA and 28 are approved in European countries. Nine of the sixteen approved filters are protective against UVB; Aminobenzoic acid (PABA), Octinoxate, Octocrylene, Oxybenzone, Octisalate, Homosalate, Cinoxate, Ensulizole, Dioxybenzone. Physical blockers such as Zinc Oxide (ZnO) and Titanium Dioxide (TiO<sub>2</sub>) are protective against both UVA and UVB rays. In general, they are much more photostable and less irritative to skin, however, they can cause acneiform breakouts. Most users complain of the “white cast” that results from the application of physical blockers [22].

### **1.5 Actinic Keratoses (AKs)**

AKs are the most common precancerous lesion, affecting up to 5.5% of women and 13.9% of men in U.S. and accounting for 5.2 million visits per year and an estimated annual cost of \$920 million [23]. Actinic Keratoses (AKs) are scaly lesions, often readily palpable and visible on the skin of affected individuals primarily on sun-exposed regions of the body. Histologically, they are characterized by epidermal dysmaturation and partial thickness basal and spinous layer atypia. In time, this atypia extends to the full thickness of epidermis eventuating in Cutaneous Squamous Cell Carcinoma (cuSCC). Ultraviolet (UV) radiation is the main etiological factor implicated in AK and cuSCC pathogenesis [24].





**Figure 1. cuSCC pathogenesis occurs through distinct lesional changes.** Progression of cuSCC consists of distinct lesions that are easily recognized both clinically and histologically. This progression sequence is depicted here : where we see a transition from Normal skin that is exposed to UV solar radiation to actinic keratosis which is regarded as the precancerous lesions, ultimately to carcinoma, which is invasive.

### 1.5.1 AK and field cancerization

AKs are an excellent example of field cancerization with wide swaths of skin that possess the potential to grow into carcinoma [25, 26]. “Field cancerization” refers to the development of multiple AKs in the UV-exposed field. Approximately 0.6% of clinically diagnosed AKs are estimated to progress to cuSCC within 1 year and 2.6% are estimated to progress within 4 year [27]. A recent study in 2014 estimated that about 6-10% of all AKs progress into cuSCC [26]. Thus, the standard practice of destroying these lesions is well founded, but there is still no rationally designed way of preventing their progression, and there are still over 250,000 cases of



cuSCC in U.S. every year [28]. Destructive therapies are effective but treatments of large surface areas are impractical and fail to control progression in high-risk populations such as organ transplant recipients [29]. Compounding this problem, aggressive surgical interventions have significant adverse effects and usually for patients with facial or acral lesions the results are grotesque and disfiguring. Understanding the genetic alterations that dictate AK formation and progression to cuSCC forms the molecular basis for rationally designed targeted secondary cancer prevention for an extremely common skin cancer.

### **1.5.2 Molecular genetics of AK**

To date, molecular genetic studies of AK have largely centered on known tumor suppressor genes. In chronically sun-damaged skin, AK and cuSCC a characteristic UVB-induced cellular changes such as increases in COX-2 activity and inflammatory cytokines in addition to signature genetic mutations in mtDNA and the tumor suppressor TP53 have been identified [30]. What dictates whether or not AKs progress to cuSCC is inadequately understood as these genetic lesions are also commonly found in cuSCC. Some efforts to discern differences by gene expression have been successful at identifying gene signatures that distinguish SCC from AK or irradiated skin but they have not been refined to identify a mechanistic basis for progression [31].

Amplifications of epidermal growth factor receptor (*EGFR*) and *c-MYC* have been identified in AK and cuSCC [32]. Using array comparative genomic hybridization (aCGH) to probe copy number variation (CNV), loss of *INPP5A* and *CKS1B* expression has been demonstrated in human cuSCC and smaller proportions of AKs [33-35]. In the SKH-1 Hairless mouse model of UV-induced cuSCC, *p53*, *RAS*, and *CDKN2A* are similarly affected [7-16]. Serial Analysis of Gene Expression (SAGE) profiling revealed changes in growth factors and stress responsive elements [7-16] and aCGH revealed some changes that map to previously reported



abnormalities in human cuSCC (chromosomes 3p, 11p, 9q) [36-39]. Given that cancers are genomically unstable, it is not surprising that it is difficult to identify pathogenic changes, the drivers of progression, when comparing tumor tissue to their normal counterparts, or when comparing unmatched samples.

### **1.5.3 Lack of diagnostic predictors of AK progression**

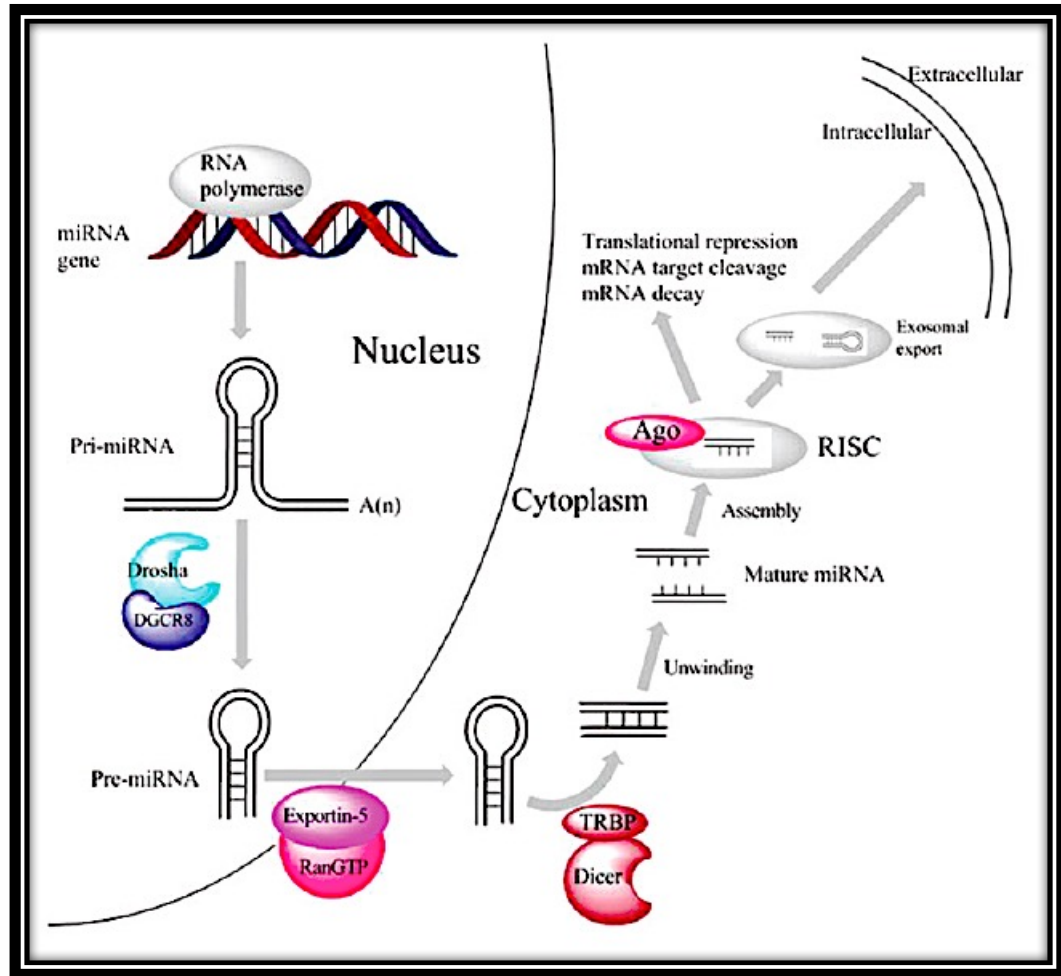
Currently, we lack diagnostic predictors of AK progression to cuSCC. We would like to identify important genetic events that determine the progression of clinically normal sun-exposed skin (NS) to AK and subsequently to cuSCC. This 3-way comparison is essential for cancer prevention; genetic events that are relevant to the progression of NS to AK and are retained in the subsequent progression to cuSCC may be necessary for this step-wise transition. Similarly, genetic changes that are unique to this last transitional step may cause AK transformation to cuSCC. In profiling studies, the key gap in methodology is the inability to rank these changes in terms of which are likely to act to drive the development of cancer and which may be biologically insignificant.

### **1.6 miRNAs role in cancer**

Over the past decade, miRNAs have been identified as important drivers of cancer pathogenesis. miRNAs have emerged as important players not only in tumorigenesis but also tumor progression. miRNAs are important modulators of tumor proliferation, transformation, invasion, and metastasis [40]. Importantly, fluctuations in abundance of a single miRNA can impact expression levels of hundreds of proteins. It is important to highlight the role of miRNAs as cardinal regulators of global cellular physiology such that a small perturbation in transcript



abundance is sufficient to disrupt the normal cell-cycle control and sway the cells down a transformed path.



**Figure 2. Biogenesis of microRNAs (miRNAs).** The miRNA gene is transcribed by RNA polymerase II/III. The transcript is called Pri-miRNA, which is cleaved by Drosha-DGCR8 complex and forms pre-miRNA. This is transported to cytoplasm from nucleus by the exportin-5 and RanGTP cofactor. Pre-miRNA is processed by the transactivating response RNA binding protein-Dicer complex into a miRNA duplex, which is unwound to form mature miRNA. The guide stand binds to Ago to form RNA-induced silencing complex (RISC). RISC complementary pairs with the target messenger RNA (mRNA) 3'-untranslated region, leading to mRNA cleavage



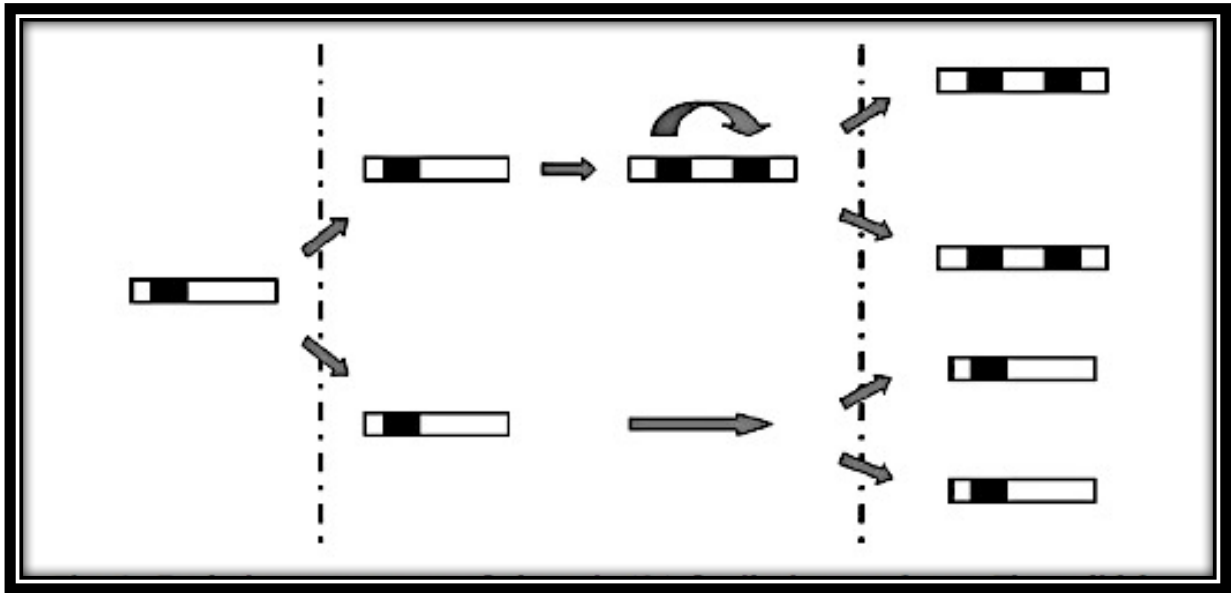
and translation repression. The passenger strand is degraded, and the surplus miRNAs are exported to extracellular matrix by exosomes. Reproduced by permission from the following article: Title: A Systematic Review of MicroRNA in Glioblastoma Multiforme: Micro-modulators in the Mesenchymal Mode of Migration and Invasion, Publication: Molecular Neurobiology, Publisher: Springer.

As a consequence of their important role in cancer initiation and progression, miRNAs have become the new target of anticancer therapy. Virtually in all cancer types, expression levels of miRNAs are deregulated in tumor tissue in comparison with their normal counterpart [41]. Dysregulation of miRNAs have been previously reported in multiple types of SCC. However, expression of Drosha, a component of microprocessor complex that has the essential role of initiation of miRNA machinery, is upregulated in cuSCC. This gives strength to the hypothesis of miRNA involvement in cuSCC pathogenesis [42]. In addition, it has been shown that tumor phenotypes can be modulated by modification of aberrantly-expressed miRNA, suggesting that miRNA may be good therapeutic targets [43].

### **1.7 miR-181 family**

miR-181 family is highly evolutionarily conserved across vertebrates [44]. This is an ancient gene family originating from *urochordate C. intestinalis*. The evolution pattern of this gene is significant for multiple rounds of duplication, segmental replication with mutation and deletion of certain genes in some species (Figure 3) [44]. miR-181 family was first identified for their role in differentiation of hematopoietic cells, including T and B cells, natural killer cells, and megakaryocytes [45]. miR-181a-1, miR-181a-2, miR-181b-1, miR-181b-1, miR-181c, and miR-181d are the six members of this family.



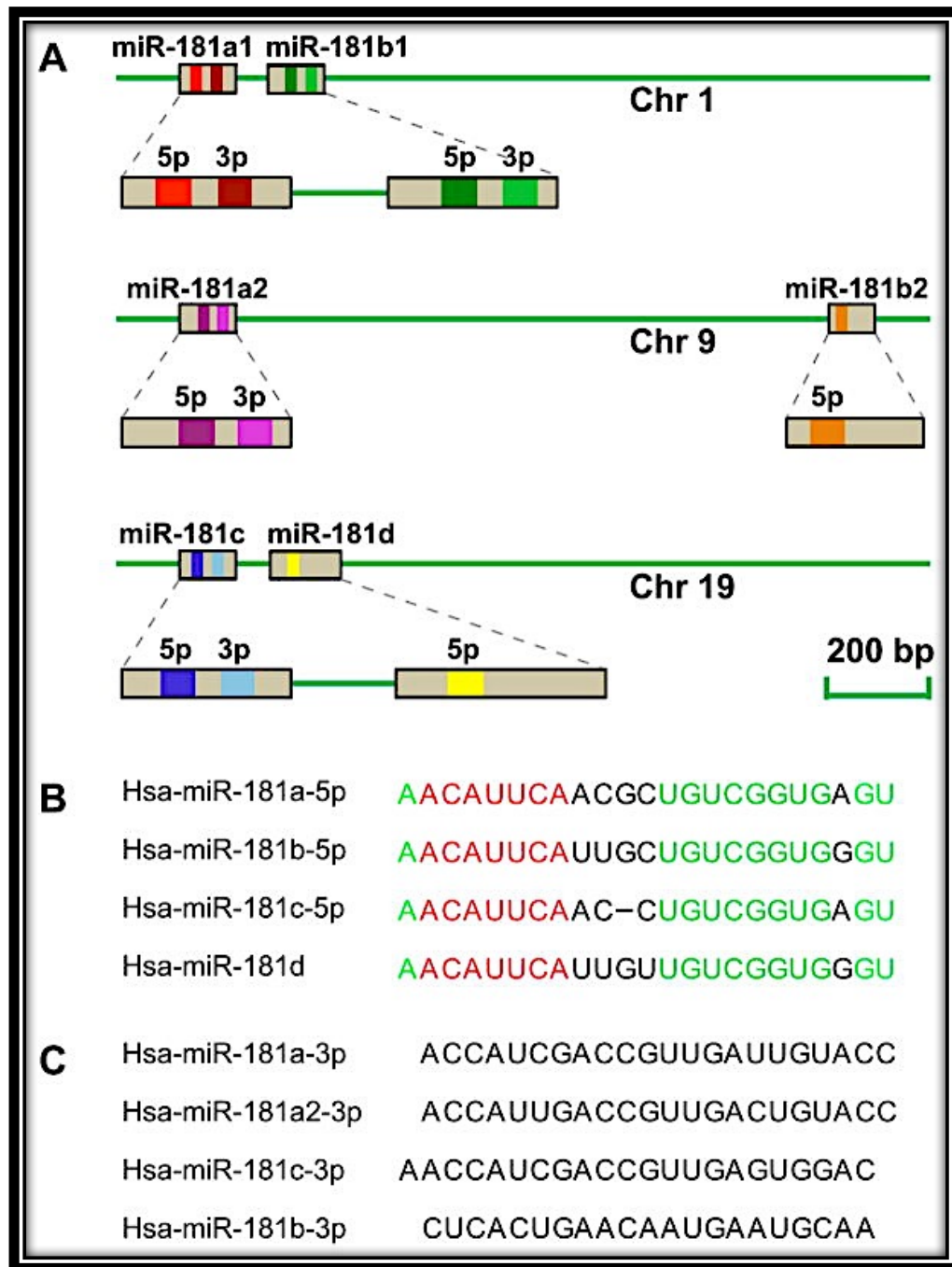


**Figure 3. Evolutionary pattern of the miR-181 family in vertebrate.** The solid bar represents miR-181 gene. Two rounds of duplications and one fragmental replication within one of the duplicates after first duplication during the vertebrate evolution shape this gene family. Reproduced by permission from the following article: Title: Evolution of the mir-181 microRNA family, Publication: Computers in Biology and Medicine, License Number: 3821610198316.

### 1.7.1 Genomic location of the miR-181 family members

In humans, miR-181 family members are clustered and located on three different chromosomes. *miR-181a* and *miR-181b* are located on chromosome 1. *miR-181a2* and *miR-181b2* are located on chromosome 9. *miR-181c* and *miR-181d* are located on chromosome 19 [46]. The seed-region is highly conserved among the individual family members [47]. Genomic location of the miR-181 family members along with their mature sequences and seed regions are depicted on (Figure 4). There is high level of redundancy in this family suggesting that they are evolutionary and functionally important.





**Figure 4. miR-181 family members and their genomic locations.** **A**, genomic location of miR-181 family members. **B**, mature sequences of miR-181 family members that arise from the 5' arm of the precursors. Nucleotides in red represent seed sequence, and green shows conserved nucleotides among the members. **C**, mature sequences of miR-181 family members that arise from the 3' arm of the precursors. Reproduced by permission from the following article: Title: Role of

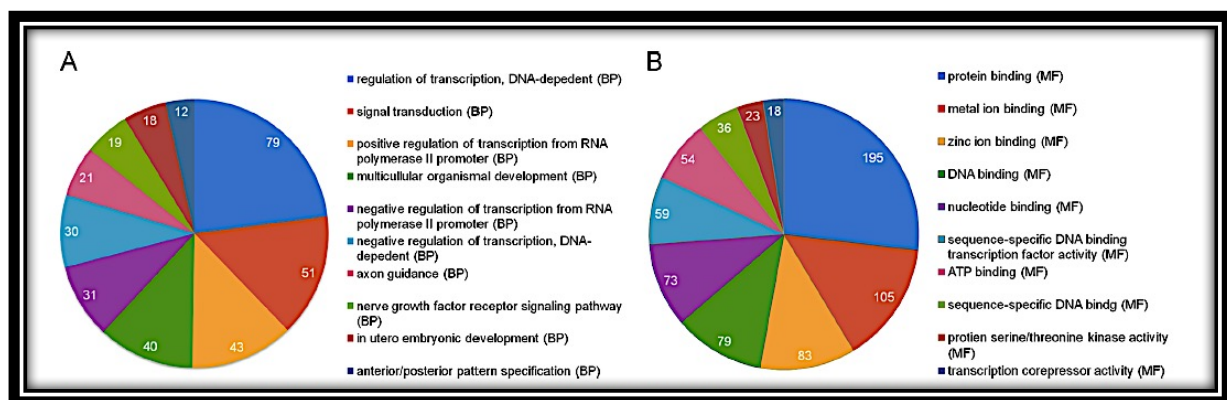


miR-181 family in regulating vascular inflammation and immunity, Publication: Trends in Cardiovascular Medicine, License Number: 3821581367364.

The distinct activities of miR-181a and miR-181c are largely determined by their unique pre-miRNA loop nucleotides [48]. Pre-miRNA loop nucleotides play a critical role in controlling the activity of miRNA genes and that members of the same miRNA gene families could have evolved to achieve different activities via alterations in their pre-miRNA loop sequences, while maintaining identical or nearly identical mature miRNA sequences.

### 1.7.2 Role of miR-181 family

Target genes of mir-181 family are involved in various cellular and biological processes, including regulation of transcription, signal transduction, metabolism and synthesis, cellular division, growth, and proliferation (Figure 5) [44]. In terms of molecular functions, miR-181 family target genes are involve in DNA, protein, transcription factor, and metal ion binding (Figure 5) [44]. Pathway analysis reveals that miR-181 family target genes play important role in cancer, axon guidance, actin cytoskeleton, MAPK singlaing, and T cell receptor signaling pathways (Table 1)[44].



**Figure 5. Gene ontology of targets of miR-181 family. A, biological process, and B, molecular function. The indicated numbers are the numbers of the target genes predicted by the Gene**



Ontology method. Reproduced by permission from the following article: Title: Evolution of the mir-181 microRNA family, Publication: Computers in Biology and Medicine, License Number: 3821610198316.

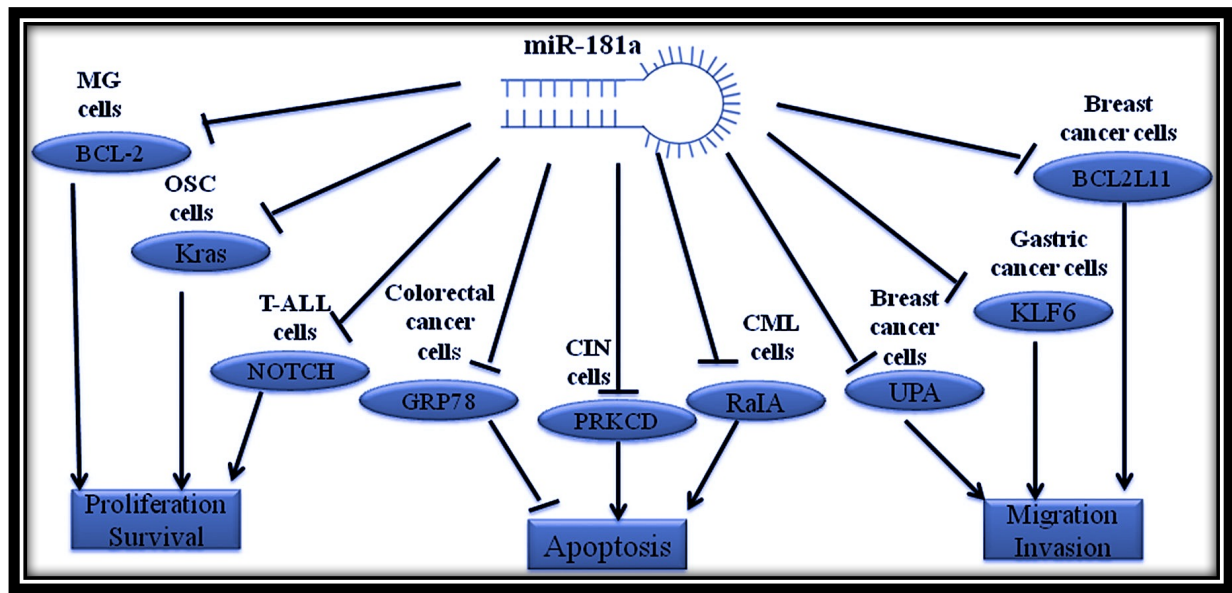
| KEGG pathway                       | Number of genes | Enriched gene ID   | P-value  |
|------------------------------------|-----------------|--|----------|
| Neurotrophin signaling pathway     | 15              | 8660 4215 11108 5580 801 5908 8503 596 3845 5594 10818 7529 818 7532 6197                          | 1.49E-09 |
| Long-term potentiation             | 11              | 801 107 5534 5908 5500 3845 2891 5594 2915 6197 818  | 1.19E-08 |
| Axon guidance                      | 14              | 23380 6092 54910 57144 1808 57715 5534 10512 3845 90249 5594 10725 10298 7869                      | 1.19E-08 |
| Pathways in cancer                 | 20              | 7184 3915 3655 868 11186 7046 3845 1050 2353 2113 5156 10401 5898 3675 8030 8503 596 861 9915 5594 | 3.89E-08 |
| T cell receptor signaling pathway  | 11              | 84433 920 57144 5534 868 8503 3845 2353 5594 10725 10298   | 7.73E-07 |
| Oocyte meiosis                     | 11              | 5529 115 801 107 5534 5500 5594 7529 6197 7532 818   | 1.13E-06 |
| Regulation of actin cytoskeleton   | 14              | 3696 3675 57144 8874 3655 8503 5500 55740 3845 5594 4628 5156 10298 10458                          | 2.63E-06 |
| MAPK signaling pathway             | 15              | 4215 5534 5908 9254 51701 7046 3845 3552 2353 5594 5156 5495 1847 4137 6197                        | 5.64E-06 |
| Focal adhesion                     | 13              | 5170 3696 3915 3675 57144 3655 5908 8503 5500 596 5594 5156 10298                                  | 5.64E-06 |
| Vascular smooth muscle contraction | 10              | 5581 3778 5580 115 801 107 5592 4660 5500 5594   | 6.94E-06 |

**Table 1. Enriched KEGG pathways of the targets of miR-181 family.** Reproduced by permission from the following article: Title: Evolution of the mir-181 microRNA family, Publication: Computers in Biology and Medicine, License Number: 3821610198316.

## 1.8 Role of miR-181a in cancer

The significant role of miR-181a in tumorigenesis is revealed by various studies that show upregulation of miR-181 in colorectal carcinoma [49], invasive cervical squamous cell carcinoma (5) and hepatocarcinoma (6). Multiple studies have evaluated the role of miR-181 in various cellular process such as cell cycle, apoptosis, proliferation, migration and invasion [50]. miR-181a have been shown to regulate Bim [47], Bcl-2 [51], ATM [52], and K-Ras [53]. Figure 6 depicts the various roles of miR-181a and its targets in different types of human cancer [54].





**Figure 6. The multiple roles of miR-181a in hallmarks of human cancer.** Reproduced by permission from the following article: Title: MiR-181a-5p inhibits cell proliferation and migration by targeting Kras in non-small cell lung cancer A549 cells, Publication: Acta Biochimica et Biophysica Sinica, License Number: 3821560608610.

### 1.8.2 miR-181a as an oncomir

miRNAs regulation of their target genes' expression is determined by cell, tissue, hormonal, and temporal effects. For this reason, it is not surprising that miR-181a has been investigated in different types of cancer. For example, it has been shown that miR-181a and its target gene, *PGR* are associated with the transition of endometrial cells to cancerous cells, in a hormonal and temporal context [55]. Authors demonstrate that in the *in vitro* model of endometrial cells, miR-181a directly regulate *PGR* and *PGRMC1* genes and influencing P4-mediated cellular processes [55].

miR-181a is overexpressed in papillary thyroid cancer (PTC) [56, 57]. Specifically, miR-181a expression was increased by 2.6 fold in PTC in comparison with normal thyroid tissue. Moreover, authors show expression data of miR-181a with 4 additional micro-RNAs (miR-221,



miR-222, miR-146, miR-21) is sufficient to accurately predict cancer status [57]. Moreover, it has been shown that in esophageal squamous cell carcinoma (ESCC) miR-181a expression is significantly up-regulated in comparison with normal adjacent specimens [58].

Overexpression of miR-181a is implicated in gastric cancer development [50]. In gastric cancer cell lines miR-181a mimic overexpression increased the proliferation and clonogenicity of the cancer cells. By using a luciferase assay reporter, authors show that miR-181a directly target *KLF6* gene, a member of zinc-finger transcription factors, and reduces the expression of this tumor suppressor gene [50]. Figure 6 depicts the various roles of miR-181a and its targets in different types of human cancer [54].

### **1.8.3 miR-181a as a tumor suppressor**

In glioblastoma multiforme (GBM), three members of miR-181 family (miR-181a, miR-181b, and miR-181c) are all identified as tumor suppressors [59]. These miRs were significantly down-regulated in glioblastoma compared to normal brain controls. miR-181a and miR-181b are enriched in brain. Authors hypothesized that since these three miR-181 genes are located on distinct chromosomes, their simultaneous downregulation may stem from their role in modulation of an important common target gene [59].

In non-small cell lung cancer (NSCLC) miR-181a expression is down-regulated. Authors show that miR-181a could significantly decrease the colony formation and decrease migration in A549 cells by targeting *KRAS* and reducing its expression at both RNA and protein levels [54].

miR-181a is expressed in various types of leukemia, specifically, in chronic myelogenous leukemia (CML) it has been shown that miR-181a has a tumor suppressor function [60]. By using K562 cells, authors show that miR-181a levels are suppressed in CML and perhaps it plays an



important role in its pathogenesis. They show that miR-181a overexpression can induce apoptosis through *RalA*, a member of Ral family small G proteins [60].

### **1.8.3 miR-181a is a prognostic marker in cancer**

In colorectal cancer (CRC) miR-181a is associated with poor prognosis [61]. Patients with high expression of miR-181a have decreased disease-free survival time and poorer prognosis. In CRC patients, miR-181a expression was not differentially expressed with respect to the gender, age, and tumor grade, including distal metastasis [61]. In CRC, miR-181a overexpression results in significant suppression of phosphatase and tensin homologue (PTEN) with ultimately resulting in downregulation of PTEN/Akt pathway [61].

In contrast to CRC, in ESCC, miR-181a expression correlates with TNM staging. Patients with metastasis to lymph nodes had higher miR-181a levels in comparison with those without any metastasis to the lymph nodes [58]. miR-181a overexpression was identified as an independent risk factor for overall survival and cancer recurrence in ESCC patients [58]. Authors suggest *Thymosin  $\beta$ 10* and *RECK*, a tumor suppressor gene, as potential direct targets of miR-181a and their role in pathogenesis of ESCC [58]. In cholangiocarcinoma (CCA), cell migration and metastasis increases as the result of *Thymosin  $\beta$ 10* suppression, which may be mediated by upregulation of Ras, ERK1/2 signaling as well as upregulation of Snail and MMPs [62].

miR-181 family has been implicated in regulating the differentiation of B, T, and NK cells. In acute myeloid leukemia (AML) miR-181a serves as both a diagnostic and a prognostic marker [45]. A 2013 meta-analysis shows that in hematological malignancies, low expression of miR-181a/b is associated with poor overall survival and can serve as an important clinical prognostic factor in those patients; however the exact mechanism of their action remains largely unknown [63].



In a recent meta-analysis of 21 studies involving 1685 patients, elevated levels of miR-181a has been identified as a prognostic molecular marker in the human head and neck squamous cell carcinoma (HNSCC) [64]. Authors, identified elevated expression of miR-181a along with a cohort of six other micro-RNAs (miR-21, miR-18a, miR-134a, miR-210, miR-19a, and miR-155) associated with poor survival in human HNSCC [64].

Similarly, in breast cancer, miR-181a has been recognized as one of the most promising prognostic miRNAs for advanced tumor. Authors show that overexpression of miR-21, miR-181a, and the miR-221/miR-222 cluster is correlated with advanced tumor stage, lymph node metastasis and poor patient survival [65].

#### **1.8.4 Role of miR-181a in epithelial-mesenchymal transition (EMT)**

In prostate cancer, direct transcriptional activation of miR-181a via Lymphoid enhancer-binding factor-1 (LEF1) promotes epithelial-mesenchymal transition (EMT) and invasion [66]. LEF1 is a key transcription factor mediating Wnt signaling pathway [66]. Authors show that combined overexpression of LEF1 and miR-181a has a synergistic effect on reduction of E-cadherin protein levels. They also show a dose-dependent enhancement of migration and invasion in androgen-sensitive human prostate adenocarcinoma cells that are transfected with miR-181a mimic [66].

In murine liver carcinoma model, authors set to investigate the role of mi-RNAs in pathogenesis of TGF- $\beta$ -induced hepatocyte cirrhosis and hepatocellular carcinoma (HCC) [67]. TGF- $\beta$  signaling has an important role in driving EMT and tissue fibrosis leading to hepatic carcinoma. Investigators show that miR-181a is highly expressed in cirrhosis and HCC and has direct effect in induction of EMT in hepatocytes [67].



| a                                   |              |       |                    | b                                   |    |      |
|-------------------------------------|--------------|-------|--------------------|-------------------------------------|----|------|
|                                     | TGF- $\beta$ | Mimic | Inh + TGF- $\beta$ | Assay                               | Up | Down |
| <b>EMT array</b>                    |              |       |                    | <b>TGF-<math>\beta</math> array</b> |    |      |
| ARHGEF9                             | up           | up    | down               | Bmp1                                | up |      |
| CALD1                               | up           | up    | down               | Bmp7                                |    | down |
| CAMK2N1                             | up           | up    | down               | Cald1                               | up |      |
| CDH2                                | up           | up    | down               | Cdkn1b                              |    | down |
| CHD1L                               | up           | up    | down               | Chd1l                               | up |      |
| FN1                                 | up           | up    | down               | Colla2                              | up |      |
| ITGA5                               | up           | up    | down               | Col Sal                             | up |      |
| ITGAV                               | up           | up    | down               | Col5a2                              | up |      |
| ITGB1                               | up           | up    | down               | Epcam                               | up |      |
| MMP2                                | up           | up    | down               | Fnl                                 | up |      |
| MMP3                                | up           | up    | down               | Gng1l                               | up |      |
| MMP9                                | up           | up    | down               | Igfbp4                              | up |      |
| MSN                                 | up           | up    | down               | Ilrn                                | up |      |
| PDGFRB                              | up           | up    | down               | Mmp2                                | up |      |
| PLEK2                               | up           | up    | down               | Mmp9                                | up |      |
| SERPINE1                            | up           | up    | down               | Notch1                              | up |      |
| SIP1                                | up           | up    | down               | Odn                                 |    | down |
| SNAI1                               | up           | up    | down               | Rad                                 | up |      |
| SNAI2                               | up           | up    | down               | Snail                               | up |      |
| TGFB1                               | up           | up    | down               | Wnt5a                               | up |      |
| VIM                                 | up           | up    | down               | Wnt5b                               | up |      |
| WNT5B                               | up           | up    | down               | <b>EMT array</b>                    |    |      |
| CDH1                                | down         | down  | up                 | Acr1                                | up |      |
| CDKN1B                              | down         | down  | up                 | Acr2a                               | up |      |
| MST1R                               | down         | down  | up                 | Bmp7                                |    | down |
| NUD11.3                             | down         | down  | up                 | Bmper                               | up |      |
| TFPI2                               | down         | down  | up                 | Bmpr2                               |    | down |
| TGFB2                               | down         | down  | up                 | Chrd                                |    | down |
| TGFB3                               | down         | down  | up                 | Cull                                | up |      |
| TSPAN13                             | down         | down  | up                 | E2f5                                |    | down |
| <b>TGF-<math>\beta</math> array</b> |              |       |                    | Ep300                               | up |      |
| BMIPER                              | up           | up    | down               | Fmod                                |    | down |
| FNTA                                | up           | up    | down               | Fnta                                |    | down |
| LTBP4                               | up           | up    | down               | Gdf2                                | up |      |
| SKP1                                | up           | up    | down               | Hipk2                               | up |      |
| TGFB1                               | up           | up    | down               | Ltbp3                               | up |      |
| TGFBRI                              | up           | up    | down               | Rbl1                                |    | down |
| TGFBRAPI                            | up           | up    | down               | Smad1                               |    | down |
| TNF                                 | up           | up    | down               | Smad2                               |    | down |
| BMIP5                               | down         | down  | up                 | Smad9                               | up |      |
| E2F5                                | down         | down  | up                 | Smurf1                              |    | down |
|                                     |              |       |                    | Tab1                                | up |      |
|                                     |              |       |                    | Tsc22d1                             |    | down |

**Table 2. Upregulated and downregulated genes in response to TGF- $\beta$  and miR-181a.** a) TGF- $\beta$  and EMT genes that were up- or down-regulated with miR-181a mimic or inhibitor in vitro or in vivo, b) Mice expressing rAAV miR-181a for 4 weeks showed up or down-regulation of TGF- $\beta$  or EMT genes. Reproduced by permission from the following article: Title: Title: miR-181a mediates TGF- $\beta$  induced hepatocyte EMT and is dysregulated in cirrhosis and hepatocellular cancer, Publication: Liver International, License Number: 3826070700895.



In ovarian cancer, miR-181a plays a critical role in EMT, resulting in ovarian cancer progression. In ovarian carcinomas, the chromosomal region of 1q is referred to as a “hotpot” due to amplification of this locus in tumors, interestingly, miR-181a gene resides in this chromosomal region [68]. Authors show that miR-181a suppresses Smad7, leading to upregulation of TGF- $\beta$  signaling pathway and resulting in enhancement of EMT [68].

miR-181a expression levels are upregulated in triple-negative breast cancers (TNBCs) and corresponds to decreased overall survival in patients. Authors show that miR-181a increases metastasis in breast cancer patients, partially by enhancing Erk1/2, Akt, and Src signaling pathways. They also show that pre-miR-181a levels are expressed in a Smad4-dependent manner; whereas, the mature miR-181a levels were modulated in Smad4-independent manner. Authors were unable to comment on the relative contribution of both transcriptional and post translational mechanisms and their effect on modulation of miR-181a levels [47].

## **1.9 TGF $\beta$ pathway**

The role of the TGF $\beta$  pathway in development of primary epithelial tumors has been well established through detection of mutations in TGF- $\beta$ , its receptors, and its downstream signaling molecules [69]. The effect of aberrant TGF $\beta$  signaling in skin carcinogenesis has been studied in a mouse model [70]. TGF $\beta$  belongs to family of growth factors that regulate cell differentiation, migration, adhesion, and cell cycle progression. TGF $\beta$  also modulates processes such as embryonic development, wound healing, and angiogenesis.

Most cells express three types of TGF $\beta$  receptors. Type I Receptor, 53 kDa, is a Serine/threonine kinase and is activated by phosphorylation by the type II receptor. Type II Receptor, 75 kDa, is a constitutive serine kinase and related in sequence to Type I receptor. Type I and II receptors are membrane-bound serine/threonine kinases and they require each other to



bind TGF- $\beta$  ligand. They form a heterodimeric complex that is essential for the signal transduction [71, 72]. The Type III receptor is a transmembrane proteoglycan with a large extracellular domain and a 43 amino acid residue cytoplasmic domain. The cytoplasmic domain of the Type III receptor lacks an obvious signaling motif and the receptor may not be involved directly in signal transduction [72].

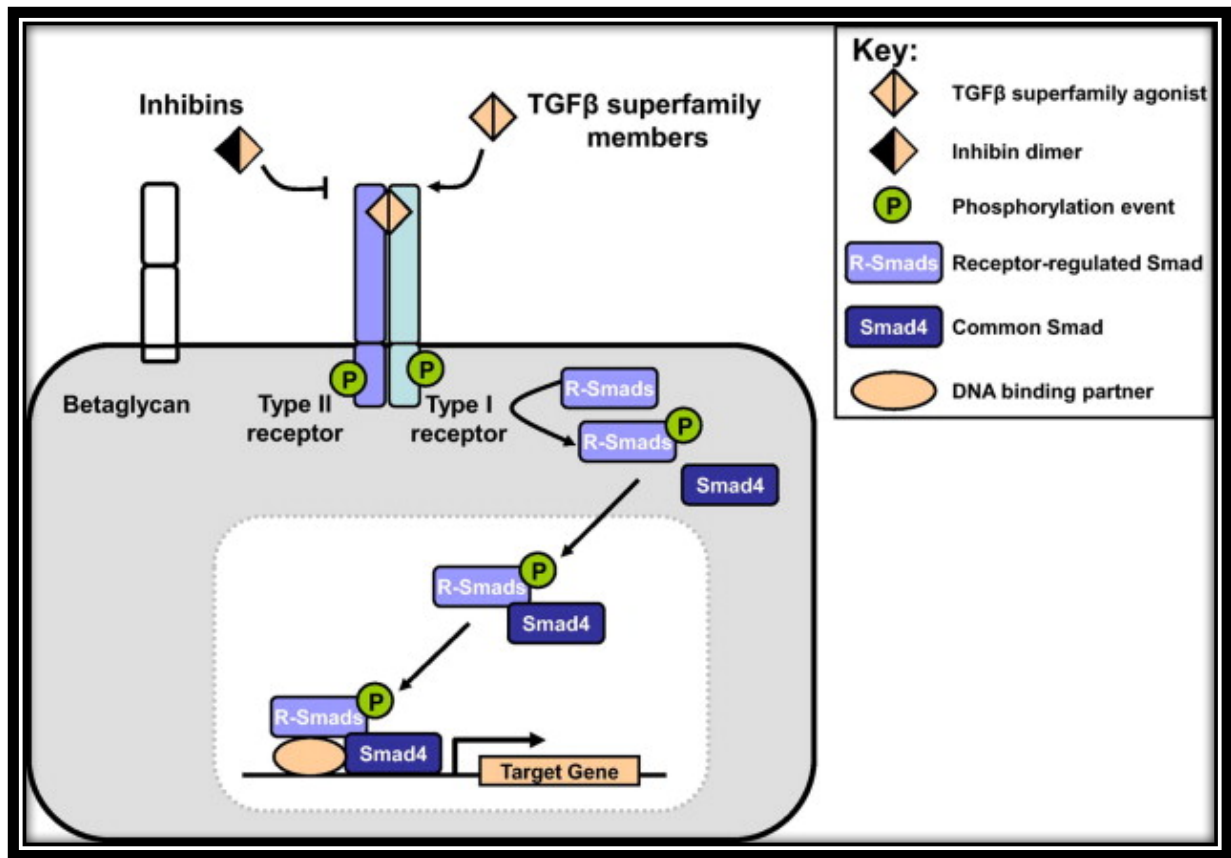
### **1.9.1 Canonical Smad TGF- $\beta$ signaling pathway**

There are 2 types of TGF- $\beta$  signaling pathways: canonical and non-canonical, and they are sometimes referred to as adhesion-independent and adhesion-dependent TGF- $\beta$  signaling pathways. Canonical TGF- $\beta$  signaling pathway is primarily mediated by rapid phosphorylation and activation of Smad proteins. Type I and type II serine/threonine-kinase transmembrane receptors hetero-dimerize and result in activation of intracellular Smads. To date, five type II and seven type I receptors have been identified. There are three groups of Smad proteins: receptor-regulated (R-Smad), common-mediator (Co-Smad), and inhibitory (I-Smad). There are three types of ligand categories: TGF- $\beta$  ligands (1, 2 and 3) result in activation of TGFBR1/ALK5 and TGFBR2. Activins signal through ACVR2A, IIB and ALK4. BMPs signal through BMPR2, ACVR2 s and ALK1/2/ 3 and 6. Inactive precursors of TGF- $\beta$  family dimerize and are cleaved by proteases, which in part impacts the the bioavailability of TGF- $\beta$  ligands. On the other hand, BMPs are secreted in their active form and interactions with extracellular antagonists impact their bioavailability. Ligand receptor interactions are regulated by two accessory receptors: namely; endoglin and betaglycan (TGFBR3).

Type I receptor recruits and phosphorylates R-Smads at their serine residues resulting in their activation. Different R-smads are activated by different receptors; for example, ALK4/5/7



receptors result in activation of R-Smads 2/3. On the other hand, ALK1/2/3/6 receptors result in activation of R-Smads 1/5/8. Activated R-Smads translocate into the nucleus with co-Smad4, where they regulate transcription of their target genes. I-Smads6/7 can result in a negative feedback loop and inhibit the activation of R-smads. I-Smads also recruit ubiquitin ligases and phosphatases and target R-smads for proteasomal degradation and dephosphorylation.



**Figure 7. TGFβ superfamily signaling pathway.** The diverse actions of the TGFβ superfamily of growth and differentiation factors are mediated by pairs of serine-threonine kinase type I and type II receptors. In the canonical signaling pathway, agonists bind to specific sets of type I and type II receptors on the cell surface, which results in the phosphorylation and activation of downstream signaling molecules, the receptor regulated (R-)SMADs. Activated R-SMADs then associate with the common co-SMAD, SMAD4, and translocate to the nucleus where, in

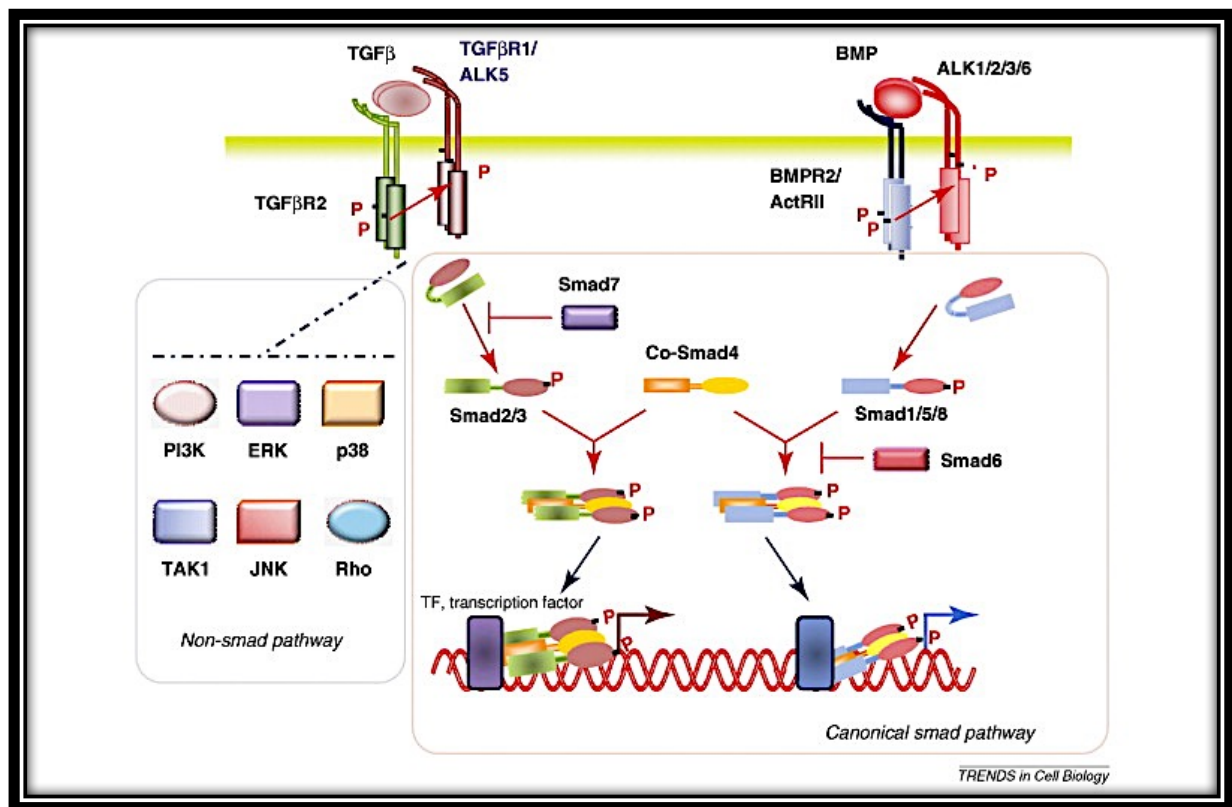


combination with cell-type specific binding partners, they regulate gene transcription and cellular function. The membrane-bound form of the accessory receptor, betaglycan, increases the binding of its ligands, the TGF $\beta$ s, inhibins, and BMPs, to their signaling receptors. This generally enhances the signaling of TGF $\beta$ s and BMPs and enhances the ability of inhibins to block the functions of other TGF $\beta$  superfamily members. Reproduced by permission from the following article: Title: Betaglycan: A multifunctional accessory, Publication: Molecular and Cellular Endocrinology, License Number: 3821680479598.

### **1.9.2 Non-canonical TGF- $\beta$ signaling pathway**

In addition to SMAD mediated pathway, TGF- $\beta$  receptor activation causes non-Smad mediated cross-talk with other signaling pathways. These pathways include: Wnt signaling through B-catenin, MAP kinase, STAT1, and NF- $\kappa$ B induced Smad7 expression, leading to inhibition of TGF- $\beta$ -induced Smad2/3 activation. JNK and p38 MAP kinase signaling leads to phosphorylation of transcription factors with which SMADs can cooperate at defined promoters. FAK autophosphorylation and activation is delayed relative to Smad signaling. It is associated with TGFB1-induced expression of both integrin subunits, fibronectin and collagens. Integrin signaling via FAK activation is essential for induction and maintenance of differentiated myofibroblast phenotype.





**Figure 8. Non-canonical signal transduction by TGF- $\beta$  family members.** In addition, to the canonical signal pathway, the activated type I receptors can activate non-Smad pathways. ALK, activin receptor-like kinase; BMP, bone morphogenetic protein; BMPR, BMP receptor; ERK, early response kinase; PI3K, phosphoinositide 3-kinase; TAK, TGF- $\beta$ -activated kinase; TGF- $\beta$ , transforming growth factor  $\beta$ ; TGFBR, TGF- $\beta$  receptor. Reproduced by permission from the following article: Title: Signaling by members of the TGF- $\beta$  family in vascular morphogenesis and disease, Publication: Trends in Cell Biology; License Number: 3824251064413.

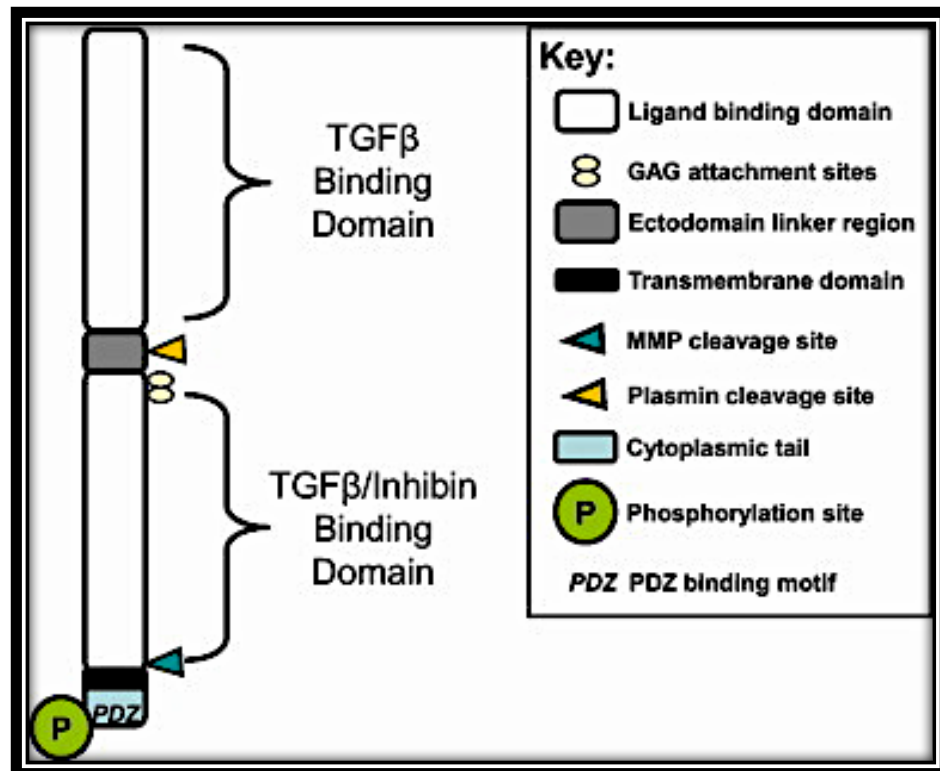
### 1.10 TGFBR3 background

TGF- $\beta$  Type III receptor (TGFBR3) is also known as betaglycan. TGFBR3 lacks a signaling domain; However, it regulates TGF $\beta$  signaling by presenting the TGF $\beta$  ligand to the type II receptor.



### 1.10.1 TGFBR3 structure

The human TGFBR3 gene has 16 coding exons and two promoters; a proximal promoter and a distal promoter. TGF- $\beta$ 1 ligand can modulate TGFBR3 expression through direct inhibition of the proximal promoter. TGFBR3 gene produces a ~4200 bp mRNA resulting in a 250 - 350 kDa protein that has multiple binding sites for activin, fibroblast growth factor and heparin. Figure 9 shows TGFBR3 (betaglycan) structure and its unique features [72].



**Figure 9. Structure of TGFBR3 (betaglycan).** Structural features of the full-length form of betaglycan, depicting key binding domains, enzymatic cleavage sites, and intracellular residues important for the association of adaptor proteins. Proteolytic cleavage events and differential post-translational modification of the GAG side chains in specific cellular contexts results in the generation of multiple forms of betaglycan, the functions of which are poorly understood. MT1-MMP, MT3-MMP, or a related protease can cleave the ectodomain near the transmembrane region to generate a soluble receptor, capable of binding ligand. Plasmin has been shown to cleave



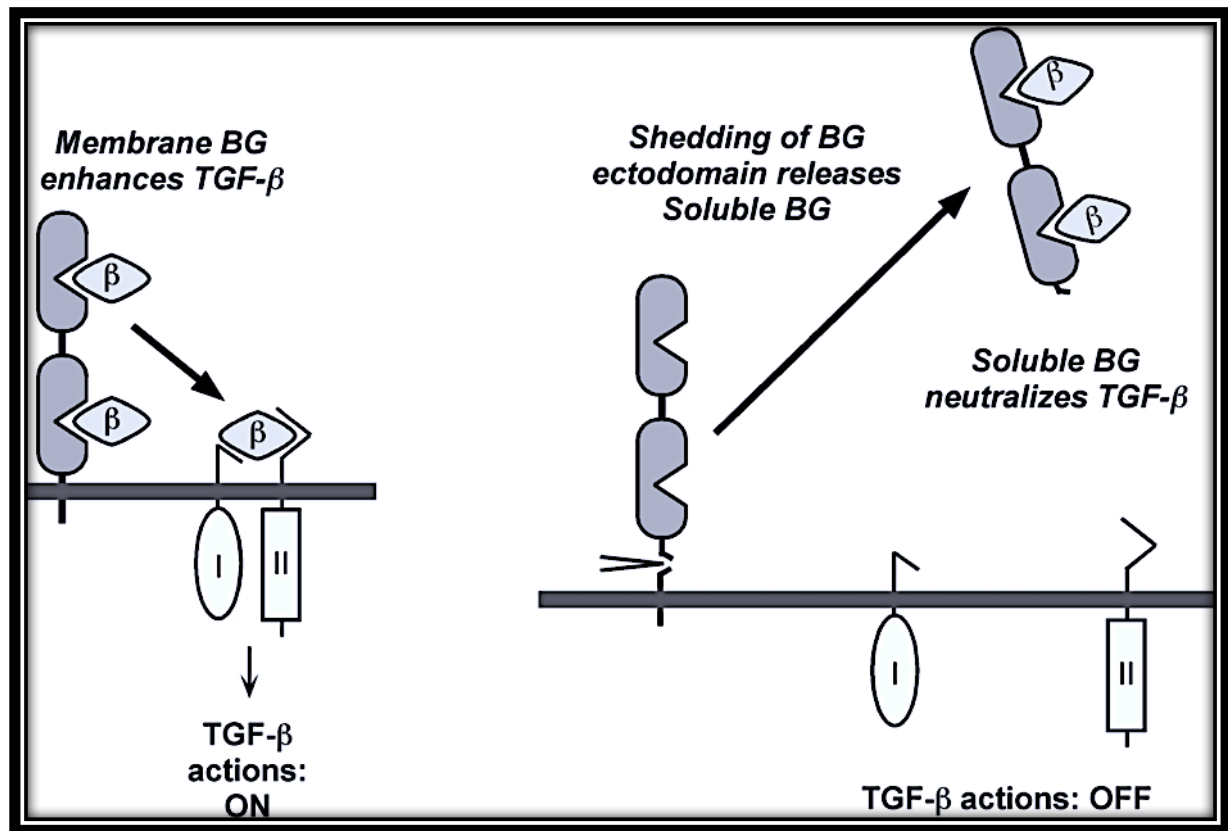
the linker region of the soluble receptor, generating two fragments with reduced ability to bind ligand. Reproduced by permission from the following article: Title: Betaglycan: A multifunctional accessory, Publication: Molecular and Cellular Endocrinology, License Number: 3821680479598.

### **1.10.2 TGFBR3 dual modulation of TGF- $\beta$ pathway through ectodomain shedding**

TGFBR3 signaling pathway has a diverse roles in human disease, with both increases and decreases in its signaling pathways resulting in human disease [71]. Dual role of TGFBR3 has resulted in a lot of confusion in the field, leading to publications such as unraveling the ‘TGF- $\beta$  paradox’ one metastamir to shine light at the discrepancies found among different studies [73].

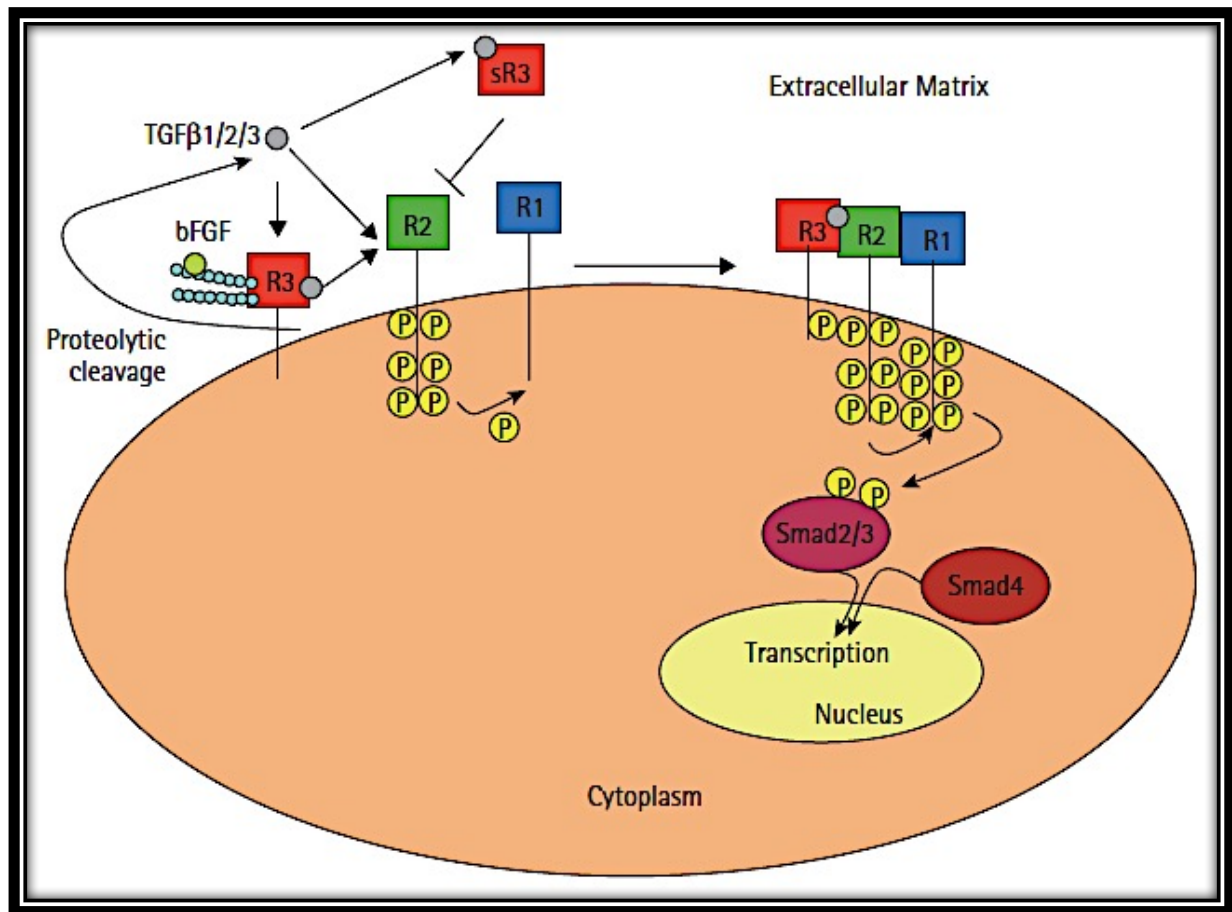
Ectodomain shedding or juxtamembrane proteolytic cleavage of TGFBR3 extracellular domain results in soluble TGFBR3 (sTGFBR3), which is a potent neutralizing agent of TGF $\beta$  [74]. Membrane betaglycan also serves as the precursor for a soluble form of the receptor. Soluble betaglycan (SBG) is shed from the membrane-bound receptor by constitutive and regulated proteolytic cleavages of its extracellular region. In contrast to membrane betaglycan, SBG inhibits TGF- $\beta$  binding to kinase receptors and thereby works as a TGF- $\beta$  antagonist.





**Figure 10. TGFBR3 dual modulation of TGF- $\beta$  pathway.** TGFBR3, potentiates TGF- $\beta$  actions when it is membrane bound. Shedding of BG extracellular region generates the soluble form of the receptor. Soluble BG still binds TGF- $\beta$  with the high affinity of the membrane BG, but instead of “presenting” it to the type II receptor, soluble BG “sequesters” it and therefore neutralizes its actions. Unique among other TGF- $\beta$  inhibitors is the fact that BG may be subject to regulated shedding of its ectodomain, making possible, in principle, control of the relative ratio of the membrane and soluble forms of the receptor, providing a way to switch TGF- $\beta$  actions on or off. Reproduced by permission from the following article: Title: Soluble betaglycan reduces renal damage progression in db/db mice, Publication: Am J Physiol-Renal Physiology, Publisher: The American Physiological Society.





**Figure 11. The role of TGFβR3 in normal cell homeostasis.** TGFβR3 binds TGFβ, and transfers the ligand to the TGFβR2 receptor followed by TGFβR1 binding and phosphorylation. This results in phosphorylation of Smads and subsequent transcription. sTGFβR3 also binds TGFβ ligand, preventing signalling through the TGFβR2 receptor, and binds bFGF through proteoglycan chains on the cytoplasmic domain. Reproduced by permission from the following article: Title: More than an accessory: implications of type III transforming growth factor-β receptor loss in prostate cancer, Publication: BJU International, License Number: 3826561293305.



### 1.10.3 Role of TGFBR3 in human cancer

In recent years, TGFBR3 role as a tumor suppressor has been recognized in breast, lung, ovarian, pancreatic and prostate cancer [75]. Most importantly, loss of TGFBR3 correlates with cancer advancement and its been shown that there is a progressive loss of TGFBR3 expression with breast cancer succession. Through allelic imbalance and loss of heterozygosity (LOH), TGFBR3 expression on average decreases about 88% from normal breast to primary breast cancer and further decreases about 61% in transformation to metastatic breast cancer [76]. TGFBR3 downregulation as a target for miR-103 in high-risk head and neck squamous cell carcinomas (HNSCCs) has been reported [77, 78].

| Cancer       | T $\beta$ RIII expression (mechanism)  | Effects on signaling | Proliferation | Migration    | Invasion     | Angiogenesis | In vivo/other T $\beta$ RIII effects   |
|--------------|--|----------------------|---------------|--------------|--------------|--------------|--|
| Breast       | Decreased (LOH)                        | Decreased            | No effect     | Decreased    | Decreased    | Decreased    | Xenograft: Reduced tumor invasiveness, angiogenesis, metastasis; sT $\beta$ RIII reduces tumor growth, angiogenesis, metastasis        |
| Lung (NSCLC) | Decreased (LOH)                        | No effect            | No effect     | Decreased    | Decreased    | Decreased    | Xenograft: Reduced tumor incidence, growth, & invasiveness   |
| Prostate     | Decreased (LOH; epigenetic regulation) | Not examined         | No effect     | Decreased    | Decreased    | Decreased    | Xenograft: Reduced tumor incidence, & growth; sT $\beta$ RIII reduced tumor growth, angiogenesis, & MMP induction, increased apoptosis |
| Pancreatic   | Decreased                              | Decreased            | Not examined  | Decreased    | Decreased    | Not examined | Decreased MMP Induction  |
| Ovarian      | Decreased (Epigenetic regulation)      | Not examined         | Not examined  | Decreased    | Decreased    | Not examined | Decreased MMP Induction  |
| Renal        | Decreased                              | Decreased (p38)      | Not examined  | Not examined | Not examined | Decreased    | Xenograft: Reduced tumor growth, increased apoptosis   |

**Table 3. Role of TGFBR3 in human cancer.** Reproduced by permission from the following article: Title: Roles for the type III TGF-B receptor in human cancer, Publication: Cellular Signalling, License Number: 3821690136482.

### 1.10.4 Role of TGFBR3 in epithelial-mesenchymal transformation (EMT)

TGFBR3 regulates epithelial-mesenchymal transformation in cardiac endothelial cells [79]



and its downregulation in capillary plexus is associated with infantile hemangioma [80]. There is evidence that loss of TGFBR3 results in increased motility and invasion both in vitro and in vivo. Mechanistic studies have shown that generation of sTGFBR3 mediates the effects of TGFBR3 in reduction of breast cancer cell invasion and metastasis [76].

#### **1.10.5 Role of TGF- $\beta$ pathway in regulation of miR-181a**

Parikh et al show that concomitant overexpression of p-Smad2 (a direct readout of TGF $\beta$  signaling intensity) and miR-181a (a trigger of TGF  $\beta$  pathway) was associated with poor response to neoadjuvant chemotherapy (NACT)[68] . miR-181a expression is upregulated by TGF- $\beta$  and correlates with the metastatic potential of breast cancer cells. Inhibition of miR-181a attenuates TGF- $\beta$ -mediated EMT, invasion, and migration. miR-181a expression enhances Erk1/2, Akt, and Src signaling in breast cancer cells [47].

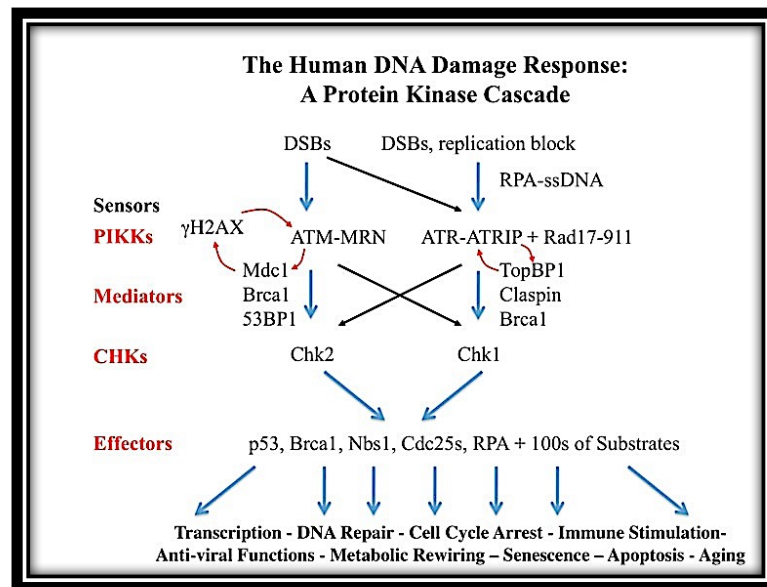
#### **1.11 The DNA Damage Response**

Environmental factors and oxidative stress can cause DNA damage, at a rate of 1,000 to 1,000,000 molecular changes per cell/day, constituting 0.000165% of the human genome's. DNA damage in important genes such as (tumor suppressors, oncogenes, and etc) can cause severe downstream consequences such as blockages of transcription/replication and mutagenesis [81-83]. UV-induced DNA damage falls into two major classes: cyclobutane-pyrimidine dimers (CPDs and 6-4 photoproducts. There are multiple types of DNA repair. In human cells, UV-induced DNA lesions are normally removed by nucleotide excision repair (NER). The NER pathway is composed of two subpathways: transcription coupled repair, which removes lesions present in the transcribed strand of actively transcribing genes, and global genomic repair (GGR), which removes lesions from the rest of the genome. NER-deficient cells are hypersensitive to UV-induced apoptosis. Also, removal of photolesions by photolyase was shown to prevent apoptosis



indicating that unrepaired DNA lesions are the main cause of UV-induced apoptosis in mammalian cells. The role played by p53 on NER has been studied extensively. p53 accumulates in a dose-dependent manner in cells exposed to UV light through post-transcriptional mechanisms. Over the past few years, it has been shown that p53, or its regulated gene products, contributes to the repair of UV-C-induced DNA damage in human cells, because it regulates the expression of XPC and DDB2, proteins belonging to the GGR pathway of NER. Figure 12 depicts the DNA damage response and all the protein kinases involved in the pathways.

Tumor suppressor, Ataxia Telangiectasia Mutated (ATM) is one of the top pathways identified that responses to DNA stress. Also, ATM regulates DNA repair factors such as Rad50, Rad51, and GADD45 [84]. As a result of ionizing radiation and in presence of DNA double strand breaks (DSBs) MRE11-Rad50-NBS1 complex or 53BP1 activate ATM; auto-phosphorylation of ATM dimer/multimer leads to its monomerization and activation. ATM regulates cell cycle through phosphorylation of Chk2 and p53. ATM regulates DNA repair through phosphorylation of SMC1 and histone H2AX [84].



**Figure 12. The human DNA damage response is a protein kinase cascade.** Reproduced by permission from the following article: [http://elledgelab.med.harvard.edu/?page\\_id=264](http://elledgelab.med.harvard.edu/?page_id=264).



# **Chapter 2**

## **Materials and Methods**



## **2.1 Human tissue samples**

We have established collaborations with multiple groups for obtaining our matched human samples including Tri Nguyen, MD (Northwest Diagnostic Clinic, Houston, TX), Valencia Thomas, MD and Michael Migden, MD (MD Anderson, Dermatology), and Aaron Joseph, MD (Skin and Laser Surgery Associates, Pasadena, TX).

We have an established laboratory IRB protocol (LAB08-0750) for collecting human skin tumor samples that has accumulated over 200 cuSCC from human patients. These samples are validated by histologic analysis, and we have successfully processed these to yield sufficient RNA appropriate for analysis (RIN > 9.0). For this study, we have already extended the protocol to enable collection of Actinic Keratoses (AKs) and adjacent normal skin as well as saliva samples for genomic DNA isolation.

## **2.2 Mouse model of UV-driven cuSCC**

To model UV-driven cuSCC under controlled conditions, we exposed SKH1-E Hairless mice to chronic low-dose UV (12.5 kJ/m<sup>2</sup> UVB total weekly divided in 3 doses M, W, F) using solar simulators (Oriel) starting at 3 months of age. In this strain, 5.0 kJ/m<sup>2</sup> UVB is about 0.5 to 1 mean erythral dose<sup>47</sup>. In this model of UV-driven cuSCC development, we irradiated the mice for 72 days. Papillomas were observed within 100 days of irradiation and were histologically well-differentiated. Some progressed to invasive cuSCC and although the kinetics of lesion development were similar.

## **2.3 DNA isolation from saliva and tissue for exome sequencing**

We used DNA Genotek ORAgene saliva collection kits and followed manufactures' collection and storage instructions (catalog # OG-500). Genomic DNA was isolated from saliva



samples using DNA Genotek prepIT•C2D (PT-C2D) extraction columns and manufacturers' protocol. PureLink Genomic DNA mini kits were used to extract DNA from tissue samples (Cat # K1820-01). Briefly, tissue specimens were minced and incubated overnight (55OC) in PureLink genomic digestion buffer and proteinase K. Manufacturer's protocol was followed for purification using the spin columns. 2ug of DNA per sample was submitted to MD Anderson DNA Analysis Facility for sequencing (Illumina HiSeq200, 76nt PE).

#### **2.4 Preparation of specimens for mRNA and miRNA Illumina Sequencing**

Tissue specimens (500-1000 mg) were homogenized with an Omni rotor stator homogenizer in Trizol (Invitrogen Cat # 15596018). Total RNA was extracted according to the manufacturer instructions. RNA purification was carried with Purelink RNA kit (Invitrogen Cat #12183018A). 4-10ug of RNA per sample was submitted to MD Anderson DNA Analysis Facility for 76-nucleotide paired-end sequencing by Illumina HiSeq2000. Also, same samples were submitted to the laboratory of Dr. Preethi Gunaratne, PhD (University of Houston, Biology & Biochemistry) for miR-sequencing.

#### **2.5 Quantitative real-time PCR validation analysis**

Separate cohorts of matched samples from patients consisting of NS, AK, and cuSCC were processed as above. Taqman (Life Technologies) probes were acquired for human miR-21, miR-31, PTPN14, FAM134B, HMG2A, TIMP3, and ARHGAP24 and used in qRT-PCR based quantitation of expression in these tissues, as benchmarked to RNU6B (microRNA) and 18S rRNA (mRNA).



|                   |          |  |
|-------------------|----------|--|
| Life Technologies | 4331182  | TaqMan mRNA probe for TIMP3 (Hs00165949_m1)    |
| Life Technologies | 4331182  | TaqMan mRNA probe for TGFBR (3Hs00234257_m1)   |
| Life Technologies | 4331182  | TaqMan mRNA probe for HMGA2 (Hs00171569_m1)    |
| Life Technologies | 4331182  | TaqMan mRNA probe for ARHGAP24 (Hs01097580_m1) |
| Life Technologies | 4331182  | TaqMan mRNA probe for PTPN14 (Hs00193643_m1)   |
| Life Technologies | 4331182  | TaqMan mRNA probe for FAM134B (Hs00375273_m1)  |
| Life Technologies | 4326317E | Human GAPDH Endogenous Control                 |
| Life Technologies | 4331182  | TaqMan mRNA probe for 18S (Hs99999901_s1)      |
| Life Technologies | 4304437  | TaqMan Universal MasterMix for mRNA            |
| Life Technologies | N8080234 | TaqMan Reverse Transcription kit for mRNA      |

**Table 4. List of TagMan mRNA probes used in the study.**

|                   |         |  |
|-------------------|---------|--|
| Life Technologies | 4427975 | ID # 001043 TaqMan QRTPCR probe for hsa-miR-497  |
| Life Technologies | 4427975 | ID # 000397 TaqMan QRTPCR probe for hsa-miR-21   |
| Life Technologies | 4427975 | ID # 000480 TaqMan QRTPCR probe for has-miR-181a |
| Life Technologies | 4427975 | ID # 000482 TaqMan QRTPCR probe for has-miR-181c |
| Life Technologies | 4427975 | ID # 000524 TaqMan QRTPCR probe for has-miR-221  |
| Life Technologies | 4427975 | ID # 000397 TaqMan QRTPCR probe for hsa-miR-21   |
| Life Technologies | 4427975 | ID #002279 TaqMan QRTPCR probe for has-miR-31    |
| Life Technologies | 4440887 | ID# 001093 RNU6B Control miRNA assay human       |
| Life Technologies | 4324018 | TaqMan Universal MasterMix for microRNA QRTPCR   |
| Life Technologies | 4366596 | TaqMan MicroRNA Reverse Transcription Kit        |

**Table 5. List of TagMan miRNA probes used in the study.**



## **2.6 Cell Lines**

A panel of eleven cutaneous squamous cell carcinoma (cuSCC) cell lines (SCC IC1, SCCT1, SCCT2, SCCT3, SCCT8, SCRDEB2, SCRDEB3, SCRDEB4, SRB1, SRB12, and COLO16) were obtained from various investigators, including Dr. Jeffrey N. Myers (MD Anderson). HaCaT cells, an immortalized human keratinocyte line cell was obtained from Norbert Fusenig (German Cancer Research Center). Normal Human Epidermal Keratinocytes (NHEK) cell line was purchased from Lonza Walkersville, Inc. Using the commercially available STR DNA fingerprinting system our cell lines we validated by the AMPFISTR SGM PlusE system according to manufacturer instructions (Applied Biosystems). We compared the STR profiles to known ATCC fingerprints (ATCC.org), to the Cell Line Integrated Molecular Authentication database (CLIMA) (<http://bioinformatics.istge.it/clima/>) and to the MD Anderson fingerprint database. The STR profiles matched known DNA fingerprints (HaCaT) or were unique (SRB1, SRB12, COLO16).

## **2.7 Culture and UV irradiation**

Cutaneous squamous cell carcinoma (cuSCC) cell lines (SRB1, SRB12, COLO16, etc) and HaCat cells were maintained and cultured in DMEM/Ham's F12 50/50 (Cellgro) supplemented with 10% Fetal Bovine Serum (FBS) (Sigma), glutamine, and Primocin (Invivogen). NHEKs (Lonza) were cultured in media according to manufacturer's instructions. All cells were maintained at 37°C in a 5% CO<sub>2</sub> incubator. UV irradiation experiments are to be carried by using an FS-40 sunlamp (0.5%UVC, 60% UVB, 40%UVA) that is dosed by an IL1700 radiometer. cuSCC cells and primary keratinocytes to be seeded at density of 400,000-750,000 cells per 10-cm diameter dishes. Following seeding, cells were allowed to attach and proliferate for 24 h. Next, cells were washed 2 times with Phosphate Buffered Saline (PBS) and irradiated at



0, 250, 500, 750, and 1000 J/m<sup>2</sup> and media replenished. Protein lysates and RNA were obtained at 6, 24, and 48hr post irradiation.

## **2.8 Flow cytometry (Fluorescence-activated cell sorting-FACS)**

TMRE (Invitrogen) was used as a measure of mitochondrial membrane potential, Annexin V-FITC or Annexin V-APC (Invitrogen) as a probe for apoptosis, and Cytox Blue (Invitrogen) as an indicator for dead cells. At 6, 24, or 48 hours post-irradiation, both floating and adherent cells were collected and stained with TMRE, Annexin V and Cytox Blue. Data were collected and analyzed using a flow cytometer (FACScalibur, Becton Dickinson) and FlowJo Software (Tree Star). Data were calculated and charts were plotted using GraphPad Prism 5 software.

## **2.9 Transfection**

All miRNA inhibitors and mimics transfections were performed using RNAiMAX (Invitrogen, Carlsbad, CA, USA) reagent following the forward transfection protocol from the manufacturer. Plasmid DNA transfection were performed using Lipofectamin 3000 reagent (Invitrogen, Carlsbad, CA, USA). To minimize toxicity, media was changed 6 h after transfections.

## **2.10 Cell invasion assay**

HaCat and RDEB2 cells were starved 48h prior to the assay. Cells ( $3.5 \times 10^5$ ) suspended in serum-free media were added into the upper compartments of Control Insert 24-well Plate (Corning 354578) and Matrigel-coated invasion chamber (Corning 354480). Complete media contain 30% FBS was added to the lower compartments as a chemo-attractant for cells.



Thereafter, cells were allowed to migrate and invade for 24 to 48 hours at 37°C. Cells remaining on the upper side of the membrane were removed with cotton swabs. Cells that migrated and invaded to the bottom side of the membrane were fixed and stained with Diff-Quik Stain Set (Siemens B4132-1A). The membranes were air-dried and mounted for photography. Cells from ten random fields were counted.

### 2.11 Overexpression of TGFBR3

pDONR223-TGFBR3 donor vector containing TGFBR3 ORF was purchased from Addgene, plasmid # 23478 [85]. The ORF were cloned into pcDNA3.1/V5 expressing vectors using Gateway technique. All vectors were validated by Sanger sequencing. TGFBR3 expression was validated by western blot.



**Figure 13. Vector backbone pDONR223.** Backbone manufacturer: Invitrogen, Backbone size w/o insert (bp): 5005, Cloning method: Gateway Cloning, Insert Size (bp): 2556 and Species: H. sapiens (human).



## 2.12 Lentiviral knockdown of TGFBR3

Lentiviral shRNA knockdown was accomplished using standard lentiviral methods using 293T cells and psPAX2/pVSV.G packaging plasmids. shRNA clones against TGFBR3 (V3LHS\_352448 TGFBR3 **Clone T1** and V3LHS\_352450 TGFBR3 **Clone T2**), as well as a non-silencing shRNA were obtained from Open Biosystems in the GIPZ vector. Following transduction, cells were puromycin-selected and FACS sorted to obtain cells with high-level suppression. Degree of mRNA suppression was quantified by qPCR using Taqman probes using internally controlled (2-color, same well) GAPDH probes to ensure proper normalization.

## 2.13 micro-RNA stable overexpression via lentiviral infection

We obtained lentivirus-based vectors for hsa-miR-181a or scramble sequence (as control) from System Biosciences lenti-miRNA vector bank. In our experiments these vectors are referred to as **Lenti-miR-181a (OE)** and **Lenti-miR-00 (control)** respectively and tagged with green fluorescent protein (GFP) were transfected into 293T cells. We used 2 mg of each vector and lentivirus packaging (pCMV-VSVG) using Fugene HD (Roche) using the manufacturer's protocol.

After transfection of 293T cells, supernatants containing the lentivirus were collected, filtered and added to target cells for 24 h in the presence of Polybrene. For some cell lines, multiple rounds of infection were necessary. At 24-48hr post infection, puromycin (or the antibiotic selection marker) was added to the media and resistant cells were selected. Infection efficiency of the cells was assessed by the % of GFP-expressing cells. Infected cells were analyzed by TaqMan assay to determine the level of miRNA overexpression. These cells were further analyzed by migration and invasion assays. All experiments were performed in triplicate.



|     |   |                 |                |
|-----|---|-----------------|----------------|
| SBI | Human pre-microRNA Expression Construct Lenti-miR-181a-2 MI0000269                | Bacterial stock | PMIRH181a2PA-1 |
| SBI | Human pre-microRNA Expression Construct Lenti-miR-181c + 181d MI0003139 MI0000271 | Bacterial stock | PMIRH181cPA-1  |
| SBI | Human pre-microRNA Expression Construct Lenti-miR-221                             | Bacterial stock | PMIRH221PA-1   |
| SBI | Human pre-microRNA Expression Construct Lenti-miR-21                              | Bacterial stock | PMIRH21PA-1    |
| SBI | Scramble control hairpin in pCDH-CMV-MCS-EF1-copGFP (CD511B-1)- miR-00            | Bacterial stock | PMIRH000PA-1   |

Table 6. List of System Biosciences lenti-miRNA vectors used in the study.

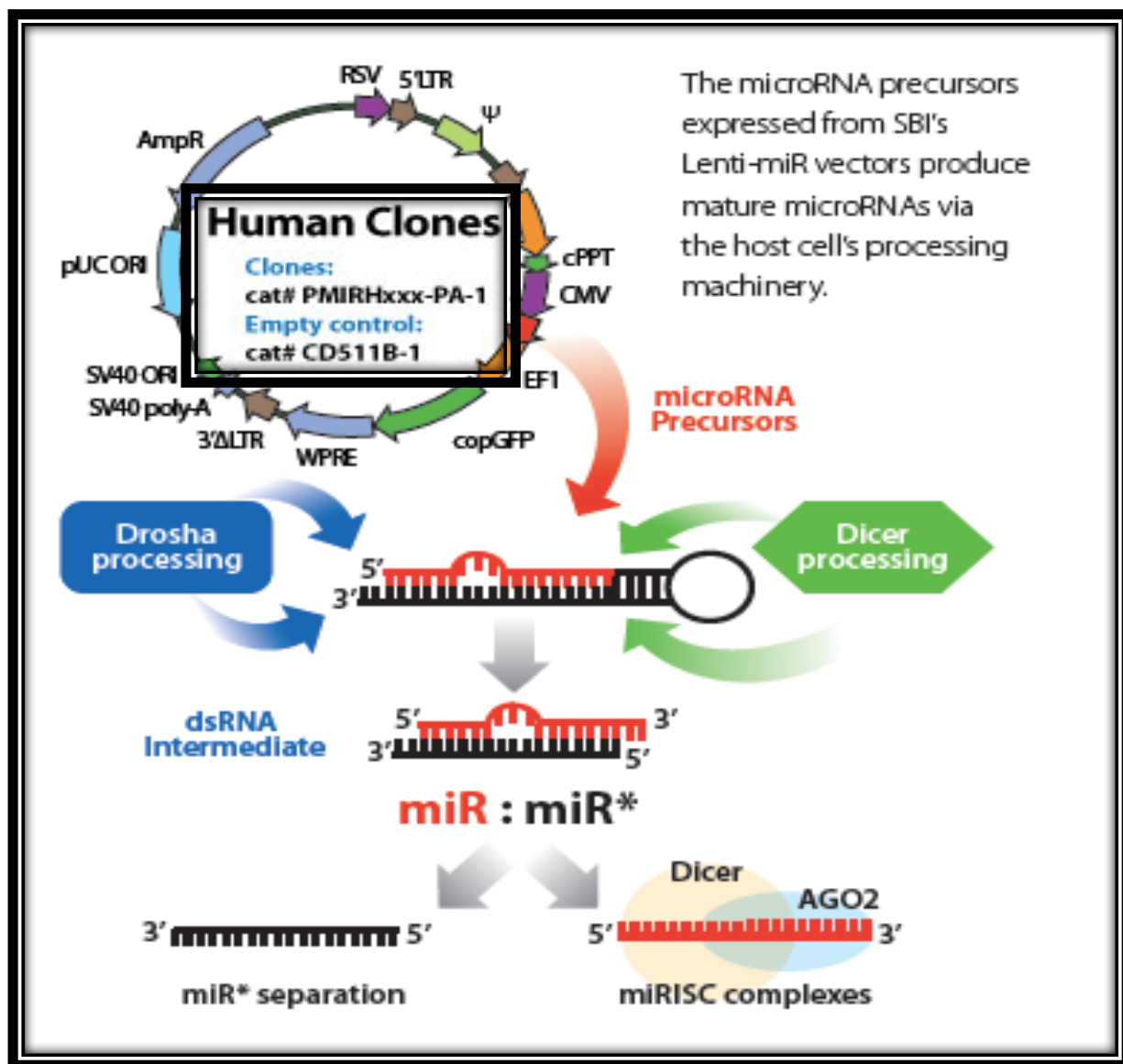
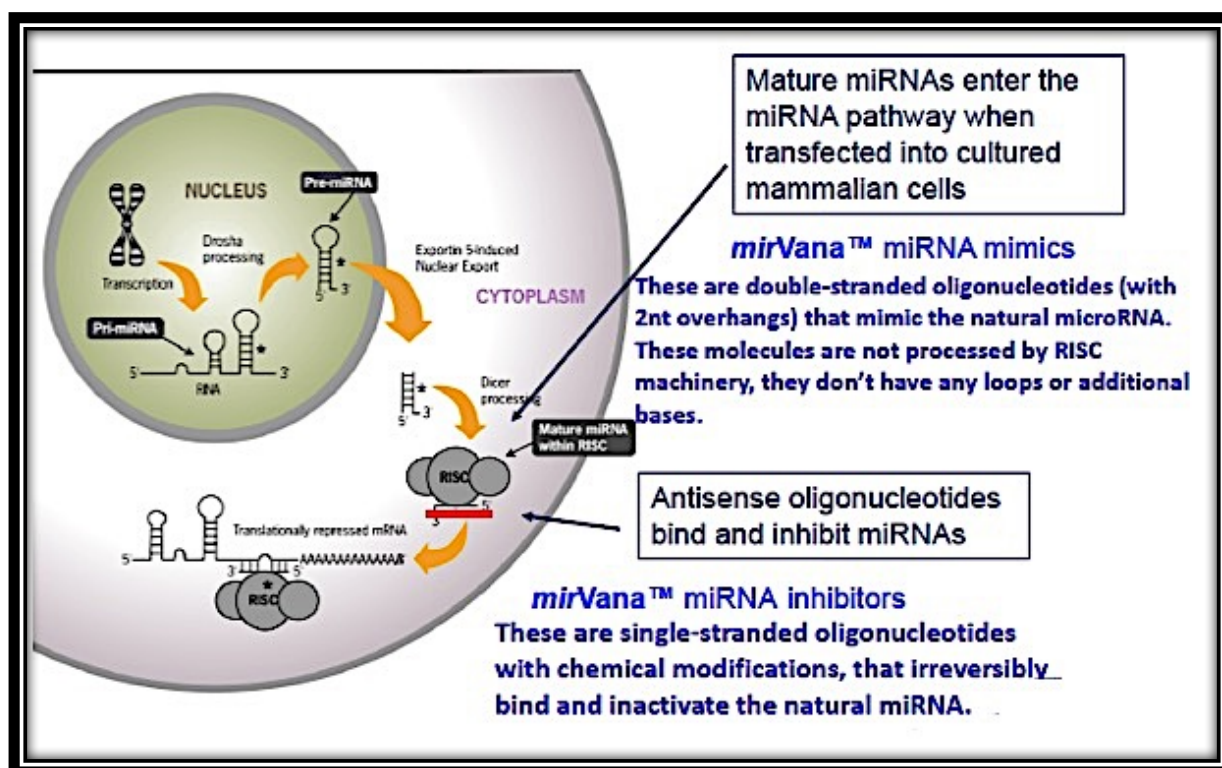


Figure 14. Schematic diagram of microRNA precursors expressed from SBI's Lenti-miR vectors. Image reproduced with permission from <https://www.systembio.com/lentimir>.



## 2.14 micro-RNA transient overexpression and inhibition

We used mirVana miRNA mimics and inhibitors along with RNAi transfection protocol and manufacturers instructions for transient overexpression of the miRs. List of all reagents and miRs used are indicated below.



**Figure 15. Schematic diagram mirVana miRNA mimics and inhibitors and their processing by the cell.** Image reproduced with permission from <https://www.thermofisher.com>.

|                   |         |   |
|-------------------|---------|---|
| Life Technologies | 4464077 | mirVana™ miRNA Inhibitor, Negative Control #1                         |
| Life Technologies | 4464084 | mirVana miR inhibitor against hsa-miR-181a-5p; Inhibitor ID # MH10421 |
| Life Technologies | 4464084 | mirVana miR inhibitor against hsa-miR-181a-3p; Inhibitor ID # MH10381 |
| Life Technologies | 4464084 | mirVana™ miRNA Mimic, Negative Control #1                             |
| Life Technologies | 4464066 | mirVana miRNA Mimic; Assay Name: hsa-miR-181a-5p; Assay ID: # MC10421 |
| Life Technologies | 4464066 | mirVana miRNA Mimic; Assay Name: hsa-miR-181a-3p ; Assay ID: #MC10381 |

**Table 7. List of mirVana miRNA mimics and inhibitors used in the study.**



## 2.15 Dual luciferase reporter assay

SEAP-Luc reporter vectors containing 3'UTR of TGFBR3 were obtained from GeneCopoeia (Rockville, MD). The entire 3'UTR region (3394, bp) of TGFBR3 (Catalogue No. HmiT066530) was cloned by Genecopoeia and divided into two clones: *First clone*: 3'UTR length 1–1883, bp (Catalogue No. HmiT066530a-MT05, Gene Accession: NM\_001195684) in our studies we refer to this clone as **3'UTR-TGFBR3-SegB**. *Second clone*: 3'UTR length 1884–3394, bp (Catalogue No. HmiT066530a-MT05, Gene Accession: NM\_001195684.1) in our studies we refer to this clone as **3'UTR-TGFBR3-SegA**. For negative control vector we used the following clone (Genecopoeia, Catalogue No. CmiT000001.MT05) and in our studies we refer to this clone as **3'UTR-Control-Vector**. These constructs were used to generate, by site-directed mutagenesis as described later, the mutant derivatives lacking miRNA-binding sites. All luciferase activity data are presented as means $\pm$ s.d. of values from at least three experiments, each performed in triplicate.

TGFBR3 3'UTR is longer than 3.5kb and for this reason the UTR was broken up into shorter fragments and cloned into two constructs with overlapping sequence. Only TGFBR3 3'UTR- Seg A had two putative binding sites for miR-181a. The putative binding sites were mutated to generate mutant reporter vectors using the site-directed mutagenesis kit. Mutagenesis was validated by Sanger DNA sequencing. HaCaT cells were transfected with wild-type and mutant reporter vectors along with scrambled control in 6-well plates. After 72 h of transfection, the supernatant was collected and the reporter assays were performed according to the manufacturer's guidelines for the Secrete Pair Dual Luminiscence Assay Kit. Luciferase activity was normalized to secreted alkaline phosphatase.



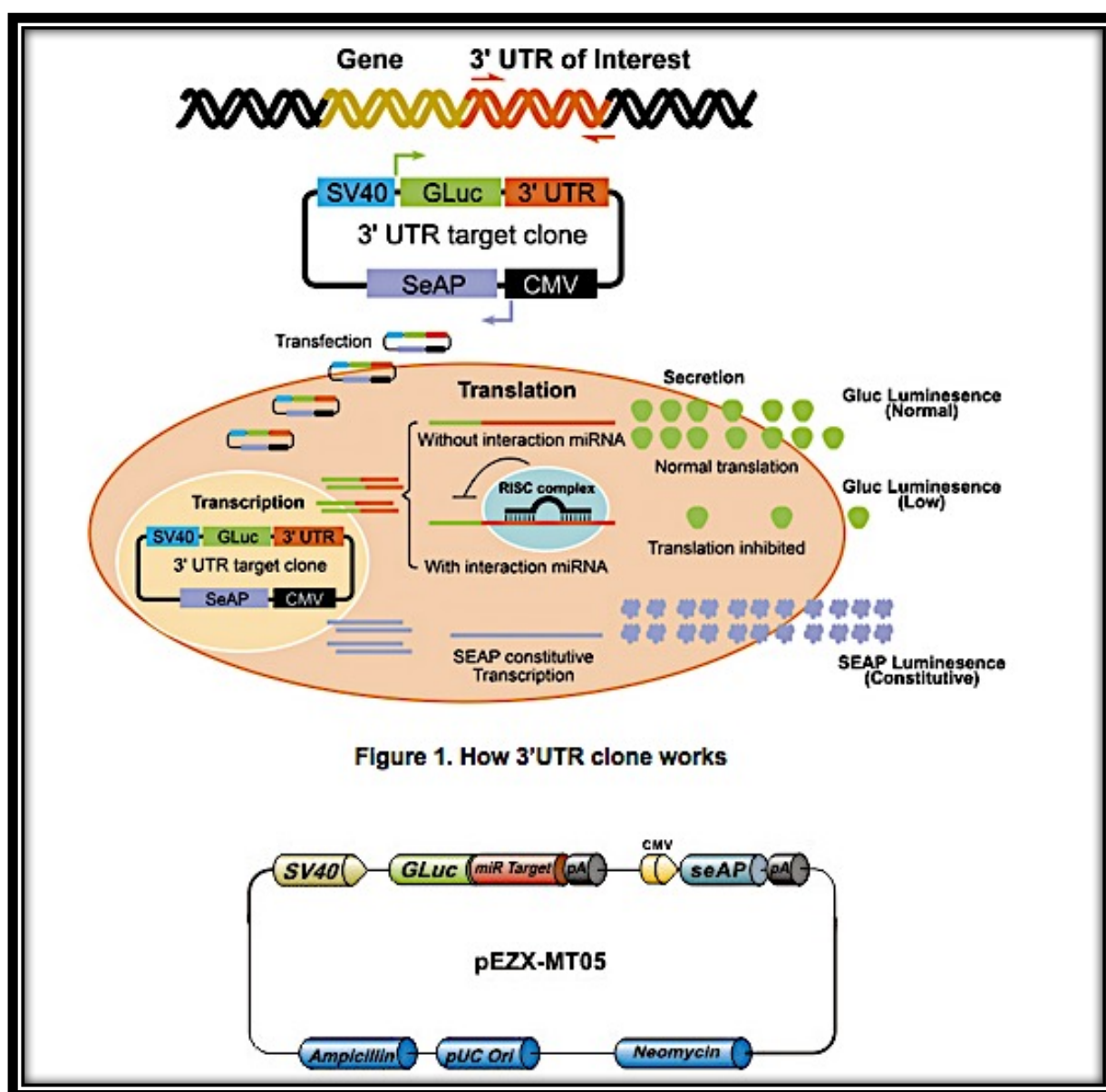


Figure 16. Schematic diagram of SEAP-Luc reporter assay and vector backbone of miTarget miRNA 3' UTR target clones. Image reproduced with permission from [www.genecopoeia.com](http://www.genecopoeia.com).

|                                 |                        |                           |                      |                               |                                     |
|---------------------------------|------------------------|---------------------------|----------------------|-------------------------------|-------------------------------------|
| Catalogue #:<br>HmiT066530aMT05 | UTR Length:<br>1905 bp | Plasmid Size:<br>10471 bp | Vector:<br>pEZXTMT05 | Selection Marker:<br>Neomycin | Reporter Genes:<br><u>Gluc,SeAP</u> |
| Catalogue #:<br>HmiT066530bMT05 | UTR Length:<br>1554 bp | Plasmid Size:<br>10120 bp | Vector:<br>pEZXTMT05 | Selection Marker:<br>Neomycin | Reporter Genes:<br><u>Gluc,SeAP</u> |

Table 8. Information for HmiT066530b-MT05 and TGFBR3-miRNA 3' UTR target clones



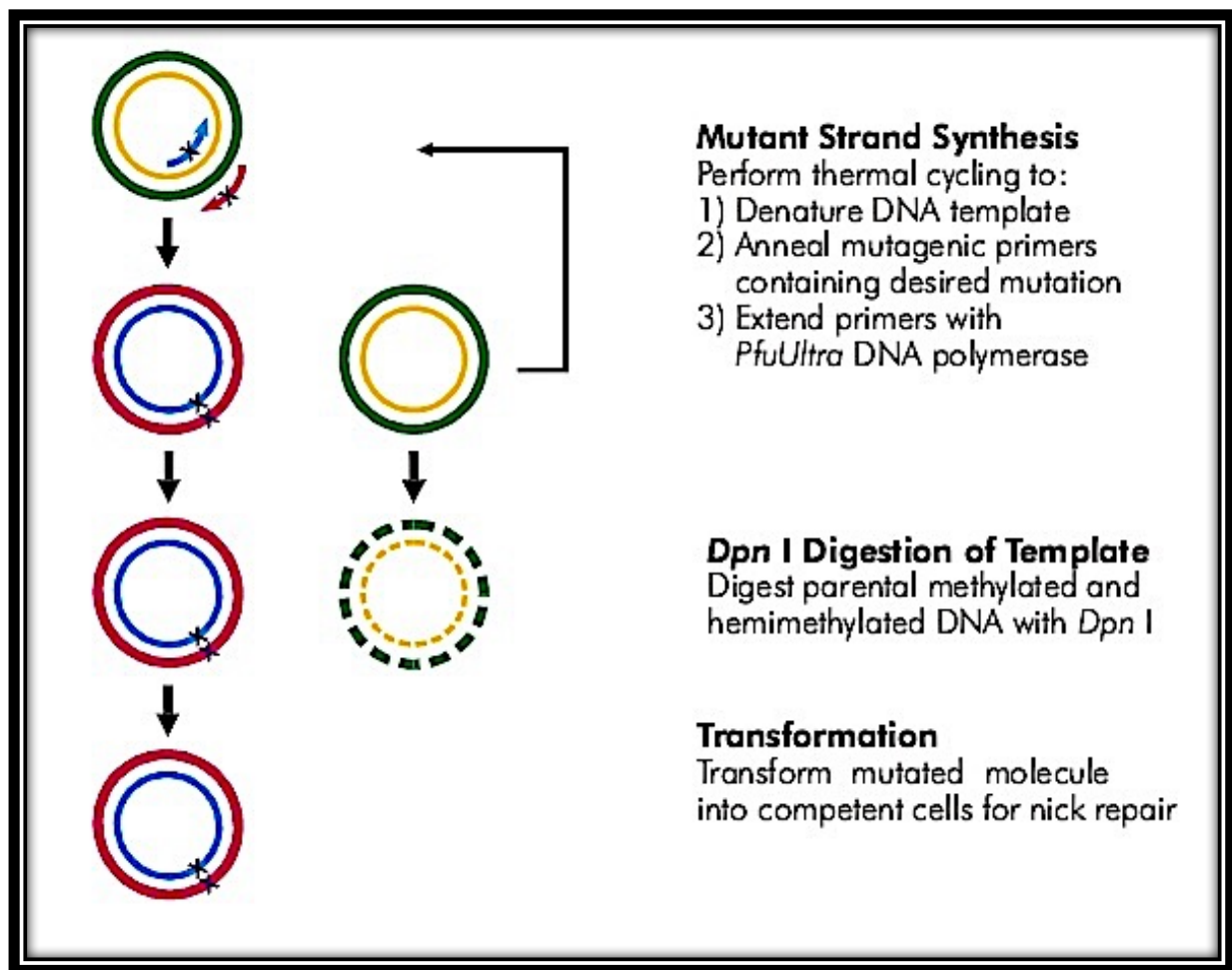
## **2.16 Stable cell line generation and single cell cloning by serial dilution**

We generated stable cell lines in stepwise fashion. First, we generated antibiotic killing for all the cell lines used and titrated the antibiotic concentration based on cell type. Next, we transfected the constructs into the cells according to the manufacturer's protocol. Following stable transfections and 2 weeks of G418 selection, we expanded our cells in a stepwise fashion. Next, we performed single cell cloning by serial dilution in 96 well plates (<http://www.corning.com>). After single cell cloning ~2 weeks and selection in G418 media, single clones were expanded into 24 well plates, 6 well plates, T25 flasks, and finally T75 flasks.



## 2.17 Site Directed mutagenesis

The pEZX-MT05 expression vector harboring the human TGFBR3 3' UTR cDNA was used as DNA template. Site-directed mutagenesis was carried out using the QuickChange II XL Site-Directed Mutagenesis Kit (Catalog #200521, Agilent Technologies), following the Manufacturer's instruction. The mutagenic primers were synthesized by IDT and the oligonucleotide sequences of these primers are listed in Table 10. The success of the designed mutations was verified by DNA sequencing.



**Figure 17. Overview of the QuickChange II XL site directed mutagenesis method.** Image from Agilent instruction manual.



|                                     | Predicted consequential pairing of target region (top) and miRNA (bottom) |
|-------------------------------------|---|
| Position 1918-1924 of TGFBR3 3' UTR | 5' ...GCCUAACCUUCGGUGG <b>AAUG</b> UAU...                                 |
| <a href="#">hsa-miR-181a-5p</a>     |   |
|                                     | 3' UGAGUGGCUGUCGCAACUUACAA  |
| Position 2441-2447 of TGFBR3 3' UTR | 5' ...UCUCAUAUUGGAGAGUG <b>AAUG</b> UC...                                 |
| <a href="#">hsa-miR-181a-5p</a>     |   |
|                                     | 3' UGAGUGGCUGUCGCAACUUACAA  |

**Table 9. Predicted binding sites of miR-181a on 3'UTR of TGFBR3.** Nucleotides bolded are seed sequence, and highlighted red nucleotide are the mutated base pairs.

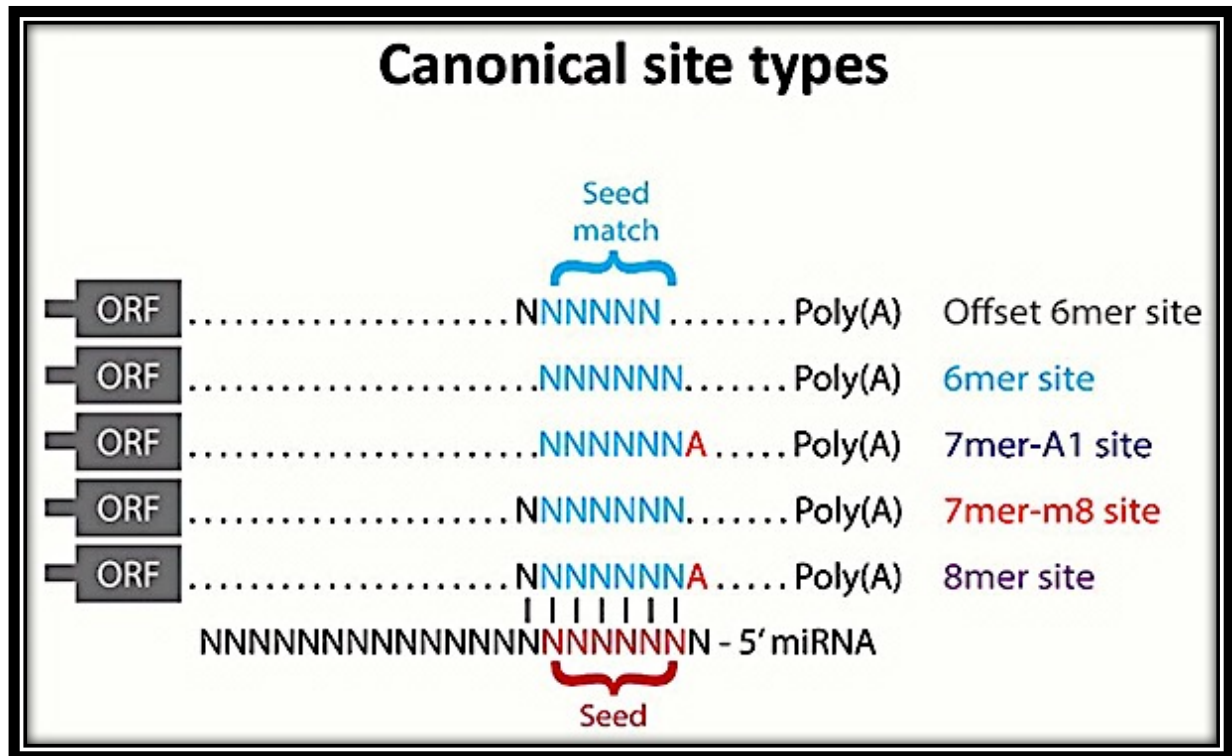
|   | Primers                         | Sequences   |
|---|---------------------------------|---|
| Mutations on position 99-102 of 3'UTR-TGFBR3-SegA           | A99T_A100T_T101A_G102C forward  | 5'- TTT TAT ACA TAG<br>AAT ATG CTG AAA CAA<br>TAG TAA CCA CCG AAG<br>GTT AGG CAA AGC GCA<br>ATA TT - 3'               |
| Corresponding to:<br>Position 1919-1922 bp of TGFBR3 3' UTR | A99T_A100T_T101A_G102C reverse  | 5'- AAT ATT GCG CTT<br>TGC CTA ACC TTC GGT<br>GGT TAC TAT TGT TTC<br>AGC ATA TTC TAT GTA<br>TAA AA - 3'               |
| <b>3'UTR-TGFBR3-SegA-Mut 1</b>                              |                                 |   |
| Mutations on position 623-626 of 3'UTR-TGFBR3-SegA          | A623T_A624T_T625A_G626C Forward | 5'- CAT TTT TTA GAA<br>ACA TTT CAG AAA TAC<br>TTA ACG AGT AAC ACT<br>CTC CAA TAT GAG ATT<br>AGG TTT TAT CGA CAC - 3'  |
| Corresponding to:<br>Position 2443-2446 bp of TGFBR3 3' UTR | A623T_A624T_T625A_G626C Reverse | 5' - GTG TCG ATA AAA<br>CCT AAT CTC ATA TTG<br>GAG AGT GTT ACT CGT<br>TAA GTA TTT CTG AAA<br>TGT TTC TAA AAA ATG - 3' |
| <b>3'UTR-TGFBR3-SegA-Mut 2</b>                              |                                 |   |

**Table 10. Mutagenic primers and their oligonucleotide sequences used in the study.**



### 2.18 TargetScan prediction of miR-181a binding sites at the 3-UTR of TGFBR3

TargetScan predicts 7mer sites of two types: 7mer-m8: An exact match to positions 2-8 of the mature miRNA (the seed + position 8) and 7mer-A1: An exact match to positions 2-7 of the mature miRNA (the seed) followed by an 'A'. Context score and features that contribute to the context score are evaluated as in Agarwal et al., 2015 [86]. Conserved branch lengths and PCT are evaluated as in Friedman et al., 2008 [87] with an expanded 84-species alignment as described in Agarwal et al., 2015 [86].



**Figure 18. Schematic of TargetScan prediction of miRNA targets.** TargetScan predicts biological targets of miRNAs by searching for the presence of conserved 8mer, 7mer, and 6mer sites that match the seed region of each miRNA.



## 2.19 Immunohistochemistry (IHC)

Staining of human and mice Formalin-Fixed, Paraffin-Embedded (FFPE) tissues would be performed by **TGF beta** Receptor III/TGFB3 antibody at 1:4000 dilution (Novus Biologicals Cat# 27030002) that shows strong cytoplasmic positivity. Human normal skin (NS), Actinic Keratosis (AK), and Cutaneous squamous cell carcinomas biopsies were obtained under IRB approval (LAB08-0750). Normal skin (NS), Actinic Keratosis (AK), and cutaneous squamous cell carcinomas from chronically irradiated Hairless mice were obtained based on our laboratory animal protocols and in accordance with institutional and National Institutes of Health guidelines. All samples were submitted to histology core at MD Anderson Cancer Center, South campus building. Dr. K.Y. Tsai performed histopathological confirmation of all lesions/biopsies. Staining levels were quantified by counting positively labeled cells and dividing by the total area of each lesion in each sample. All samples were photographed, total pixel numbers were calculated using included image analysis tools in (Adobe Photoshop) and standardized to a hemacytometer to convert to mm<sup>2</sup>.

## 2.20 Western Blot Analysis

Cell lysates were prepared by using standard buffers including protease inhibitors (Roche) and phosphatase inhibitors (Santa Cruz). Cell extracts were ran on SDS/polyacrylamide gels (50-100ug of protein/lane) and transferred to Immobilon-P transfer membrane (Millipore). Blots were blocked in TBST (10mM Tris-HCL pH8, 150mM NaCl, 0.5% Tween) containing 5% milk or using 2.5% Bovine Serum Albumin (BSA). Membranes were probed with primary antibodies, incubated at 4 degree C over night. We used corresponding HRP-conjugated secondary antibodies and ECL kit (Amersham) was used for signals detection.



## **2.21 Antibodies**

Primary antibodies for western blot analysis includes all those listed on Table 11. We used GAPDH antibody to ensure even sample protein loading.



| Vendor             | catalog # | item name/description                            |
|--------------------|-----------|--|
| Cell Signaling     | S2873     | ATM (D2E2) Rabbit mAb                            |
| Cell Signaling     | 3195S     | E-Cadherin (24E10) Rabbit mAb                    |
| Cell Signaling     | 2880P     | FoxO1 (C29H4) Rabbit mAb 40 microliters          |
| Cell Signaling     | 2118L     | GAPDH (14C10) Rabbit mAb                         |
| Cell Signaling     | 9107S     | Mouse tERK ab                                    |
| Cell Signaling     | 14215S    | N-Cadherin (13A9) Mouse mAb                      |
| Cell Signaling     | S4526     | Phospho-ATM (Ser1981) (10H11.E12) Mouse mAb      |
| Cell Signaling     | 9919S     | Phospho-p53 Antibody Sampler Kit                 |
| Cell Signaling     | 3108S     | Phospho-Smad2 (Ser465/467) (138D4) Rabbit mAb    |
| Cell Signaling     | 9520S     | Phospho-Smad3 (Ser423/425) (C25A9) Rabbit mAb    |
| Cell Signaling     | 9559S     | PTEN antibody                                    |
| Cell Signaling     | 12656S    | Smad 1/5/9 Antibody Sampler Kit                  |
| Cell Signaling     | 5339S     | Smad2 (D43B4) XP® Rabbit mAb                     |
| Cell Signaling     | 12747S    | Smad2/3 Antibody Sampler Kit                     |
| Cell Signaling     | 9523S     | Smad3 (C67H9) Rabbit mAb                         |
| Cell Signaling     | 3108S     | Phospho-Smad2 (Ser465/467) (138D4) Rabbit mAb    |
| Cell Signaling     | 9520S     | Phospho-Smad3 (Ser423/425) (C25A9) Rabbit mAb    |
| Cell Signaling     | 2519S     | TGF- $\beta$ Receptor III Antibody               |
| Cell Signaling     | 5673      | TIMP3 (D74B10) Rabbit mAb                        |
| Cell Signaling     | 8342S     | UV induced damage response sampler kit           |
| Cell Signaling     | 9919S     | Phospho-p53 Antibody Sampler Kit                 |
| Cell Signaling     | 5741P     | Vimentin (D21H3) XP® Rabbit mAb                  |
| Cell Signaling     | 9775S     | Vimentin Antibody Sampler Kit                    |
| Cell Signaling     | 9285      | Phospho-p53 (Ser6) Antibody                      |
| Cell Signaling     | 9288      | Phospho-p53 (Ser9) Antibody                      |
| Cell Signaling     | 9286      | Phospho-p53 (Ser15) (16G8) Mouse mAb             |
| Cell Signaling     | 2676      | Phospho-p53 (Thr81) Antibody                     |
| Cell Signaling     | 9287      | Phospho-p53 (Ser20) Antibody                     |
| Cell Signaling     | 2527      | p53 (7F5) Rabbit mAb                             |
| Cell Signaling     | 2529      | Phospho-p53 (Thr18) Antibody                     |
| Cell Signaling     | 2521      | Phospho-p53 (Ser46) Antibody                     |
| Cell Signaling     | 9281      | Phospho-p53 (Ser392) Antibody                    |
| Cell Signaling     | 7074      | Anti-rabbit IgG, HRP-linked Antibody             |
| Cell Signaling     | 7077      | Anti-rat IgG, HRP-linked Antibody                |
| Cell Signaling     | 4120      | Microcephalin-1/BRIT1 (D38G5) Rabbit mAb         |
| Cell Signaling     | 2853      | Phospho-ATR (Ser428) Antibody                    |
| Cell Signaling     | 2737      | ATRIP Antibody                                   |
| Cell Signaling     | 9718      | Phospho-Histone H2A.X (Ser139) (20E3) Rabbit mAb |
| Cell Signaling     | 4901      | Phospho-cdc25C (Ser216) (63F9) Rabbit mAb        |
| Cell Signaling     | 2208      | RPA32 (4E4) Rat mAb                              |
| Cell Signaling     | 2348      | Phospho-Chk1 (Ser345) (133D3) Rabbit mAb         |
| Santa Cruz         | sc-11392  | Smad7 Antibody                                   |
| Santa Cruz         | sc-15393  | twist (H-81)                                     |
| abcam              | ab39184   | Anti-TIMP3 antibody - Loop 1 ab39184             |
| abcam              | ab85926   | Anti-TIMP3 antibody                              |
| abcam              | ab140371  | ETS2 antibody                                    |
| EMD Millipore Corp | ASK10-1EA | ASK10 MMP/TIMP Family Antibody Sampler Kit I     |
| Novus Biologicals  | 27030002  | TGF-beta RIII Antibody                           |
| R&D Systems        | AF-242-PB | Human TGF- $\beta$ RIII Antibody                 |

**Table 11. List of all antibodies used in the study**



## **2.22 Soft agar and colony formation assays**

Following plating of bottom agar (0.6% Bacto Agar) with media we plated 2500 to 10,000 cells per well and they were embedded in top agar (0.3%) and plated in 24-well plates. Control or lenti-miR-overexpression media was replaced every 48 hr for 4 to 6 weeks. We stained the colonies with 1% crystal violet and they were imaged and counted by bright-field microscopy.

## **2.23 Statistical analysis**

Our data analysis was performed in collaboration with various groups including Dr. Xiaoping Su (Dept. of Bioinformatics and Computational Biology at The University of Texas M.D. Anderson Cancer Center), Dr. Preethi Gunaratne (University of Houston, Biology & Biochemistry) and Dr. Cristian Coarfa (Baylor College of Medicine Department of Bioinformatics).

### **2.23.1 Exome-seq analysis**

For any given patient, if their saliva samples were available, they were used as the paired control for the mutation detection. Otherwise, NS samples were used as controls. Four precapture libraries were pooled together and hybridized according to the manufacturer's Exome Analysis. For any given patient, if their saliva samples were available, they were used as the paired control for the mutation detection. Otherwise, NS samples were used as controls. Four precapture libraries were pooled together and hybridized according to the manufacturer's protocol NimbleGen SeqCap EZ Exome Version 3. Exomes were sequenced on an Illumina HiSeq 2000 platform to an average coverage of 135X. Sequencing runs generated approximately 300-400 million successful reads on each lane of a flow cell, yielding 9-12 Gb per sample. Initial sequence analysis was performed using the HGSC Mercury analysis pipeline,



(<https://www.hgsc.bcm.edu/software/mercury>). First, the primary analysis software on the instrument produces .bcl files that are transferred off-instrument into the HGSC analysis infrastructure by the HiSeq Real-time Analysis module. Next, the vendor's primary analysis software (CASAVA) demultiplexes pooled samples and generates sequence reads and basecall confidence values (qualities).

Reads are mapped to the GRCh37 Human reference genome (<http://www.ncbi.nlm.nih.gov/projects/genome/assembly/grc/human/>) using the Burrows-Wheeler aligner (BWA, <http://bio-bwa.sourceforge.net/>) and producing a BAM file. Finally, quality is recalibrated (GATK, <http://www.broadinstitute.org/gatk/>), and separate sequence-event BAMs are merged into a single sample-level BAM. BAM sorting, duplicate read marking, and realignment to improve in/del discovery all occur at this step. DNPs were collapsed with their neighbors and annotated by using Provean ([provean.jcvi.org](http://provean.jcvi.org)). Identification of significantly mutated genes essentially paralleled our previously established pipeline<sup>51</sup>.



### 2.23.2 RNA-seq analysis

mRNA sequencing using RNA-Seq yielded 30-40 million read pairs for each sample. The mRNA-Seq human specimens reads were mapped using TopHat [88] onto the human genome build UCSC hg19 (NCBI 37) and the RefSeq human genes; The mRNASeq mouse sample reads were mapped using TopHat [88] onto the mouse genome build UCSC mm10 (NCBI 38) and the RefSeq mouse genes. Gene expression was computed using Cufflinks [89]. A combined profile of all samples was computed and quantile normalization was applied separately for the human specimens and the mouse samples. To reduce potential batch effects due to sample collection and preparation at different times, the combat normalization algorithm [90] was applied to the human data. Analysis of differentially expressed genes was performed using the t-test statistics via the R statistical system (fold change exceeding 1.5x,  $p < 0.05$ ). Significant genes were analyzed through the Gene Set Enrichment (GSEA)(Broad Institute) data analysis [91], and GSEA implementation at the Molecular Signature Database (MSigDB) to screen for pathways and processes [92]. Principal component analysis (PCA), hierarchical clustering, and heatmaps were generated using the R statistical system. Another analysis of gene expression was also undertaken and gave largely concordant results. The raw paired-end reads were aligned to the human reference genome, GRCh37/hg19, using MOSAIK alignment software [93]. The mRNA-Seq mouse sample reads were mapped onto the mouse genome build UCSC mm10 (NCBI 38). The overlaps between aligned reads and annotated genomic features, such as genes/exons were counted using HTSeq software [94]. The counts were normalized using the scaling factor method [95]. A hierarchical clustering analysis was performed using the Pearson correlation coefficient as the distance metrics and the ward's linkage rule. Principal component analysis (PCA) was also applied to discover the multivariate structure.

To identify differentially expressed genes, a negative binomial generalized linear model



was fit to each gene expression with patients, disease stages and experiment batches as covariates. Then a likelihood-ratio test was applied to examine if there is any difference in the expression of a gene among three stages. The Benjamin-Hochberg method was used to control false discovery rate (FDR). The pairwise comparisons were performed to compare the gene expressions between any two stages using Wald's tests. The Holm's method was used to calculate adjusted p-value to correct for multiple testing.

All analyses of identification of differential expressions were performed using the R package, DESeq2 [96]. To quantify chromosomal instability (CIN), CIN70 score was calculated by summing up the normalized counts of all CIN70 genes [97].

### **2.23.3 miRNA-seq Analysis**

This work was performed with collaboration with laboratory of Dr. Preethi Gunaratne, PhD (University of Houston, Biology & Biochemistry). As previously described [98], Illumina small RNA adapter sequences were trimmed from the reads, and reads of length below 10nt or ending in homopolymers of length 9 nt or above were discarded. Total usable number of reads for each sample was calculated. The reads were mapped to the miRBase [99, 100] reference using BLAST; the abundance of each expressed microRNA was quantified as a fraction of the usable reads, and expressed as parts per million

To reduce potential batch effects due to sample collection and preparation at different times, the combat normalization algorithm [90] was applied for the human data. We determined differentially expressed microRNAs imposing a fold-change of 1.5x and t-test comparison ( $p < 0.05$ ) using the R statistical system. We employed principal component analysis (PCA) to examine sample structure; further visualization of microRNA significant in one or multiple comparisons was carried out using the R statistical system.



#### **2.23.4 Integrative mRNA-miRNA functional pair analysis**

We determined enriched miRNA-mRNA pairs using the SigTerms methodology. Essentially, by applying a one-sided Fisher exact test and using the TargetScan [86, 87] predicted microRNA targets, we determined the miRNAs for which the gene targets are significantly enriched (FDR-adjusted  $q < 0.25$ ) in the gene signature, separately for the human specimens and the mouse samples. Finally, we determined the conserved enriched miRNAs alongside the SCC progression model, and the conserved miRNA-mRNA pairs conserved alongside the SCC progression model. Conserved enriched microRNA-mRNA pairs were visualized using the Cytoscape software [101].

#### **2.23.5 Cross-species linear mixed effects model**

This analysis was confined to human samples that had complete matched sets of lesion types (21 samples from 7 patients). Samples from all six mice were used. Using the output of differentially expressed genes from the HTseq-based analysis, LME models were constructed [102] and genes designated as early, late, stepwise (both), or none (blank) in each dataset, with associated ANOVA nominal p and FDR q values, t statistics, and signed linear fold changes (Appendix 6). HUGO identifiers were converted to Entrez Gene identifiers. Most (>95%) of the identifiers could be translated in this manner (16,155 out of 16,952 human features and 14,084 out of 14,542 mouse features); features that did not map to an Entrez Gene ID were discarded.

GATHER (Gene Annotation Tool to Help Explain Relationships) [103] was used to identify TRANSFAC identifiers that were significantly overrepresented in three settings: EARLY (NS/CHR to AK/PAP), LATE (AK/PAP to cuSCC), and STEPWISE (both EARLY and LATE), with the data consisting of the TRANSFAC identifier and description, p-value, Bayes Factor, and associated genes (Appendix 7). The two tabs containing GATHER results from genes with



discordant behavior between species also contain a column that computes the maximum Bayes Factor between the two species. The rows in the two "concordant" tabs are sorted in ascending order by human p value and filtered to show only those motifs for which the Bayes Factor is greater than 3 in both species. The rows in the two "discordant" tabs are sorted in descending order by maximum Bayes Factor and filtered to show only those motifs for which the maximum Bayes Factor is greater than 3.

### **2.23.6 Gene Set Enrichment Analysis for TCGA tumor signatures**

Gene Set Enrichment Analysis (GSEA) was carried out using the GSEA software package [91] to assess the degree of similarity among the studied gene signatures. For each of the human or the mouse SCC progression transcriptome response, all genes were ranked by the fold change alongside the SCC progression model. To assess comparative association with multiple tumor progression signatures, we downloaded from the Cancer Genome Atlas (TCGA) (<https://tcgadata.nci.nih.gov/tcga/>) gene expression data for 19 cancer cohorts, performed, quantile normalized using the R statistical analysis system, and then inferred tumor progression transcriptome signature by imposing a fold change exceeding 2 ( $p < 0.05$ ). We utilized separately the down-regulated genes and the up-regulated genes. Normalized Enrichment Score (NES) and adjusted q-values ( $q < 0.25$ ) were computed utilizing the GSEA method, based on 1000 random permutations of the ranked genes. We visualized combined NES scores for all the TCGA tumor development gene signatures and for our human and mouse SCC progression signatures using the Circos software [104].



### **2.23.7 Survival analysis for TCGA Head and Neck Squamous Cell Carcinoma with TP53 mutant tumors**

We evaluated the survival prognostic power of cuSCC progression-associated gene signature using human specimen cohorts from the Cancer Genome Atlas (TCGA) (<https://tcgadata.nci.nih.gov/tcga>), specifically Head and Neck Squamous Cell Carcinoma (HNSCC) which are TP53-mutant. We first replaced the gene expression of each gene with the z-score within the cohort, then we computed the sum of z-scores for each sample, as described previously [105], by adding the z-score for up-regulated genes and subtracting the z-score from down-regulated genes. Specimens were sorted according to the sum z-score of the respective SCC progression gene signature; association with survival ( $p < 0.05$ , log-rank test) was evaluated by using the package survival in the R statistical system.

### **2.23.8 Bioinformatic prediction for miR-181a-5p targeted genes**

TargetScan (<http://www.targetscan.org>), miRanda (<http://www.microrna.org>) and PicTar (<http://pictar.bio.nyu.edu/>) online searching programs was used for the prediction of miR-181a-5p target genes



# **Chapter 3**

## **Genomic drivers of squamous cell carcinoma development**

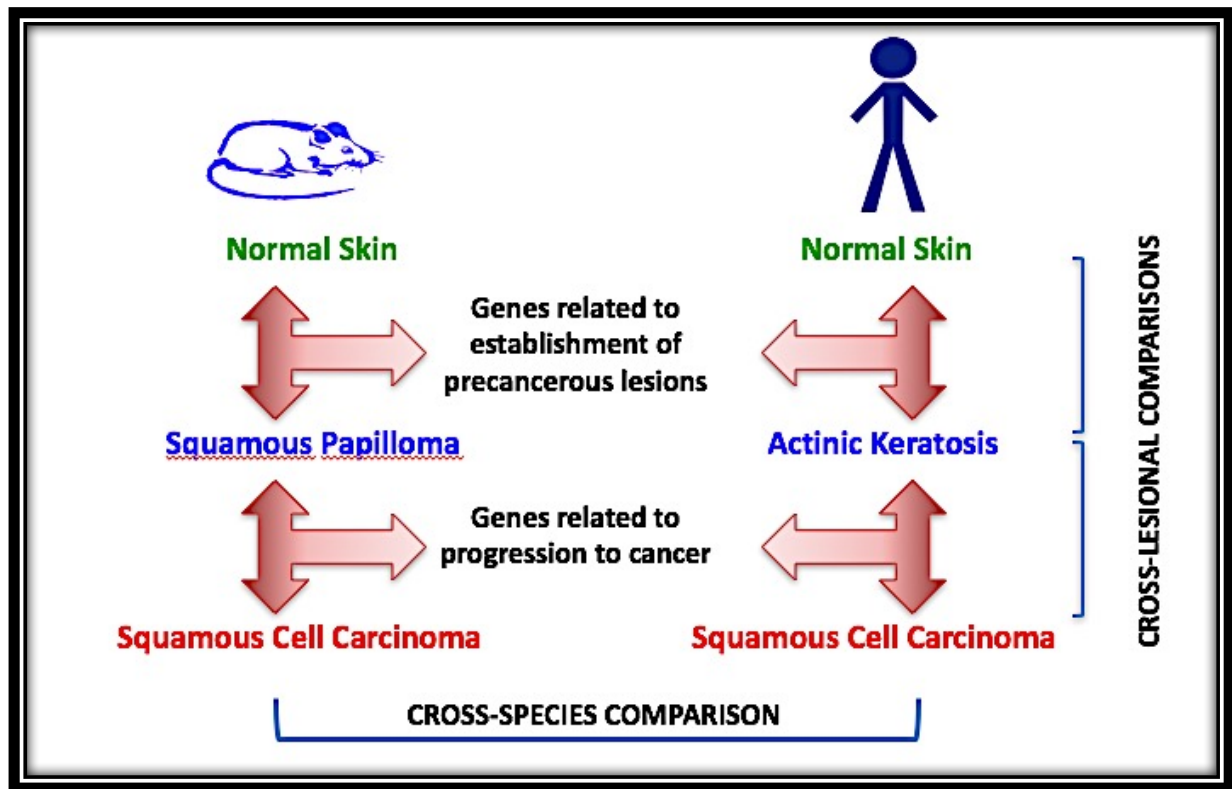


### **3.1 Our approach: Genomic analysis of cutaneous squamous cell carcinoma (cuSCC)**

We have used an integrated approach by combining RNA-Seq, miR-Seq, and reference exome sequencing [106-110]. Our method is novel in that it employs tissue-specific, matched samples at three stages of tumor development to identify changes between the different stages. Our goal is to identify mutations or other variations that are most relevant to the formation of AKs and their subsequent progression to cuSCC. We expected that the preliminary data gathered from this approach would yield a tractable number of genetic targets to validate mechanistically. Comparing lesions that are closely related in the evolution of NS to AK to cuSCC is important for a number of reasons. Many studies have been performed comparing tumor cells to normal cells of the same lineage; these typically yield hundreds to thousands of differentially expressed genes or genetic alterations.

We have used matched samples acquired from the same individual. By performing inter-lesional analysis on internally-controlled lesions on the path to carcinoma, our approach minimizes variation thus enriching for changes that are more likely to be causal [111]. This proposal is innovative because it couples the integrated high-resolution detection of large-scale chromosomal abnormalities, mutations, differentially expressed genes, non-coding RNAs, and microRNAs to the methodologies of inter-lesional comparisons to identify the genetic events that dictate the well-defined progression of clinically normal sun-exposed skin (NS) to AK to cuSCC (Figure 19).





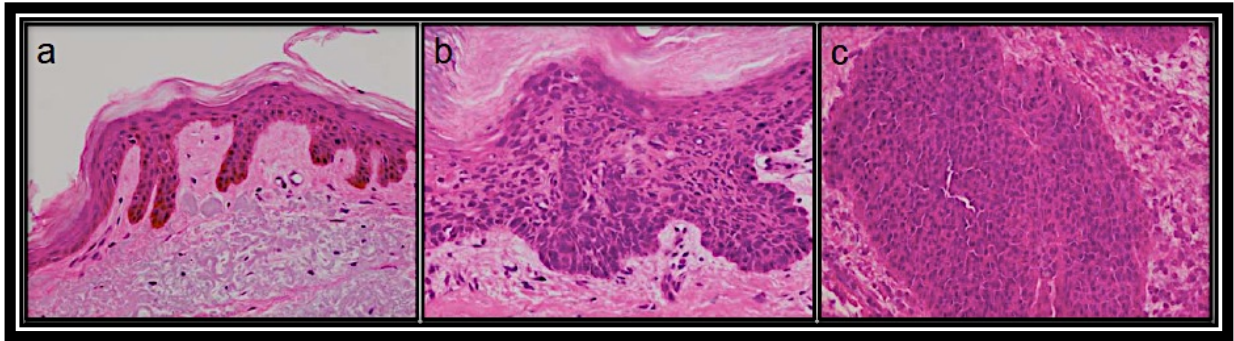
**Figure 19. Schematic diagram of our experimental approach.** We have used a novel approach that combines RNA-Seq, miR-Seq, and reference exome sequencing on tissue-specific, matched samples at three stages of tumor development, in both human and mouse. The power of our study rests in performing inter-lesional analysis on internally-controlled lesions on the path to carcinoma.

### 3.1.1 Isogenic matched human samples

Isogenic matched human samples have a key advantage in minimizing inter-individual variability. A total of 27 tissue samples were isolated from 9 patients who were treated for invasive cuSCC with Mohs surgery (Table 12). cuSCC tumor cores were extracted prior to Mohs surgery with matched samples of peritumoral clinically-normal skin (NS) within 1 cm the tumor removed in the course of reconstruction. For most patients, a distinct AK was also isolated, often from the



same general field (Figure 20).



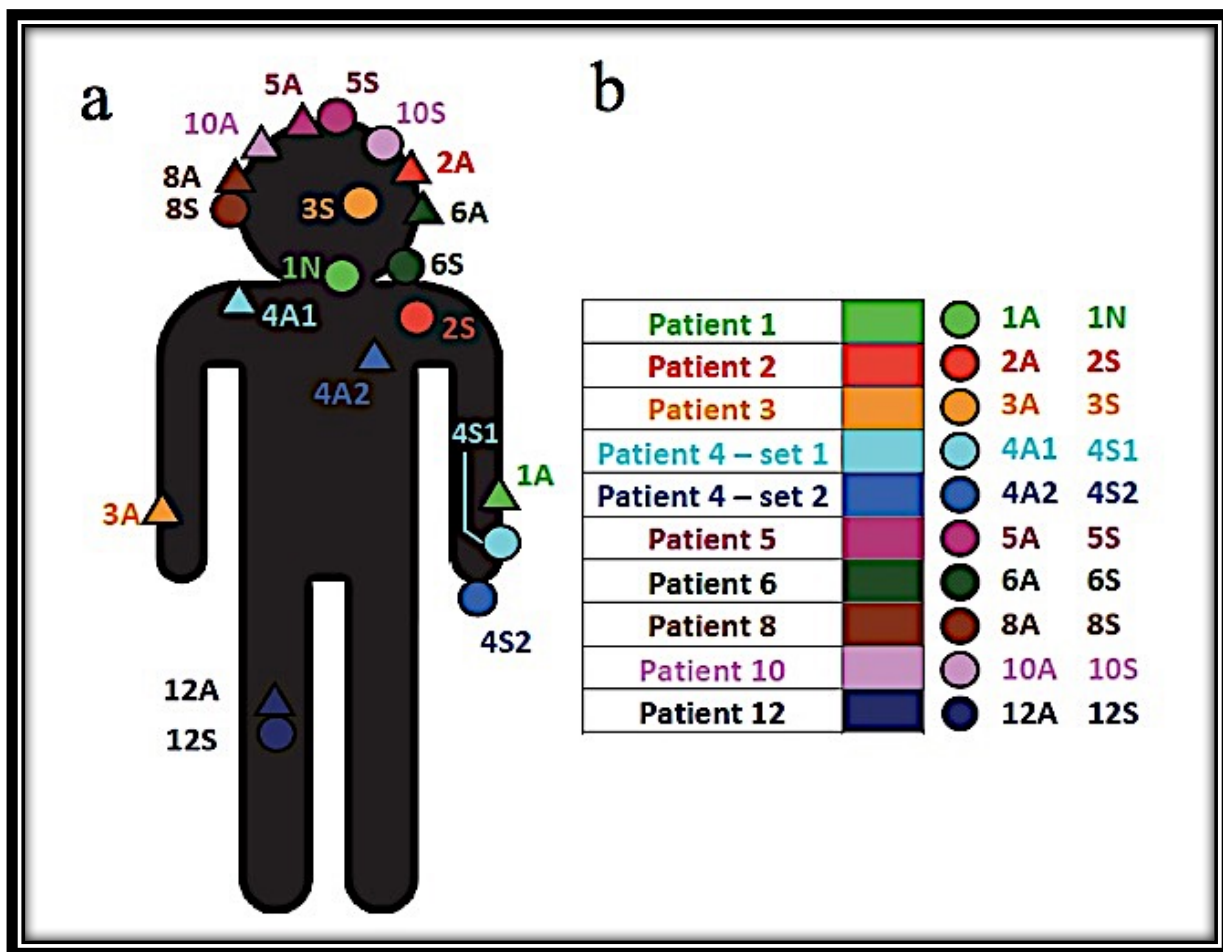
**Figure 20. Histology of representative tissues isolated from patients. a)** Normal (peri-tumoral) skin, **b)** actinic keratosis, and **c)** invasive cuSCC, respectively, are shown from human patients. Human samples were processed following combined RNAlater and formalin fixation, resulting in significant cytoplasmic shrinkage.



| patient # | sample | Immune status | Gender | Location                 | Age (years) | Tobacco use | Alcohol use  | Skin Cancer Hx                           | Fam. Hx skin Cancer |
|-----------|--------|---------------|--------|--------------------------|-------------|-------------|--------------|--|---------------------|
| 1         |        | IC            | M      |                          | 56          | 1ppd        | 6 drinks/day | melanoma - scalp                         | none                |
|           | NS     |               |        | Left dorsal forearm      |             |             |              |  |                     |
|           | AK     |               |        | Left dorsal forearm      |             |             |              |  |                     |
|           | Saliva |               |        |                          |             |             |              |  |                     |
| 2         |        | IC            | M      |                          | Deceased    | unknown     | unknown      | none                                     | none                |
|           | NS     |               |        | Left anterior shoulder   |             |             |              |  |                     |
|           | AK     |               |        | Left temple              |             |             |              |  |                     |
|           | SCC    |               |        | Left anterior shoulder   |             |             |              |  |                     |
|           | Saliva |               |        |                          |             |             |              |  |                     |
| 3         |        | IC            | M      |                          | 70          | 1ppd        | N            | BCC - Upper R Limb, SCC - L lower eyelid | GM - melanoma       |
|           | NS     |               |        | Left infraorbital cheek  |             |             |              |  |                     |
|           | AK     |               |        | Right dorsal forearm     |             |             |              |  |                     |
|           | SCC    |               |        | Left infraorbital cheek  |             |             |              |  |                     |
|           | Saliva |               |        |                          |             |             |              |  |                     |
| 4         |        | IC            | F      |                          | 60          | N           | Y            | SCC - R upper limb                       | father and sister   |
|           | NS     |               |        | Left ulnar forearm       |             |             |              |  |                     |
|           | AK1    |               |        | Right anterior shoulder  |             |             |              |  |                     |
|           | AK2    |               |        | Left chest sternum       |             |             |              |  |                     |
|           | SCC1   |               |        | Left ulnar forearm       |             |             |              |  |                     |
|           | SCC2   |               |        | Left dorsal hand         |             |             |              |  |                     |
|           | Saliva |               |        |                          |             |             |              |  |                     |
|           |        |               |        |                          |             |             |              |  |                     |
| 5         |        | IC            | M      |                          | 75          | former      | unknown      | AK scalp, NMSC                           | none                |
|           | NS     |               |        | Crown of scalp           |             |             |              |  |                     |
|           | AK     |               |        | Scalp                    |             |             |              |  |                     |
|           | SCC    |               |        | Crown of scalp           |             |             |              |  |                     |
|           | Saliva |               |        |                          |             |             |              |  |                     |
| 6         |        | IC            | M      |                          | 82          | former      | N            | AK - nose, BCC - arms, SCC - back        | Brother - BCC ,SCC  |
|           | NS     |               |        | Left sternocleidomastoid |             |             |              |  |                     |
|           | AK     |               |        | Left zygomatic arch      |             |             |              |  |                     |
|           | SCC    |               |        | Left sternocleidomastoid |             |             |              |  |                     |
|           | Saliva |               |        |                          |             |             |              |  |                     |
| 8         |        | IC            | M      |                          | 83          | N           | unknown      | BCC - nose                               | none                |
|           | NS     |               |        | Right temple             |             |             |              |  |                     |
|           | AK     |               |        | Right temple             |             |             |              |  |                     |
|           | SCC    |               |        | Right temple             |             |             |              |  |                     |
|           | Saliva |               |        |                          |             |             |              |  |                     |
| 10        |        | IC            | M      |                          | 79          | N           | Y            | SCC x2 (s/p removal)                     | none                |
|           | NS     |               |        | Left temporal hairline   |             |             |              |  |                     |
|           | AK     |               |        | Right scalp              |             |             |              |  |                     |
|           | SCC    |               |        | Left temporal hairline   |             |             |              |  |                     |
|           | Saliva |               |        |                          |             |             |              |  |                     |
| 12        |        | IC            | F      |                          | 74          | unknown     | unknown      | unknown                                  | unknown             |
|           | AK     |               |        | Right knee               |             |             |              |  |                     |
|           | SCC    |               |        | Right pretibia           |             |             |              |  |                     |
|           | Saliva |               |        |                          |             |             |              |  |                     |

**Table 12. Clinical characteristics of patient cohort.** Clinicopathological characteristics of the patients with AK and cuSCC (n=9) included in this study.





**Figure 21. Anatomic locations of matched samples from human patients.** Tabular list of matched samples from human patients: (S) denotes the cuSCC with adjacent NS and (A) denotes the AK. For patient 1, only NS and AK were available for analysis.

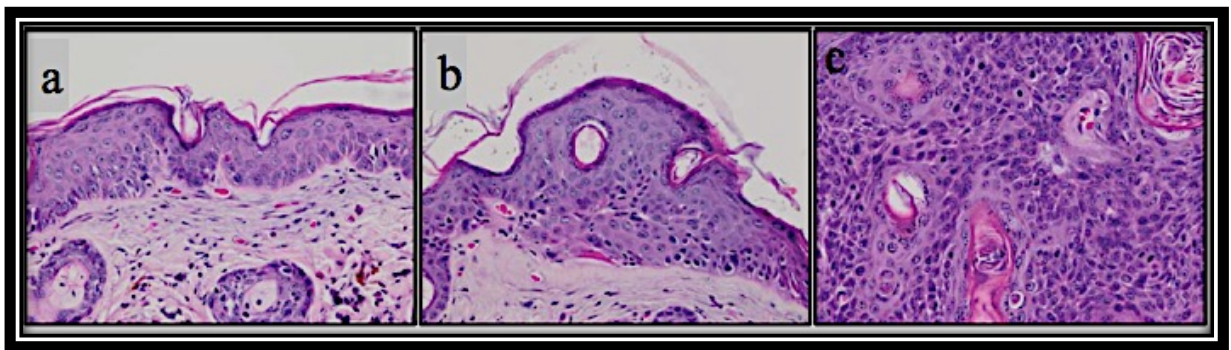
### 3.1.2 SKH-1 Hairless mouse model of UV-induced cuSCC

In parallel to our human model, we established a mouse model using chronically UV-irradiated SKH-1E Hairless mice with solar simulators (Oriol). This model is regarded as a highly relevant model for UV-induced human cuSCC [7, 112] (Figure 22). SKH-1E hairless mice are highly susceptible to UV-induced skin tumors, UV-induced immunosuppression and DNA damage [7]. Our solar simulators much more accurately simulate terrestrial UV exposure than do



standard UV bulbs [113]. Thus our model ensures a useful platform in which we can test potential chemoprevention approaches. These mice develop p53 hotspot mutations [13, 114], overexpression of RAS [8, 12] and mutation of CDKN2A in similar proportions to human cuSCC [14]. SAGE mRNA gene expression data from this model, comparing UV-induced cuSCC to normal skin epidermis, shows substantially similar patterns of changes to our human data including overexpression of matrix metalloproteinases and hyperproliferative keratins [115]. Importantly, these mice develop precancerous papillomas (PAP) and ultimately cuSCC following chronic low-dose UV exposure [7] .

Six littermate female Hairless mice were chronically irradiated with 12.5 kJ/m<sup>2</sup> of UVB weekly (ILT1700/73) for 100 days, and 14 days following cessation of irradiation, sacrificed at which time, chronically irradiated skin (CHR), PAP, and cuSCC were isolated. All papillomas were grade 1 or 2 (not grade 3) and all cuSCC were grade 1 or 2 [26]. All human and mouse samples were histologically validated with estimated 80% tumor cellularity for AK/PAPs and cuSCCs. The chronically UV-exposed samples from both patients (NS) and mice (CHR) exhibited clear histologic evidence of solar damage including elastosis, fibrosis, and chronic inflammation (Figure 20 and 22).



**Figure 22. Histology of representative tissues isolated from Hairless mice. a)** Normal (peri-tumoral) skin, **b)** papillomas, and **c)** invasive cuSCC, respectively, are shown from Hairless mice.





**Figure 23. Representative skin samples from Hairless mice.** are shown, which include smaller papillomas and a smaller number of invasive carcinoma.

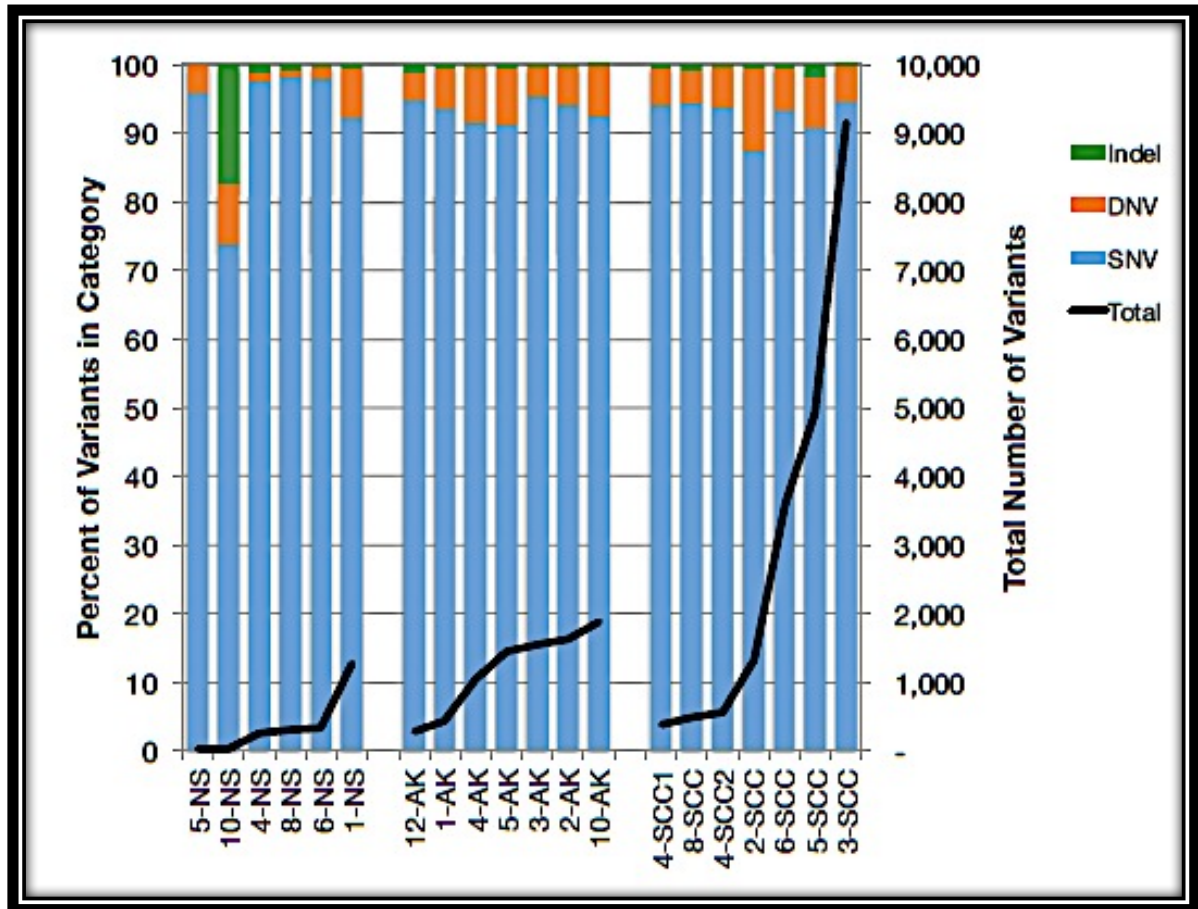
### 3.2 Mutational analysis

Exome sequencing (Illumina Hi-Seq) was performed on a subset (Table 12) of collected samples with an average coverage of  $135X \pm 22$ . The mutational load varied widely across our cohort of well-differentiated primary cuSCC, averaging 2,927 somatic variants (range 385-9,156) or 45.7 variants per Mb (Figure 24), which is congruent with previously reported results of about 50 mutations per Mb for cuSCC [116], keeping in mind that some AKs and cuSCCs were referenced to UVR-exposed peritumoral NS and not germline. AKs had substantially fewer variants, with an average of 1,186 variants (range 290-1,873) or 18.5 per Mb.

To our surprise, the clinically normal, chronically UV exposed skin of patients harbored an average of 372 somatic variants (range 23-1,264) across the exome, corresponding to an



average of 5.8 variants per Mb, indicating that the skin sustains substantial mutagenic insults in the course of chronic UV exposure (Figure 24).



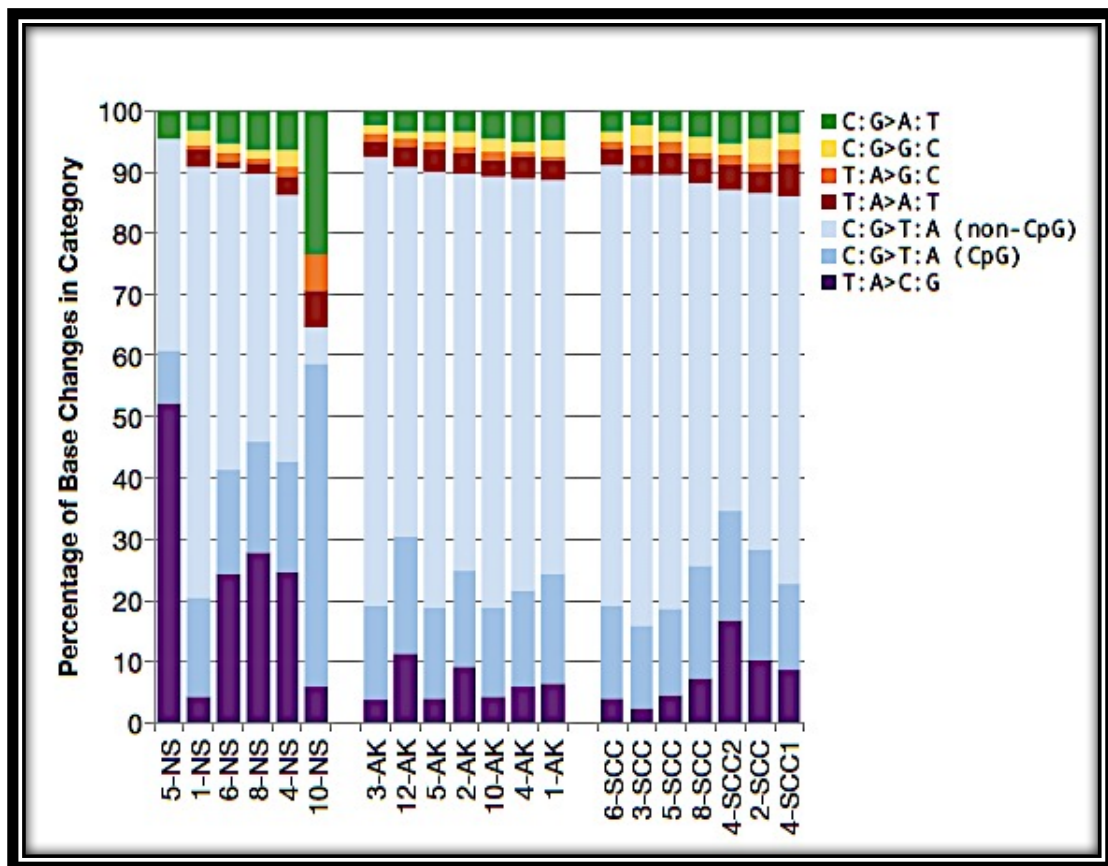
**Figure 24. The spectrum of mutations in human NS, AK, cuSCC show increasing mutation burden across cuSCC development.** cuSCC display very high mutational loads of 47.5 variants per Mb, with NS and AK samples harboring an average of 5.8 and 18.5 variants per Mb, respectively. There are strongly dominated by single nucleotide variants.

TP53 mutations have been described before in UV exposed skin; however, it was not known if this represented ongoing selection specifically for TP53 mutation [117]. High-depth targeted sequencing of 74 genes has demonstrated an estimated 5 mutations per Mb in chronic



UV exposed skin, with a strong preponderance of NOTCH1-3, TP53, and FGFR3 mutations suggesting positive selection for these mutations [118].

The spectrum of mutations is very strongly dominated by transitions between cytosine and thymine, in particular from cytosine to thymine (C→T) (Figure 25). These distributions are most heterogeneous for the NS samples, suggesting that chronic UV exposure may generate a greater spectrum of mutations initially from which classic UVB signature C→T transitions are then enriched perhaps through selection or acquired deficiencies in DNA (nucleotide excision) repair. Interestingly, the larger proportion of T→C transitions in NS (Figure 25), may reflect them increased influence of POL $\eta$ -dependent mutagenesis following UV exposure, before AK and cuSCC development [119].

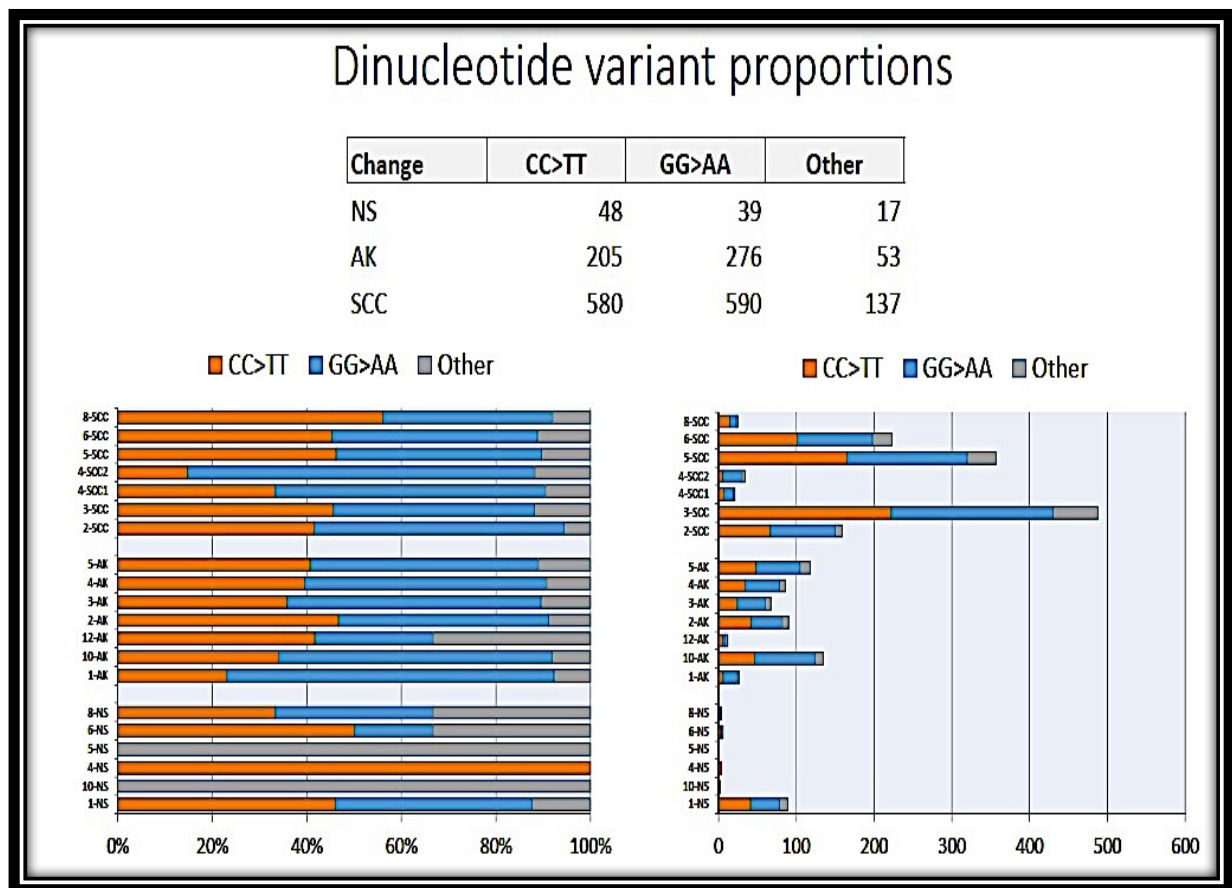


**Figure 25.** The spectrum of mutations in human NS, AK, cuSCC is dominated by C→T transitions. AK and cuSCC have mutational spectra strongly dominated by C→T transitions at



CpG sites, whereas NS show a substantially a more heterogeneous pattern, with a greater proportion of T→C transitions.

UV exposure is known to generate oxidative damage at time scales well beyond initial photoproduct generation [120]. The proportion of dinucleotide variants that are CC→TT is 90% for both AK and cuSCC and 84% for NS (Figure 26). Given the relative statistical rarity of CpG islands across the human genome, the high proportion of C→T transitions at CpG sites reflects the enhanced susceptibility of methylated CpG to deamination and to photoproduct formation [121].

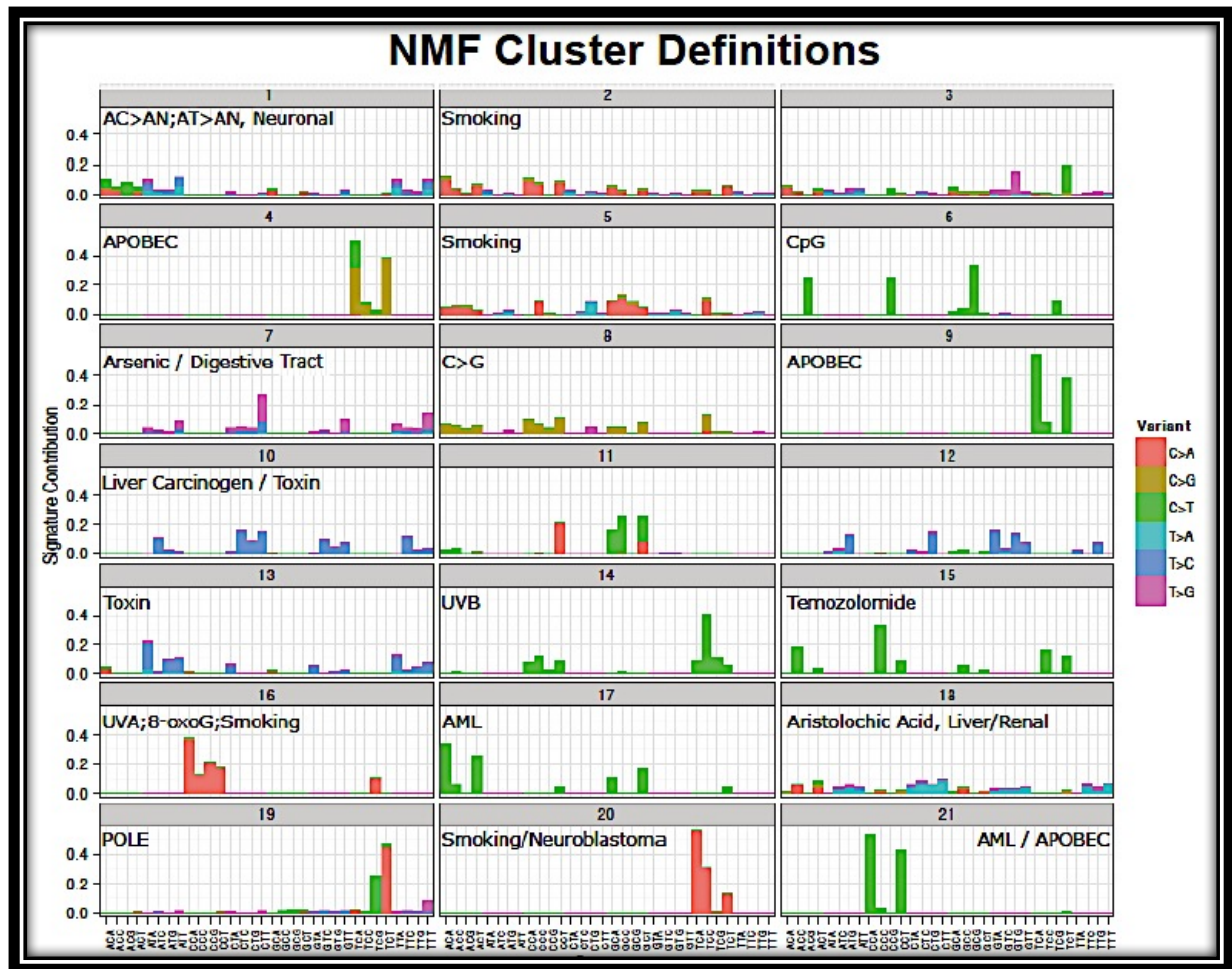


**Figure 26. Dinucleotide variant proportions.** These are described and quantitated for each lesion type.

By using non-negative matrix factorization (NMF)-based spectral deconvolution, 21 orthogonal mutation signatures were derived from over 6000 specimens across 32 cancer types



profiled in TCGA. This enabled the classification of mutational patterns within trinucleotide contexts, among which three signatures predominated in our samples, all of them strongly enriched for C→T transitions (Figure 27 and Figure 28 ). By these criteria, AK and cuSCC are also clearly driven by UV exposure, with substantial enrichment for the classic UVB C→T transition signature at dipyrimidines [122]. As suggested by the mutational spectrum (Figure 25), NS samples had more heterogeneous mutation signatures, including those associated with temozolomide exposure<sup>60</sup> and CpG sites [121], and there is a subsequent enrichment for the classic UVB signature in AK and cuSCC (Figure 28).

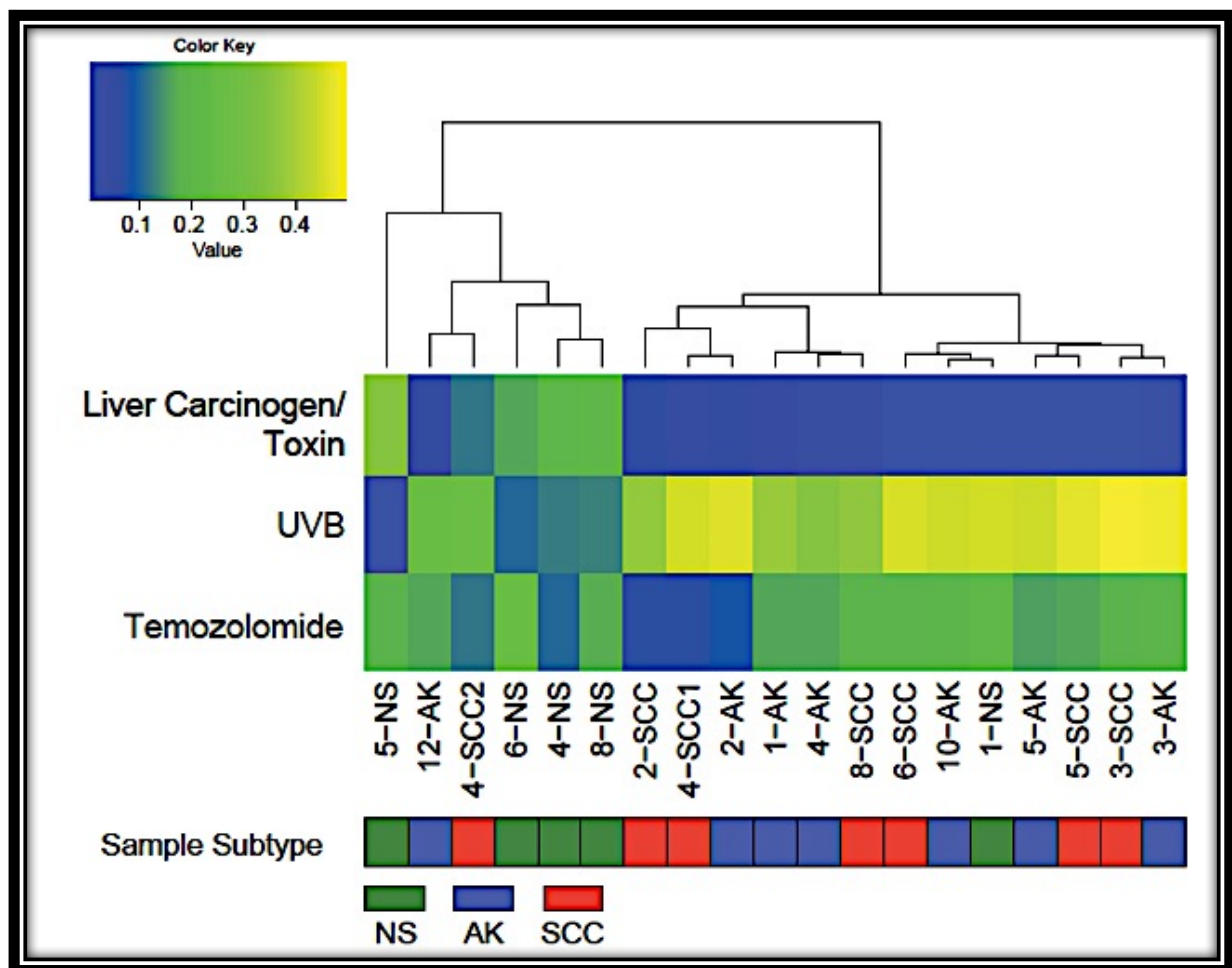


**Figure 27. Non-negative matrix factorization-derived orthogonal mutational profiles.** Our strategy employed non-smooth NMF, a variant which approximates the data using the basis and

85



coefficient matrices as above with the addition of a third smoothing matrix which serves to absorb noise within the data driving the coefficient and basis matrices to increase sparseness. The resulting basis matrix generated with  $k=21$  signatures from a diverse set of over 6000 cancers (data from Alexandrov, et al. Nature 2013).

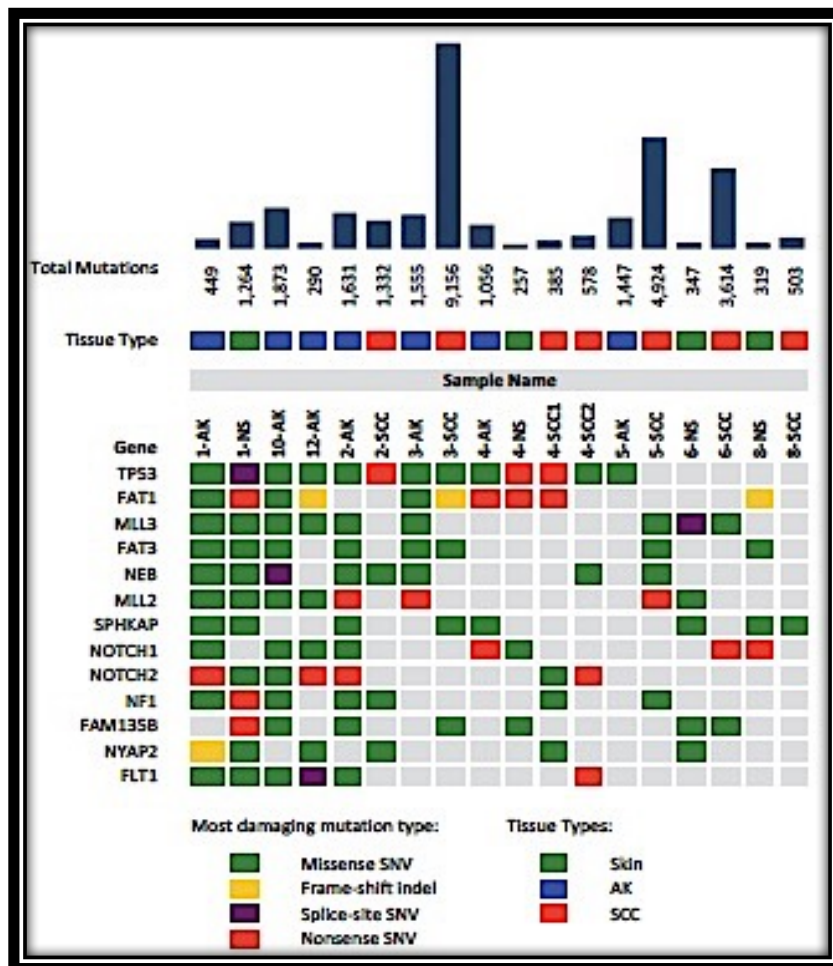


**Figure 28. Enrichment for specific NMF-derived orthogonal** mutational profiles derived from over 6,000 human cancers confirm a strong enrichment for CpG-associated C→T transitions classically associated with UVB-exposure, particularly for AK and cuSCC. Two other profiles dominated by C→T transitions are significantly represented in the mutational data and selectively enriched in NS, including one first described in the context of temozolamide exposure.



To identify significantly mutated genes (SMG), we identified those that were recurrently mutated in at least 7 pairings and that were either previously implicated in cuSCC or have COSMIC frequencies over 400 (Figure 29, Appendix 1). Given the exceptionally high mutational load, we were not able to identify new SMGs based upon recurrence with statistical confidence.

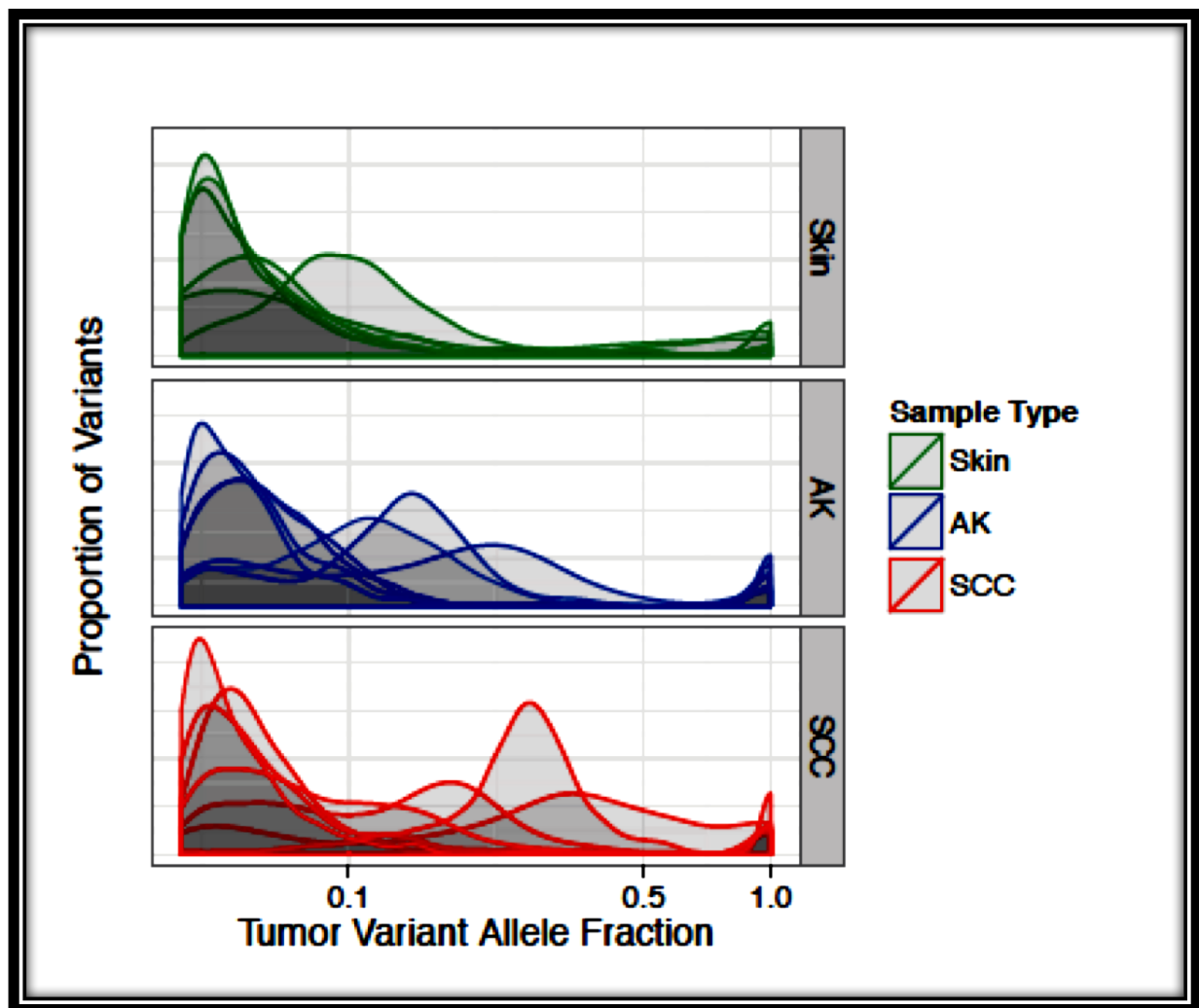
There is substantial overlap, as expected, with genes also mutated in cuSCC, including metastatic and aggressive cuSCC (Figure 29) [123, 124], most prominently, TP53, NOTCH1-2, FAT1, and MLL2. We identified a non-silent KNSTRN missense mutation (resulting in p.P28S) in one cuSCC and one AK from our cohort. Although this is not the previously reported hotspot change at p.S25F [125], it appears to be within the same functional domain. Importantly, AKs not only have mutations in all of the known SMGs, but AKs have the greatest proportion of SMGs represented.





**Figure 29. Significantly mutated genes (SMG) from this cohort, match those identified previously studied cohorts of cuSCC.**

This is consistent not only with the notion that AKs have acquired the mutational events necessary for cuSCC formation, but that AKs may harbor multiple clones that have the capacity to ultimately give rise to cuSCC (Figure 30). Given the knowledge that mutations exist in many hundreds of clones within normal, UV-exposed skin<sup>54</sup> (Figure 24), our data further suggest that dominant clones may be emerging only in the context of AK and cuSCC, particularly in the latter (Figure 30 and Figure 31).

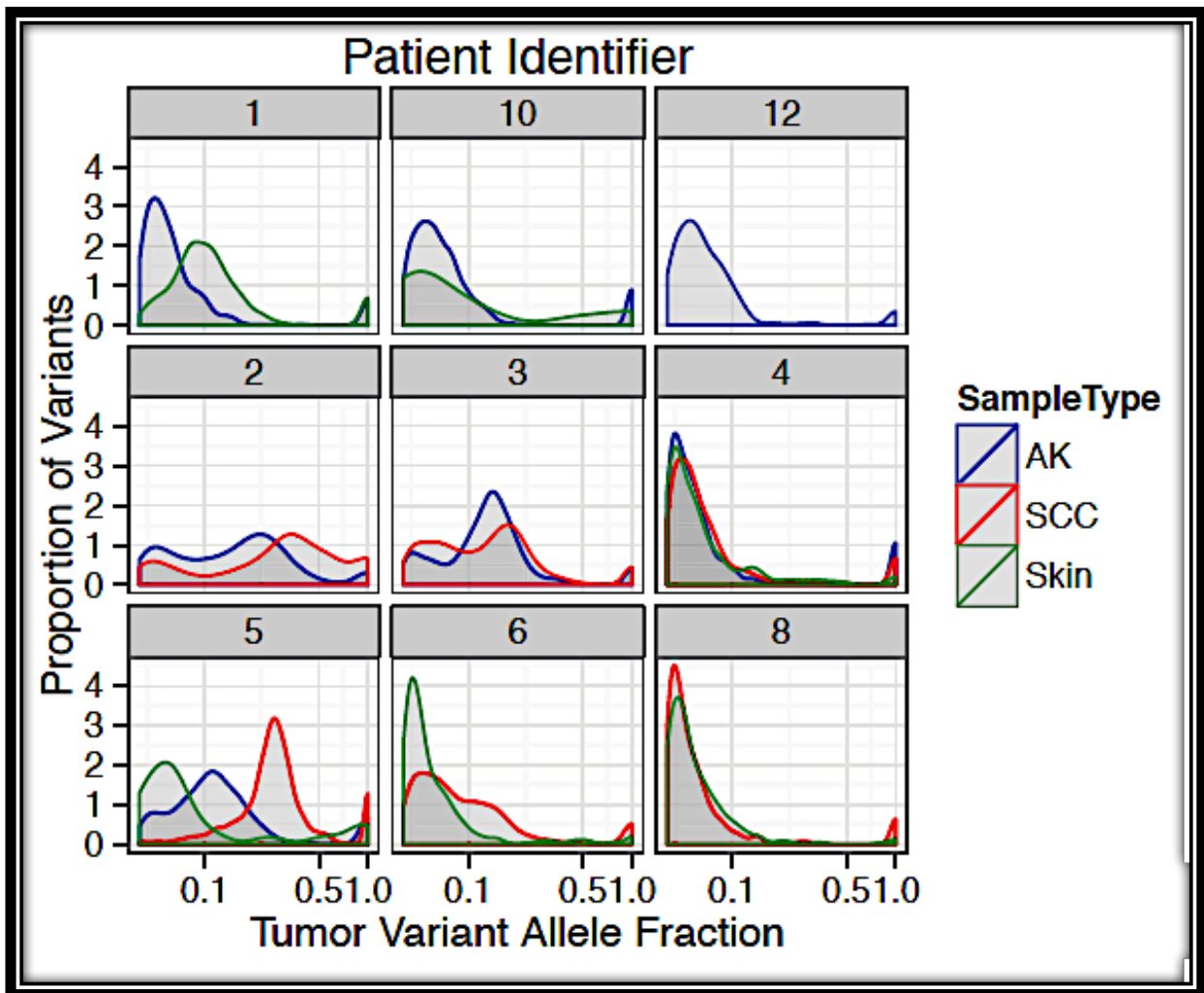


**Figure 30. Significant mutational heterogeneity and overlap exists between AK and cuSCC.**

Histograms of variant allele frequencies in NS, AK, and cuSCC, show that NS have a large



number of low-frequency variants. AK and cuSCC have a more heterogeneous distribution of variant frequencies, with a higher frequency variants, indicative of a trend towards the emergence of dominant clones.

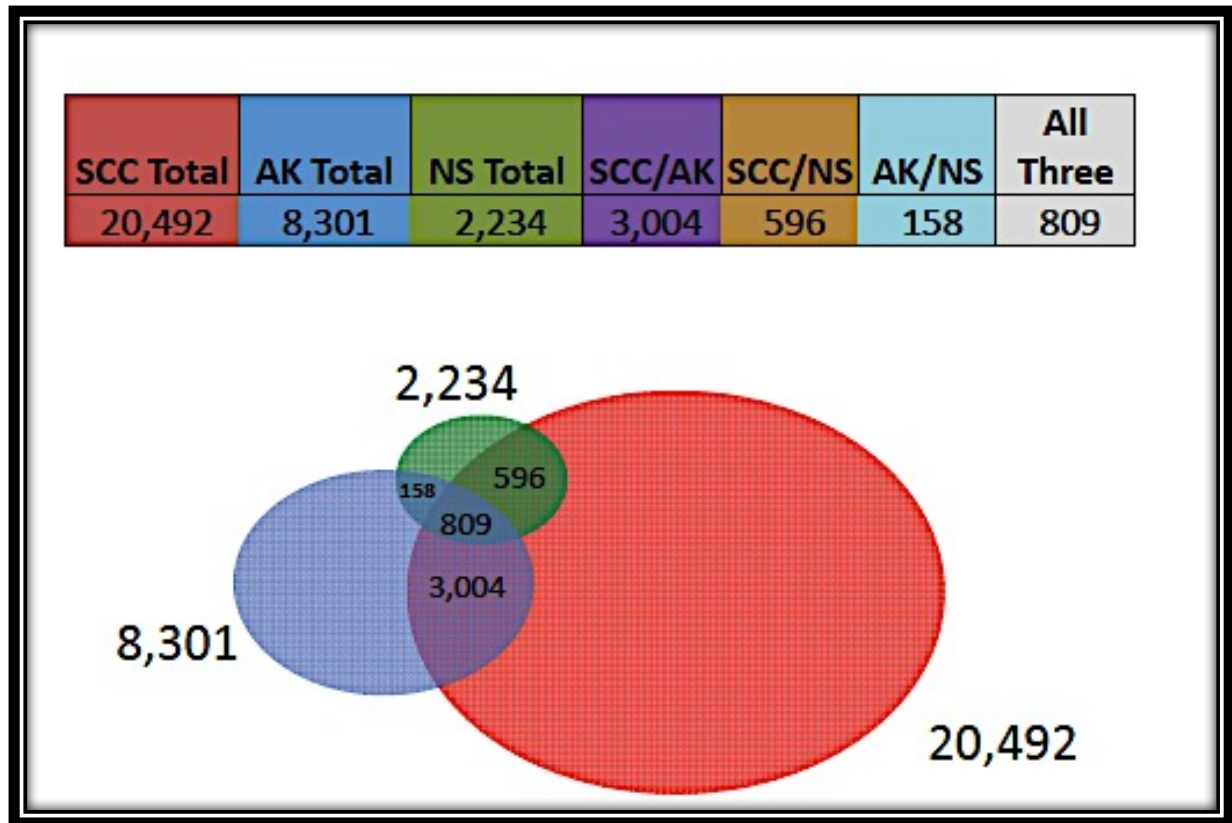


**Figure 31. Histograms of variant allele frequencies of samples grouped by patient.**

We then probed whether these specific SMGs (Figure 29) overlapped between the three groups of samples. Globally, this was rare, and the number of overlaps between AK and cuSCC far exceeded those between NS and AK or NS and cuSCC, by over 19 and 5-fold, respectively (Figure 32). When viewed within patients, functionally significant genes were mutated in multiple samples, including TP53 (4 patients), FAT1 (3 patients), and MLL3 (3 patients) (Figure 33 and



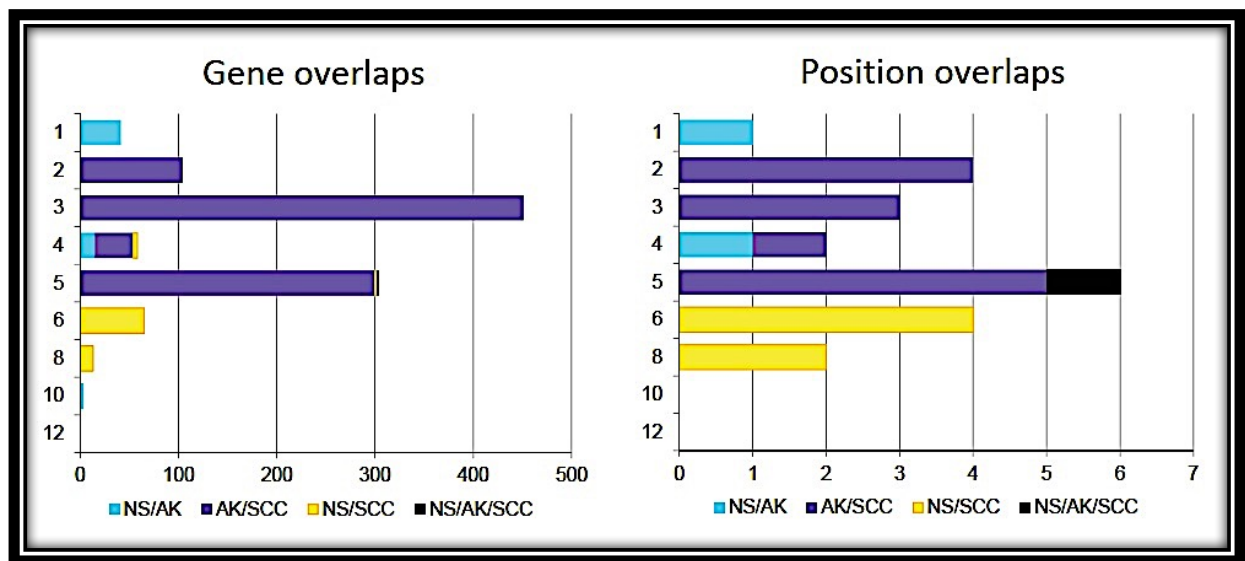
Appendix 2). Surprisingly, these overlaps occurred regardless of spatial proximity (Figure 21), as overlaps in AK-cuSCC were the most common even among these genes (Figure 32 and Figure,33), suggesting that they are specifically targeted in the development of cuSCC.



**Figure 32. Significant mutational heterogeneity and overlap exists between AK and cuSCC.**

The overlap of genes that were mutated in NS, AK, cuSCC shows that the greatest amount of overlap, by far, occurs between AK and cuSCC. This overlap is 5-fold lower in the NS/cuSCC comparison and 19-fold lower in the NS/AK comparison, consistent with the concept that the relevant variants for forming cuSCC are likely to have been acquired early in the transition from NS to AK.

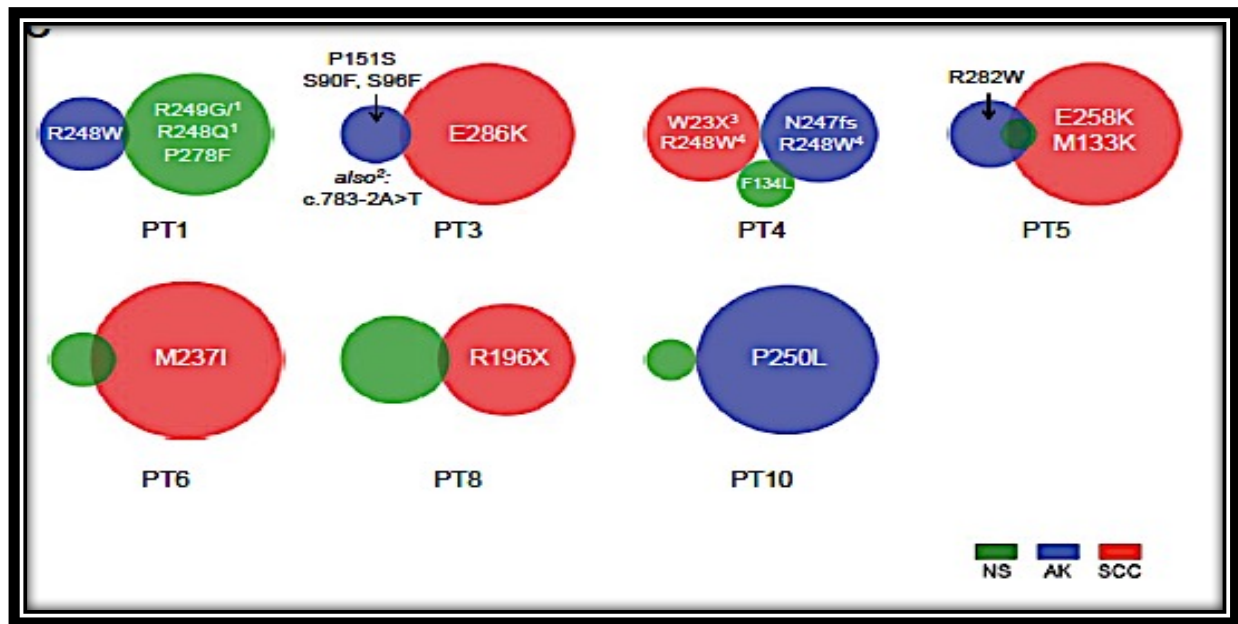




**Figure 33. Enumeration of overlaps between mutated genes and variant positions within mutated genes within samples.** Overlaps in non-silent SNVs at the gene and position level are enumerated here.

The overlap of variants at specific nucleotides within mutated genes between sample types was rare. An illustrative example is provided by TP53, in which multiple mutations were present across the coding region (Figure 34). Among all the human tumor samples sequenced, only amino acid R248, which is a mutational hotspot in cuSCC [126], was multiply altered within 2 patients (patients 1 and 4). These findings are consistent with the concept that mutations that inactivate tumor suppressor genes are often distributed across the entire coding region [127].





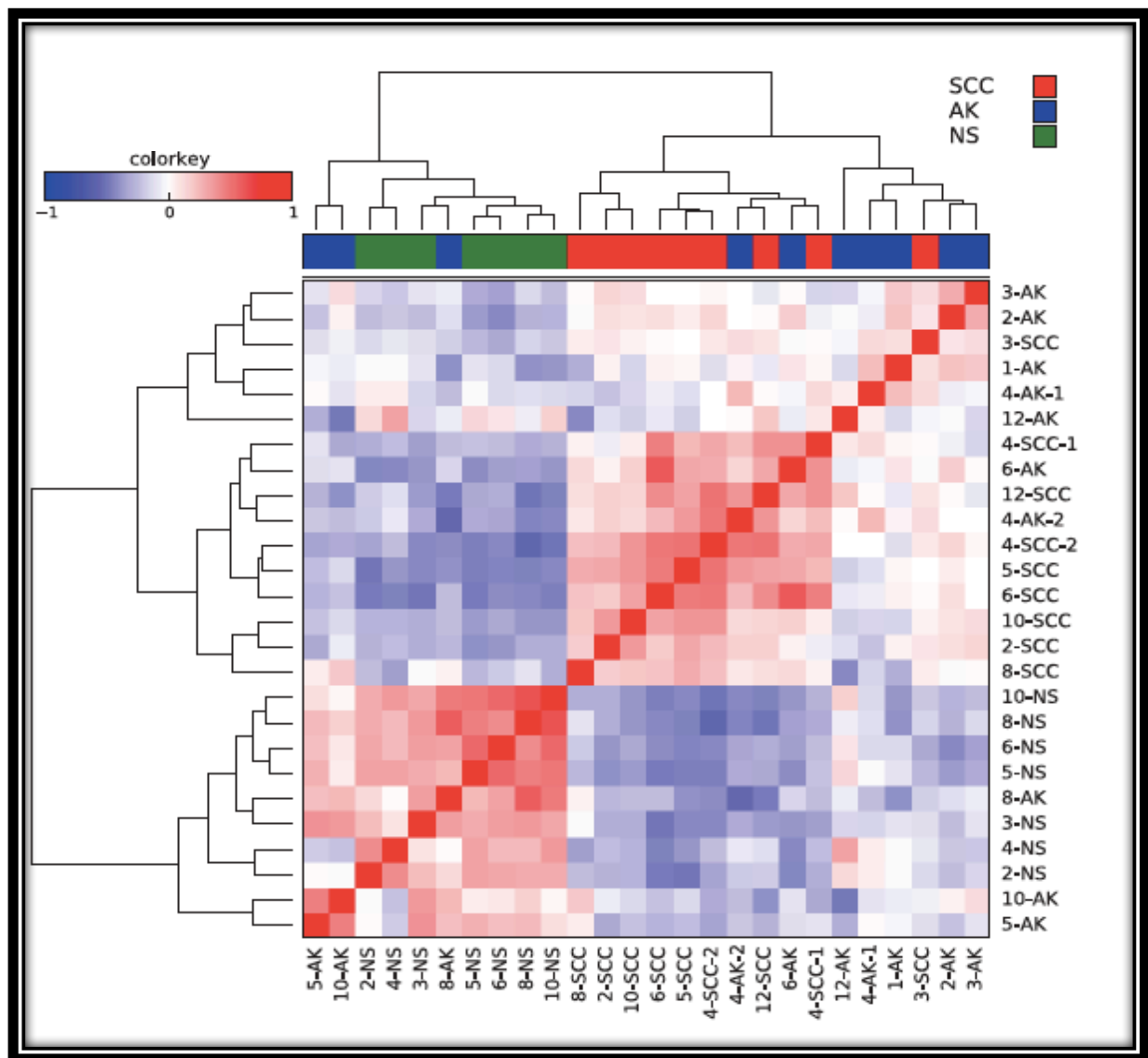
**Figure 34. Significant mutational heterogeneity and overlap exists between AK and cuSCC.**

Specific positional overlap in mutated genes, such as TP53, is rare, showing a wide spectrum of inactivating mutations across this tumor suppressor gene. R248 is the only amino acid changed in multiple samples within patients 1, 4. Notes regarding specific findings: 1: complex variant at R248/9 hotspot; 2: splice-site variant, 3: appears in both SCC-1 and SCC-2, 4: base change differs between AK and SCC-1 (c.GG741AA in AK, and c.C742T in SCC-1).

### 3.3 Transcriptomic analysis

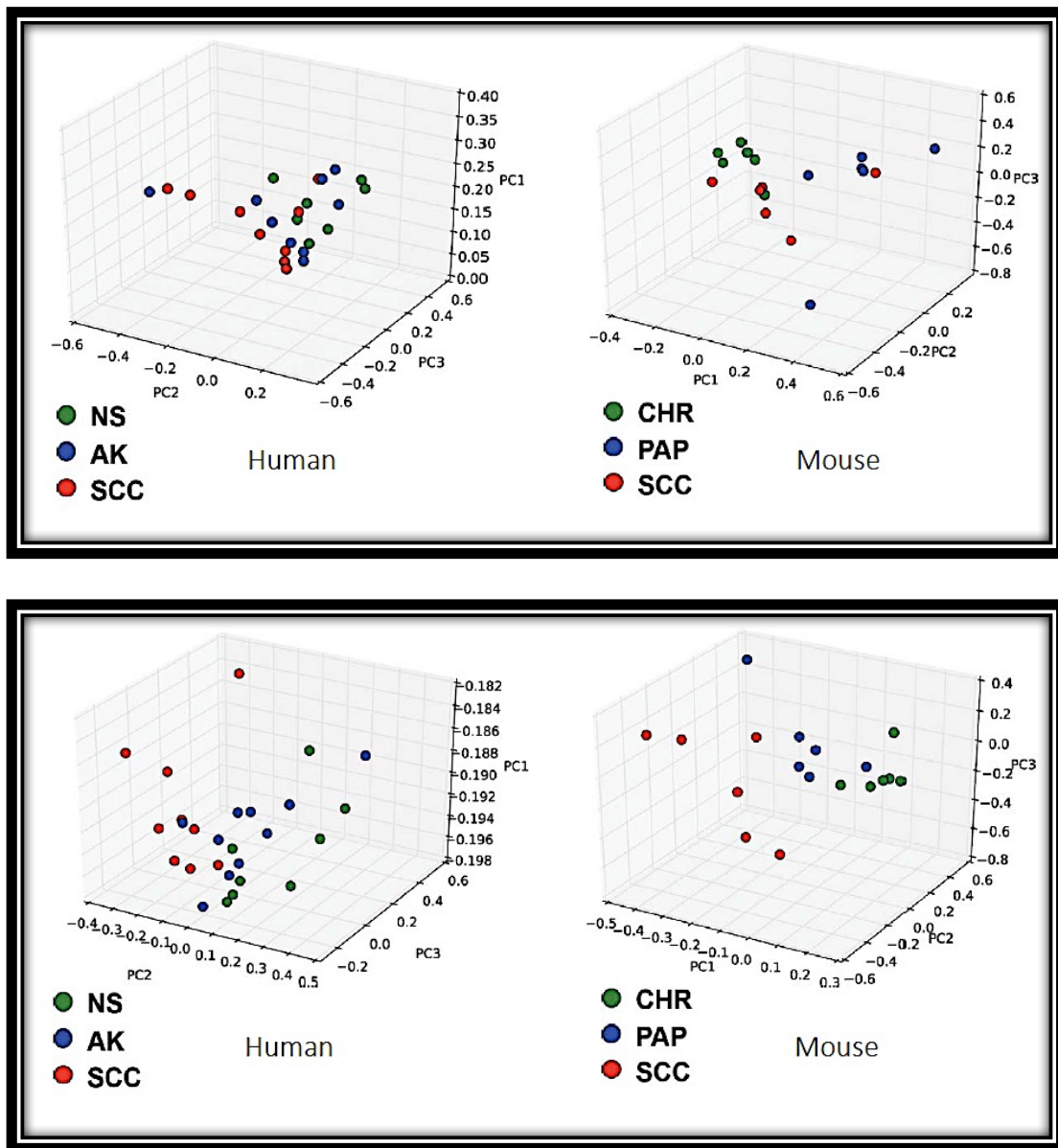
RNA and miRNA-seq were performed on the Illumina Hi-Seq platform to yield an average of 64 million and 6.1 million reads, respectively. No significantly expressed fusion or viral transcripts were detected. Hierarchical clustering of mRNA expression of genes differentially expressed in at least one pairwise comparison demonstrated a clear distinction between NS and cuSCC with AKs interspersed across the spectrum (Figure 35 and Figure 36). This shows that even given uniform histologic criteria, there is a spectrum of AK that transcriptomically resembles UV exposed NS vs. some that resemble cuSCC.





**Figure 35. mRNA profiling across AK / papilloma and cuSCC development.** Hierarchical clustering of mRNA expression of genes differentially expressed in at least one signature in human samples shows that AKs span the spectrum of NS to cuSCC samples.





**Figure 36. Principal component analysis of unsupervised mRNA and miRNA expression.**

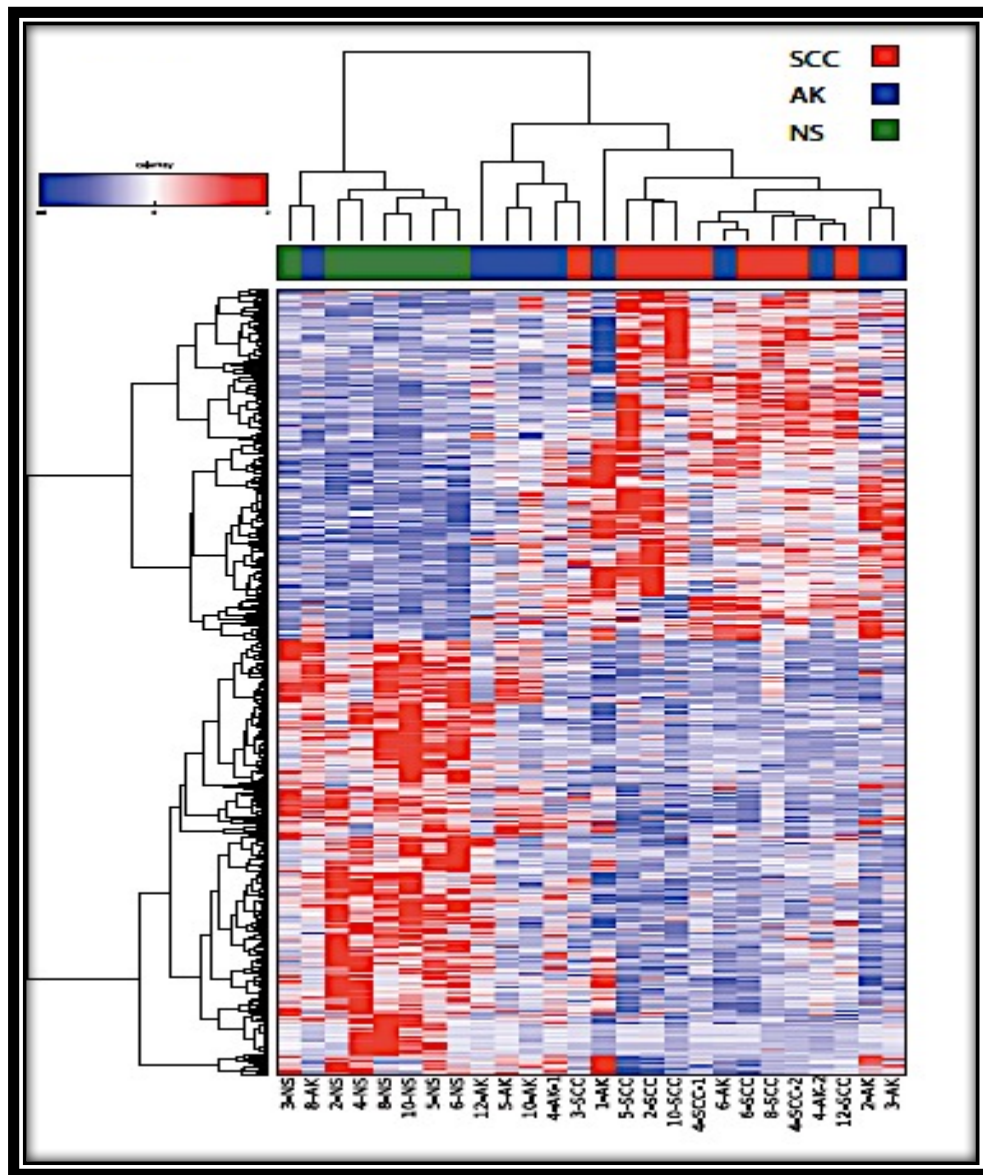
**Top panel)** Using principal component analysis across three dimensions as an alternative means of organizing the transcriptional profiles, the results of the unsupervised clustering are largely recapitulated: cuSCC and AK/PAP segregate away from NS most prominently.

**Bottom panel)** Using principal component analysis across three dimensions as an alternative means of organizing the microRNA profiles, the results of the unsupervised clustering are largely recapitulated: while NS/CHR are very distinctly separated from cuSCC, segregation of AK/PAP



as a distinct group is more clearly seen here as compared to the principal component analysis of mRNA profiles, particularly in mouse.

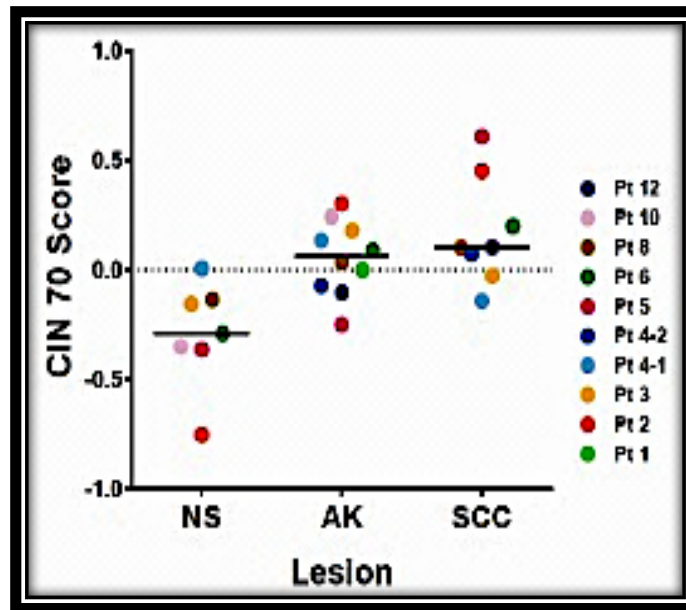
Using recurrently differentially expressed genes in at least 2 of 3 possible pairwise comparisons between NS, AK, and cuSCC to classify samples, clustering showed that AKs predominantly cluster with cuSCC, consistent with the notion that they are largely transcriptomically indistinguishable from cuSCC (Figure 37, Appendix 3).



**Figure 37. Pairwise analysis mRNA profiles primarily distinguish NS and cuSCC, but not AK.** Using only genes differentially expressed in at least 2 of 3 pairwise comparisons ( $p < 0.05$ ),



excellent discrimination is achieved between NS and AK/cuSCC only. AK and cuSCC are both significantly enriched to a similar degree over peritumoral NS for a 70-gene chromosomal instability signature (Figure 38), again reinforcing the idea that AKs have acquired key genomic features of invasive cuSCC [97].

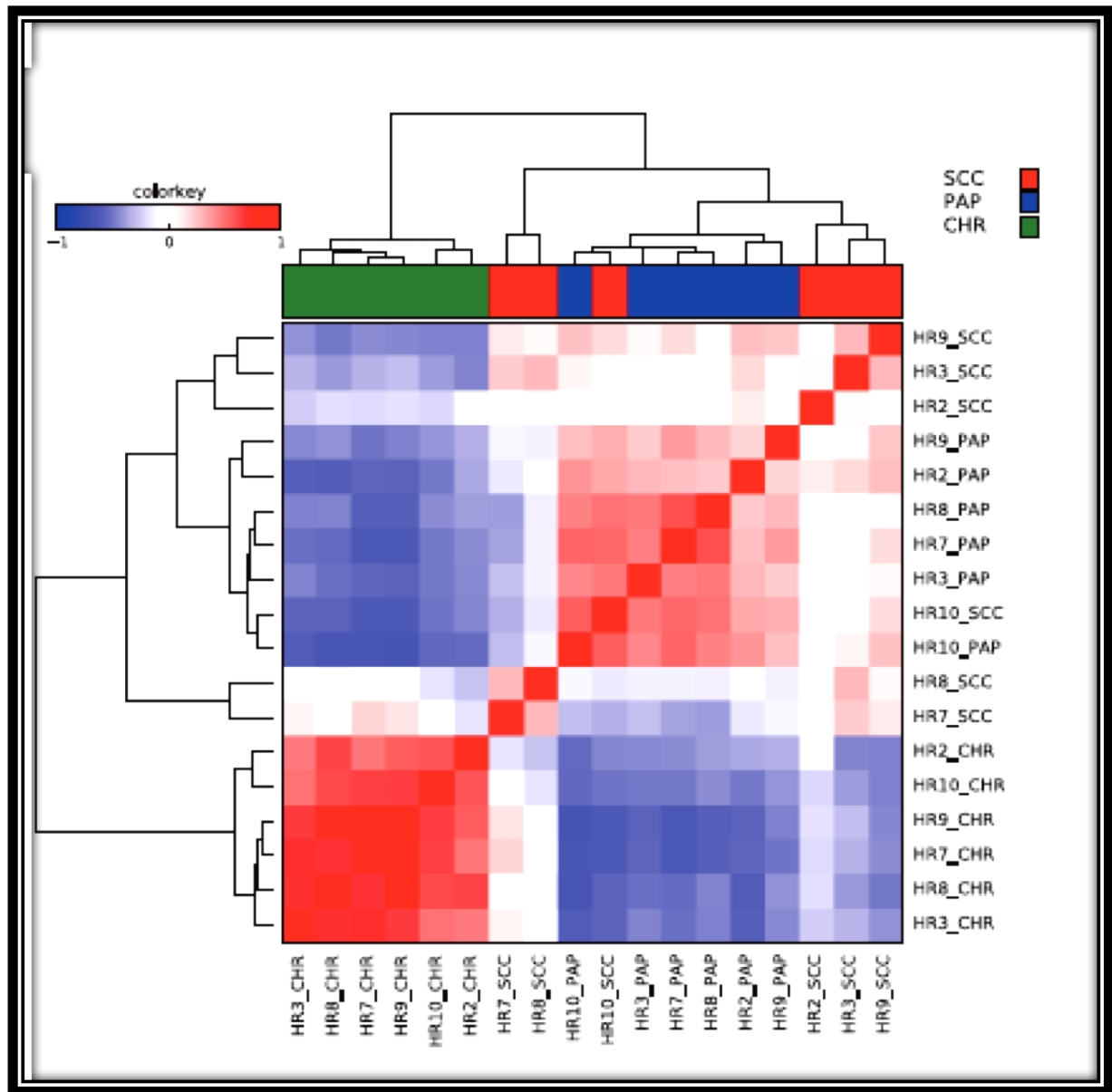


**Figure 38. AKs and cuSCCs have significant chromosomal instability signature.** A 196-gene signature of chromosomal instability derived from human cancers is highly enriched in AK and cuSCC to a similar degree, but not NS. Hierarchical clustering of mRNA expression of genes differentially expressed in at least one signature in mouse samples demonstrates that papillomas much more closely resemble cuSCC than CHR.

RNA-seq results performed on 6 sets of samples from Hairless mice corroborated this concept even more strongly, even though they are an outbred strain (Figure 40). Unsupervised clustering of these samples very clearly delineates CHR away from PAP and cuSCC (Figure 40 and Figure 36). Using recurrently differentially expressed genes in at least 2 of 3 possible pairwise comparisons between CHR, PAP, and cuSCC to classify samples, clustering revealed again that

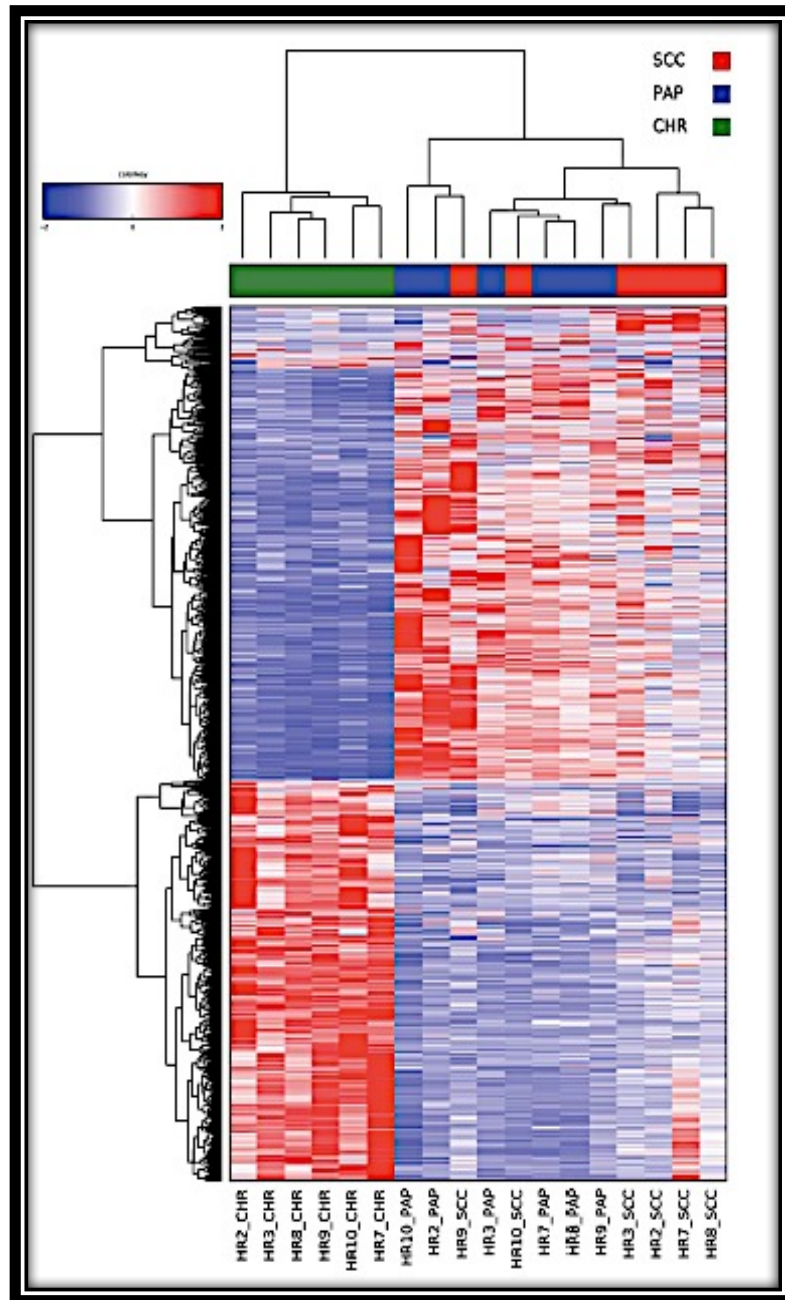


PAP are essentially indistinguishable from cuSCC (Figure 39 and Appendix 4).



**Figure 39. mRNA profiling across AK / papilloma and cuSCC development.** Hierarchical clustering of mRNA expression of genes differentially expressed in at least one signature in mouse samples demonstrates that papillomas much more closely resemble cuSCC than CHR.



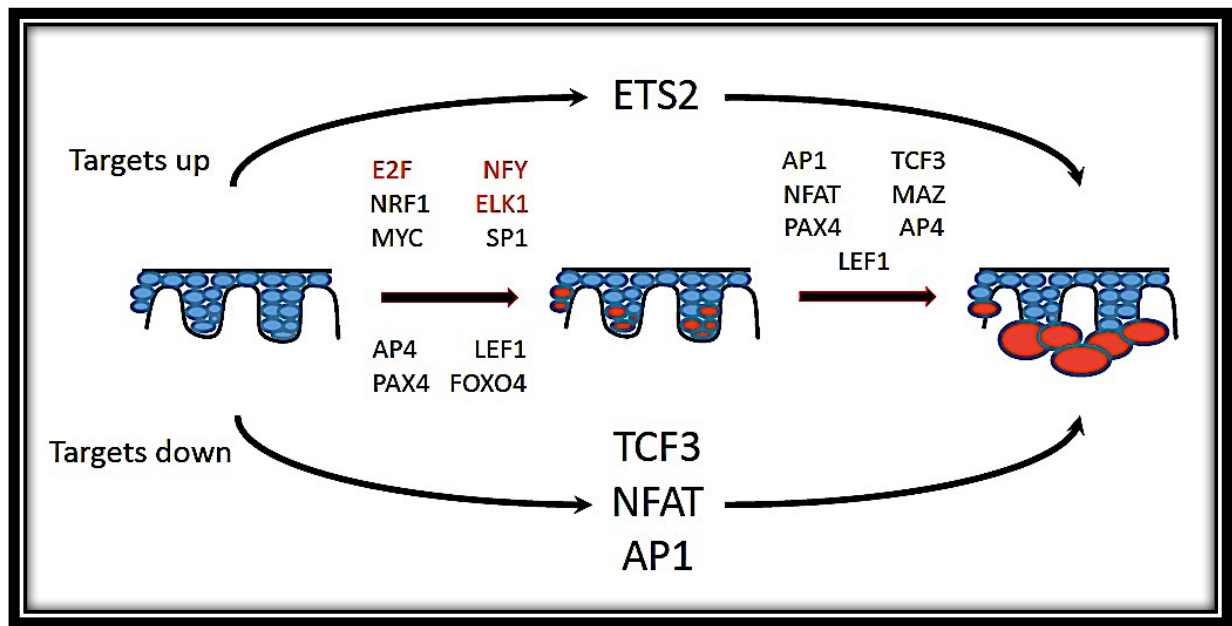


**Figure 40. Pairwise analysis mRNA profiles primarily distinguish CHR and cuSCC, but not PAP.** Using only genes differentially expressed in at least 2 of 3 pairwise comparisons ( $p < 0.05$ ), discrimination is still only achieved between CHR and papilloma/cuSCC, as is the case with human samples.



Next we sought to identify transcription factors that could be responsible for the gene expression changes observed in the course of AK and cuSCC development. Using TRANSFAC based motif analysis [128], we identified significantly represented motifs and their associated transcription factors for all three pairwise comparisons in both human and mice. We identified significant candidate factors by first ranking them by their enrichment scores (Appendix 5).

They were then selected only if their targets were enriched in genes sets that changed in the same direction, for both species, in any one of the adjacent pairwise comparisons: NS/CHR to AK/PAP or AK/PAP to cuSCC. These changes also had to be present and significantly enriched in the NS/CHR to cuSCC comparison. This analysis yielded a total of 16 transcription factors likely to be significant in the development of cuSCC of which were significant early, and 7 of which were significant late (Figure 41).

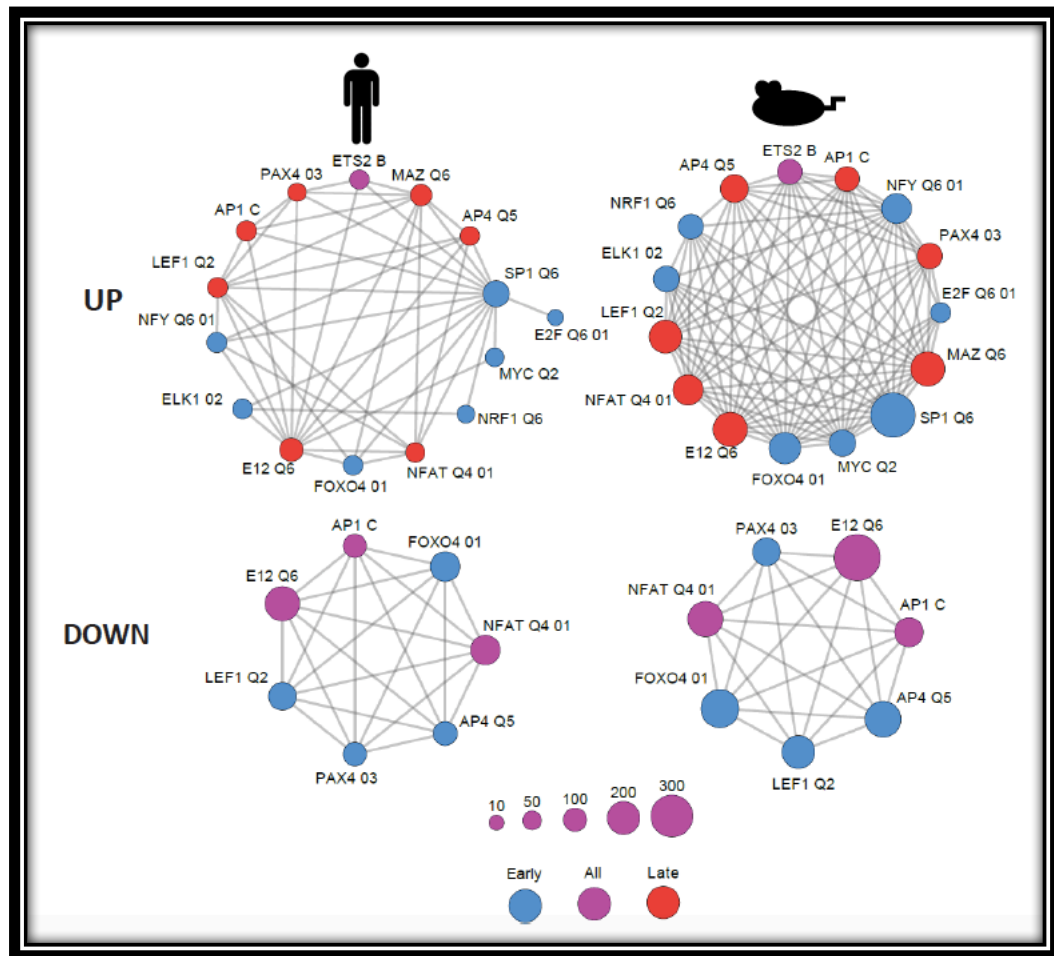


**Figure 41. Cross-species transcription factor motif analysis reveals major drivers of cuSCC development.** Global view of transcription factors with target genes enriched across the entire NS/CHR to AK/PAP to cuSCC progression sequence. Directionality reflects the significant upregulation (above the line) or downregulation (below the line) of predicted targets of the listed



transcription factors. Some factors have targets that are enriched in opposite directions across multiple transitions.

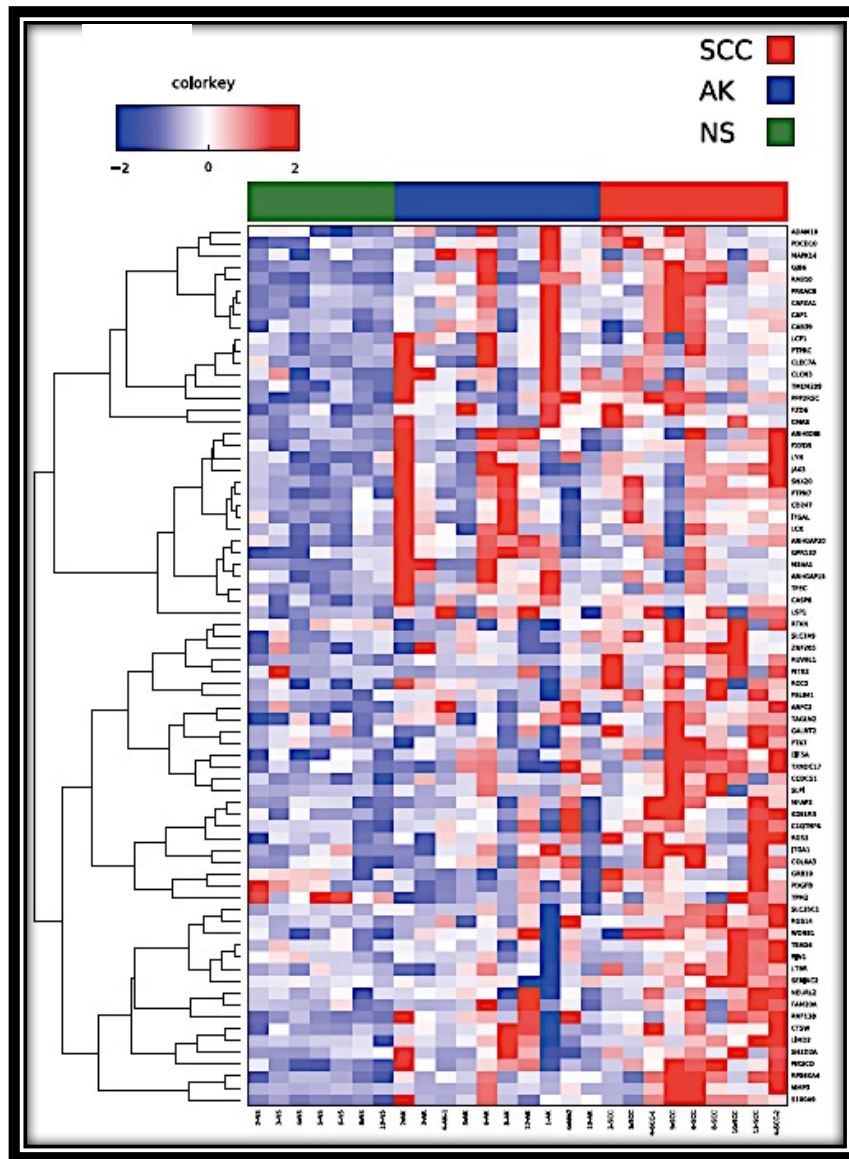
Four such factors were globally important across all pairwise comparisons: ETS2, TCF3, NFAT, and AP1. Gene interaction networks reveal that these transcription factors are highly interconnected, co-regulating up to several hundred genes in concert (Figure 42). Importantly, some transcription factors, such as ETS2 showed unidirectional target modulation, but others such as TCF3, had significant target modulation in opposite directions, reflecting pairwise transition-specific target changes (Figure 43).



**Figure 42. Network analysis demonstrates that core transcriptional drivers are highly interconnected in both human (left) and mouse (right).**



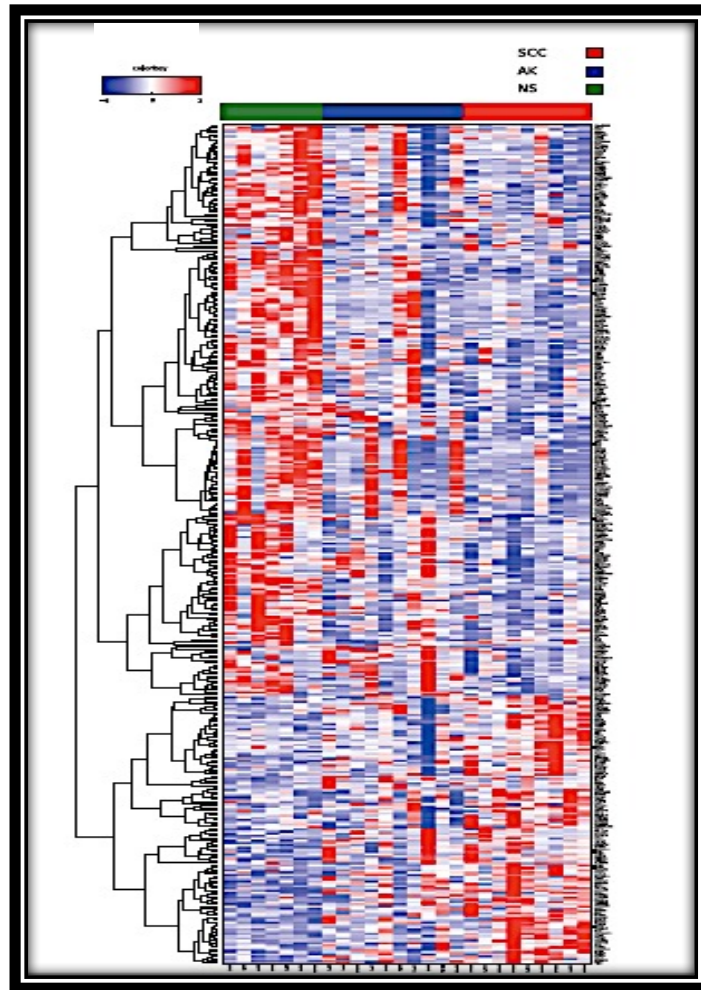
Profiles of the four globally important transcription factors showed significant upregulation of ETS2 and downregulation of TCF3, NFAT, and AP1 targets across the entire progression sequence (Figure 41 and Appendix 5). ETS2 is pro-oncogenic in multiple other contexts, and is downstream of the ERK MAP kinase signaling module [129], which is known to be important in sporadic and BRAF-inhibitor-induced cuSCC development [130, 131].



**Figure 43. ETS2 targets are upregulated across the continuum of samples.** As expected,  $\beta$ -catenin/Wnt signaling plays an important role in cuSCC pathogenesis and this is reflected in the importance in this analysis of both TCF3 and LEF1 activity. TCF3 can function



as a transcriptional repressor and activator and has been implicated in skin homeostasis and wound healing [132, 133]. Our data suggest an important role in cuSCC development as well (Figure 44).



**Figure 44. TCF3 gene targets pattern of expression.** TCF3 gene targets that are overall downregulated have greater significance across the continuum than those that are upregulated in the late stage transition (AK/PAP to cuSCC).

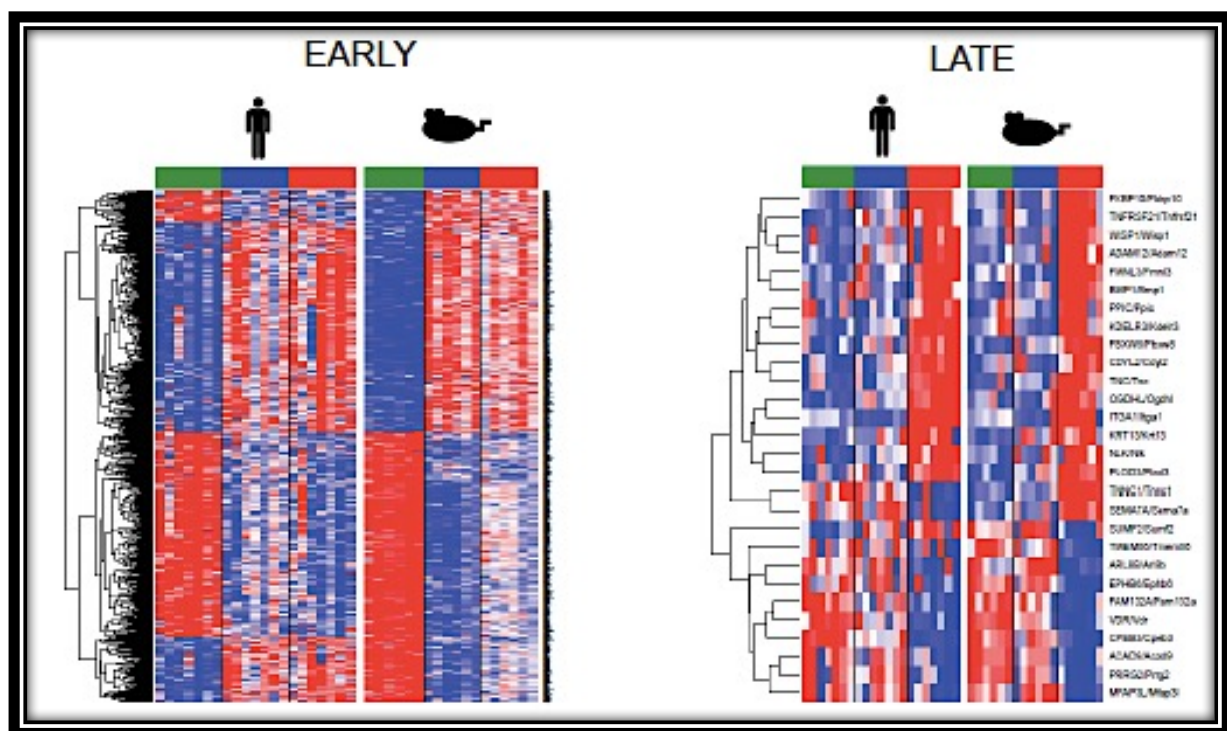
LEF1 is activated across the spectrum of samples, with targets significantly downregulated early and upregulated late (Figure 45- left panel), and is an established effector of  $\beta$ -catenin/WNT signaling [134]. The downregulation of NFAT targets may reflect an inhibition of keratinocyte differentiation programs that may be modulated by NOTCH signaling and further compromise TP53-dependent tumor suppression [135, 136].







Similarly, the downregulation of AP1 target genes across the continuum of cuSCC development (Figure 45- right panel) suggests a similar compromise of normal epidermal differentiation [137]. Consistent with our global transcriptomic data, most of the transcriptional drivers act early to induce changes in the NS to AK/PAP transition, and include NFY, E2F, and MYC activation, the latter two of which have been implicated in cuSCC development [130] (Figure 46).



**Figure 46. Significant gene expression changes occur in the early transition.** The linear effects model of mRNA expression changes across cuSCC development in both species demonstrates that the vast majority of significant gene expression changes occur in the early transition from NS/CHR to AK/PAP.

In GATHER-based analysis of TRANSFAC motifs within concordantly differentially-expressed genes [103] by this analysis, E2F and NFY (Appendix 7) were again highlighted in the early stage transition from NS to AK/PAP in both mouse and human. ELK1, which is likewise



regulated by the ERK MAPK pathway, was also indicated as significant by both analyses (Figure 41 and Appendix 7). No enriched transcription factor signatures were identified for the late stage transition from AK/PAP to cuSCC.

Based upon these sets of differentially expressed genes, Ingenuity Pathway Analysis of both human and mouse data was performed individually (Appendix 13) and identified strongly overlapping key pathways including cell cycle progression, mitotic roles of polo-like kinase, and DNA damage checkpoint functions, as well as upstream regulators E2F1, E2F4, CDK4, TP53, RABL6, and ERBB2. While the E2Fs, CDK4, and TP53 are further identified here as critical regulators of cuSCC development, RABL6 and ERBB2 (HER2), both of which are expressed in skin, may yield novel targets for intervention [138, 139].

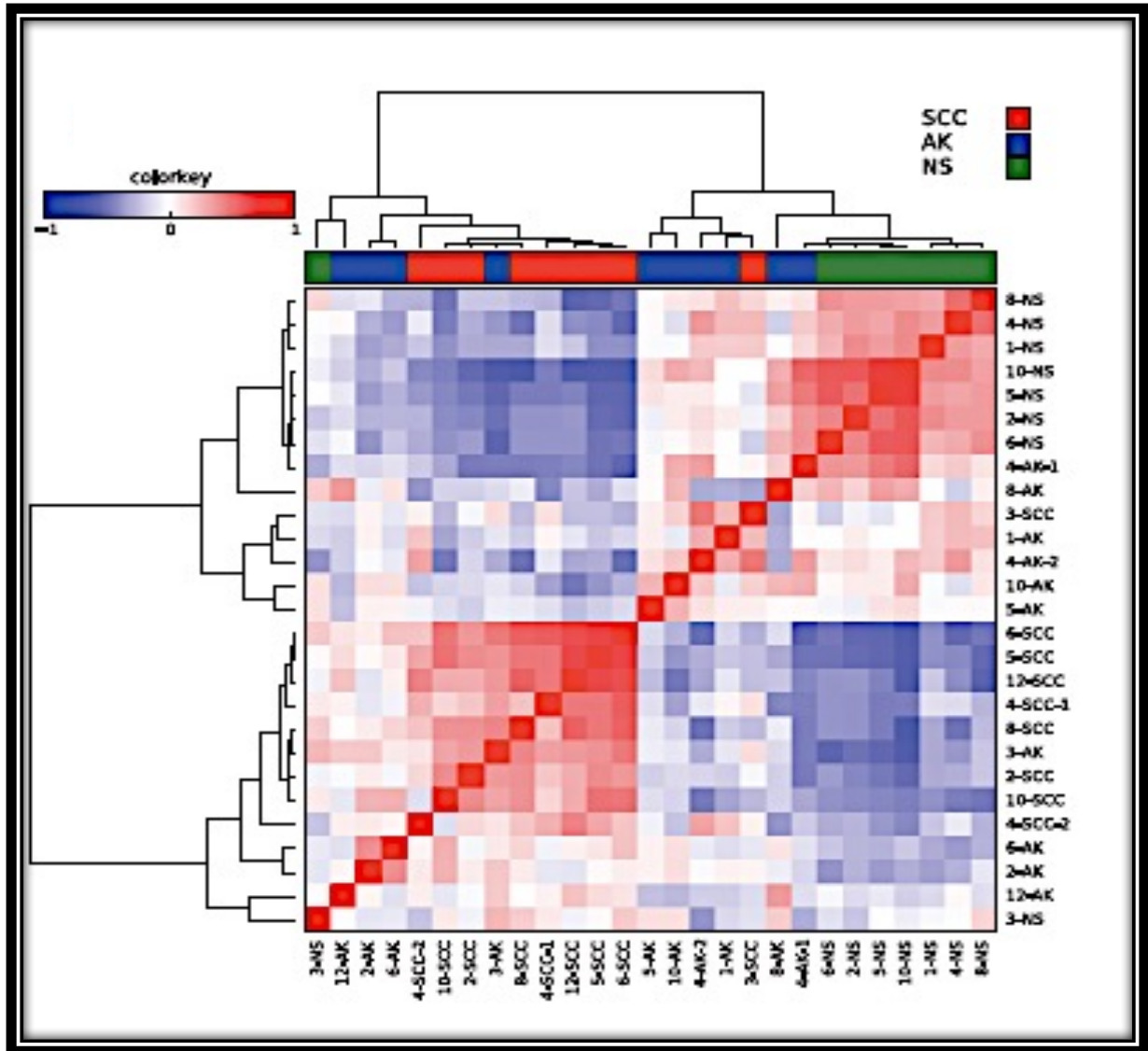
The transcriptional networks identified in both the pairwise analyses and the progression model analysis implicate pathways important in cuSCC development, mostly early in the NS/CHR to AK/PAP transition, notably E2F, MYC, ELK1, and NFY. ERK signaling through ETS2,  $\beta$ -catenin signaling through TCF3 and LEF1, and pathways regulated by NFAT and AP1 that likely impinge upon keratinocyte differentiation, were implicated globally across the entire development sequence (Figure 41 and Figure 42).

The majority of both NFAT and AP1 targets are downregulated in the course of cuSCC development, with less significant upregulation of targets in the late transition (AK/PAP to cuSCC). Targets of E2F and NFY are significantly upregulated early (NS to AK/PAP) and these were also highlighted in the linear mixed effects model of progression which are highlighted in red in panel.



### 3.4 MicroRNA sequencing and integrated analysis

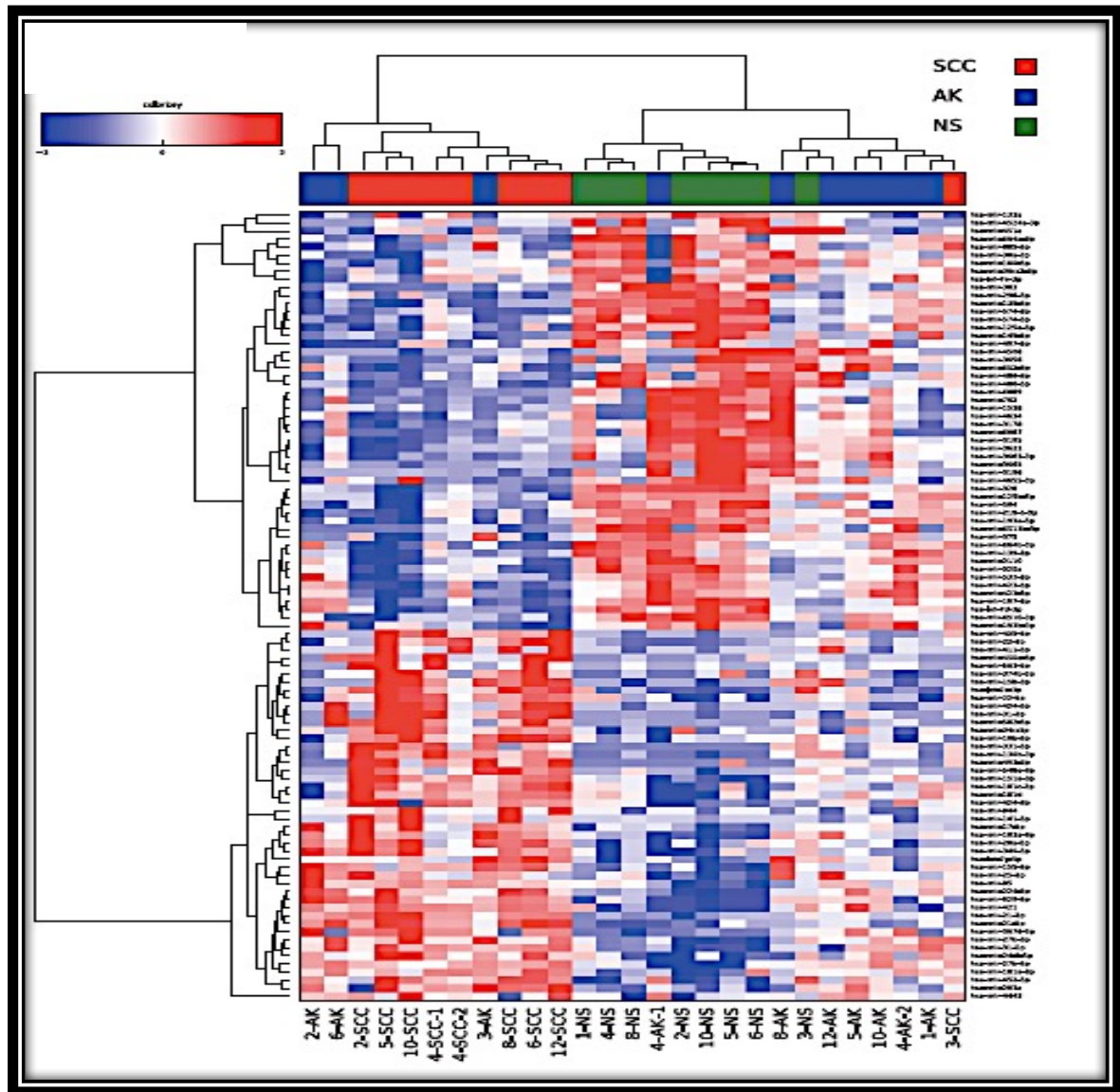
Relative to mRNA, clustering of microRNAs differentially expressed in at least one pairwise comparison among the matched human samples showed a better ability to distinguish the three sample classes (Figure 47).



**Figure 47. microRNA profiling across AK / papilloma and cuSCC development.** Hierarchical clustering of microRNAs differentially expressed in at least one signature in human samples shows that significantly improved discrimination between three sample types is achieved as compared to mRNA profiles.



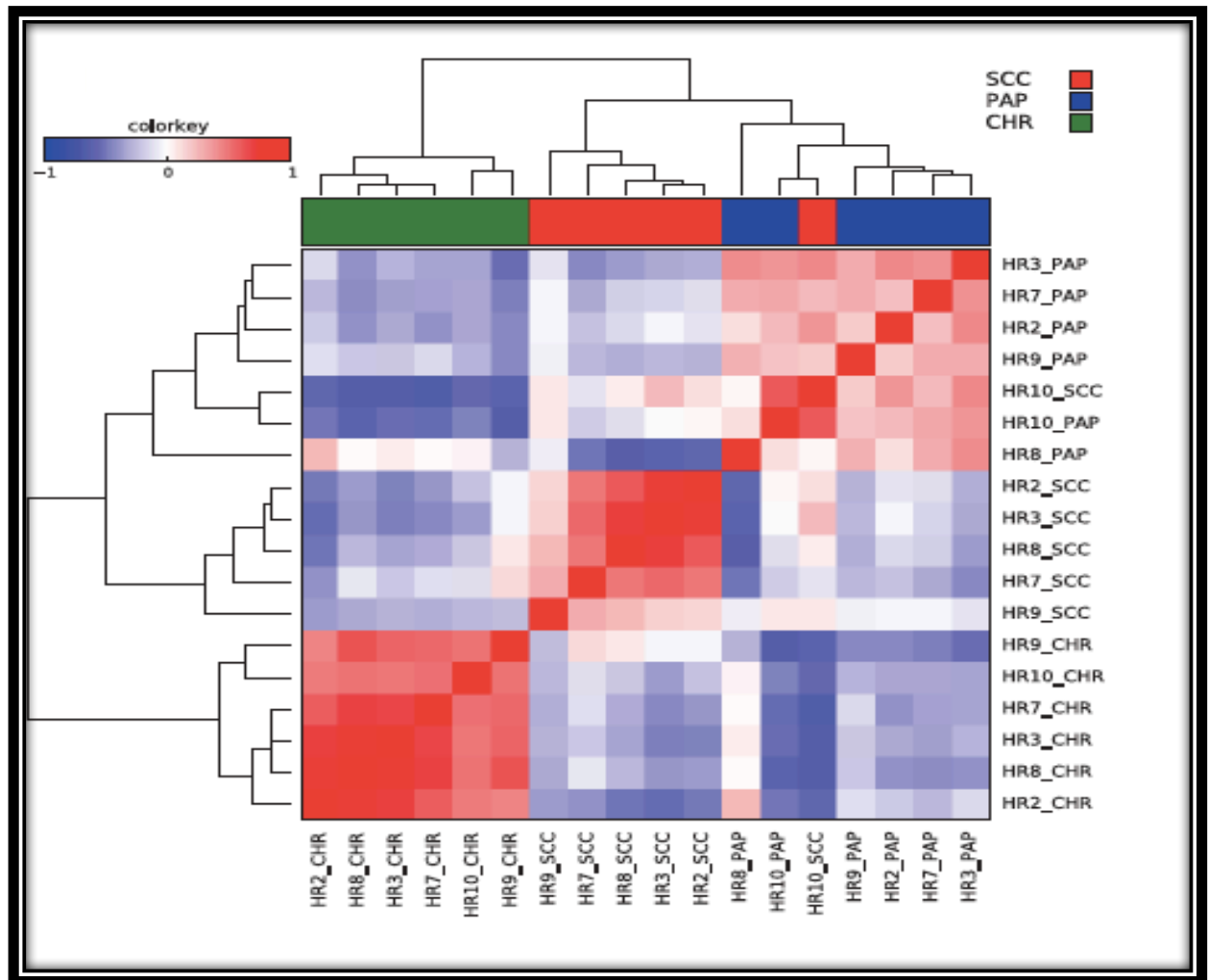
When recurrent statistically significant changes occurring in at least 2 of 3 pairwise comparisons are used, it is clear that AKs now define a pattern of microRNA expression that is intermediate between NS and cuSCC, with improved discrimination among all three sample types (Figure 48, Appendix 8).



**Figure 48. Human micro-RNA profiles have significantly higher discriminatory power.** Using only microRNAs differentially expressed in at least 2 of 3 pairwise comparisons ( $p < 0.05$ ), robust discrimination is achieved between NS and cuSCC with most AKs occupying an intermediate expression pattern.

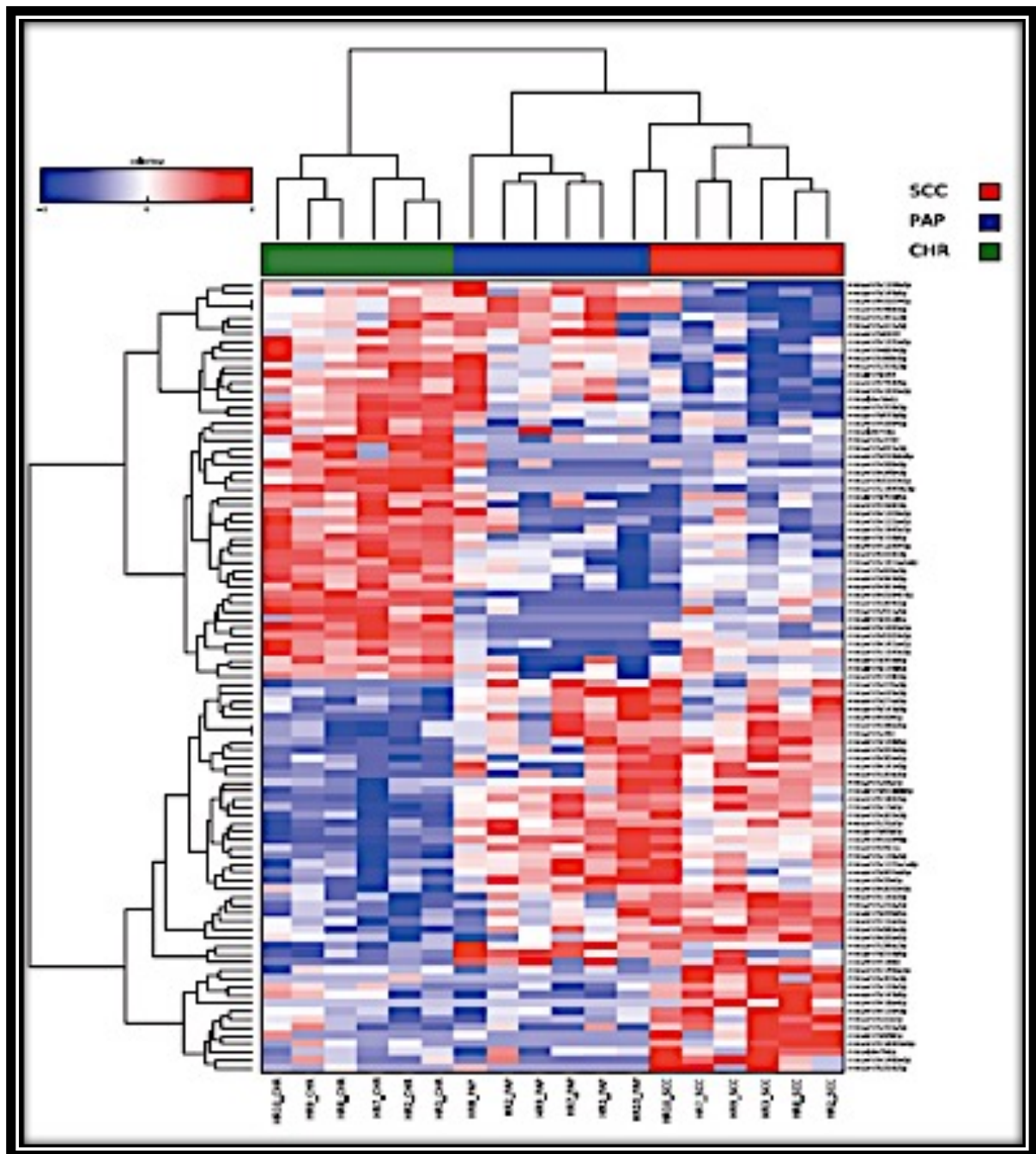


Whereas unsupervised clustering of mRNA expression in the Hairless mouse model failed to distinguish papillomas from cuSCC (Figure 49 and Figure 50), unsupervised clustering of microRNA expression more clearly separates all three sample types (Figure 49,50 and Appendix 9). Therefore, in both humans and the UV-driven mouse model, microRNAs appear to have more discriminatory power compared to mRNA to segregate the main sample types.



**Figure 49. Mouse micro-RNA profiles have significantly higher discriminatory power.** Hierarchical clustering of microRNAs differentially expressed in at least one signature in mouse samples shows distinct patterns among the three sample types as compared to mRNA profiles.

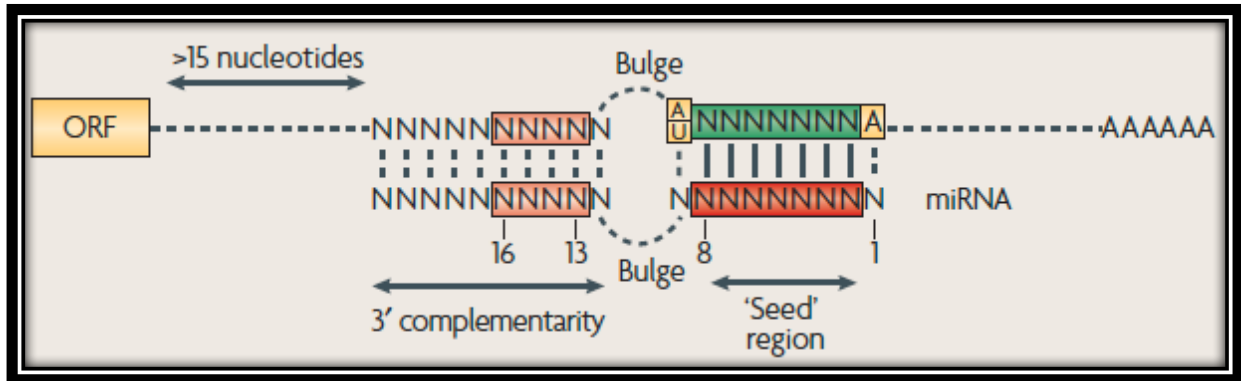




**Figure 50. Mouse pairwise micro-RNA profiles can distinguish the 3 lesion types.** Using only microRNAs differentially expressed in at least 2 of 3 pairwise comparisons ( $p < 0.05$ ), CHR and cuSCC are very strongly segregated with an intermediate group dominated by PAP.



Given that microRNAs can negatively regulate their target mRNA expression by Watson-Crick pairing over a 7-8 nucleotide seed region, these targets can be computationally predicted [140] (Figure 51).



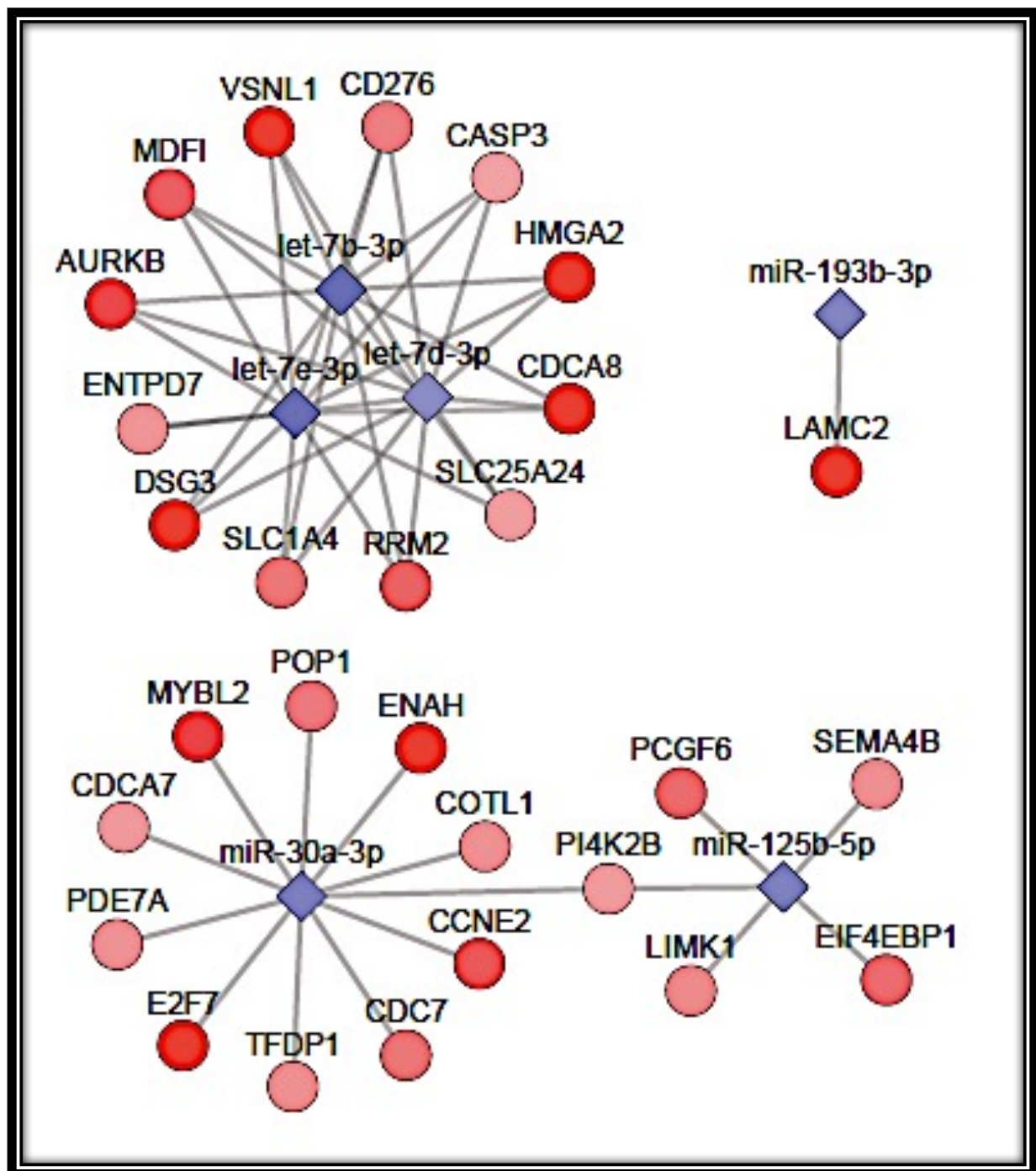
**Figure 51. MicroRNAs (miRNAs) interact with their mRNA targets by base pairing.** For miRNA–mRNA base pairing there must be a contiguous base pairing of 2 to 8 nucleotide, also known as 'seed' region (shown in dark red and green). The A residue across position 1 of the miRNA, and an A or U across position 9 (shown in yellow), improve the site efficiency, although they do not need to base pair with miRNA nucleotides. Reproduced by permission from the following article: Title: Mechanisms of post-transcriptional regulation by microRNAs: are the answers in sight? Publication: Nature Reviews Genetics, License Number: 3822801068546.

We performed functional pair analysis by identifying miRNA-mRNA pairs predicted to be linked by a seed sequence in the 3'UTR of the mRNA and that were significantly anti-correlated in expression changes [141]. Corresponding analysis was done for mouse samples as well. Functional pairs in both species were ranked by all possible pairwise comparisons in which they were significantly differentially expressed (rather than by stage), and an integrated network map was generated to identify several key microRNAs with multiply-targeted mRNAs (Figure 52 and 53).









**Figure 53. Functional pair analysis of downregulated miRNA and upregulated d mRNA.**

Functional pair analysis identifies conserved, highly interconnected microRNA-mRNA regulatory networks. This graph shows downregulated miRs and thier upregulated target mRNAs.

The microRNAs significantly upregulated in this analysis included miRs-17, 20a, 21, 31, 93, 106b, and 200a (Figure 52), and those significantly downregulated included let-7 family



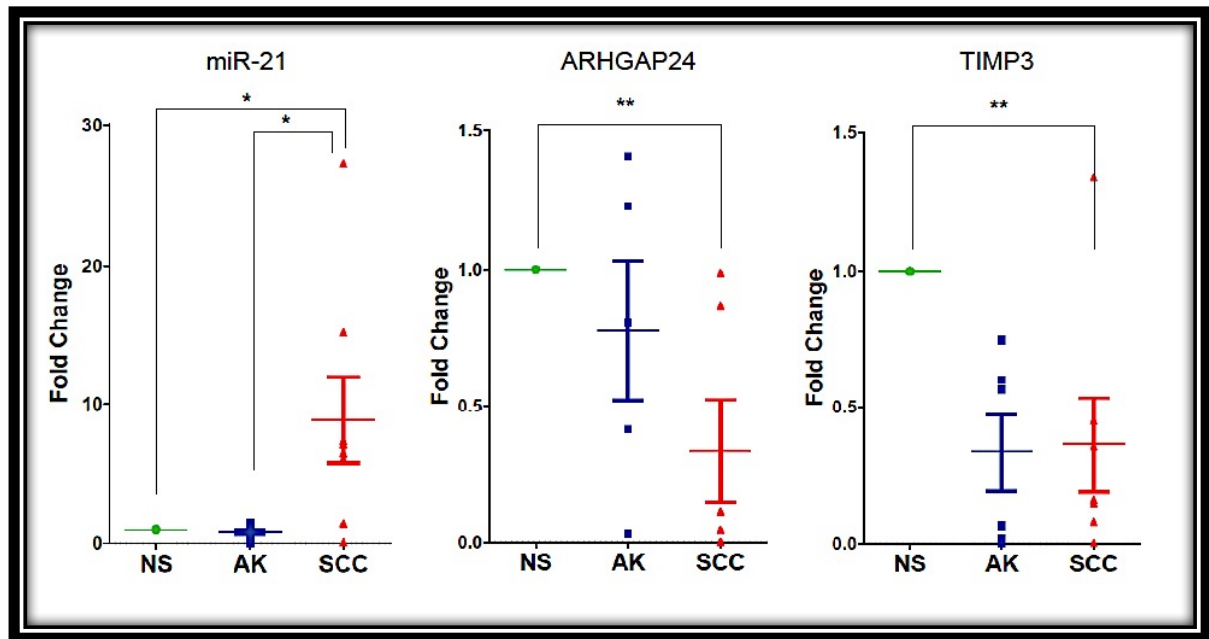
members and miRs-30a and 125b (Figure 53). Some of these microRNAs are confirmed in our data to be significant in cuSCC. miR-21 and miR-31 have been shown to be upregulated in a number of cancers including cuSCC [142-144], although the identity of the most relevant mRNA targets is not known. In many instances, functionally paired mRNAs were predicted to be targeted by multiple microRNAs.

We validated the expression levels of miR-21 and miR-31 and of selected predicted target genes in additional sets (n=21) of matched human samples of NS, AK, and cuSCC (Figure 54, 55, and Appendix 10). PTPN14 is a tumor suppressor tyrosine phosphatase which plays a role in the regulation of lymphangiogenesis, cell-cell adhesion, cell-matrix adhesion, cell migration, cell growth and also regulates TGF-beta gene expression, thereby modulating epithelial-mesenchymal transition [145]. PTPN14 also mediates beta-catenin dephosphorylation at adhesion junctions. PTPN14 acts as a negative regulator of the oncogenic property of YAP, a downstream target of the hippo pathway, in a cell density-dependent manner [145]. ARHGAP24 encodes a negative regulator of Rho GTPases involved in actin remodeling, cell polarity, and cellular migration [146]. TIMP3 is metalloproteinase inhibitor and its differential expression affects tumor progression and angiogenesis in melanomas through regulation of endothelial cell migration. TIMP3 inhibits angiogenesis by blockage of VEGF binding to VEGF receptor-2 [147].

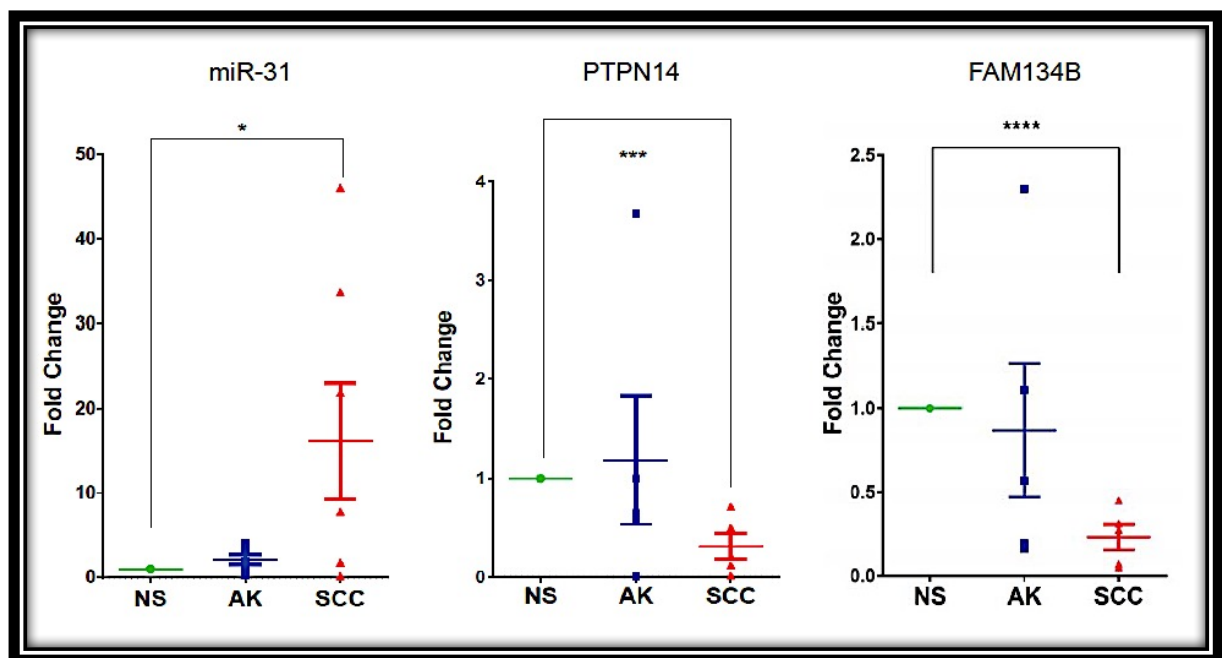
miR-21 was substantially upregulated by  $8.9 \pm 3.1$ -fold across the progression sequence, with respective downregulation of the predicted targets ARHGAP24 ( $2.9 \pm 0.6$ -fold) and TIMP3 ( $3.0 \pm 0.4$ -fold) (Figure 54). ARHGAP24 is a RAC1 GAP [148], and TIMP3 suppresses metalloproteinase function, both of which are consistent with tumor suppressive functions. miR-31 was also upregulated ( $16.2 \pm 6.8$ -fold) across cuSCC development and predicted to downregulate PTPN14 ( $3.2 \pm 0.4$ -fold), a phosphatase involved in protein trafficking [149] and



which downregulates YAP signaling [145] (Figure 55). In addition, FAM134B, a putative tumor suppressor [150, 151] was identified as a potential target of miR-31 (Figure 55).



**Figure 54. Validation of miR-21 in a distinct set of human matched samples.** miR-21 is upregulated between NS and cuSCC and it's predicted targets ARHGAP24 and TIMP3 are downregulated.

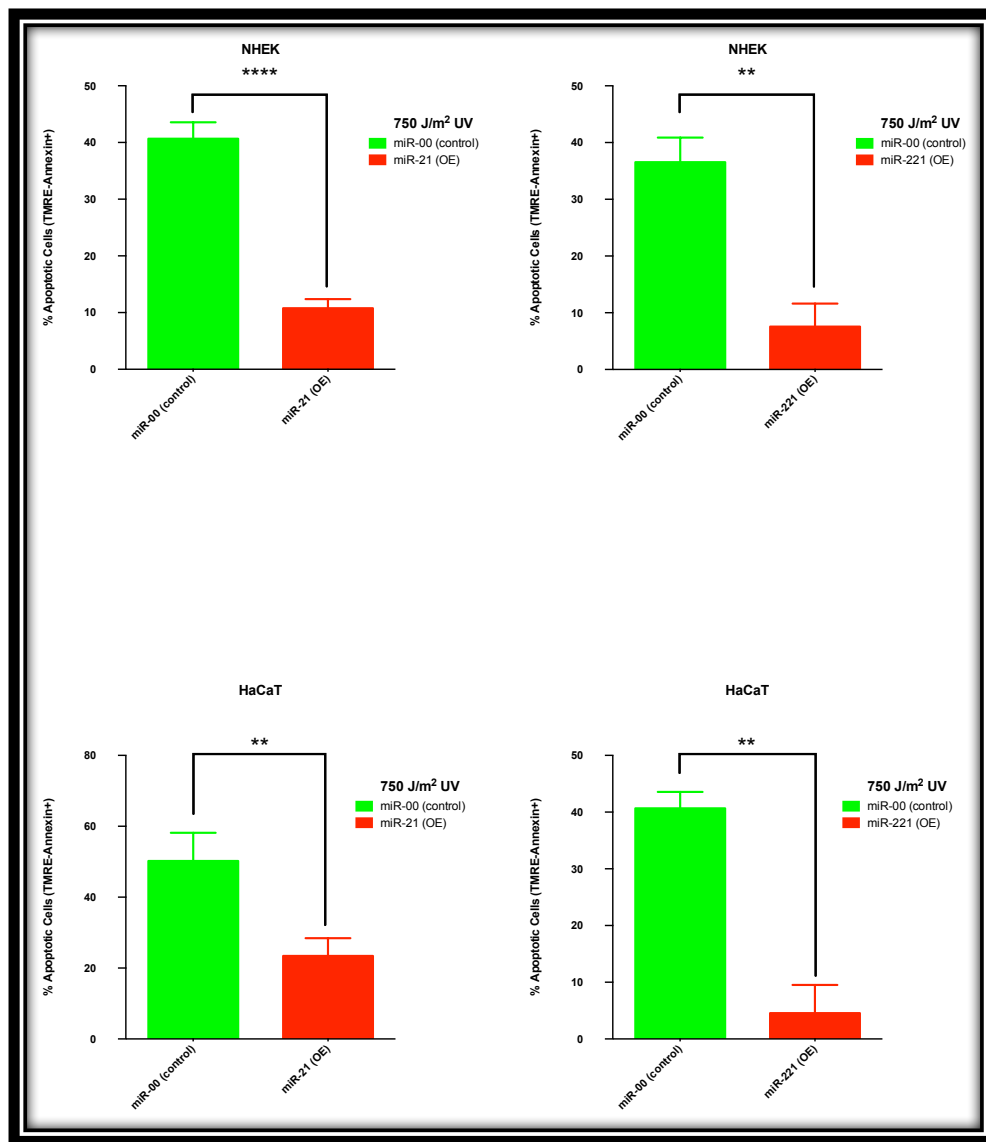


**Figure 55. Validation of miR-31 in a distinct set of human matched samples.** miR-31 is



upregulated between NS and cuSCC and it's predicted targets PTPN14 and FAM134B are downregulated.

Next, we validated the role of miR-21 and miR-221 in UV-induced apoptosis. We used lenti-miRNA vector for stable over expression of miR-21, miR-221 or miR-00 control vector (SBI). Using Flow cytometry (FACS) we show that overexpression miR-21 and miR-221 significantly suppresses UV-induced apoptosis. We are investigating the mechanism by which this occurs.



**Figure 56. Overexpression of miR-21 and miR-221 suppresses UV induced apoptosis.**



Interestingly, the let-7 family of microRNAs are prominently represented in downregulated microRNAs, consistent with their putative tumor suppressor roles [152], and one of the predicted targets, HMG2A was substantially upregulated in a validation cohort by  $45.4 \pm 14.5$ -fold. These specific pairs would need to be functionally validated as well to provide mechanistic links, but these data show that our cross-species functional pair analysis is robust.

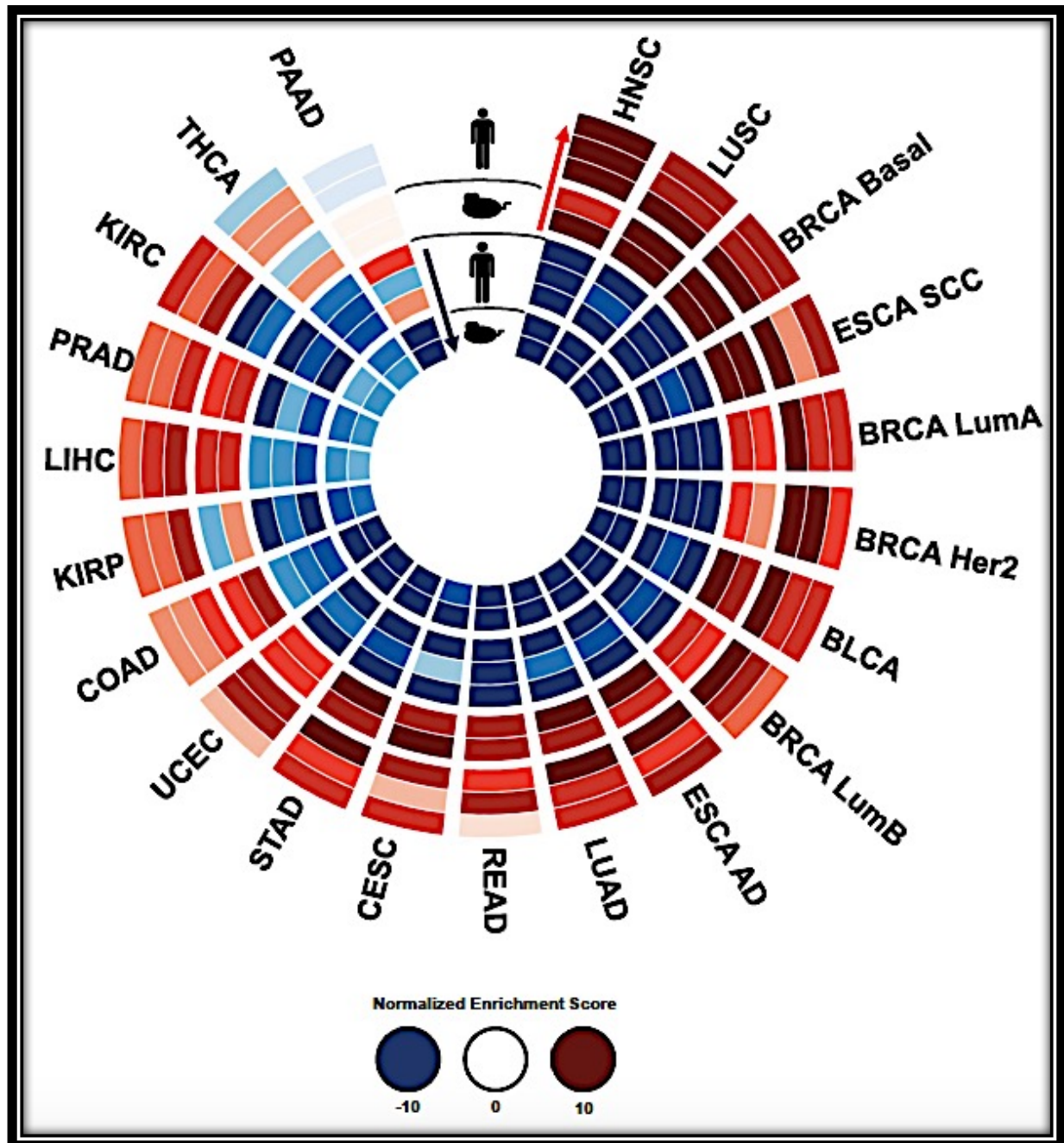
### **3.5 Relationship of cuSCC to other SCC**

Many tumor types have been subjected to large scale genomic profiling including through the TCGA effort, including multiple types of SCC arising in diverse sites, such as lung, esophagus, bladder, cervix, and head & neck SCC. Recently several profiling efforts have concentrated on exome sequencing of cutaneous SCC. These combined efforts have collectively identified common pathway alterations for many SCCs. TP53 mutations occur at over 70% frequency in all SCCs; NOTCH family genes are mutated in over 70% of cuSCC [49,50], 10-20% of head & neck SCC (HNSCC) [153-155], 13% of lung SCC [156], and 10% of esophageal SCC [157]; and SOX2 amplification is a common lineage-specific driver of SCC [158].

To test the hypothesis that mRNA expression profiles would reveal molecular commonalities between all SCC, we profiled our NS/cuSCC signature against cancers in the TCGA using gene set enrichment analysis (GSEA). Furthermore, we surmised that there would be major differences between carcinogen-driven vs. virally-driven SCC, as has been observed in HNSCC [124, 153]. We found that cuSCC is most similar to HNSCC, followed by lung SCC, triplenegative breast cancer (basal type), and esophageal SCC and not closely related to cervical SCC, which is overwhelmingly human papillomavirus (HPV)-driven (Figure 57, Appendix 11). This establishes transcriptomic evidence that deep molecular commonalities exist between carcinogen-driven SCCs of multiple tissue sites, a concept supported by the mutational data, and



suggests that common molecular strategies for prevention and treatment of multiple types of SCCs may exist.



**Figure 57.** cuSCC is molecularly related to carcinogen-driven SCCs of multiple sites. GSEA analysis of all significant pairwise comparisons in both mouse (CHR vs. PAP, CHR vs. cuSCC) and human (NS vs. AK, AK vs. cuSCC, NS vs. cuSCC) represented as a CIRCOS plot. For all



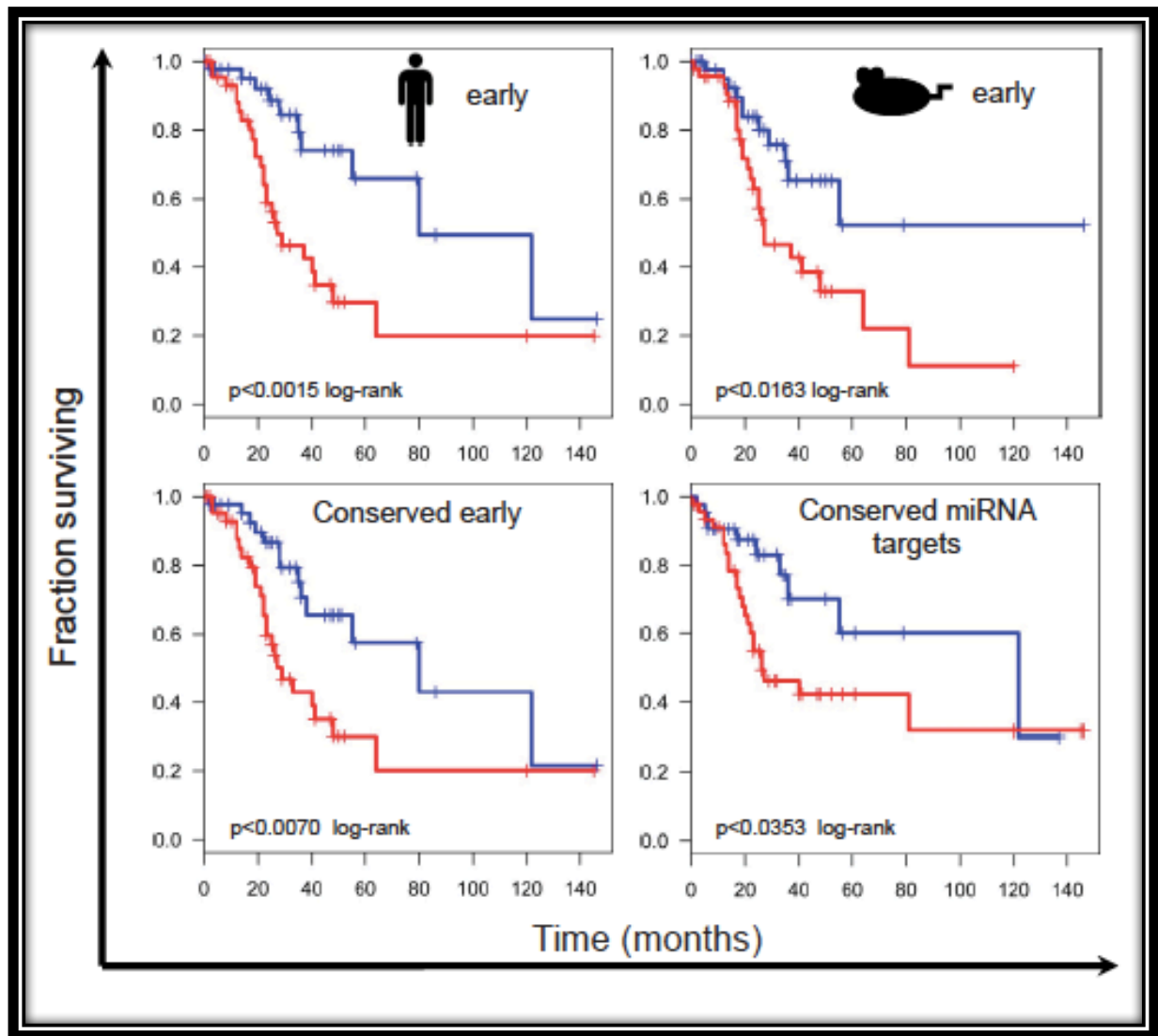
cancers profiled in the TCGA, normalized enrichment scores for each signature were determined and cancer types ranked by descending order (clockwise) of the sum of squares of all the scores with a penalty . By this measure, cuSCC is most closely related to head & neck SCC (HNSC), lung SCC (LUSC), basal subtype of breast cancer (BRCA), and esophageal SCC (ESCA).

Given that HNSCC is consistently the most closely related tumor to cuSCC, we asked whether cuSCC-derived signatures from our cohort of well-differentiated tumors could also be used to predict outcome in carcinogen-driven (non-HPV) HNSCCs, which have TP53 mutations and high mutational loads. Indeed, cuSCC-associated gene expression changes were associated with significantly worse survival outcome in patients with TP53-mutant HNSCC tumors [155](Figure 58). When we restricted the cuSCC signatures to early genes identified in the LME progression model for either human or mouse independently, both signatures were significantly predictive of overall survival (Figure 58 top row).

Similarly, when we used only the cross-species intersection of these two signatures of early genes, this was again significantly predictive of overall survival (Figure 58 – bottom left), a finding further corroborated by the fact that both NS/AK and CHR/PAP signatures also individually predicted outcome in HNSCC.

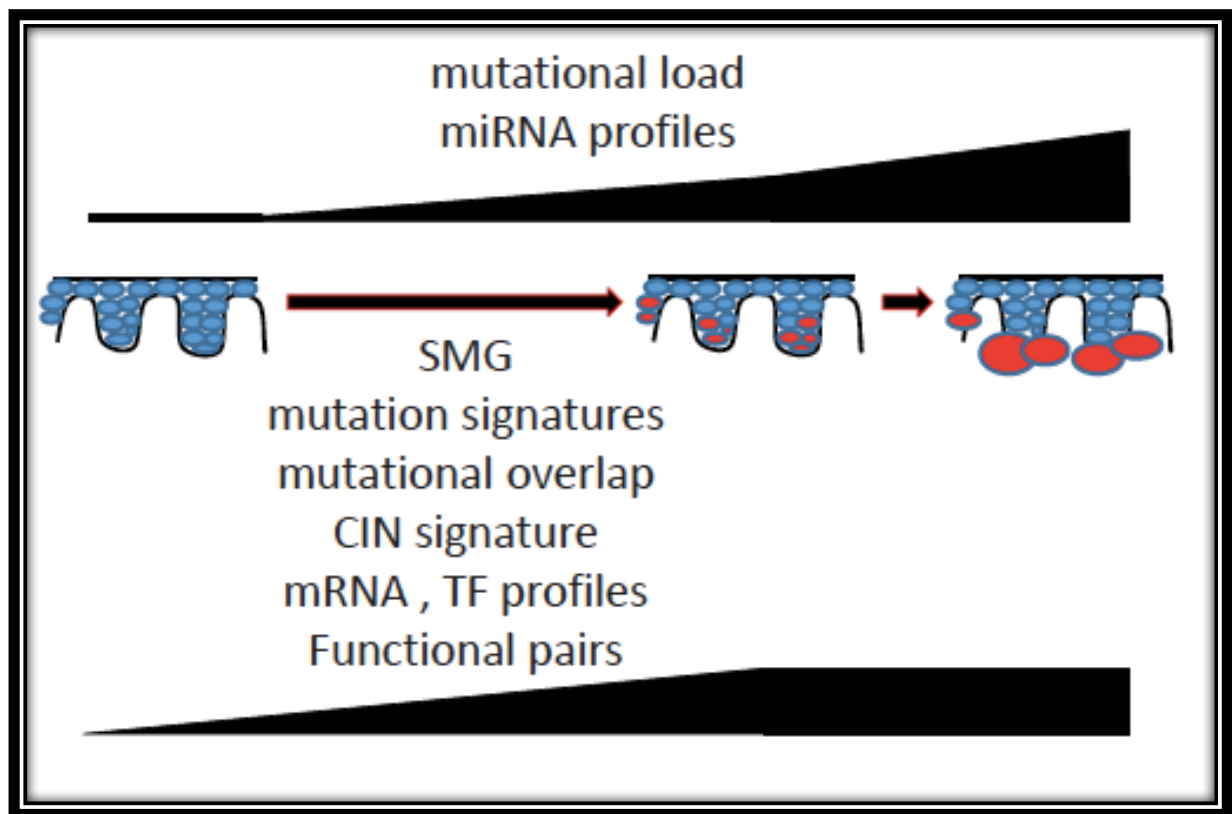
Most importantly, a 196-gene signature derived solely from the crossspecies microRNA functional pair analysis (Figure 52 and 53) had significant predictive power for overall survival (Figure 58 – bottom right), showing that these microRNA target genes likely regulate not only important processes in cuSCC development, but also drivers of disease outcome in HNSCC.





**Figure 58. cuSCC signature acts as a prognostic marker in a cancer subtype specific manner.** Given that HNSC is most closely related to cuSCC by this measure, we show that cuSCC signatures can predict outcome (overall survival) in HNSC with TP53 mutation, used here as a proxy for identifying tumors that do not express high-risk HPV. The cross-species early signatures derived from the linear mixed effects model and the cross-species microRNA functional analysis all predict survival in HNSCC for the top and bottom 25% of outcomes.





**Figure 59. Schematic diagram of our data summary.** Our data show that AKs have acquired many of the properties of cuSCC as assessed by SMG, mutational overlap, mutational signatures, chromosomal instability signature, mRNA and transcription factor profiles, and functional pair analysis, although overall mutational load and unsupervised microRNA clustering do enable separation of the three sample types.



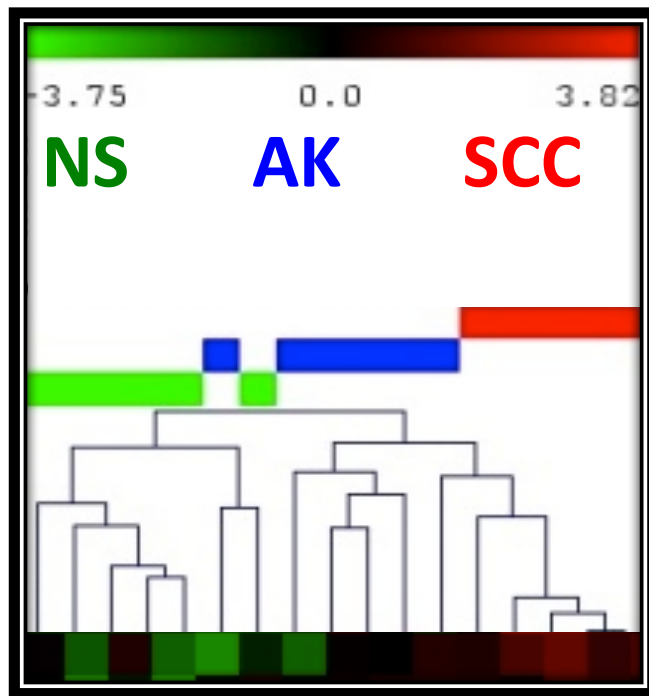
## **Chapter 4**

# **Functional characterization of miR-181a and TGFBR3**



#### 4.1 miR-181a a potential novel diagnostic biomarker and therapeutic target in cuSCC

miR-181a is significantly upregulated in multiple carcinomas. Through initial analysis of 9 sets of matched samples, miR-181a was identified as a potential novel diagnostic biomarker and therapeutic target. Expression of the miR-181 family gradually increases throughout cuSCC progression. Figure 60 is a blown up heat map from miRNA data of our human patient samples, showing steadily increase in miR-181a levels; over 6 folds as we transition from NS in green to AK in blue and subsequently to cuSCC in red.



**Figure 60. Supervised hierarchical clustering reveals differential expression of miR-181a.** Partial heat map (first 6 set of paired samples) reveals expression changes of miR-181a that correlate highly ( $P < 0.009$ ) with sample class (normal skin in green, AKs in blue, and cuSCC in red).

Bioinformatics screening of mRNA targets of miR-181a revealed multiple putative targets (Table 13). We utilized three online software and databases (Targetscan, miRanda, PicTar) to elucidate potential mRNA targets of miR-181a. mRNA targets that were predicted in at least two



of the databases are depicted in Table 13. Additionally, among the many possible targets predicted and listed, TGFBR3 as a tumor suppressor has been recognized in breast, lung, ovarian, pancreatic and prostate cancer [75].

|          |          |        |        |         |
|----------|----------|--------|--------|---------|
| AFTPH    | FAM160A2 | LBR    | PDX3X  | SLC37A3 |
| ANKRD13C | FBX011   | LCLAT1 | PITPNB | SLC7A11 |
| ARF6     | FBX028   | METAP1 | PLAG1  | STCH    |
| ATP8A1   | FBXO33   | MTMR12 | PLCL2  | TGFBR3  |
| BAPX1    | GATA6    | NFYB   | PLXDC2 | TIAL1   |
| BCL2     | GIGYF1   | NLK    | PROX1  | TM9SF3  |
| BTBD3    | GPR137B  | NOCH2  | PUM1   | TMED4   |
| CCDC6    | HMGB2    | NOL4   | RLF    | TMEM64  |
| CCNG1    | K-ras    | NR6A1  | RNF34  | YOD1    |
| CDX2     | KIAA     | NRP1   | SCD    | ZNF148  |
| DDIT4    | KLADCS   | NUPL1  | SFRS7  | ZNF445  |

**Table 13. miR-181a-5p target genes predicted by Targetscan, miRanda, PicTar.**

Using with Ingenuity Pathway Analysis (IPA) core analysis we input the mRNA expression data of all the genes in our cohort that are targets of miR-181a. The most highly modulated transcripts were input to the system. The most statistically significant enriched categories and networks identified by IPA were associated with gene expression, cellular movement, cellular assembly and organization, cell-to-cell signaling, and cellular growth and proliferation.



| Molecular and Cellular Functions       |                     |
|--|---------------------|
| Name                                   | p-value             |
| Gene Expression                        | 4.91E-07 - 2.45E-02 |
| Cellular Movement                      | 5.70E-07 - 3.24E-02 |
| Cellular Assembly and Organization     | 1.74E-05 - 3.00E-02 |
| Cell-To-Cell Signaling and Interaction | 4.26E-05 - 3.50E-02 |
| Cellular Growth and Proliferation      | 4.59E-05 - 3.50E-02 |

**Table 14. Top molecular and cellular functions of miR-181a targets identified by IPA.**

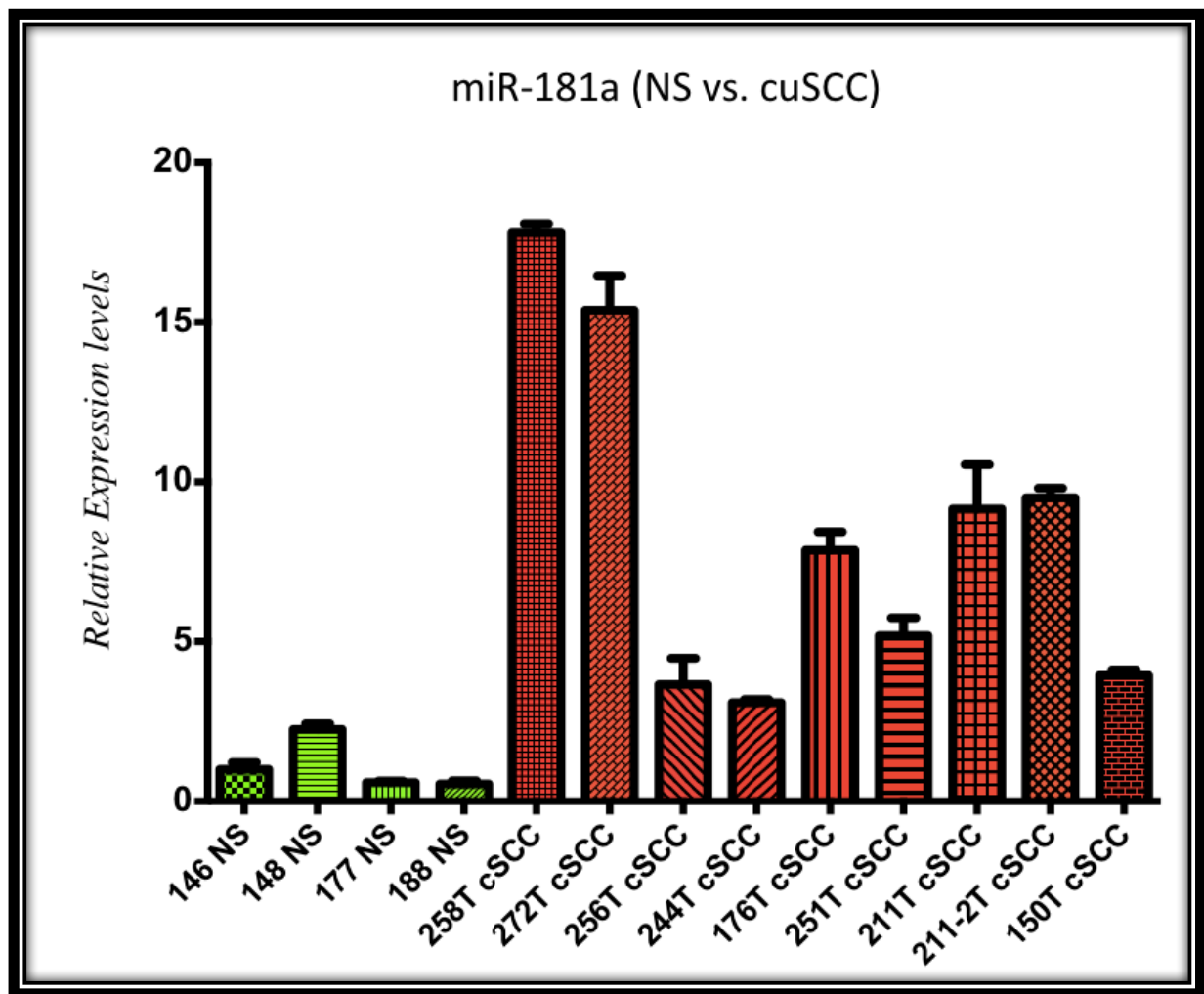
Initially, the focus has been on the function of TGFBR3, which is downregulated by miR-181 and has a tumor suppressor role in many contexts. This study tests the hypothesis that upregulation of miR-181a promotes initiation and progression of keratinocyte transformation by targeting TGFBR3.

#### **4.2 Validation of miR-181a upregulation and TGFBR3 downregulation in human cuSCC**

In interlesional comparisons of clinically normal irradiated skin (NS) and cuSCC in humans, miR-181a is upregulated. Our RNA-Seq and miR-Seq analysis of internally controlled samples have revealed a progressive upregulation of miR-181a with concurrent downregulation of TGFBR3 in interlesional analysis of human NS, AK, and cuSCC..

We confirmed upregulation of miR-181a in unmatched human cuSCC samples in comparison to the NS specimens by using qRT-PCR, *in vivo*. We took a cohort of n=13 unmatched samples where we compared miR-181a levels of NS ( n=4) in comparison to cuSCC (n=9) and found on average 9 fold increase in miR-181a levels ( Figure 61).



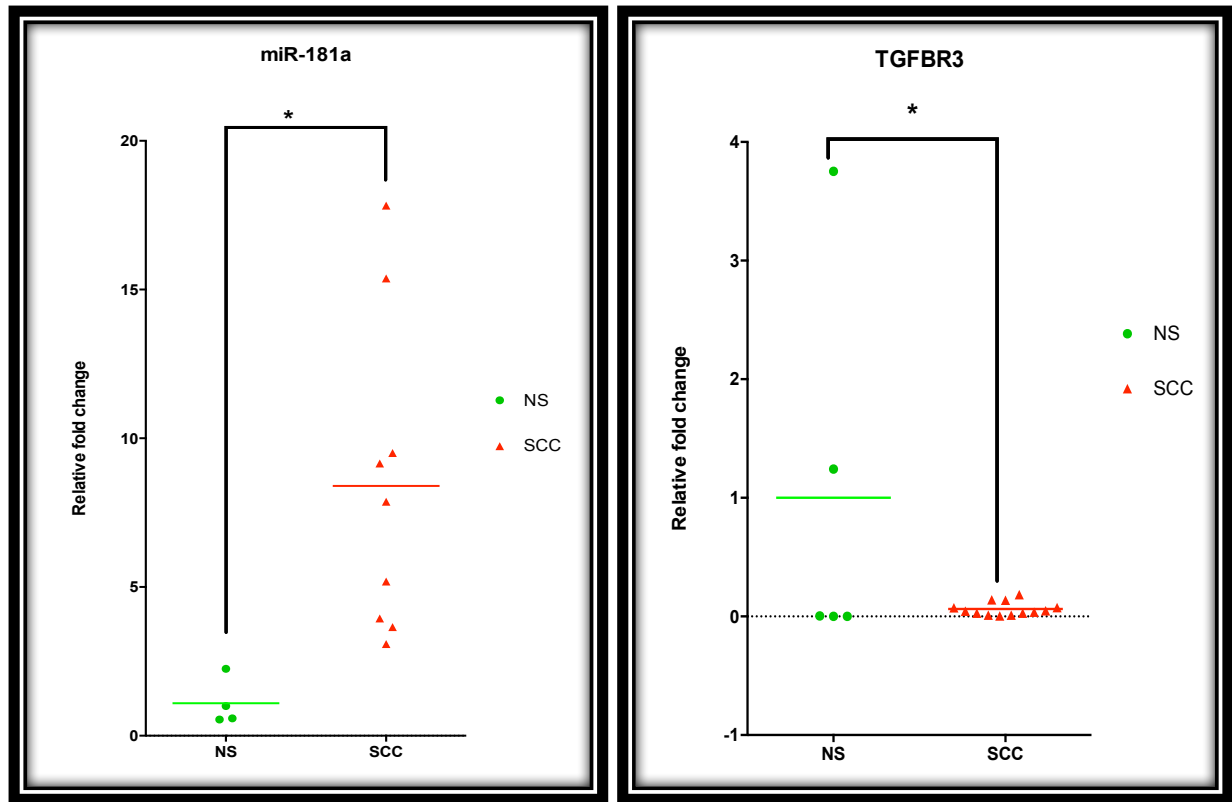


**Figure 61. miR-181a is significantly more highly expressed in unmatched cuSCC (red, n=9 right) as compared to normal skin (green, n=4 left) by 8.4-fold.** TaqMan MicroRNA two-step RT-PCR was performed. Levels of miR-181 were measured in triplicates and normalized by RNUB6 snRNA level. Relative levels of each sample is shown as the mean  $\pm$  standard deviation.

We validated the expression levels of miR-181a in additional sets (n=13) of matched human samples. miR-181a was substantially upregulated by  $7.305 \pm 2.702$ -fold ( $p=0.0205$ ) across the progression sequence.



We validated the expression levels of TGFBR3 in additional sets (n=18) of matched human samples. We show downregulation of TGFBR3 by 93% ( $-0.9371 \pm 0.4296$ ) in cuSCC samples in comparison to NS with  $p=0.0444$  (Figure 62).



**Figure 62. qRT-PCR analysis of miR-181a and TGFBR3 in NS and cuSCC matched human samples.** TaqMan microRNA two-step RT-PCR was performed and levels of miR-181a were measured in triplicate and normalized to RNUB6 level. Quantitative RT-PCR was used to determine mRNA levels of TGFBR3. Expression of TGFBR3 was normalized to 18S.

TGFR3 does not appear to be a target for mutational inactivation in breast cancer, and somatic mutations in TGFR3 have not been reported in other cancers [55]. TGFR3 regulation at the mRNA level has been reported in breast, colon, and renal cell carcinoma. Similarly, in our SNV and CNV variants analysis, we did not find any TGFR3 inactivating mutations.

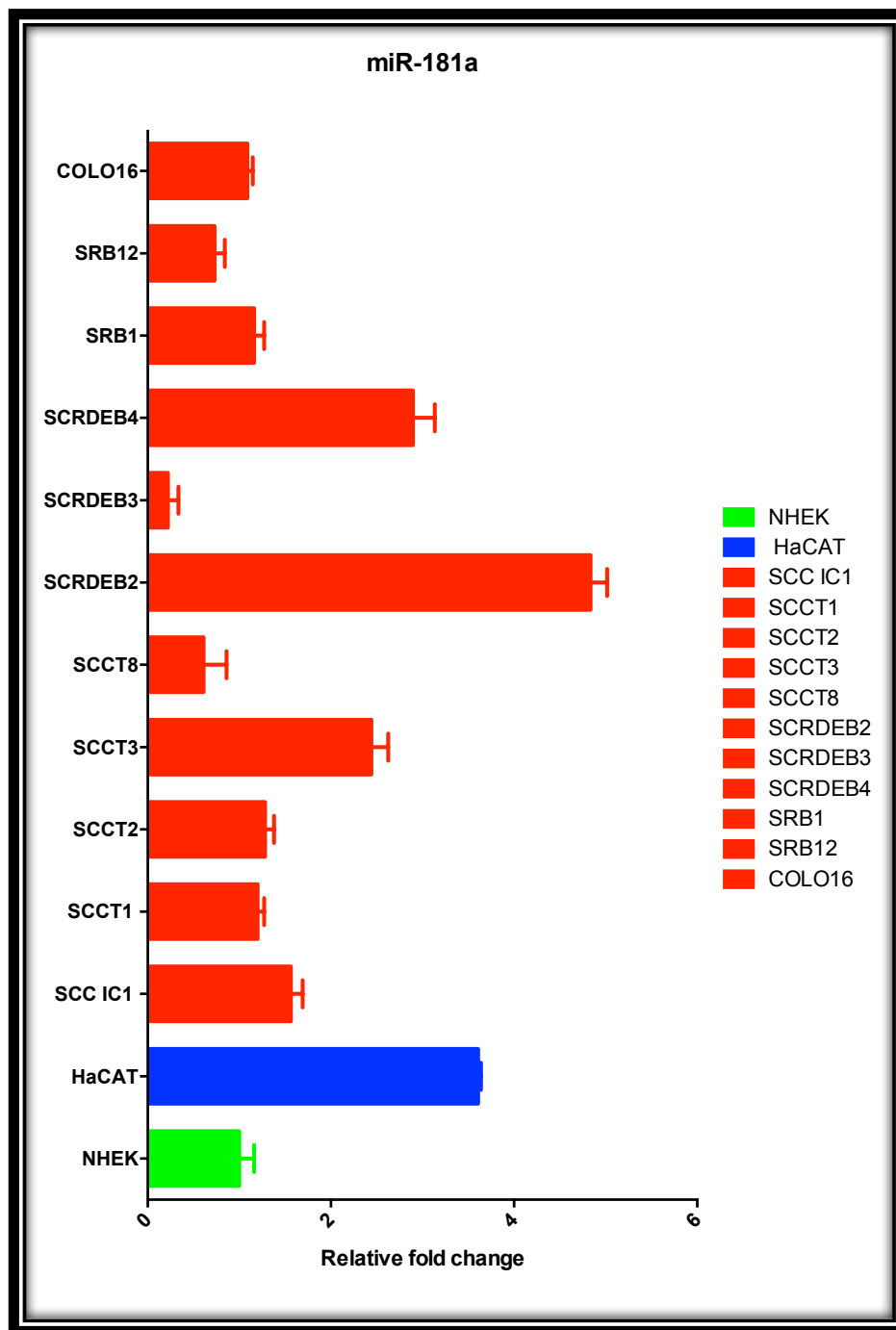


### **4.3 Basal expression of miR-181a in primary human keratinocytes (NHEK) and cuSCC cell lines**

We examined the basal expression of miR-181a and TGFBR3 in our panel of human cell lines. We measured miR-181a levels in primary normal human epidermal keratinocytes (NHEKs) and a panel of eleven cuSCC cell lines (SCC IC1, SCCT1, SCCT2, SCCT3, SCCT8, SCRDEB2, SCRDEB3, SCRDEB4, SRB1, SRB12, and COLO16). miR-181a is expressed in variable levels in cuSCC lines, we identified few cell lines with very high expression of miR-181a as well as few cell lines with very low expression of miR-181a (Figure 63).

miR-181a levels were increased in SCRDEB4 (RDEB4) by a  $2.895876 \pm 0.24$  fold in comparison to NHEK. In addition, miR-181a levels were increased in SCRDEB2 (RDEB2) by a  $4.836623 \pm 0.181$  fold in comparison to NHEK. As a result of these data, for experiments requiring miR-181a suppression we used SCRDEB2 (RDEB2) and SCRDEB4 (RDEB4) cell lines. For experiments requiring miR-181a overexpression we used NHEK, SRB1, and COLO16.





**Figure 63.** Basal expression of miR-181a in our panel of human cuSCC cell lines, NHEK and HaCaT.



#### 4.4 Specific and direct regulation of TGFBR3 by miR-181a

First, we determined the binding sites in 3'UTR of TGFBR3 by examining the number of unique binding sites on its 3'UTR and the evolutionary conservation of those sites. The Targetscan algorithm predicts TGFBR3 as a target of miR-181a with 2 different binding sites. The first (7mer-1A; context score=-0.07, PCT=0.52) and the second binding site (7mer-m8; context score=-0.02, PCT=0.18) are depicted in Table 15. As described in materials and methods section, context score is determined by six unique factors: contribution or site-type, 3' pairing, local AU, position, target site abundance, seed-pairing stability. A more negative context score reflects a higher probability of mRNA binding. The probability of conserved targeting, PCT, refers to the likelihood of the sequence being conserved so as to allow regulation by the miRNA. The higher the PCT, the higher the chance of miRNA:mRNA binding. TGFBR3 has 3 transcripts which are all targeted by miR-181a.

|                                     | Predicted consequential pairing of target region (top) and miRNA (bottom) | Site type | Context++ score | Context++ score percentile | Weighted context++ score | Conserved branch length | P <sub>CT</sub> |
|-------------------------------------|---|-----------|-----------------|----------------------------|--------------------------|-------------------------|-----------------|
| Position 1918-1924 of TGFBR3 3' UTR | 5' ...GCCUAACCUUCGGUGGAAUGUAU...<br>                                      | 7mer-A1   | -0.07           | 68                         | -0.07                    | 6.653                   | 0.52            |
| <a href="#">hsa-miR-181a-5p</a>     | 3' UGAGUGGCUGUCGCAACUUAACA  |           |                 |                            |                          |                         |                 |
| Position 2441-2447 of TGFBR3 3' UTR | 5' ...UCUCAUAUUGGAGAGUGAAUGUC...<br>                                      | 7mer-m8   | -0.02           | 30                         | -0.02                    | 2.721                   | 0.18            |
| <a href="#">hsa-miR-181a-5p</a>     | 3' UGAGUGGCUGUCGCAACUUAACA  |           |                 |                            |                          |                         |                 |

**Table 15. TGFBR3 3'UTR binding sties of miR-181a as predicted by Targetscan.** Schematic representation of 3'UTR sequence from human TGFBR3 indicating the putative miRNA-binding sites (shown in bold) and their nucleotide (nt) position on the sequence.

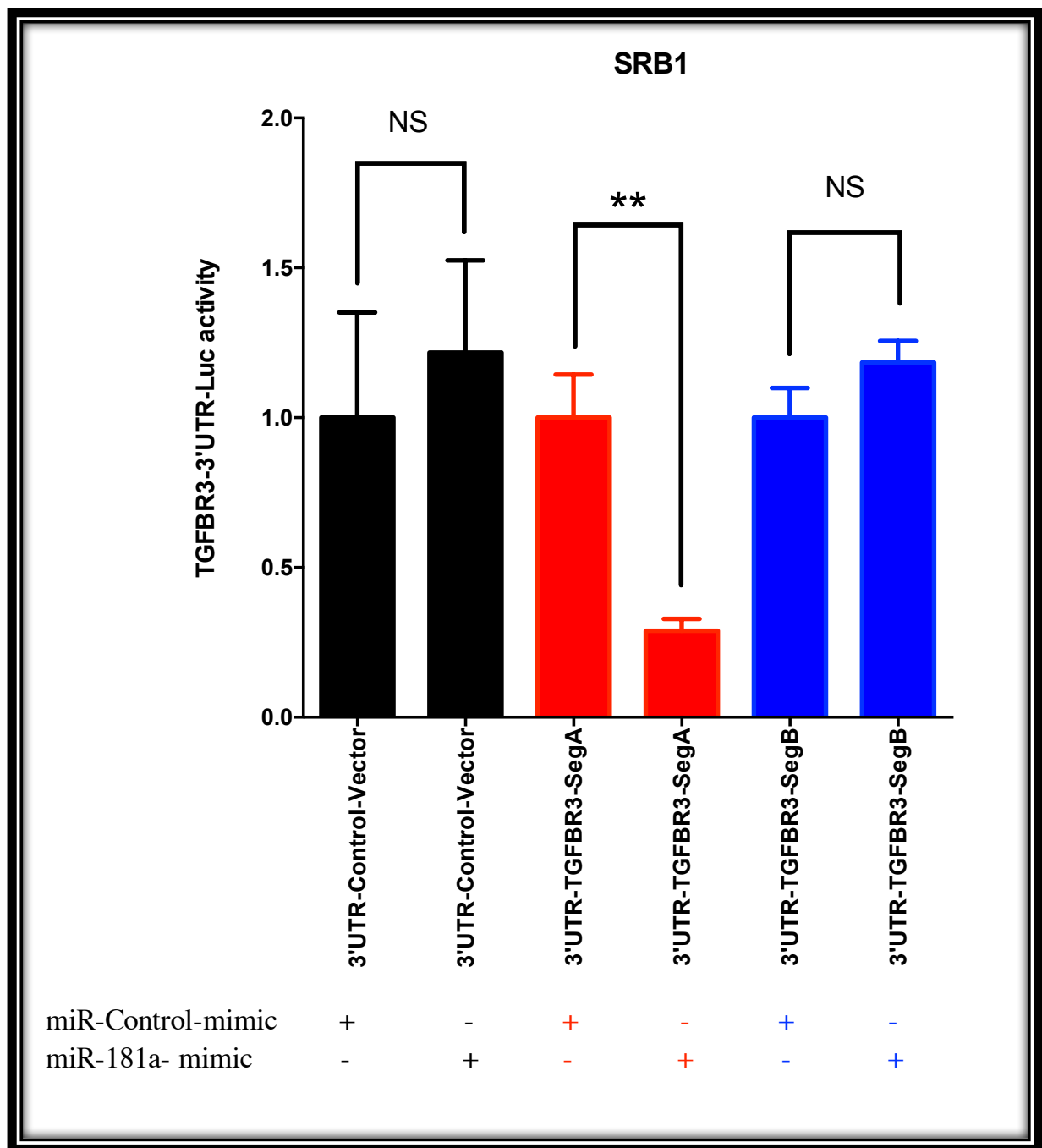


Second, we utilized a dual luciferase reporter assay for *in vitro* binding confirmation of miR-181a to the 3'UTR of TGFBR3. To determine whether miR-181a directly binds to the TGFBR3 3' UTR, we utilized a Gaussia luciferase (GLuc)-secreted alkaline phosphatase (SEAP) dual-reporter pEZX-MT05 vector (GeneCopoeia). We transfected human cuSCC SRB1 cell line with cloning plasmids containing the 3'UTR predicted binding site of TGFBR3 and miR-181a-mimic. TGFBR3 3'UTR was cloned into 2 separate vectors, 3'UTR-TGFBR3-SegA, which contains 2 miR-181a binding sites and 3'UTR-TGFBR3-SegB, which contains no miR-181a binding sites. Figure 16 and Table 8 in the material and methods section shows the plasmids we used in this study.

To show direct regulation of TGFBR3 by miR-181a we generated stable SRB1 cell lines expressing 3'UTR-TGFBR3-SegA and SegB or control vector. Next we transfected these cell lines with miR-181a-mimic or a negative control, 48hr post miR-mimi transfection we measured the SEAP/Gluc activity. Our results show that miR-181a modulates TGFBR3 expression. Specifically, miR-181a overexpression suppressed the luciferase activity from the TGFBR3 3' UTR-Seg A clone by more than 71% ( $-0.7116 \pm 0.08607$  FC) with  $p=0.0012$  in comparison to the control vector (Figure 64).

Similarly, we generated stable cell lines expressing each of the 3 vectors (3'UTR-TGFBR3-SegA, SegB or control vector) in cuSCC RDEB2 cell line. Next we transfected these cell lines with miR-181a-inhibitor or a negative control, 48hr post miR-inhibitor transfection we measured the SEAP/Gluc activity. Our results show that miR-181a modulates TGFBR3 expression. Specifically, miR-181a inhibition results in an increase of the luciferase activity from the TGFBR3 3' UTR-Seg A clone by more than 57% ( $0.5715 \pm 0.1738$  FC) with  $p=0.0462$  in comparison to the control vector (Figure 65).



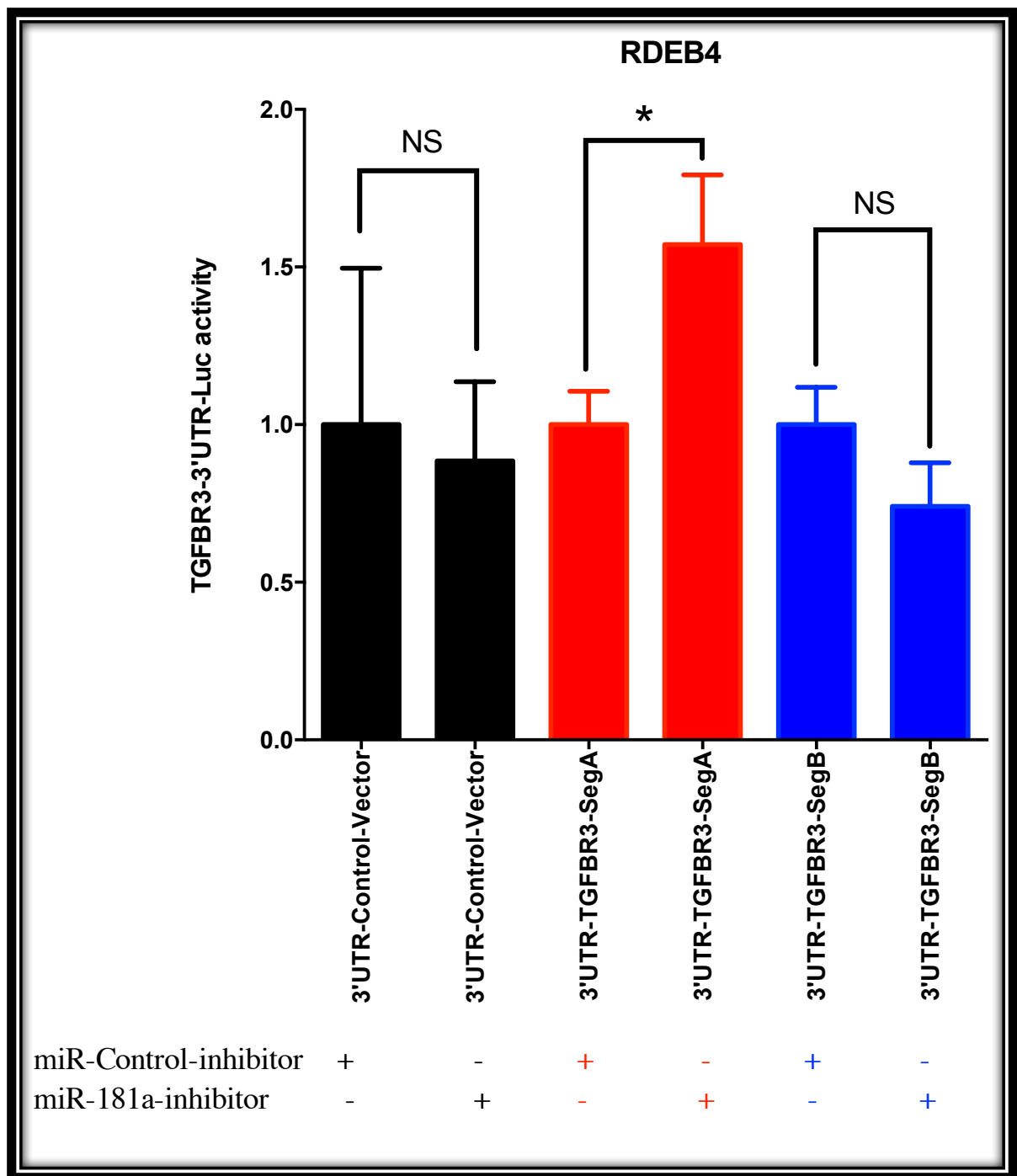


**Figure 64. The inhibitory effect of miR-181a overexpression on TGFB3 3'UTR expression.** SRB1 cells were transfected with pEZX-MT05-3'UTR-Control-Vector (black bars), or TGFB3 3' UTR-Seg A (red bars), or TGFB3 3' UTR-Seg B (blue bars). Stable cell lines expressing these plasmids were generated using single cell cloning. Next these lines were transfected with miR-control-mimic or miR-181a-mimic. GLuc activity and SEAP activity were



determined 48 hours post-transfection. The activity ratio of GLuc to SEAP was set to 1 for the transfection samples with 3'UTR-Control-Vector and miR-control-mimic (left black bar), against which the activity of the other samples was compared. The result shows that miR-181a suppressed the luciferase activity from the TGFBR3 3' UTR-Seg A clone by more than 71% (right red bar). miR-181a did not suppress the luciferase activity from the 3' UTR-Seg B (right blue bar). Bars represent the mean of three independent experiments  $\pm$ s.d. \*\*P<0.01 versus control.





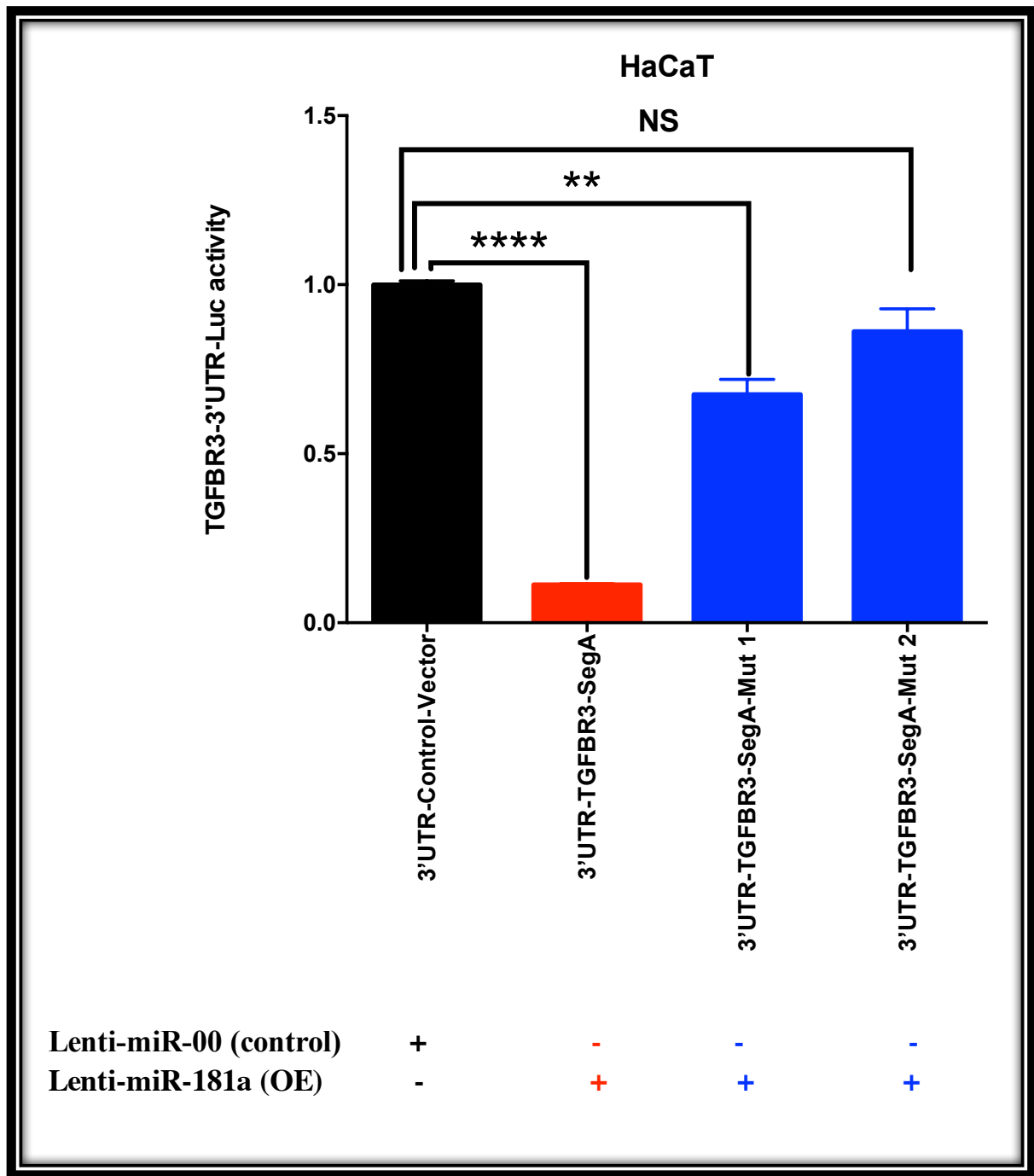
**Figure 65. The release of miR-181a inhibitory effect on TGFB3 3'UTR expression.** RDEB2 cuSCC cells were transfected with pEZX-MT05-3'UTR-Control-Vector (black bars), or TGFB3 3' UTR-Seg A (red bars), or TGFB3 3' UTR-Seg B (blue bars). Stable cell lines expressing these plasmids were generated using single cell cloning. Next these lines were transfected with miR-control-inhibitor or miR-181a-inhibitor. GLuc activity and SEAP activity



were determined 48 hours post-transfection. The activity ratio of GLuc to SEAP was set to 1 for the transfection samples with 3'UTR-Control-Vector and miR-control-inhibitor (left black bar), against which the activity of the other samples was compared. The result shows that miR-181a inhibition results in an increase of luciferase activity from the TGFBR3 3' UTR-Seg A clone by more than 57% (right red bar). miR-181a inhibition did not affect the luciferase activity from the 3' UTR-Seg B (right blue bar). Bars represent the mean of three independent experiments  $\pm$ s.d. \*P<0.05 versus control.

To demonstrate specificity of TGFBR3 downregulation by miR-181a, we generated HaCaT stable cell lines overexpressing lenti-miR-181a or lenti-miR-00 (control). Next we transfected these lines with TGFBR3 3'UTR constructs with or without mutations that perturb the mRNA-miRNA binding site. Utilizing site-directed mutagenesis we generated two mutant constructs targeting each of the miR-181a binding sites of TGFBR3 3' UTR-Seg A; namely, TGFBR3 3' UTR-Seg A Mut 1 and Mut 2. We measured the SEAP-Gluc activity was measured 72 hours post transfection. Our data show that miR-181a regulates TGFBR3 in a specific manner. In lenti-miR-181a over expressing HaCaT cell line, transfection of wild-type TGFBR3-3'UTR-SegA results in suppression of luciferase activity by 88% ( $-0.8876 \pm 0.01183$  P  $\leq 0.0001$ ) which is significantly blunted by the mutation of the binding sites, as evident in TGFBR3-3'UTR-SegA-Mut1 where we see a reduction of luciferase activity by 32% ( $-0.3252 \pm 0.04633$  P < 0.01) and in TGFBR3-3'UTR-SegA-Mut2 by only 13% (P=NS).





**Figure 66. miR-181a regulation of TGFB3 is site specific.** This graph shows the luciferase activity of TGFB3 3'UTR-control-vector, 3'UTR-SegA wild-type vector or its mutant derivatives (SegA Mut1 and Mut2) lacking the mRNA-miRNA binding sites in HaCaT cell line overexpressing the indicated lenti-miRNA. The activity ratio of GLuc to SEAP was set to 1 for the transfection samples with 3'UTR-Control-Vector and lenti-miR-00 (black bar), against which



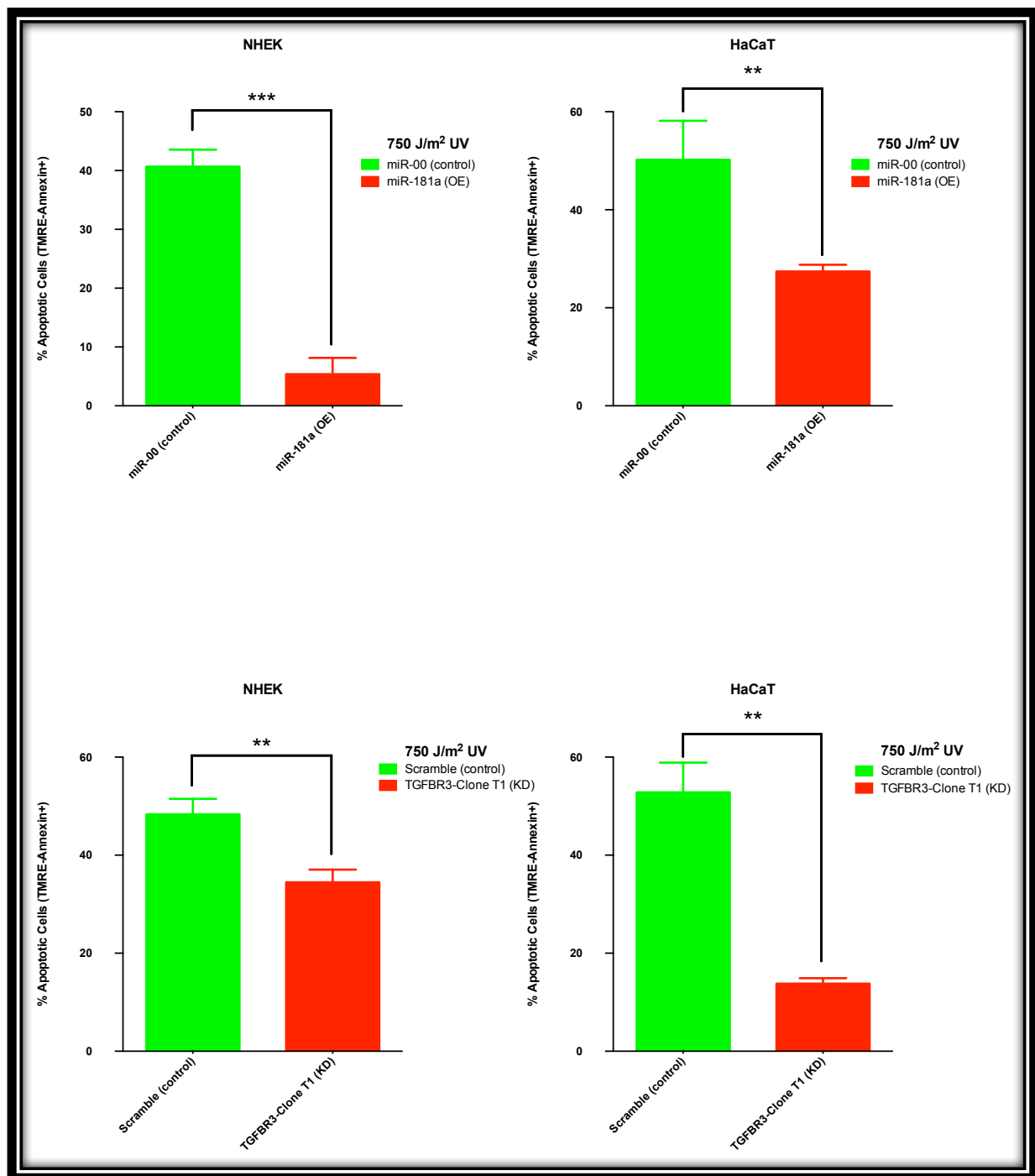
the activity of the other samples was compared. Our results show that in lenti-miR-181a over expressing HaCaT cell line, transfection of 3'UTR-SegA wild-type (red bar) results in suppression of luciferase activity by 88% ( $P \leq 0.0001$ ) which is significantly blunted by the mutation of the binding sites, as evident in Mut1 (32%  $P < 0.01$ ) and Mu2 (13%  $p = \text{NS}$ ) columns (blue bars). Graph error bars indicate s.d. calculated on at least three independent experiments. \*\*\*\*  $P \leq 0.0001$  and \*\* $P < 0.01$  versus control.

#### **4.5 miR-181a overexpression suppresses UV-induced apoptosis**

The most important risk factor for development of AK and cuSCC is chronic exposure to UV radiation. Preliminary data from other labs have shown that miR-181a levels are modulated in response to acute UV exposure in mice (unpublished data from Flores lab). To assess the effects of miR-181a on UV-induced apoptosis, we used retrovirally-transduced keratinocytes (NHEK and HaCaT) overexpressing miR-181a and control miR-00. We used lenti-miRNA vector for stable over expression of miR-181a or miR-00 control vector (SBI). We show that overexpression miR-181a significantly modulates the responses of cells to UV-induced apoptosis. Using Flow cytometry (FACS) we show that overexpression of miR-181a suppresses UV-induced apoptosis in NHEK by 35% ( $-35.28 \pm 2.309$ ,  $P \leq 0.001$ ) and in HaCaT by 22% ( $-22.80 \pm 4.662$ ,  $P = 0.0081$ ) (Figure 67).

Similarly, to examine the susceptibility of retrovirally-infected cells to UV-induced apoptosis Lentiviral shRNA was used for TGFBR3 knockdown. Using Flow cytometry (FACS) we show that TGFBR3 knockdown suppresses UV-induced apoptosis in NHEK by 13% ( $-13.87 \pm 2.354$ ,  $P = 0.0041$ ) and in HaCaT by 39% ( $-39.00 \pm 3.311$ , with  $P = 0.0013$ ).



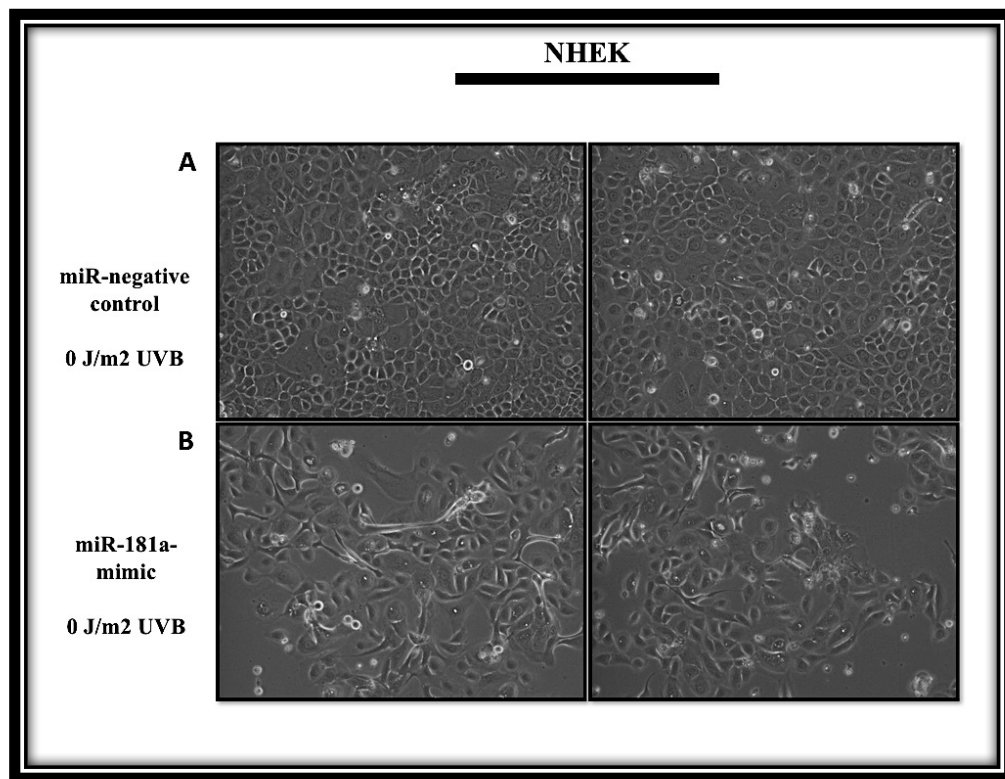


**Figure 67. miR-181a overexpression and TGFBR3 knockdown suppresses UV-induced apoptosis in HaCaT and NHEK.** HaCaT and NHEK cells were transfected with lenti-miRNA vector for miR-181a overexpression or miR-00 control (SBI). Next, they were either irradiated with 750 J/m<sup>2</sup> of UVB or unirradiated and isolated 48 hours post treatment for FACS analysis. HaCaT and NHEK cells show 22% and 35% suppression of apoptosis in the presence of miR-

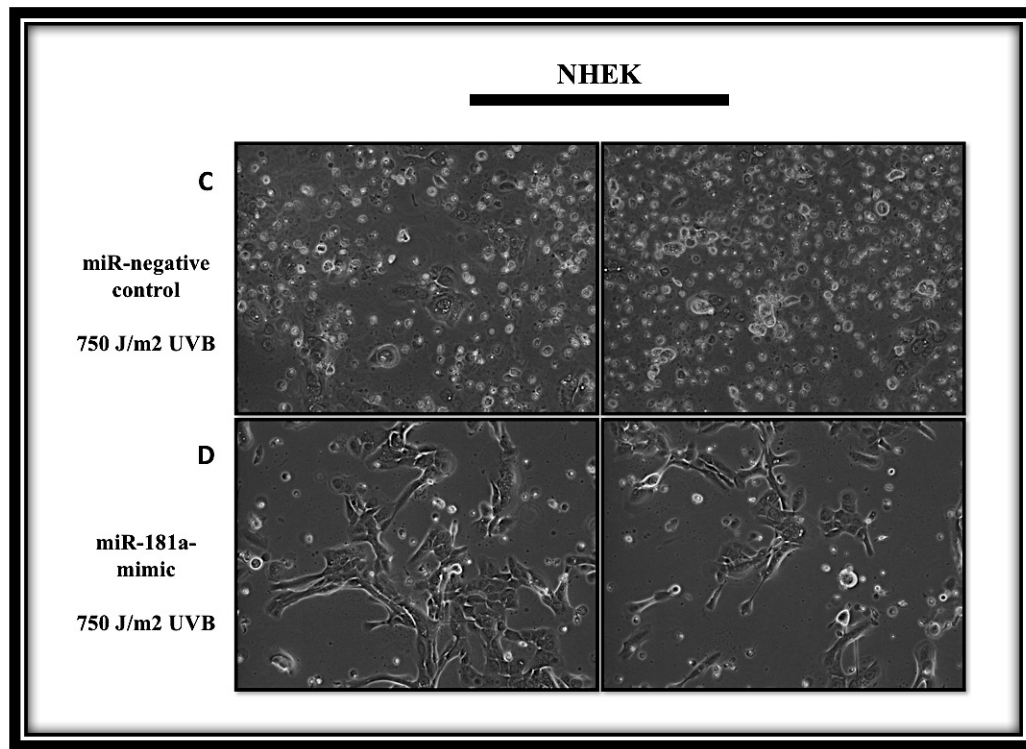


181a overexpression, respectively, as measured by FACS for Annexin V<sup>+</sup>, TMRE-low cells (n=6 for each condition, \*\*\* p<0.001, \*\*P<0.01). Similarly, HaCaT and NHEK cells were transfected with lentiviral shRNA or scramble control for TGFBR3 knockdown. Next, they were either irradiated with 750 J/m<sup>2</sup> of UVB or unirradiated and isolated 48 hours post treatment for FACS analysis. HaCaT and NHEK cells show 39% and 13% suppression of apoptosis as result of TGFBR3 knockdown, respectively, as measured by FACS for Annexin V<sup>+</sup>, TMRE-low cells (n=6 for each condition, \*\*\* p<0.001, \*\*P<0.01).

We observed similar effects with NHEK cell lines that were transiently transfected with miR-negative control or miR-181a-mimic (mirVana) and were are either sham irradiated or irradiated with 750 J/m<sup>2</sup> of UVB. Figure 68 shows the microscopic morphological changes that were observed in NHEK cell lines in response to UV.







**Figure 68 - Phase-contrast microscopy of the morphological changes of NHEK in response to UV-induced apoptosis.** NHEK cells were transiently transfected with miR-negative control or miR-181a-mimic (mirVana) and were either sham irradiated (A and B) or irradiated with 750 J/m<sup>2</sup> of UVB (C and D). In panel B we can appreciate the morphological changes as result of miR-181a-mimic transient overexpression, cells acquire a spindle-type morphology and that the number of cell-cell contacts are reduced in comparison to control (A). In panel C, numerous characteristic morphological features of apoptotic cells such as, cell rounding, cytoplasmic condensation, and apoptotic bodies/blebs can be identified in NHEK cells that were transiently transfected with miR-negative control and exposed to 750 J/m<sup>2</sup> of UVB. In panel D, less of these apoptotic features can be appreciated in NHEK cells transfected with miR-181a-mimic and exposed to 750 J/m<sup>2</sup> of UVB. All images were obtained at a magnification of  $\times 100$ .

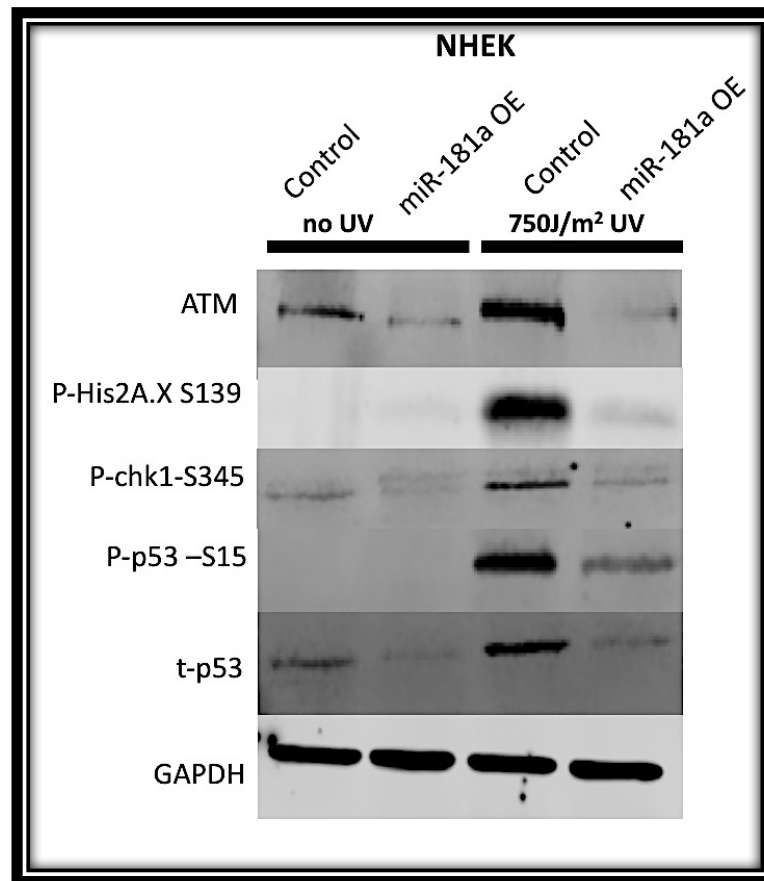


#### **4.6 miR-181a overexpression suppresses basal levels of ATM and p-P53 without recovery in response to UV exposure**

Ataxia telangiectasia mutated (ATM) is a validated miR-181a target [52]. Our single-nucleotide variant analysis identified mutations in ATM that have been previously reported in breast cancer [159], in addition to deleterious mutations in ATM interactor protein (ATMIN). ATM is a key regulator of DNA damage signaling pathway that activates p53 [160, 161]. ATM regulates cell cycle progression through phosphorylation of Chk2 and p53, and DNA repair through phosphorylation of SMC1 and histone H2AX [162].

miR-181a is a negative regulator of the DNA damage response in breast cancer, and negatively impacts the expression and activity of the stress-sensor kinase ATM [163]. Perhaps one mechanism of suppressed UV-induced apoptosis in miR-181a over expressing cell lines is down regulation of ATM. DNA double-strand-breaks activation of ATM is crucial to initiate an efficient DNA damage response and to induce DNA repair by homologous recombination [163]. We show that basal levels of ATM and p53 are reduced in miR-181a overexpressing NHEK and modulation of the pathway with UV exposure does not affect the levels of ATM, p-p53 (S15), and pH2AX in miR-181a over expressing cell.





**Figure 69. miR-181a overexpression suppresses UV-induced levels of ATM and p-P53.**

NHEK cells were transiently transfected with miR-negative control or miR-181a-mimic (mirVana) and were either sham irradiated or irradiated with 750 J/m<sup>2</sup> of UVB. We performed immunoblotting using lysates from each group 24hr post UV exposure. miR-181a overexpression impairs the proper induction of ATM, p-P53, p-His2AX, and p-Chk1 in response to UV exposure.

#### **4.7 miR-181a overexpression enhances epithelial mesenchymal transition (EMT) through TGFBR3**

Given the findings that miR-181a can regulate cellular movement and the critical role of TGFβ signaling in EMT, we investigated whether modulation of miR-181a and TGFBR3 can significantly impact cellular motility and EMT in cuSCC. EMT is a critical embryonic and developmental process that is characterized by loss of cellular junctions and increased cellular

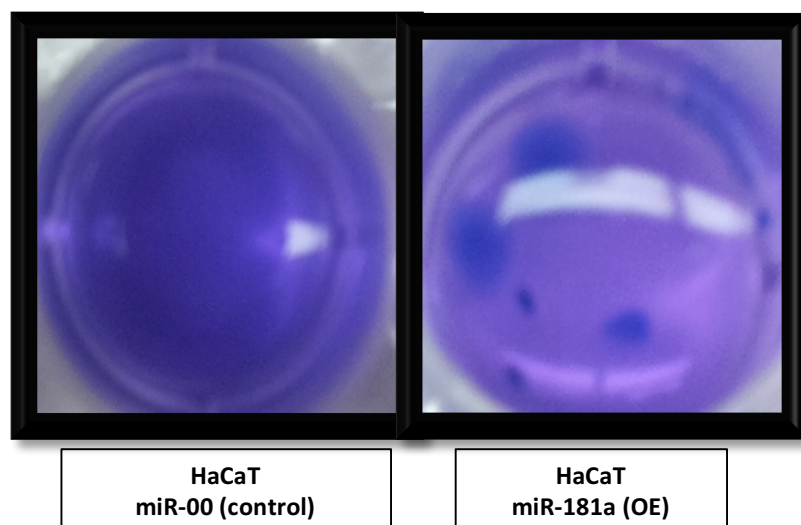
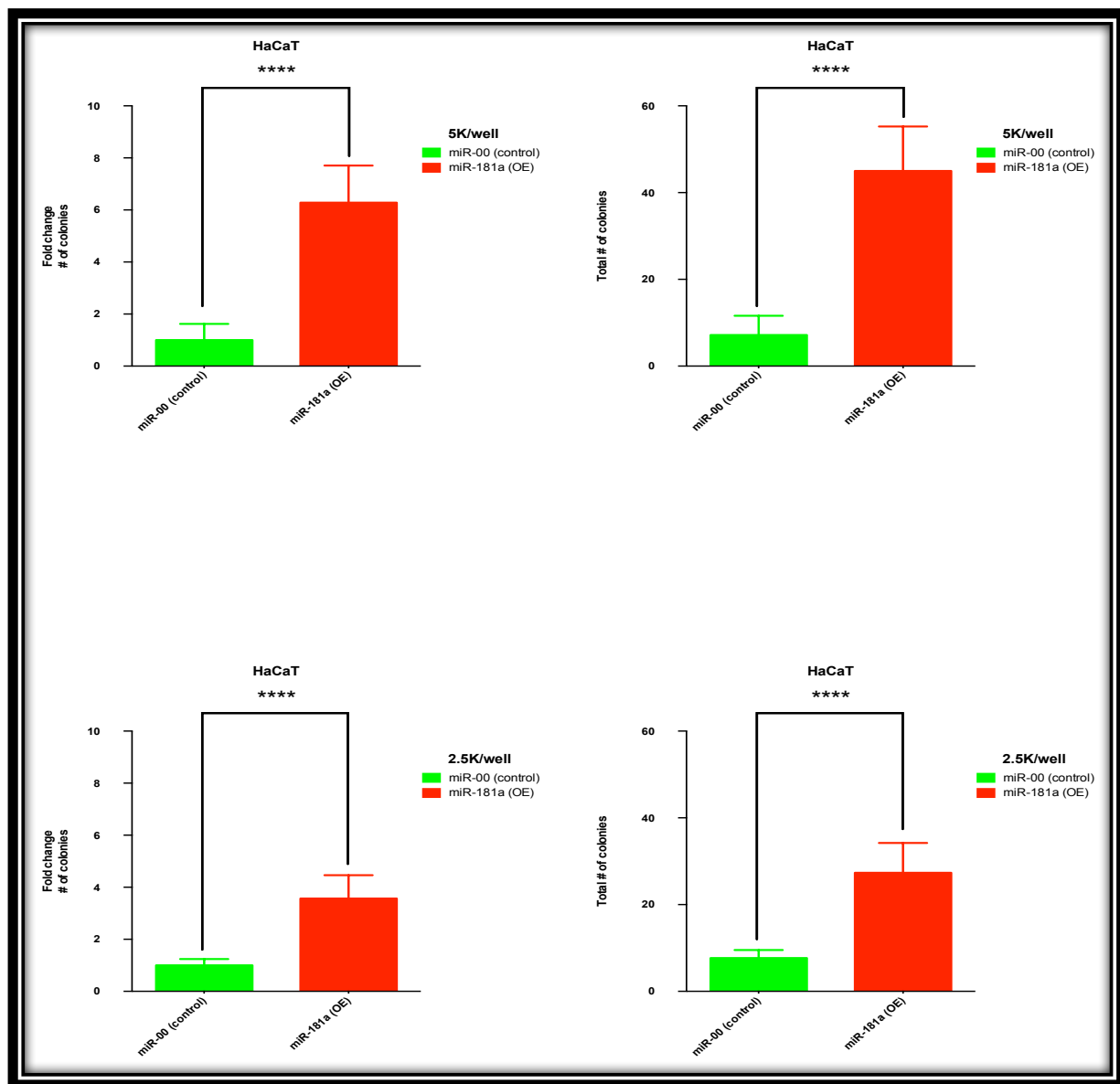


mobility. Furthermore, EMT is involved in multiple pathological processes such as fibrosis and cancer metastasis [164-166]. Anchorage-independent survival is an important characteristic of metastatic solid tumors.

We ascertained whether overexpression of miR-181a or direct knockdown of TGFBR3 by shRNA is necessary and sufficient for enhanced anchorage-independent survival of keratinocytes. HaCaT stable cell lines overexpressing lenti-miR-181a or lenti-miR-00 (control) were tested for their survival in liquid culture and enhance colony formation in soft agar. As a positive control we used Ha-RasV12 transformed HaCaT cells, which readily form colonies and tumors in-vivo [167].

Our results show that HaCaT miR-181a overexpressing cell lines have an increased capability of colony formation that is cell density dependent. At 2.5 K/ well seeding, miR-181a overexpressing HaCaTs show an increase in absolute number of colony by  $19.67 \pm 2.914$  and a fold change increase in number of colonies by  $2.565 \pm 0.3800$  folds  $p < 0.0001$ . Similarly, at 5K/ well seeding, miR-181a overexpressing HaCaTs show an increase in absolute number of colony by  $37.83 \pm 4.556$  and a fold change increase in number of colonies by  $5.279 \pm 0.6358$  folds,  $p < 0.0001$  (figure 70). The fold-change in colony counts of miR-181a overexpressing HaCaTs show a dose-dependent increase in colony formation. We also, measured the effects of miR-181c (a member of miR-181 family member with significant seed sequence homology to miR-181a) on colony formation capacity of HaCaT cells, where we saw no enhancement in survival of HaCaT cells in forced suspension culture (Figure 71).

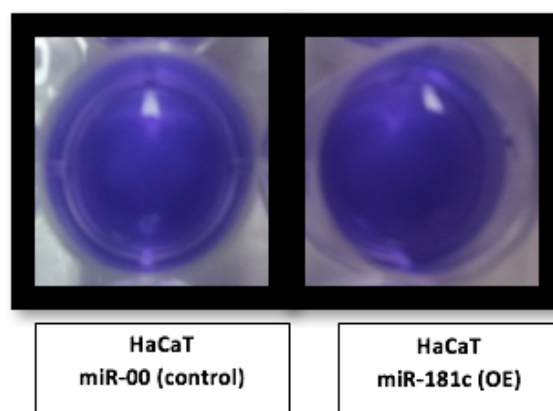
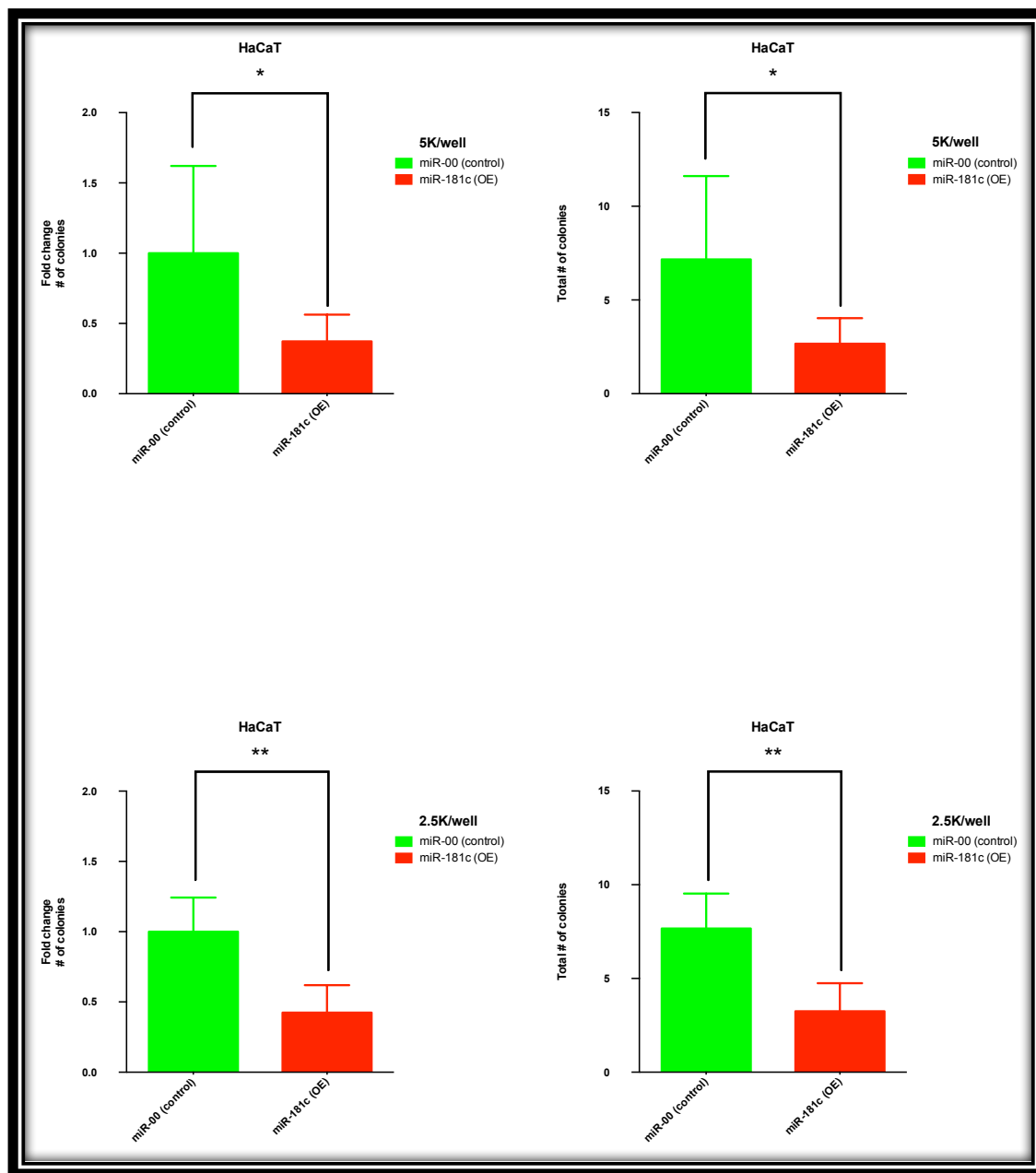






**Figure 70. miR-181a overexpression confers significant colony-forming advantages to HaCaT keratinocyte cell lines.** We tested the anchorage independent growth ability of a miR-181a overexpressing cell line using two-layer soft agar assay. miR-181a overexpression, over 4-6 weeks, results in significant acceleration of soft agar colony formation in-vitro. Representative soft agar colonies of HaCaT-miR-181a overexpressing and control vector miR-00 transformed cell lines (bottom panel). Colony formation assay were performed at various cell densities (2.5 and 5 K/well in triplicates) subsequently stained with crystal violet and quantified. Ha-RasV12 transformed HaCaT cells were used as positive control. (n=12 for each condition, “\*\*\*”,  $p<0.001$ )







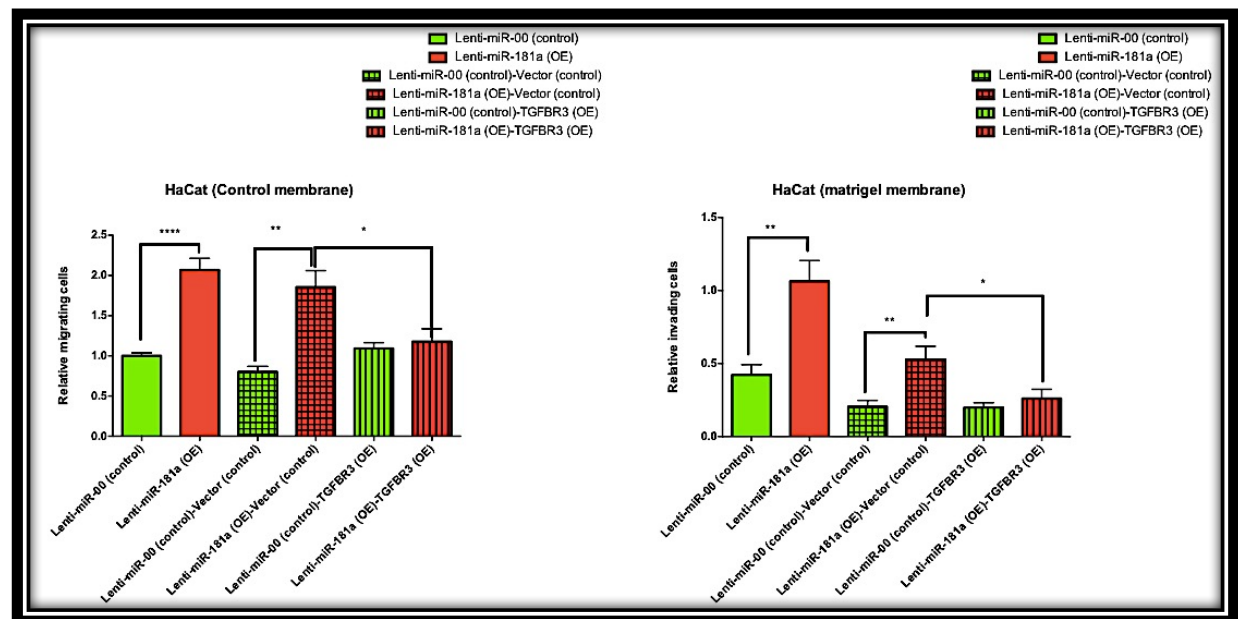
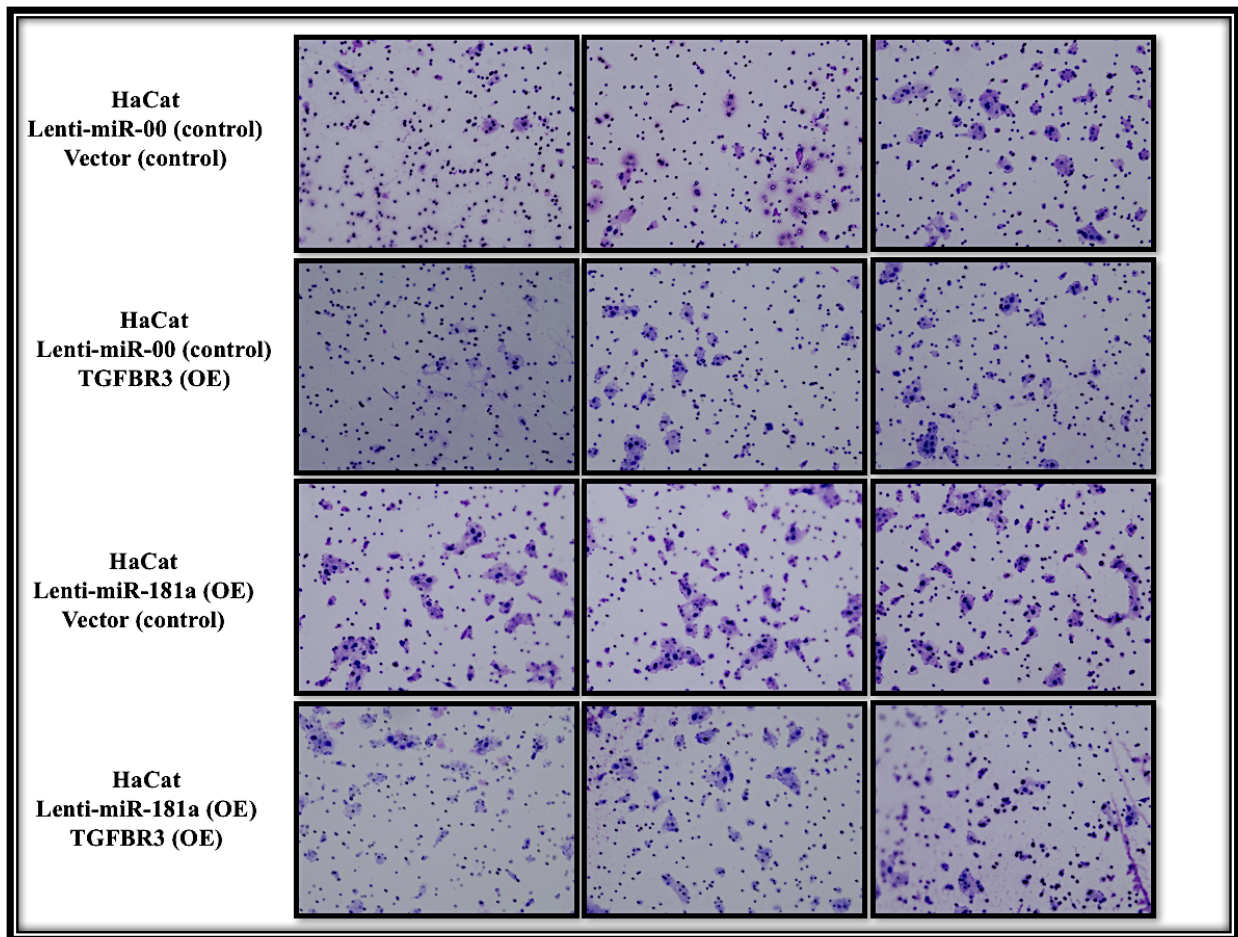
**Figure 71. miR-181c overexpression does not confer significant colony-forming advantages to HaCaT keratinocyte cell lines.** Similar to figure 70, we also measured the effects of miR-181c (a member of miR-181 family member with significant seed sequence homology to miR-181a) on colony formation capacity of HaCaT cells, where we saw no enhancement in anchorage-independent survival in miR-181c overexpressing cells in comparison to control.

EMT is characterized by increased expression of transcription factors Snail, Slug, and Twist. In addition to nuclear localization of beta-catenin, increased expression of mesenchymal markers such as vimentin and N-cadherin are hallmarks of EMT [164-166]. The essential triggering event for EMT is downregulation of E-cadherin that results in downregulation of the adherens junctions. Members of Snail family; Snail1 (Snail) and Snail2 (Slug), bHLH factors, Twist and ZEB family (ZEB1 and ZEB2) are transcriptional repressors of E-cadherin. TGFBR3 is required for epithelial to mesenchymal transition (EMT), during cardiac development [79] and palate fusion [168, 169]. In a pancreatic model of EMT, expression levels of TGFBR3 decreases prior to loss of E-cadherin and other cytoskeletal proteins. Loss of TGFBR3 expression correlates with increased invasion and motility [170].

We investigated whether miR-181a overexpression, by negatively regulating the expression of TGFBR3 could promote EMT in cuSCC. EMT induction can be measured in cultured keratinocytes by assessing morphological changes, [66-68]. Keratinocytes typically maintain an epithelioid-round appearance in culture and we show that miR-181a overexpression in NHEK cells results in a more spindle-shaped appearance (Figure 68).

We assessed the effects of miR-181a overexpression in regulation of cuSCC cell invasion and migration. Immortalized but non-tumorigenic human keratinocytes, HaCaT cells were stably transfected with lenti-miR-181a (OE) or lenti-miR-00 (control) and subjected to Boyden chamber assays, using matrigel coated membranes.







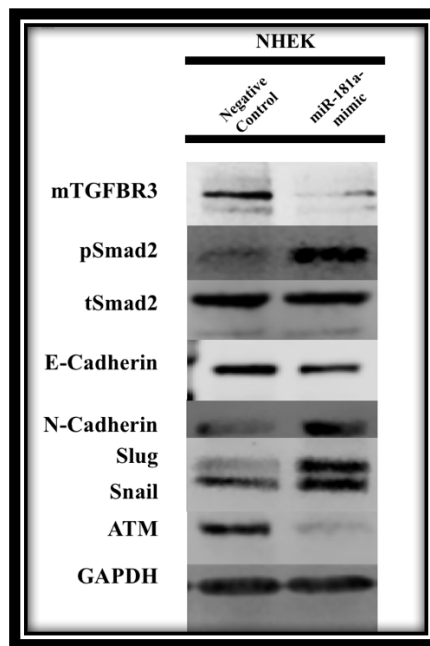
**Figure 72. miR-181a overexpression significantly promotes invasion of HaCaT keratinocyte cell lines *in vitro*.** We have examined the effects of miR-181a overexpression and TGFBR3 knockdown on cellular motility, using a matrigel coated PET membrane. Cell invasion assays were performed using 24-well transwell chambers with a pore size of 8  $\mu\text{m}$  (BD BioCoat Matrigel invasion chambers, Bioscience Franklin Lakes, NJ, United States). We planted  $2.5 \times 10^5$  cells in serum-free media. The lower chambers were filled with medium that contained 30% fetal bovine serum as the chemo-attractant. After 24 h culture, the cells on the upper membrane surface were removed by scraping with a cotton swab, and the cells that passed through the filter were fixed and stained using the hematoxylin-eosin reagent. The invading cells were counted in 10 representative fields using a microscope. All the experiments were performed in triplicate with 3 replicates and the total number of invading cells were calculated. Top panel) Representative images of invasion and migration assay in miR-181a overexpressing cell lines in addition to the rescue with TGFBR3 overexpression. Left bottom panel) We generated HaCaT stable cell lines overexpressing lenti-miR-181a (OE) or lenti-miR-00 (control). We show that lenti-miR-181a overexpression enhances cellular migration and invasion. miR-181a overexpression enhances cellular migration by 100% in comparison to the control ( $1.069 \pm 0.1489$ ,  $P < 0.0001$ ). Next we overexpressed TGFBR3 in our cell lines, using pDONR223-TGFBR3 vector. We show that control vector overexpression has no significant effect on level of cellular migration. We show that overexpression of TGFBR3 in miR-181a overexpressing can rescue the phenotype and decrease migration by 60% ( $-0.6780 \pm 0.2598$ ,  $P = 0.0311$ ). Left right panel) Using generated HaCaT stable cell lines overexpressing lenti-miR-181a (OE) or lenti-miR-00 (control), we show that miR-181a overexpression enhances cellular invasion by 60% ( $0.6399 \pm 0.1588$ ,  $P = 0.0024$ ), we also show that vector control overexpression has no effect on cellular invasion. We show that



overexpression of TGFBR3 in miR-181a overexpressing cells can rescue the phenotype and decrease invasion by 26% ( $-0.2669 \pm 0.1101$ ,  $P= 0.0358$ ).

We show that miR-181a overexpression greatly enhances HaCaT cells migration and invasion. miR-181a enhancement of cellular invasion and migration is blunted by TGFBR3 overexpression. In these rescue experiments, (Figure 72) we show that overexpression of the TGFBR3 can rescue the migration phenotype almost completely and the invasion phenotype partially.

Consistent with the effects on morphology change, we show loss of E-cadherin in cell lines transfected with miR-181a mimic with concurrent increase in vimentin expression; hallmark of a mesenchymal phenotype as shown by western blot (figure 73). Further analysis of EMT markers demonstrated significant increases in *Snail*, *slug*, and *N-cadherin* [66-68] in NHEK cells overexpressing miR-181a (Figure 73).

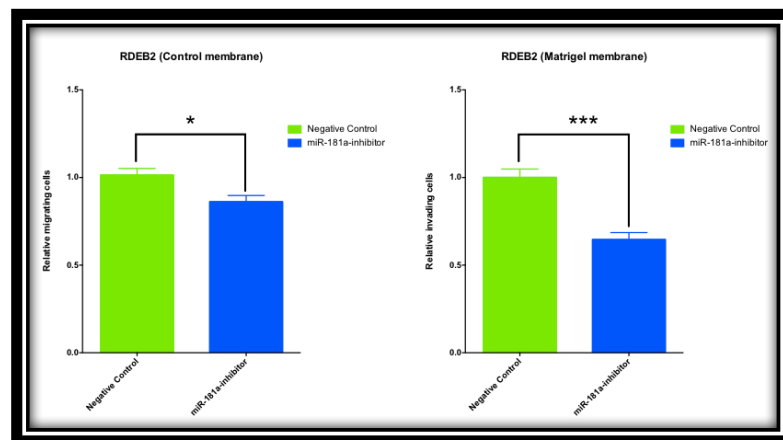
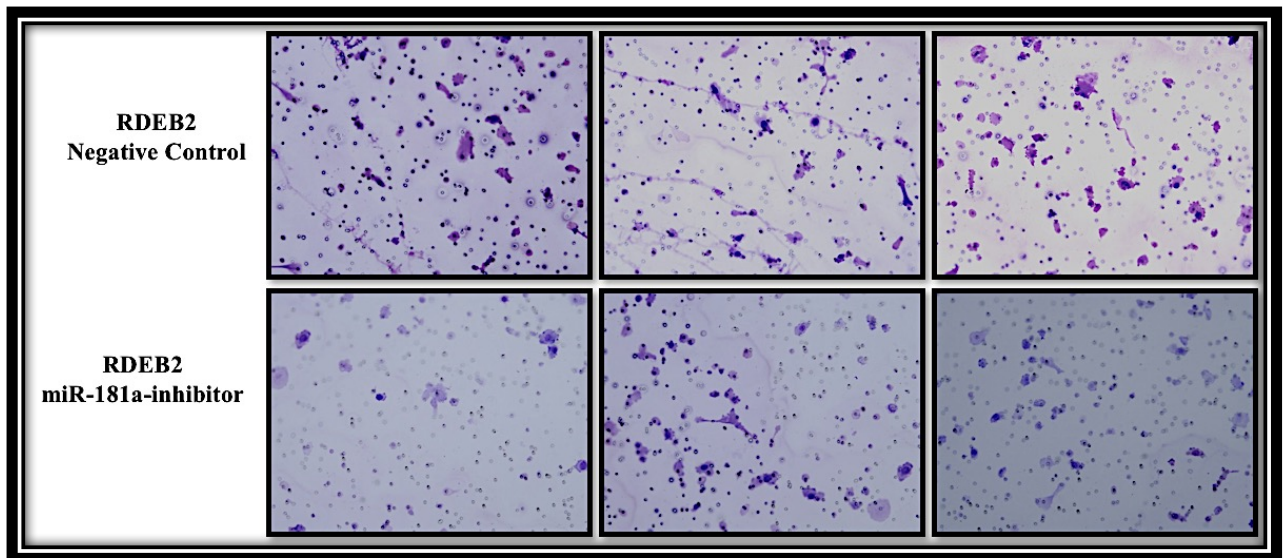


**Figure 73. Overexpression of miR-181a results in upregulation of TGF- $\beta$  pathway and mesenchymal markers.** Overexpression of miR-181a in NHEK cells was confirmed with



downregulation of ATM and downregulation of mTGFBR3, Results show upregulation of TGF- $\beta$  pathway markers pSmad and mesenchymal markers such as *Snail/Slug* and *Vimentin*.

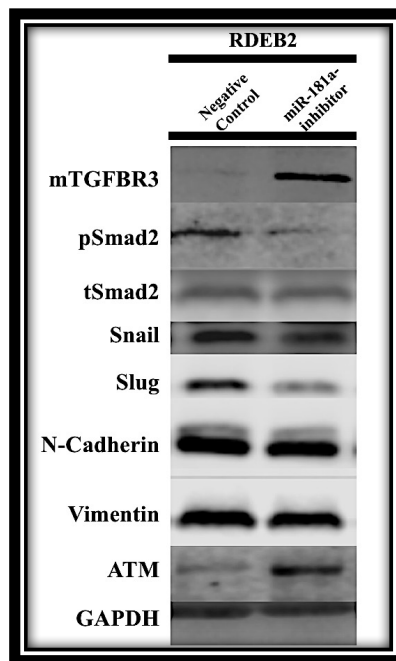
Conversely, we assessed the effect of inhibiting miR-181a in cuSCC cell lines to see if cellular migration and invasion are decreased. We used mirVana miR-inhibitors against miR-181a to decrease miR-181a levels in RDEB2 cell line. As shown above in Figure 63, RDEB2 is one of the cuSCC cell lines that has the highest expression of miR-181a. We subjected RDEB2 control and RDEB2- miR-181a inhibitor cells to Boyden chamber assays, using matrigel coated membranes. We show in Figure 74 that miR-181a inhibition decreases cellular invasion and migration.





**Figure 74. miR-181a inhibition significantly suppresses invasion of HaCaT keratinocyte cell lines *in vitro*.** We show that miR-181a inhibitor decreases cellular invasion in RDEB2 cell lines by 15% ( $-0.1526 \pm 0.05273$ ,  $P= 0.0160$ ) in comparison to the control. More significantly, miR-181a inhibition results reduces cellular invasion by 35% ( $-0.3539 \pm 0.06267$ ,  $P= 0.0002$ ). This is also reflected in the calculation of the invading index, miR-181a inhibitor ( $-0.1526 \pm 0.05273$ ,  $P= 0.0160$ ).

Consistent with the effects on morphology change, we show loss of *vimentin* in cell lines transfected with miR-181a inhibitor with concurrent decrease in expression of *N-cadherin*; hallmarks of mesenchymal phenotype are reduced as shown by western blot (Figure 75). Further analysis of EMT markers demonstrated significant decrease in *Snail*, and *slug* [66-68] in RDEB2 cells treated with miR-181a inhibitor (Figure 75).



**Figure 75. Inhibition of miR-181a results in downregulation of TGF- $\beta$  pathway and mesenchymal markers.** Inhibition of miR-181a in RDEB2 cells was confirmed with



upregulation of ATM and upregulation of mTGFB3, Results show downregulation of TGF- $\beta$  pathway markers pSmad and mesenchymal markers such as Snail/Slug and Vimentin.

## **Discussion**

Our understanding of the molecular events that lead from normal skin to AK to cuSCC is very poor and represents a fundamental gap in our understanding of this progression sequence. Such an understanding would be of enormous importance. While destructive modalities such as cryotherapy, topical immunomodulators (imiquimod), topical chemotherapy (5-fluorouracil), and photodynamic therapy are the mainstay of treatment of AK with clearance rates of about 80%, they must be repetitively used and can cause significant pain and morbidity; factors that limit their use [31, 171-175]. Furthermore, in high-risk patients such as organ transplant recipients, the sheer multiplicity of lesions makes widespread use of these therapies impractical. Chemo-preventive agents such as oral retinoids have significant systemic adverse effects[31, 171-175]. Therefore, there is a tremendous need for rationally designed targeted diagnostics and therapy for AKs, which presents an ideal opportunity for secondary skin cancer screening and prevention.

Currently, limiting sun-exposure, wearing protective clothing, and sunscreen application are the primary preventive measures against AK and cuSCC. However, these approaches have remained ineffective in reducing the overall incidence of AK and cuSCC [176]. Currently, we lack reliable diagnostic predictors of AK progression to cuSCC and its subsequent potential for metastasis. For this reason, secondary cancer prevention is of utmost importance. We propose that tumor miR-181a levels correlated with TGFB3 expression can be used as a noninvasive biomarker to predict AK behavior (distinguish AKs that will progress to cuSCC) and an independent prognostic factor in cuSCC pathogenesis [177].



We have confirmed upregulation of miR-181a in human cuSCC samples in comparison to a cohort of unmatched and matched NS specimens by using qRT-PCR, *in vivo*. Our results show that miR-181a has a significantly higher expression in unmatched cuSCCs as compared to NS (Figure 62).

We have shown that miR-181a overexpression and TGFBR3 knockdown significantly suppresses UV-induced apoptosis in HaCaTs. We have shown similar suppression of UV induced apoptosis in primary normal human epidermal keratinocytes (NHEK) ( Figure 67). We have evaluated the basal expression of miR-181a and TGFBR3 in primary keratinocytes and cuSCC cell lines through RNA-Seq and miR-Seq and their modulation with UV-exposure. We show that miR-181a suppression of UV-induced apoptosis can be partially explained with downregulation of ATM and DNA damage response cascade (Figure 69).

We have show that overexpression of miR-181a or direct knockdown of TGFBR3 by sh-RNA is sufficient for enhanced anchorage independent survival of HaCaTs. We have examined the effects of miR-181a overexpression or TGFBR3 knockdown on cellular motility and using a matrigel coated PET membrane and show that miR-181a overexpression significantly enhances invasion capacity of HaCaTs.

We show that even transient miR-181a overexpression in keratinocytes play critical role in the progression of cuSCC by suppressing UV-induced apoptosis and enhancement of migration and invasion. By developing constructs containing WT miR-181a binding sites in TGFBR3 3'UTR and mutated versions, we have demonstrated specific and direct regulation of TGFBR3 by miR-181a with luciferase reporter assay, *in vitro* (Figure 64,65, and Figure 66).

We assessed the effects of transient miR-181a overexpression and miR-181a antagonism, and we show that miR-181a overexpression, results in downregulation of TGFBR3 and upregulation of TGF- $\beta$  singling pathway as evident from upregulation of p-Smad2 and p-Smad3.



Our results validate upregulated levels of miR-181a and altered TGFBR3 signaling as important drivers of cuSCC progression. miR-181a and TGFBR3 be used as biomarkers for progression of cuSCC. This would be a tremendous advance in identifying lesions most likely to cause morbidity and mortality, particularly in high-risk populations. Therefore, treatment could be more easily optimized and targeted. miR-181a levels and TGFBR3 signaling could potentially be measured in-vivo by various non-invasive methods such as tape stripping or ultrasound-driven epidermal sampling, without the need for biopsy [159].

Importantly we would validate our findings in vivo using the SKH-1 mouse model described above by assessing whether miR-181a expression and that of the predicted targets vary with progression. We would also see whether AKs (papillomas) that are associated contiguously with cuSCC could be distinguished molecularly from AKs that arise in isolation.



# **Chapter 5**

## **Discussion and future direction**



Cutaneous squamous cell carcinoma (cuSCC) comprises 15-20% of all skin cancers, accounting for over 700,000 cases in the U.S. annually. Most cuSCC arise in association with a distinct precancerous lesion, the actinic keratosis (AK). In order to identify potential targets for molecularly targeted chemoprevention, we performed integrated cross-species genomic analysis of cuSCC development through the preneoplastic AK stage using matched isogenic human samples and a solar UV-driven Hairless mouse model. We identified transcriptional drivers of this sequence showing that the key genomic changes in cuSCC development occur in the normal skin to AK transition. Our data validate the use of this UV-driven mouse cuSCC model and demonstrate that cuSCC bears deep molecular similarities to multiple carcinogendriven SCCs from diverse sites, suggesting that cuSCC may serve as an effective, accessible model for multiple SCC types and that common treatment and prevention strategies may be feasible.

We sought to identify important genetic events that drive squamous cell carcinoma development through combined analysis of next generation sequencing of isogenic matched patient samples with a UV-driven mouse model to identify key pathways. Our approach has the key advantages of minimizing inter-individual variability and annotation errors, while enabling identification of the most biologically significant pathways. We compared non-lesional, chronically UV-exposed skin (“NS” in human, “CHR” in mouse) to preneoplastic AK (human) / papilloma (mouse) and subsequently to cuSCC using successive pairwise comparisons as well as progression models to highlight potential targets for cancer prevention.

Our analysis is the first comprehensive characterization of genomic changes that drive the development of cuSCC through its preneoplastic intermediate, the AK, employing the combination of matched isogenic human patient samples, next generation sequencing, and cross species analysis. Despite the clear clinical and histologic distinctions between cuSCC, AK, and peri-lesional UV-damaged skin, AK/PAP are most closely related to cuSCC, by many measures



including mRNA expression (unsupervised clustering and LME model), transcription factor motif analysis, mutational signatures and overlap, chromosomal instability signature expression, and microRNA-mRNA functional pair analysis (Figure 59).

Our data confirm the dramatically high mutational burden of these skin cancers and, for the first time, also show the large degree of mosaicism present across the entire exome in non-lesional UV-exposed peritumoral skin (Figure 24). Surprisingly, there is very little overlap in either the genes mutated or the positions at which those mutations occur despite close spatial proximity, but those that do overlap are significantly enriched in genes likely to be important in cuSCC pathogenesis.

Conversely, one of the most frequently mutated genes previously identified in sun-exposed skin, FGFR3, was not found to be mutated in our cohort, suggesting that this genetic lesion, frequently found in seborrheic keratoses, may be specifically critical for benign keratosis and not non-melanoma skin cancers<sup>54</sup>. Our findings are consistent with the notion that tumor suppressor genes, which represent the largest class of cancer genes known to be recurrently targeted in cuSCC, can often be inactivated by mutational insults spread across their entire coding regions<sup>64</sup>.

The subsequent expansion in overall mutational load which occurs in progression to AK and cuSCC despite expected equivalent UV exposure, combined with maintenance of the overall proportion of UVB-signature mutations, suggests an ultimate enrichment for UVB signature mutations. This may reflect compromised repair and / or the continual generation of these types of mutations in the absence of UV exposure.

SCCs of diverse sites often arise at interfaces with the environment, thus making them susceptible to sustained carcinogenic insults. Our data support the notion that cuSCC, HNSCC, lung SCC, and esophageal SCC share deep molecular commonalities (Figure 57) at the mutational



and transcriptional levels, and include deregulation of key pathways such as those driven by altered RB1, TP53 and TP63 pathways function. Therefore, for the subsets of these SCCs driven by UV, alcohol, and tobacco exposure, common molecular treatment and prevention strategies may potentially be developed and modeled on cuSCCs, which are substantially more accessible and common.

In early-stage breast cancer, even in the presence of surgery, chemotherapy, hormonal therapy, and radiotherapy, about 30% of patients have recurrence of their disease. Until now, the biological mechanism for recurrence and resistance to treatment are poorly understood. In standard prognostic factors of breast cancer classification, physicians usually take into account, histologic subtype, axillary lymph node status, tumor size and grade, patient's age and other comorbidities. There are various histological subtypes of breast cancer; however, in general, breast cancers were divided into hormone receptor positive and negative tumors.

In-situ breast cancer is divided into ductal (comedo, cribriform, micro-papillary, papillary, solid) or lobular subtypes. Invasive/infiltrating breast cancer is divided into tubular, ductal lobular, invasive lobular, infiltrating ductal, mucinous/colloid, medullar, and infiltrating ductal subtypes. About 50% of hormone receptor positive breast cancers are none-responsive to endocrine treatment intrinsically and furthermore, they develop resistance over time (acquired resistance).

Perou and colleagues, analyzed the gene expression of 65 surgical specimens of human breast tumors from 42 different individuals [178]. They show that tumors show great variation in their patterns of gene expression are mainly independent patterns of variation. They also show various subtypes of the breast cancer. Furthermore, Sorlie and colleagues show that different molecular subtypes were associated with distinct clinical outcomes and that molecular classification have prognostic relevance [179].



In the past decade, gene expression profiling has been extensively applied to the study of breast cancer [180] in order to understand its metastatic propensity [181, 182], prognosis [183], and response to therapy [184].

Luminal A is the most common subtype of breast cancer and has a higher expression of the ER and estrogen-associated genes ESR1, GATA3 and FOXA1. It does not express HER2/neu and it has a low Ki-67 proliferation index and associated with a better prognosis [185, 186]. Luminal B subtype of breast cancer express ER and has variable HER2/neu expression. It has a high Ki-67 proliferation index and has increased frequency of TP53 mutations. Luminal B tumours are associated with worse prognosis compared to Luminal A [185, 186].

Basal-like subtype of breast cancer is negative for hormone receptors (ER and PR) and HER2/neu receptor [187-190]. It has high expression of genes associated with myoepithelial cells: KRT5 (keratin 5), KRT17 (keratin 17), CNN1 (calponin 1), CAV1 (caveolin) and LAMB1 (laminin). It is aggressive and associated with a poorer disease-free and overall survival than the other breast cancer subtypes [191].

HER2/neu over-expressing subtype of breast cancer has increased expression of genes located in the same region on chromosome 17q: human epidermal growth factor receptor 2, ERBB2, and growth factor receptor bound protein 7, GRB7. It is associated with a high histological grade, low expression of ER and PR and a poor clinical outcome [185, 186]. The unexpected molecular similarity of cuSCC to specific subtypes of breast cancer may also highlight similar molecular vulnerabilities such as ERBB2/HER2.

Interestingly, there was much less similarity between cuSCC and cervical SCC (Figure 57). cuSCC does not appear to require HPV transcription for tumor maintenance, whereas cervical SCC is overwhelmingly driven by high-risk  $\alpha$ HPV infection and may warrant virus-directed strategies [192-194].



While AKs appear already to harbor the majority of events that are retained in cuSCC, at least two alternative explanations are possible for our findings: (1) consistent mutational or transcriptomic events that separate AKs vs. cuSCC could be present, and/or (2) there are distinct molecular classes of AKs with different risks of progression to cuSCC. Either of these explanations would require much larger numbers of samples to demonstrate. Nevertheless, data from multiple groups suggest that extant clinical criteria for predicting the behavior of AKs are inadequate [195]. Our data show that microRNA expression distinguishes the three sample classes and may serve as a basis for distinguishing different types of AKs. In addition, our cross-species functional pair analysis has identified a handful of highly interconnected microRNA-mRNA networks that drive cuSCC development through preneoplastic AKs (Figure 52 and Figure 53), highlighting specific microRNA targets for potential intervention.

Nevertheless, given the many significant similarities between AK and cuSCC, our data suggest that non-lesional carcinogen-exposed fields of tissue may represent the most effective point of intervention for molecularly-targeted chemoprevention. The development of cancer through a preneoplastic intermediate has been studied in greatest detail at the genomic level in Barrett's esophagus and esophageal adenocarcinoma. For the most part, these lesions have little mutational overlap and progression to carcinoma is thought to result from catastrophic genome doublings within 4 years of progression [196, 197]. Recently, this was confirmed and extended with the identification of rare sweeps of initial clonal expansion in Barrett's esophagus, with frequent polyclonality, and subsequent genome doublings, with specific oncogenic amplifications [198, 199].

In many respects, Barrett's esophagus that eventually evolves into adenocarcinoma is largely indistinguishable from carcinoma, although some that do so appear genomically stable, consistent with our conclusion that for a subset of patients, field-based treatment is most



appropriate. AKs are typically too small to allow for repeated sampling, thus removing the possibility for longitudinal follow-up and clinical discernment between AKs that ultimately progress and those that do not. Nevertheless, it appears that at least in comparing AKs to cuSCCs, it is likely that AKs are polyclonal reservoirs from which cuSCCs can arise (Figure 30), and it is as yet unclear whether catastrophic genomic instability is a further driver in this late transition.

Our data substantiate the power of cross-species analysis to identify biologically-important pathways in cuSCC development and also validates the use of the solar UV-exposed Hairless mouse model as an accurate and useful testbed for novel chemo-preventive and treatment modalities. The key transcriptional drivers we identified in both pairwise signatures and the LME model are important early in the NS/CHR to AK/PAP transition and include E2F, ELK1, and NFY. Globally, we also identified ERK signaling through ETS2 and ELK1,  $\beta$ -catenin signaling through TCF3 and LEF1, and potential differentiation pathways regulated by NFAT and AP1 as important drivers of cuSCC development (Figure 41 and Figure 42).

Wnt signaling is mediated by Tcf/Lef transcription factors and  $\beta$ -catenin [200]. Wnt signaling plays an important role in embryogenesis, stem cell renewal, and cancer progression. Unique Tcf/Lef transcription factors mediate distinct responses to Wnt signaling [200]. Lui and colleagues show that TCF1 and TCF3 genes are required in *Xenopus* mesoderm induction for transcriptional activation and repression, respectively.

Transcription factor T-cell factor-3 (TCF3) encodes a member of the E protein family of helix-loop-helix transcription factors [201, 202], which activates transcription by binding to regulatory E-box sequences. TCF3 is required for B and T lymphocyte development. TCF3 deletion or downregulation results in lymphoid malignancies. TCF3 is frequently involved in chromosomal translocations resulting in various lymphoid malignancies [201, 202]. Based on the human protein atlas, most cancer cells have very weak or negative TCF3 nuclear



immunoreactivity. On the other hand, testis cancers, lymphomas, and skin cancers show moderate to strong immunoreactivity.

Oct4, Sox2, and Nanog are the key transcription factors that regulate the unique cellular pathways such as pluripotency and self-renewal of embryonic stem cells (ES) [203]. Cole and colleagues show that TCF3 is an integral component of the core regulatory circuitry of ES cells. They show that TCF3 downregulation and Wnt pathway activation causes enhancement of pluripotency factors and ES cells refract to differentiation. Wnt signaling through TCF3 influences the balance of pluripotency and differentiation in ES cells [203].

The significant enrichment of signatures from both patient samples and the UV-driven Hairless model in multiple carcinogen-driven SCCs arising in diverse sites is important in many respects (Figure 57). Furthermore, early cuSCC signatures were able to predict survival in TP53-mutant (non-HPV) HNSCC (Figure 58). Coupled with previously-reported mutational data, it indicates that a common set of biological processes underlie the development of multiple SCC types, and that cuSCC may serve as an accurate and extremely accessible model for exploring pathogenesis and testing interventions.

Currently, we lack diagnostic predictors of AK progression to cuSCC. We proposed that miR-181a levels, correlated with TGFBR3 expression, drive disease progression and can be used as a noninvasive biomarker to both predict AK behavior and prognosis in cuSCC pathogenesis. This would be a tremendous advance in identifying lesions most likely to cause morbidity and mortality, leading to better treatment strategies. Importantly, miR-181a and TGFBR3 could serve as therapeutic targets. Restoring TGFBR3 signaling or suppressing miR-181a expression could be used to reverse or stop cuSCC progression, thus functioning as targeted chemoprevention for cuSCC in high risk patients.

In our study, miR-181a was shown to be significantly up-regulated in cuSCC samples in



comparison to NS. miR-181a has been shown to be involved in several processes, including hematopoiesis [204], adipogenesis [205], myoblast differentiation[206] and endothelial cell differentiation [207]. In addition, miR-181a is a master regulator in hematological and non-hematological cancers [208, 209].

Li and colleagues demonstrated that the downregulation of miR-181a is associated with adverse overall survival in cytogenetically abnormal acute myeloid leukemia, which suggests a tumor suppressive function [210]. Conversely, miR-181a overexpression has been associated with poor survival in oral squamous cell carcinoma, which supports an oncogenic function [211]. Recently, miR-181a expression was found to be transcriptionally regulated by the activation of Wnt/ $\beta$ -catenin signalling in hepatocellular carcinoma [212] a signaling pathway that is also commonly deregulated in CRC [213].

Given the therapeutic potential of this regulatory miRNA and the pivotal role of miR-181a in different cancer types necessitates further research to elucidate its role in pathogenesis of human cuSCC. Until now, the role of miR-181a in human cuSCC and its prognostic significance have not been explored systematically. To elucidate the role of miR-181a in cuSCC, we tested whether miR-181a overexpression influences cuSCC EMT pathway through TGFBR3.

The diverse effects of TGF-beta are mediated by the TGF-beta receptors and cell surface-binding proteins. Three TGF-beta receptors exist: type I, type II, and type III (TGFBR3) [214]. TGFBR3 regulates epithelial-mesenchymal transformation in cardiac endothelial cells. Some evidence suggests that TGFBR3 is involved in regulation of cellular apoptosis. TGF- $\beta$  induces apoptosis in numerous cell types. TGF- $\beta$  can induce apoptosis through the SMAD pathway or the DAXX pathway. TGFBR3 has a dichotomous role in human cancers; it functions both as a tumor suppressor and as a tumor promoter. TGFBR3 is downregulated in various human cancers. In early-stage human cancer, it has a tumor suppressor role and it serves as a regulator of homeostatic



functions of the TGF- $\beta$  pathway. On the other hand, in late-stage human tumors it increases TGF- $\beta$  expression, resulting in tumor progression [215]. TGFBR3 has been shown to enhance tumor progression by suppressing immune surveillance, inducing epithelial to mesenchymal transition, and promoting tumor invasiveness, angiogenesis, and metastasis [71].

TGF- $\beta$  pathway plays a crucial role in the regulation of the cell cycle. TGF- $\beta$  causes synthesis of p15 and p21 proteins, which block the cyclin:CDK complex responsible for Retinoblastoma protein (Rb) phosphorylation. Thus TGF- $\beta$  blocks advance through the G1 phase of the cycle. In doing so, TGF- $\beta$  suppresses expression of c-myc, a gene which is involved in G1 cell cycle progression [216]. TGF-B superfamily has a dual role in human cancer where it can either suppress or promote progression of carcinoma in a cell type and context dependent manner. TGFBR3 is a cancer suppressor and regulates cellular functions such as proliferation, migration and invasion [216].

Loss of TGFBR3 and its important role as a regulator of cellular migration, invasion, and proliferation has been demonstrated in multiple cancers such as breast, lung, prostate and renal cancer [71, 72]. TGFBR3 may have a role as the guardian of the epithelial phenotype and tumor suppressor. TGFBR3 expression is regulated at transcriptional, epigenetic, and protein level. TGFBR3 null mice is embryonically lethal, pointing to the importance of highly regulated mRNA levels during development [217].

Our results show that primary human keratinocytes and HaCaT cells that overexpress miR-181a or have TGFBR3 knockdown are less susceptible to UV-induced apoptosis, readily form colonies in soft agar, and exhibit hypermotility as well as adhesion defects. Based on our results, we propose that miR-181a is a useful therapeutic target for prevention of cuSCC.

In addition, miR-181a and TGFBR3 could serve as therapeutic targets. Restoring TGFBR3 signaling (through manipulation of downstream molecules) or suppressing miR-181a



expression could be used to reverse or stop cuSCC progression. Thus, functioning as targeted chemoprevention for cuSCC in individuals with multiple AKs or high-risk factors such as excessive UV exposure or immunosuppression. We would evaluate how the manipulation of miR-181a and associated target expression would affect cuSCC progression in vivo by using the SKH-1 mouse model.

A thesis project from F. Wang at Yale University, investigates the role of TGFBR3 in head and neck SCC development [218]. They show that HNSCC lines expressing low levels of wt-p53 have suppressed levels of TGFBR3 in comparison to cell lines that have mut-p53 expression. They demonstrate that TGFBR3 overexpression enhances TGF- $\beta$  signaling through stimulation of Smad-dependent pathway and results in upregulation of PAI-1 and p21Cip1 [218]. They also show that TGFBR3 enhances NF- $\kappa$ B and AP-1 reporter activity, downstream IL-6 and IL-8 cytokine production, and p65 and p38 MAPK phosphorylation [218]. In addition, TGFBR3 overexpression induces a microspike/filopodia-like phenotype in HNSCC cells. In contrast to our results, they show that TGFBR3 overexpression enhances TGF- $\beta$  and NF- $\kappa$ B signaling and reduces cell proliferation and migration in HNSCC.

In another study, authors show that TGFB2 and TGFBR3 signaling through p38alpha/beta regulates disseminated tumor cells dormancy and defines restrictive versus permissive microenvironments for HNSCC metastasis, such as bone marrow versus lung metastasis [219].

A recent meta-analysis in 2015, investigated the prognostic value of different microRNAs in human head and neck squamous cell carcinoma (HNSCC) [64]. In this study they included 21 publications and data from 1685 patients to assess the relationship between miRNA and HNSCC prognosis. The results of this study is very similar to microRNAs we identified to be important in cuSCC progression. They show that elevated expressions of miR-21, miR-18a, miR-134a, miR-210, miR-181a, miR-19a, and miR-155 were associated with poor survival in human HNSCC



[64]. Of important note, similar to our findings, they identify miR-21 and miR-181a as two very important microRNAs that are associated with HNSCC poor prognosis.

On the other hand, this meta-analysis identifies that low expressions of miR-153, miR-200c, miR-363, miR-203, miR-17, miR-205, miR-Let-7d, Let-7g, miR-34a, miR-126a, miR-375, miR-491-p53, miR 218, miR-451 and miR-125b were associated with poor prognosis. Based on these results and our TCGA data results we can conclude that miRs are promising markers for prognosis prediction in HNSCC [64].

In addition, various individual studies have identified miR-181a to be upregulated in HNSCC [220]. Moreover, miR-181a serves as a putative biomarker for lymph-node metastasis of oral squamous cell carcinoma [211]. Consistently, in another HNSCC study, authors show that four miRNA: miR-181a, miR-181b, miR-21, and miR-7 demonstrate dramatic upregulation in HNSCC tumor tissues comparing to their patient-matched normal controls [221].

Tumor suppressor, Ataxia Telangiectasia Mutated (ATM) is one of the top pathways identified in cell cycle regulation and cellular stress. From SNV variant analysis we found out that in multiple samples, as predicted by the SIFT tool, we have deleterious mutations in ATM and ATM interactor (ATMIn). From miR-Seq data we found out that overexpression of miR-181a family paralleled the transition from NS to AK to cuSCC. ATM is a target of miR-181 family.

ATM is a key regulator of DNA damage signaling pathway. ATM targets multiple downstream signaling molecules such as Chk1, Chk2, p53 and BRCA. Also, ATM regulates DNA repair factors such as Rad50, Rad51, and GADD45 [195]. As a result of ionizing radiation and in presence of DNA double strand breaks (DSBs) MRE11-Rad50-NBS1 complex or 53BP1 activate ATM; auto-phosphorylation of ATM dimer/multimer leads to its monomerization and activation. ATM regulates cell cycle through phosphorylation of Chk2 and p53. ATM regulates DNA repair through phosphorylation of SMC1 and histone H2AX [84]. ATM has various roles: it responds



to DNA damage by DSB signal amplification. ATM controls cell-cycle checkpoints, maintains telomere length and integrity, and it is involved in V(D)J recombination: T-cell receptor and immunoglobulin genes rearrangement.

We tested whether overexpression of miR-181a is sufficient to induce cuSCC-like phenotype in primary feeder-dependent keratinocytes. We measured the effect on proliferation, apoptosis, and/or DNA damage responses. Results of our experiments provided insights into the cellular factors regulating the transformation of AK to cuSCC. It also elucidated a novel role for the tumor suppressor ATM and mir-181a family in pathogenesis of cuSCC development. Our results show that miR-181a by targeting ATM dampens the response to the UV-induced apoptosis and results in downregulation of p-H2AX. We concluded that in part, the targeting of ATM by miR-181a is the likely event that causes UV-induced suppression in miR-181a overexpressing cell lines and cuSCCs. In addition, Bisso and colleagues have demonstrated that ATM is down-regulated by miR-181a/b in triple negative breast cancer [163].

Moreover, our bioinformatics analysis also showed that miR-30a varied consistently across cuSCC progression, steadily decreasing from NS to AK to cuSCC. miR-30a has been implicated in ocular disease processes and through downregulation of catalase it halts the cytoprotective mechanisms against reactive oxygen species [222]. In addition, downregulation of miR-30 has been implicated in myocardial matrix remodeling [223], idiopathic pulmonary fibrosis [224], and promotion of EMT in thyroid carcinoma [225] as well as pancreatic islet cells [226]. We will conduct similar analyses as described above to validate the function of miR-30a and its potential targets in regulating the progression of cuSCC. We have identified multiple targets of miR-30a for further functional validation.

Our cross-species analyses show that miR-497 and let-7b are downregulated in cuSCC samples in comparison to normal skin. Our functional pair analysis revealed that both miRNAs



regulate High Mobility Group A2 (HMGA2), which is upregulated in various cancers and prolactinomas [227]. HMGA2 protein has been demonstrated to be a biomarker of dysplasia in intraductal papillary mucinous neoplasms (IPMN) and its concentration in cystic fluid serves as a biomarker to differentiate high-risk IPMNs versus low-risk IPMNs [228]. It has been shown that HMGA2 epigenetically silences the *Cdh1* gene during EMT [229]. HMGA2 is an oncogenic protein that regulated epithelial to mesenchymal transformation, cell proliferation and apoptosis. More specifically, it has been shown that in CRC, HMGA2 induces transcription factor Slug expression to promote EMT and colon cancer progression [230]. In lung cancer, HMGA2 is overexpressed in tumor samples as compared with normal tissue [231]. In breast cancer, HMGA2/TET1/HOXA9 signaling pathway enhances metastasis [232]. In addition, both miR-195 and miR-497 are significantly downregulated in breast cancer and their target genes Raf-1 and *Ccnd1* play important inhibitory roles in breast cancer [233]. Moreover, miR-497 acts as a tumor suppressor by targeting *Bcl-w* in breast cancer [234].

Drawing parallels between our cuSCC findings and basal-like subtype of breast cancer, a recent study examines the gene signature of 25-miRNA to effectively distinguish triple-negative breast cancers from normal tissues [235]. Overall, they identified seven polycistronic miRNA clusters that is significantly dysregulated and two of those clusters are miR-143-145 at 5q32 and miR-497-195 at 17p13.1 which are significantly down-regulated in triple-negative breast cancer [235]

As a future goal, we would like to investigate the role of miRNA-497 and let-7b in cuSCC progression by targeting *HMGA2*. The Let-7 miRNA family was among of the first miRNAs to be discovered. Across species, Let-7 family members are highly conserved in both sequence and function. Let-7 is regulated both transcriptionally and post-transcriptionally [236]. HMGA2 is a functionally validated target of Let-7 [237]. Let-7 downregulation promotes a stem-cell-



phenotype via regulation of HMGA2 [238]. We would like to assess the degree by which lLet-7 and miR-497 cooperatively modulate the levels of HMGA2 and resulting in cuSCC progression.

Because of their small size, delivery of miRNAs *in vivo* is much easier than proteins. Chitosan-based hydrogel can be used for local delivery of miRNA [239]. This method utilizes a thermosensitive, low-toxic, biodegradable polymer that can be introduced *in vivo* that solidifies at higher temperatures [240]. With this tool, we can have localized and tissue-specific overexpression or inhibition of miRNAs target genes. Our lab has been utilizing this model for further *in vivo* validation of our dysregulated miRNAs.



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## **Vita**

Vida Chitsazzadeh was born in Mashhad, Iran on March 10, 1985, the daughter of Mansoureh A. Shajari and Mohammad Chitsazzadeh. When she was sixteen years old, her family immigrated to the United States and settled in Southern California. After completing her work at Canoga Park High School, LA, California in 2003, she entered University of California, Los Angeles (UCLA). She received her Bachelor of Science with a major in biology from UCLA in May, 2007. For the next year, she worked as a research assistant in the Department of Neurology and Pediatrics at Harvard Medical School and Boston Children's Hospital. In May of 2008 she entered the MD/PhD dual degree program of the The University of Texas Medical School at Houston and The University of Texas Graduate School of Biomedical Sciences at Houston.

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# Appendix 1.

## Significantly mutated genes



|    | Gene  | Classification | Type | Sample | AAChange  | TVarRat | FATHMM_score<br>LRT<br>MutationAssessor<br>MutationTaster<br>Polyphen2_HDIV<br>Polyphen2_HVAR<br>SIFT_score |   |         |   |     |     |      | Type |
|----|-------|----------------|------|--------|-----------|---------|---|---|---------|---|-----|-----|------|------|
|    |       |                |      |        |           |         |   |   |         |   |     |     |      |      |
| 0  | USH2A | Missense       | SNV  | 1-NS   | c.G7310A  | 0.050   | 1.35  | D | medium  | D | D   | D   | 0.05 | NS   |
| 3  | USH2A | Missense       | SNV  | 10-AK  | c.A3831T  | 0.095   | 0.92  | D | medium  | D | D;D | D;D | 0.31 | AK   |
| 4  | USH2A | Missense       | SNV  | 2-AK   | c.C4717A  | 0.126   | -0.6  | D | medium  | D | D   | D   | 0.21 | AK   |
| 5  | USH2A | Missense       | SNV  | 2-SCC  | c.G13295A | 0.376   | 0.7   | U | medium  | D | D   | P   | 0.04 | SCC  |
| 6  | USH2A | Missense       | SNV  | 3-SCC  | c.G14288A | 0.160   | 0.9   | U | medium  | D | D   | D   | 0    | SCC  |
| 7  | USH2A | Missense       | SNV  | 3-SCC  | c.C11411T | 0.074   | 1.19  | D | medium  | D | D   | D   | 0.36 | SCC  |
| 8  | USH2A | Missense       | SNV  | 3-SCC  | c.C10633T | 0.138   | 1.4   | N | medium  | N | D   | P   | 0.01 | SCC  |
| 9  | USH2A | Missense       | SNV  | 3-SCC  | c.C7916T  | 0.050   | 0.6   | N | medium  | D | D   | D   | 0.08 | SCC  |
| 10 | USH2A | Missense       | SNV  | 3-SCC  | c.G6172A  | 0.041   | 1.4   | N | medium  | N | B   | B   | 0.49 | SCC  |
| 11 | USH2A | Missense       | SNV  | 3-SCC  | c.G5146A  | 0.179   | -0.8  | D | medium  | D | D   | D   | 0.02 | SCC  |
| 12 | USH2A | Missense       | SNV  | 3-SCC  | c.C5087T  | 0.137   | 2.58  | N | neutral | N | P   | P   | 0.01 | SCC  |
| 13 | USH2A | Missense       | SNV  | 3-SCC  | c.G3034A  | 0.074   | 1.95  | U | neutral | N | B;P | B;B | 0.66 | SCC  |
| 14 | USH2A | Missense       | SNV  | 3-SCC  | c.C914T   | 0.065   | 2.2   | D | medium  | D | D;D | D;D | 0.02 | SCC  |
| 15 | USH2A | Missense       | SNV  | 4-SCC2 | c.G10321A | 0.061   | 2.65  | N | low     | N | B   | B   | 0.61 | SCC2 |
| 16 | USH2A | Missense       | SNV  | 5-SCC  | c.C9355T  | 0.213   | 1.35  | N | low     | N | D   | B   | 0.07 | SCC  |
| 17 | USH2A | Missense       | SNV  | 5-SCC  | c.C7774T  | 0.265   | 0.3   | D | medium  | D | D   | D   | 0.02 | SCC  |
| 18 | USH2A | Missense       | SNV  | 5-SCC  | c.G5147A  | 0.293   | -0.8  | D | medium  | D | D   | D   | 0.02 | SCC  |
| 19 | USH2A | Missense       | SNV  | 5-SCC  | c.G2558A  | 0.295   | 2.83  | D | high    | D | D;D | D;D | 0    | SCC  |
| 20 | USH2A | Missense       | SNV  | 6-NS   | c.G5008A  | 0.049   | -0.7  | N | medium  | N | D   | D   | 0.03 | NS   |
| 21 | USH2A | Missense       | SNV  | 6-SCC  | c.G14855A | 0.072   | 2.55  | U | medium  | N | B   | B   | 0.25 | SCC  |
| 22 | USH2A | Missense       | SNV  | 6-SCC  | c.G13993A | 0.097   | 0.63  | U | medium  | D | D   | D   | 0    | SCC  |
| 23 | USH2A | Missense       | SNV  | 6-SCC  | c.G10501A | 0.139   | 1.41  | U | medium  | D | D   | D   | 0.08 | SCC  |
| 24 | USH2A | Nonsense       | SNV  | 6-SCC  | c.G9120A  | 0.111   | .   | . | .       | . | .   | .   | .    | SCC  |
| 25 | USH2A | Missense       | SNV  | 6-SCC  | c.G389A   | 0.062   | 2.82  | U | low     | N | B;B | B;B | 0.31 | SCC  |
| 26 | USH2A | Missense       | DNV  | 6-SCC  | c.GG161AA | 0.124   | .   | . | .       | . | .   | .   | .    | SCC  |

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|    | Gene   | Classification | Type | Sample | AAChange   | TVarRat | FATHMM_score<br>LRT<br>MutationAssessor<br>MutationTaster<br>Polyphen2_HDIV<br>Polyphen2_HVAR<br>SIFT_score |   |        |   |       |       |      | Type |
|----|--------|----------------|------|--------|------------|---------|---|---|--------|---|-------|-------|------|------|
|    |        |                |      |        |            |         |   |   |        |   |       |       |      |      |
| 28 | SPHKAP | Missense       | SNV  | 2-AK   | c.C1532T   | 0.091   | 2.68  | D | medium | D | D;D   | D;D   | 0    | AK   |
| 30 | SPHKAP | Missense       | SNV  | 2-AK   | c.C350T    | 0.045   | 2.01  | D | low    | D | D;D   | D;D   | 0    | AK   |
| 31 | SPHKAP | Missense       | SNV  | 3-AK   | c.G3412A   | 0.196   | 2.8   | D | low    | D | D;D;D | D;D;D | 0.34 | AK   |
| 32 | SPHKAP | Missense       | SNV  | 3-SCC  | c.T2413C   | 0.067   | 2.79  | N | medium | N | B;B   | B;B   | 0.64 | SCC  |
| 33 | SPHKAP | Missense       | SNV  | 3-SCC  | c.G2263A   | 0.107   | 2.44  | N | medium | N | B;P   | B;B   | 0.11 | SCC  |
| 34 | SPHKAP | Missense       | SNV  | 4-AK   | c.G3412A   | 0.196   | 2.8   | D | low    | D | D;D;D | D;D;D | 0.34 | AK   |
| 35 | SPHKAP | Missense       | SNV  | 5-SCC  | c.A4905T   | 0.257   | 3.1   | D | medium | D | D;D   | D;D   | 0.01 | SCC  |
| 36 | SPHKAP | Missense       | SNV  | 5-SCC  | c.G3686A   | 0.455   | 2.64  | D | medium | D | D;D;D | D;D;D | 0.01 | SCC  |
| 37 | SPHKAP | Missense       | DNV  | 6-SCC  | c.GG1366AA | 0.058   | .   | . | .      | . | .     | .     | .    | SCC  |
| 38 | SPHKAP | Missense       | SNV  | 8-NS   | c.G754A    | 0.071   | 2.62  | N | low    | N | B;B   | B;B   | 0.55 | NS   |
| 39 | SPHKAP | Missense       | SNV  | 12-AK  | c.G733A    | 0.119   | 2.73  | N | medium | N | D;D   | D;D   | 0.03 | AK   |

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|    | Gene    | Classification | Type | Sample | AAChange  | TVarRat | FATHMM_score<br>LRT<br>MutationAssessor<br>MutationTaster<br>Polyphen2_HDIV<br>Polyphen2_HVAR<br>SIFT_score |   |         |   |       |       |      | Type |
|----|---------|----------------|------|--------|-----------|---------|---|---|---------|---|-------|-------|------|------|
|    |         |                |      |        |           |         |   |   |         |   |       |       |      |      |
| 41 | FAM135B | Missense       | SNV  | 2-AK   | c.G832T   | 0.074   | 2.5   | N | low     | N | B     | B     | 0.74 | AK   |
| 43 | FAM135B | Nonsense       | SNV  | 3-SCC  | c.C2155T  | 0.066   | .   | . | .       | . | .     | .     | .    | SCC  |
| 44 | FAM135B | Missense       | SNV  | 3-SCC  | c.G1012A  | 0.061   | 2.51  | D | low     | N | D     | D     | 0.24 | SCC  |
| 45 | FAM135B | Missense       | SNV  | 3-SCC  | c.C32T    | 0.048   | 1.78  | U | low     | D | D     | D     | 0.38 | SCC  |
| 46 | FAM135B | Missense       | DNV  | 3-SCC  | c.TC865CT | 0.224   | .   | . | .       | . | .     | .     | .    | SCC  |
| 47 | FAM135B | Missense       | SNV  | 4-AK   | c.G3556A  | 0.053   | 0.58  | D | low     | D | D;D   | D;D   | 0    | AK   |
| 48 | FAM135B | Missense       | SNV  | 4-AK   | c.G167A   | 0.045   | 2.49  | U | low     | N | B     | B     | 0.5  | AK   |
| 49 | FAM135B | Missense       | SNV  | 6-NS   | c.C3193T  | 0.040   | 2.07  | D | medium  | N | D;D;D | D;D;D | 0.02 | NS   |
| 50 | FAM135B | Missense       | SNV  | 6-SCC  | c.G3695A  | 0.151   | 1   | D | neutral | N | D     | D     | 0.23 | SCC  |
| 51 | FAM135B | Missense       | SNV  | 6-SCC  | c.A883G   | 0.148   | 2.45  | N | low     | N | B     | B     | 0.22 | SCC  |
| 52 | FAM135B | Missense       | SNV  | 8-SCC  | c.C2198G  | 0.075   | 1.81  | D | medium  | N | D;D;D | D;D;P | 0.16 | SCC  |



|    |         |          |     |       |          |       |      |   |         |   |       |       |      |     |
|----|---------|----------|-----|-------|----------|-------|------|---|---------|---|-------|-------|------|-----|
| 53 | FAM135B | Missense | SNV | 8-SCC | c.G1876A | 0.074 | 2.42 | N | low     | D | D;P;P | P;P;B | 0.12 | SCC |
| 54 | FAM135B | Missense | SNV | 10-AK | c.G3506A | 0.136 | 1    | D | neutral | N | D;D   | D;D   | 0.05 | AK  |

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|      |                |          |        |          |          | FATHMM_score | LRT | MutationAssessor | MutationTaster | Polyphen2_HDIV | Polyphen2_HVAR | SIFT_score |  |      |
|------|----------------|----------|--------|----------|----------|--------------|-----|------------------|----------------|----------------|----------------|------------|--|------|
| Gene | Classification | Type     | Sample | AACHange | TVarRat  |              |     |                  |                |                |                |            |  | Type |
| 56   | ABCA13         | Missense | DNV    | 10-AK    | p.P4883L | 0.042        |     |                  |                |                |                |            |  | AK   |
| 57   | ABCA13         | Missense | SNV    | 2-AK     | p.D3259N | 0.134        |     |                  |                |                |                |            |  | AK   |
| 58   | ABCA13         | Missense | SNV    | 2-AK     | p.L819F  | 0.139        |     |                  |                |                |                |            |  | AK   |
| 59   | ABCA13         | Missense | SNV    | 3-SCC    | p.G4838E | 0.042        |     |                  |                |                |                |            |  | SCC  |
| 60   | ABCA13         | Missense | SNV    | 3-SCC    | p.A932V  | 0.044        |     |                  |                |                |                |            |  | SCC  |
| 61   | ABCA13         | Missense | SNV    | 3-SCC    | p.S522F  | 0.044        |     |                  |                |                |                |            |  | SCC  |
| 62   | ABCA13         | Missense | SNV    | 3-SCC    | p.F2849L | 0.063        |     |                  |                |                |                |            |  | SCC  |
| 63   | ABCA13         | Missense | SNV    | 3-SCC    | p.G2179D | 0.072        |     |                  |                |                |                |            |  | SCC  |
| 64   | ABCA13         | Missense | SNV    | 3-SCC    | p.E4960K | 0.114        |     |                  |                |                |                |            |  | SCC  |
| 65   | ABCA13         | Missense | SNV    | 3-SCC    | p.P1751L | 0.152        |     |                  |                |                |                |            |  | SCC  |
| 66   | ABCA13         | Missense | SNV    | 3-SCC    | p.P4406L | 0.158        |     |                  |                |                |                |            |  | SCC  |
| 67   | ABCA13         | Missense | SNV    | 3-SCC    | p.E1553K | 0.161        |     |                  |                |                |                |            |  | SCC  |
| 68   | ABCA13         | Missense | SNV    | 3-SCC    | p.I3884F | 0.165        |     |                  |                |                |                |            |  | SCC  |
| 69   | ABCA13         | Missense | SNV    | 3-SCC    | p.E3730K | 0.188        |     |                  |                |                |                |            |  | SCC  |
| 70   | ABCA13         | Missense | SNV    | 3-SCC    | p.E909K  | 0.217        |     |                  |                |                |                |            |  | SCC  |
| 71   | ABCA13         | Missense | SNV    | 3-SCC    | p.L933F  | 0.231        |     |                  |                |                |                |            |  | SCC  |
| 72   | ABCA13         | Nonsense | SNV    | 4-SCC2   | p.W2837X | 0.064        |     |                  |                |                |                |            |  | SCC2 |
| 73   | ABCA13         | Missense | DNV    | 5-AK     | p.L1670F | 0.081        |     |                  |                |                |                |            |  | AK   |
| 74   | ABCA13         | Missense | SNV    | 5-AK     | p.E2986K | 0.040        |     |                  |                |                |                |            |  | AK   |
| 75   | ABCA13         | Missense | SNV    | 5-AK     | p.H4032Q | 0.064        |     |                  |                |                |                |            |  | AK   |
| 76   | ABCA13         | Missense | SNV    | 5-AK     | p.K161R  | 0.119        |     |                  |                |                |                |            |  | AK   |
| 77   | ABCA13         | Missense | SNV    | 5-SCC    | p.M567I  | 0.092        |     |                  |                |                |                |            |  | SCC  |
| 78   | ABCA13         | Missense | SNV    | 5-SCC    | p.P605S  | 0.396        |     |                  |                |                |                |            |  | SCC  |
| 79   | ABCA13         | Missense | SNV    | 6-SCC    | p.E4748K | 0.041        |     |                  |                |                |                |            |  | SCC  |
| 80   | ABCA13         | Missense | SNV    | 6-SCC    | p.G3720R | 0.059        |     |                  |                |                |                |            |  | SCC  |
| 81   | ABCA13         | Missense | SNV    | 6-SCC    | p.E4960K | 0.080        |     |                  |                |                |                |            |  | SCC  |
| 82   | ABCA13         | Missense | SNV    | 6-SCC    | p.E3852K | 0.135        |     |                  |                |                |                |            |  | SCC  |
| 83   | ABCA13         | Nonsense | SNV    | 6-SCC    | p.W179X  | 0.072        |     |                  |                |                |                |            |  | SCC  |
| 84   | ABCA13         | Missense | SNV    | 8-SCC    | p.G1780S | 0.044        |     |                  |                |                |                |            |  | SCC  |

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| Gene | Classification | Type       | Sample | AACHange | TVarRat        |       |  |  |  |  |  |  |  | Type |
|------|----------------|------------|--------|----------|----------------|-------|--|--|--|--|--|--|--|------|
| 87   | FAT1           | Frameshift | DEL    | 1-NS     | p.3138_3139del | 0.131 |  |  |  |  |  |  |  | NS   |
| 88   | FAT1           | Missense   | SNV    | 1-NS     | p.P1560S       | 0.045 |  |  |  |  |  |  |  | NS   |
| 89   | FAT1           | Nonsense   | DNV    | 1-NS     | p.P4580*       | 0.080 |  |  |  |  |  |  |  | NS   |
| 90   | FAT1           | Missense   | SNV    | 10-AK    | p.D1131Y       | 0.068 |  |  |  |  |  |  |  | AK   |
| 91   | FAT1           | Frameshift | DEL    | 12-AK    | p.A2920fs      | 0.067 |  |  |  |  |  |  |  | AK   |
| 92   | FAT1           | Nonsense   | SNV    | 3-AK     | p.Q3192X       | 0.167 |  |  |  |  |  |  |  | AK   |
| 93   | FAT1           | Missense   | SNV    | 3-SCC    | p.C281S        | 0.149 |  |  |  |  |  |  |  | SCC  |
| 94   | FAT1           | Nonsense   | SNV    | 3-SCC    | p.R2597X       | 0.159 |  |  |  |  |  |  |  | SCC  |
| 95   | FAT1           | Frameshift | DEL    | 4-AK     | p.G4034fs      | 0.072 |  |  |  |  |  |  |  | AK   |
| 96   | FAT1           | Nonsense   | SNV    | 4-AK     | p.Q3379X       | 0.042 |  |  |  |  |  |  |  | AK   |
| 97   | FAT1           | Nonsense   | SNV    | 4-SCC1   | p.R1096X       | 0.061 |  |  |  |  |  |  |  | SCC1 |
| 98   | FAT1           | Missense   | DNV    | 5-AK     | p.A3000T       | 0.074 |  |  |  |  |  |  |  | AK   |
| 99   | FAT1           | Missense   | SNV    | 5-AK     | p.T2558S       | 0.056 |  |  |  |  |  |  |  | AK   |
| 100  | FAT1           | Missense   | SNV    | 5-AK     | p.T1937S       | 0.084 |  |  |  |  |  |  |  | AK   |
| 101  | FAT1           | Missense   | SNV    | 5-SCC    | p.R1543G       | 0.264 |  |  |  |  |  |  |  | SCC  |
| 102  | FAT1           | Nonsense   | SNV    | 8-SCC    | p.R2726X       | 0.060 |  |  |  |  |  |  |  | SCC  |

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| Gene | Classification | Type     | Sample | AACHange | TVarRat  |       |  |  |  |  |  |  |  | Type |
|------|----------------|----------|--------|----------|----------|-------|--|--|--|--|--|--|--|------|
| 105  | FAT3           | Missense | SNV    | 10-AK    | p.S896F  | 0.077 |  |  |  |  |  |  |  | AK   |
| 106  | FAT3           | Missense | SNV    | 10-AK    | p.G585E  | 0.079 |  |  |  |  |  |  |  | AK   |
| 107  | FAT3           | Missense | SNV    | 12-AK    | p.R3674Q | 0.066 |  |  |  |  |  |  |  | AK   |
| 108  | FAT3           | Missense | SNV    | 2-SCC    | p.S2675L | 0.451 |  |  |  |  |  |  |  | SCC  |
| 109  | FAT3           | Missense | SNV    | 3-SCC    | p.S844L  | 0.041 |  |  |  |  |  |  |  | SCC  |
| 110  | FAT3           | Missense | SNV    | 3-SCC    | p.I3160V | 0.052 |  |  |  |  |  |  |  | SCC  |
| 111  | FAT3           | Missense | SNV    | 3-SCC    | p.S1667F | 0.062 |  |  |  |  |  |  |  | SCC  |



|     |      |          |     |       |          |       |  |  |  |  |  |  |  |  |  |  |     |
|-----|------|----------|-----|-------|----------|-------|--|--|--|--|--|--|--|--|--|--|-----|
| 113 | FAT3 | Missense | SNV | 3-SCC | p.E4470K | 0.124 |  |  |  |  |  |  |  |  |  |  | SCC |
| 114 | FAT3 | Missense | SNV | 3-SCC | p.T1101I | 0.131 |  |  |  |  |  |  |  |  |  |  | SCC |
| 115 | FAT3 | Missense | SNV | 3-SCC | p.S1025F | 0.161 |  |  |  |  |  |  |  |  |  |  | SCC |
| 116 | FAT3 | Missense | SNV | 4-AK  | p.S1341F | 0.051 |  |  |  |  |  |  |  |  |  |  | AK  |
| 117 | FAT3 | Missense | SNV | 5-AK  | p.S189F  | 0.066 |  |  |  |  |  |  |  |  |  |  | AK  |
| 118 | FAT3 | Missense | SNV | 5-AK  | p.N980I  | 0.069 |  |  |  |  |  |  |  |  |  |  | AK  |
| 119 | FAT3 | Missense | SNV | 5-AK  | p.L3274F | 0.140 |  |  |  |  |  |  |  |  |  |  | AK  |
| 120 | FAT3 | Missense | SNV | 5-SCC | p.R1011Q | 0.222 |  |  |  |  |  |  |  |  |  |  | SCC |
| 121 | FAT3 | Missense | SNV | 5-SCC | p.I3120M | 0.234 |  |  |  |  |  |  |  |  |  |  | SCC |
| 122 | FAT3 | Missense | SNV | 5-SCC | p.L1946F | 0.308 |  |  |  |  |  |  |  |  |  |  | SCC |
| 123 | FAT3 | Missense | SNV | 5-SCC | p.R3674Q | 0.308 |  |  |  |  |  |  |  |  |  |  | SCC |
| 124 | FAT3 | Missense | SNV | 6-SCC | p.D1949N | 0.053 |  |  |  |  |  |  |  |  |  |  | SCC |
| 125 | FAT3 | Missense | SNV | 6-SCC | p.E3280K | 0.159 |  |  |  |  |  |  |  |  |  |  | SCC |

126

| Gene | Classification | Type        | Sample | AACHange | TVarRat |       |  |  |  |  |  |  |  |  |  |  | Type |
|------|----------------|-------------|--------|----------|---------|-------|--|--|--|--|--|--|--|--|--|--|------|
| 127  | FLT1           | Nonsense    | SNV    | 1-AK     | p.R781X | 0.051 |  |  |  |  |  |  |  |  |  |  | AK   |
| 128  | FLT1           | Splice Site | SNV    | 1-NS     | .       | 0.087 |  |  |  |  |  |  |  |  |  |  | NS   |
| 130  | FLT1           | Missense    | SNV    | 10-AK    | p.G727S | 0.061 |  |  |  |  |  |  |  |  |  |  | AK   |
| 131  | FLT1           | Missense    | SNV    | 3-SCC    | p.R275K | 0.089 |  |  |  |  |  |  |  |  |  |  | SCC  |
| 132  | FLT1           | Missense    | SNV    | 5-SCC    | p.Q52H  | 0.304 |  |  |  |  |  |  |  |  |  |  | SCC  |
| 133  | FLT1           | Missense    | SNV    | 5-SCC    | p.A635V | 0.333 |  |  |  |  |  |  |  |  |  |  | SCC  |
| 134  | FLT1           | Missense    | SNV    | 6-SCC    | p.E569K | 0.096 |  |  |  |  |  |  |  |  |  |  | SCC  |

135

| Gene | Classification | Type     | Sample | AACHange | TVarRat  | FATHMM_score | LRT  | MutationAssessor | MutationTaster | Polyphen2_HDIV | Polyphen2_HVAR | SIFT_score |  |  |  |  | Type |
|------|----------------|----------|--------|----------|----------|--------------|------|------------------|----------------|----------------|----------------|------------|--|--|--|--|------|
| 136  | MLL2           | Missense | SNV    | 1-NS     | p.P4005L | 0.092        | 0.93 | neutral          | .              | B              | B              | 0          |  |  |  |  | NS   |
| 137  | MLL2           | Missense | DNV    | 1-NS     | p.P4578L | 0.165        |      |                  |                |                |                |            |  |  |  |  | NS   |
| 139  | MLL2           | Missense | SNV    | 1-NS     | p.Q3599R | 0.042        | -1.2 | neutral          | .              | D              | P              | 0          |  |  |  |  | NS   |
| 140  | MLL2           | Missense | SNV    | 10-AK    | p.P5469S | 0.066        | -0.8 | low              | .              | D              | D              | 0          |  |  |  |  | AK   |
| 141  | MLL2           | Missense | SNV    | 2-AK     | p.P4745S | 0.311        | 0.81 | medium           | .              | D              | D              | 0          |  |  |  |  | AK   |
| 142  | MLL2           | Missense | SNV    | 2-SCC    | p.E5506G | 0.130        | -1.6 | high             | .              | D              | D              | 0          |  |  |  |  | SCC  |
| 143  | MLL2           | Missense | SNV    | 2-SCC    | p.G5505R | 0.142        | -2   | high             | .              | D              | D              | 0          |  |  |  |  | SCC  |
| 144  | MLL2           | Missense | DNV    | 2-SCC    | p.P493F  | 0.520        |      |                  |                |                |                |            |  |  |  |  | SCC  |
| 145  | MLL2           | Nonsense | DNV    | 2-SCC    | p.R2915* | 0.520        |      |                  |                |                |                |            |  |  |  |  | SCC  |
| 146  | MLL2           | Missense | SNV    | 2-SCC    | p.R4978C | 0.146        | 0.87 | neutral          | .              | D              | B              | 0          |  |  |  |  | SCC  |
| 147  | MLL2           | Missense | SNV    | 3-SCC    | p.A4550V | 0.084        | -0.8 | low              | .              | D              | P              | 0          |  |  |  |  | SCC  |
| 148  | MLL2           | Nonsense | SNV    | 5-AK     | p.R4536X | 0.250        |      |                  |                |                |                |            |  |  |  |  | AK   |
| 149  | MLL2           | Missense | SNV    | 5-SCC    | p.E1540V | 0.355        | 0.91 | medium           | .              | D              | D              | 0          |  |  |  |  | SCC  |
| 150  | MLL2           | Missense | SNV    | 5-SCC    | p.H4306Y | 0.143        | 0.84 | neutral          | .              | P              | P              | 0          |  |  |  |  | SCC  |
| 151  | MLL2           | Missense | SNV    | 5-SCC    | p.P2930L | 0.345        | -0.8 | neutral          | .              | B              | B              | 0          |  |  |  |  | SCC  |
| 152  | MLL2           | Missense | SNV    | 5-SCC    | p.P893L  | 0.362        | -1   | neutral          | .              | D              | P              | 0          |  |  |  |  | SCC  |
| 153  | MLL2           | Nonsense | SNV    | 6-SCC    | p.E922X  | 0.178        |      |                  |                |                |                |            |  |  |  |  | SCC  |

154

| Gene | Classification | Type        | Sample | AACHange | TVarRat  | FATHMM_score | LRT  | MutationAssessor | MutationTaster | Polyphen2_HDIV | Polyphen2_HVAR | SIFT_score |  |  |  |  | Type |
|------|----------------|-------------|--------|----------|----------|--------------|------|------------------|----------------|----------------|----------------|------------|--|--|--|--|------|
| 155  | MLL3           | Splice Site | SNV    | 2-AK     | .        | 0.160        |      |                  |                |                |                |            |  |  |  |  | AK   |
| 157  | MLL3           | Missense    | DNV    | 2-SCC    | p.G2601S | 0.248        |      |                  |                |                |                |            |  |  |  |  | SCC  |
| 158  | MLL3           | Missense*   | SNV    | 5-AK     | p.G4632V | 0.057        |      |                  |                |                |                |            |  |  |  |  | AK   |
| 159  | MLL3           | Missense    | SNV    | 5-SCC    | p.H2950Y | 0.309        | -1.4 | low              | N              | P;B;B          | B;B;B          | 0.8        |  |  |  |  | SCC  |
| 160  | MLL3           | Missense    | SNV    | 1-NS     | p.L2036F | 0.110        | -1.5 | neutral          | N              | B;P            | B;B            | 0.7        |  |  |  |  | NS   |
| 161  | MLL3           | Missense    | SNV    | 6-NS     | p.P3302S | 0.041        | 0.89 | low              | N              | B;B;B          | B;B;B          | 0.58       |  |  |  |  | NS   |
| 162  | MLL3           | Missense    | SNV    | 6-SCC    | p.P3452L | 0.054        | 0.79 | medium           | D              | D;D;D          | D;D;D          | 0.46       |  |  |  |  | SCC  |
| 163  | MLL3           | Missense    | SNV    | 3-SCC    | p.P4655S | 0.175        | 0.94 | medium           | D              | B;P;P          | B;B;B          | 0.05       |  |  |  |  | SCC  |
| 164  | MLL3           | Missense    | SNV    | 10-AK    | p.S4601F | 0.060        | -0.8 | medium           | D              | D;D;D          | D;D;D          | 0.01       |  |  |  |  | AK   |

165



|     | Gene   | Classification | Type | Sample | AAChange | TVarRat | FATHMM_score | LRT | MutationAssessor | MutationTaster | Polyphen2_HDIV | Polyphen2_HVAR | SIFT_score | Type |
|-----|--------|----------------|------|--------|----------|---------|--------------|-----|------------------|----------------|----------------|----------------|------------|------|
| 166 | NF1    | Missense       | SNV  | 10-AK  | p.T700I  | 0.051   | 1.87         | D   | neutral          | N              | B;B;B          | B;B;B          | 0.54       | AK   |
| 167 | NF1    | Missense       | SNV  | 2-SCC  | p.E716K  | 0.506   | 1.66         | D   | low              | D              | D;D;D          | D;D;D          | 0          | SCC  |
| 168 | NF1    | Nonsense       | SNV  | 3-SCC  | p.W696X  | 0.237   |              |     |                  |                |                |                |            | SCC  |
| 169 | NF1    | Splice Site    | SNV  | 4-SCC1 | p.D1237N | 0.048   |              |     |                  |                |                |                |            | SCC1 |
| 170 | NF1    | Splice Site    | SNV  | 4-SCC2 | p.D1237N | 0.041   |              |     |                  |                |                |                |            | SCC2 |
| 171 | NF1    | Missense       | SNV  | 5-SCC  | p.S1470N | 0.225   | 2.71         | N   | neutral          | N              | B;B;B          | B;B;B          | 0.47       | SCC  |
| 172 | NF1    | Missense       | SNV  | 6-SCC  | p.P1809S | 0.135   | 2.47         | D   | neutral          | D              | B;D;B          | B;D;B          | 0.85       | SCC  |
| 173 |        |                |      |        |          |         |              |     |                  |                |                |                |            |      |
| 174 |        |                |      |        |          |         |              |     |                  |                |                |                |            |      |
|     | Gene   | Classification | Type | Sample | AAChange | TVarRat | FATHMM_score | LRT | MutationAssessor | MutationTaster | Polyphen2_HDIV | Polyphen2_HVAR | SIFT_score | Type |
| 175 | NOTCH1 | Missense       | DNV  | 1-NS   | p.E2071K | 0.167   |              |     |                  |                |                |                |            | AK   |
| 176 | NOTCH1 | Missense       | SNV  | 10-AK  | p.S385F  | 0.059   | -2.5         |     | low              | D              | D              | P              | 0          | SCC  |
| 177 | NOTCH1 | Nonsense       | SNV  | 12-AK  | p.C762X  | 0.102   |              |     |                  |                |                |                |            | NS   |
| 178 | NOTCH1 | Nonsense       | SNV  | 3-AK   | p.W745X  | 0.045   |              |     |                  |                |                |                |            | SCC  |
| 179 | NOTCH1 | Missense       | SNV  | 5-SCC  | p.G384C  | 0.500   | -2.6         |     | high             | D              | D              | D              | 0.01       | SCC  |
| 180 | NOTCH1 | Missense       | SNV  | 6-NS   | p.S458L  | 0.135   | -2.6         |     | medium           | D              | D              | D              | 0.03       | SCC  |
| 181 | NOTCH1 | Nonsense       | SNV  | 6-NS   | p.W1497X | 0.074   |              |     |                  |                |                |                |            | SCC  |
| 182 | NOTCH1 | Missense       | SNV  | 6-SCC  | p.D464N  | 0.365   | -2.7         |     | neutral          | D              | D              | D              | 0.56       | AK   |
| 183 | NOTCH1 | Missense       | SNV  | 6-SCC  | p.F930I  | 0.132   | -3.6         |     | neutral          | D              | B              | B              | 0.32       | AK   |
| 184 | NOTCH1 | Missense       | DNV  | 6-SCC  | p.S356F  | 0.267   |              |     |                  |                |                |                |            | NS   |
| 185 | NOTCH1 | Missense       | SNV  | 8-SCC  | p.G472W  | 0.089   | -6           |     | medium           | D              | D              | D              | 0          | NS   |
| 186 |        |                |      |        |          |         |              |     |                  |                |                |                |            |      |
| 187 | NOTCH2 | Nonsense       | DNV  | 1-AK   | p.R1838* | 0.107   |              |     |                  |                |                |                |            | SCC  |
| 188 | NOTCH2 | Nonsense       | SNV  | 1-NS   | p.E1148X | 0.087   |              |     |                  |                |                |                |            | NS   |
| 189 | NOTCH2 | Missense       | SNV  | 10-AK  | p.P578S  | 0.049   | -4.2         |     | medium           | D              | D;D;P          | D;D;B          | 0.03       | SCC1 |
| 190 | NOTCH2 | Missense       | SNV  | 3-SCC  | p.L2116F | 0.184   | -2.4         |     | low              | N              | D              | P              | 0.1        | SCC  |
| 191 | NOTCH2 | Missense       | SNV  | 3-SCC  | p.P939S  | 0.168   | -3.7         |     | low              | D              | B;B            | P;B            | 0.31       | SCC  |
| 192 | NOTCH2 | Missense       | SNV  | 4-SCC1 | p.L1709F | 0.058   | -2.7         |     | medium           | D              | D              | D              | 0.01       | SCC  |
| 193 | NOTCH2 | Frameshift     | DEL  | 5-SCC  | p.G676fs | 0.249   |              |     |                  |                |                |                |            | AK   |
| 194 | NOTCH2 | Missense       | SNV  | 5-SCC  | p.S1468F | 0.260   | -2           |     | medium           | D              | D              | D              | 0.03       | SCC  |
| 195 | NOTCH2 | Nonsense       | SNV  | 5-SCC  | p.W1529X | 0.250   |              |     |                  |                |                |                |            | SCC  |
| 196 | NOTCH2 | Missense       | SNV  | 6-SCC  | p.C1292S | 0.132   | -4.4         |     | high             | D              | D              | D              | 0          | AK   |
| 197 | NOTCH2 | Nonsense       | SNV  | 6-SCC  | p.S104X  | 0.065   |              |     |                  |                |                |                |            | SCC  |
| 198 |        |                |      |        |          |         |              |     |                  |                |                |                |            |      |
| 199 |        |                |      |        |          |         |              |     |                  |                |                |                |            |      |
|     | Gene   | Classification | Type | Sample | AAChange | TVarRat |              |     |                  |                |                |                |            | Type |
| 200 | TP53   | Missense       | DNV  | 1-AK   | p.R248W  | 0.065   |              |     |                  |                |                |                |            | AK   |
| 201 | TP53   | Missense       | DNV  | 1-NS   | p.P278F  | 0.190   |              |     |                  |                |                |                |            | NS   |
| 202 | TP53   | Missense       | SNV  | 1-NS   | p.R249G  | 0.205   |              |     |                  |                |                |                |            | NS   |
| 203 | TP53   | Missense       | SNV  | 1-NS   | p.R248Q  | 0.211   |              |     |                  |                |                |                |            | NS   |
| 204 | TP53   | Missense       | SNV  | 10-AK  | p.P250L  | 0.088   |              |     |                  |                |                |                |            | AK   |
| 205 | TP53   | Missense       | SNV  | 3-AK   | p.E286K  | 0.287   |              |     |                  |                |                |                |            | AK   |
| 206 | TP53   | Missense       | SNV  | 3-SCC  | p.S90F   | 0.078   |              |     |                  |                |                |                |            | SCC  |
| 207 | TP53   | Missense       | SNV  | 3-SCC  | p.P151S  | 0.148   |              |     |                  |                |                |                |            | SCC  |
| 208 | TP53   | Missense       | SNV  | 3-SCC  | p.S96F   | 0.169   |              |     |                  |                |                |                |            | SCC  |
| 209 | TP53   | Splice Site    | SNV  | 3-SCC  | .        | 0.250   |              |     |                  |                |                |                |            | SCC  |
| 210 | TP53   | Frameshift     | DEL  | 4-AK   | p.N247fs | 0.072   |              |     |                  |                |                |                |            | AK   |
| 211 | TP53   | Missense       | DNV  | 4-AK   | p.R248W  | 0.065   | *            |     |                  |                |                |                |            | AK   |
| 212 | TP53   | Missense       | SNV  | 4-NS   | p.F134L  | 0.063   |              |     |                  |                |                |                |            | NS   |
| 213 | TP53   | Missense       | SNV  | 4-SCC1 | p.R248W  | 0.050   |              |     |                  |                |                |                |            | SCC1 |
| 214 | TP53   | Nonsense       | SNV  | 4-SCC1 | p.W23X   | 0.293   |              |     |                  |                |                |                |            | SCC1 |
| 215 | TP53   | Nonsense       | SNV  | 4-SCC2 | p.W23X   | 0.141   |              |     |                  |                |                |                |            | SCC2 |
| 216 | TP53   | Missense       | DNV  | 5-AK   | p.R282W  | 0.160   |              |     |                  |                |                |                |            | AK   |
| 217 | TP53   | Missense       | SNV  | 5-SCC  | p.M133K  | 0.295   |              |     |                  |                |                |                |            | SCC  |
| 218 | TP53   | Missense       | SNV  | 5-SCC  | p.E258K  | 0.304   |              |     |                  |                |                |                |            | SCC  |
| 219 | TP53   | Missense       | SNV  | 6-SCC  | p.M237I  | 0.337   |              |     |                  |                |                |                |            | SCC  |
| 220 | TP53   | Nonsense       | SNV  | 8-SCC  | p.R196X  | 0.051   |              |     |                  |                |                |                |            | SCC  |
| 221 |        |                |      |        |          |         |              |     |                  |                |                |                |            |      |



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|     |      |                |      |        |             | FATHMM_score | LRT  | MutationAssessor | MutationTaster | Polyphen2_HDIV | Polyphen2_HVAR | SIFT_score |      | Type |
|-----|------|----------------|------|--------|-------------|--------------|------|------------------|----------------|----------------|----------------|------------|------|------|
| 223 | Gene | Classification | Type | Sample | AAChange    | TVarRat      |      |                  |                |                |                |            |      |      |
| 224 | NEB  | Missense       | SNV  | 1-AK   | c.C5692T    | 0.057        | 3.24 | D                | medium         | D              | D              | D          | 0.11 | AK   |
| 225 | NEB  | Splice         | SNV  | 10-AK  | c.402+1G>A  | 0.079        | .    | .                | .              | .              | .              | .          | .    | AK   |
| 226 | NEB  | Missense       | DNV  | 10-AK  | c.CC11763TT | 0.104        | .    | .                | .              | .              | .              | .          | .    | AK   |
| 227 | NEB  | Missense       | SNV  | 2-SCC  | c.T253A     | 0.046        | 2.94 | D                | medium         | N              | P              | P          | 0.22 | SCC  |
| 228 | NEB  | Missense       | SNV  | 3-SCC  | c.G23702A   | 0.082        | 3.21 | N                | neutral        | N              | B;B;D          | B;B;D      | 0.98 | SCC  |
| 229 | NEB  | Missense       | SNV  | 3-SCC  | c.G18704A   | 0.079        | 3.17 | N                | neutral        | N              | P;P            | B;D        | 0.4  | SCC  |
| 230 | NEB  | Missense       | SNV  | 3-SCC  | c.G10141A   | 0.220        | 2.08 | D                | medium         | D              | D              | D          | 0.01 | SCC  |
| 231 | NEB  | Missense       | SNV  | 3-SCC  | c.C10111T   | 0.041        | 3    | D                | medium         | N              | P              | P          | 1    | SCC  |
| 232 | NEB  | Missense       | SNV  | 3-SCC  | c.C4972T    | 0.056        | 3.22 | D                | medium         | N              | D              | D          | 0.65 | SCC  |
| 233 | NEB  | Missense       | DNV  | 4-SCC2 | c.CC10545TT | 0.050        | .    | .                | .              | .              | .              | .          | .    | SCC2 |
| 234 | NEB  | Missense       | SNV  | 5-AK   | c.G23689A   | 0.104        | 3.05 | D                | medium         | D              | D;D;D          | D;D;D      | 0.24 | AK   |
| 235 | NEB  | Missense       | SNV  | 5-AK   | c.A6291T    | 0.111        | 2.55 | D                | medium         | D              | D              | D          | 0.03 | AK   |
| 236 | NEB  | Missense       | SNV  | 5-SCC  | c.G21010A   | 0.241        | 2.99 | N                | neutral        | D              | B;P            | B;D        | 0.13 | SCC  |
| 237 | NEB  | Missense       | SNV  | 5-SCC  | c.C10582T   | 0.389        | 2.82 | D                | medium         | D              | D              | D          | 0    | SCC  |
| 238 | NEB  | Missense       | SNV  | 6-SCC  | c.G20304A   | 0.186        | 3.32 | D                | neutral        | N              | B;B            | B;B        | 0.37 | SCC  |
| 239 | NEB  | Missense       | SNV  | 6-SCC  | c.C8395T    | 0.069        | 2.82 | D                | medium         | D              | D              | D          | 0    | SCC  |
| 240 | NEB  | Missense       | SNV  | 6-SCC  | c.A2932C    | 0.093        | 3.53 | D                | neutral        | N              | P              | P          | 0.92 | SCC  |
| 241 |      |                |      |        |             |              |      |                  |                |                |                |            |      |      |



| Hugo_Symbol | Chromosome | Start_position | End_position | Variant_Classification | Variant_Type | Reference_Allele | Tumor_Seq_Allele2 | dbSNV_RS    | dbSNV_Val_Status         |
|-------------|------------|----------------|--------------|------------------------|--------------|------------------|-------------------|-------------|--------------------------|
| FAM135B     | 8          | 139207508      | 139207508    | Missense_Mutation      | SNV          | T                | C                 | novel       | unknown                  |
| FAM135B     | 8          | 139207509      | 139207509    | Missense_Mutation      | SNV          | C                | T                 | novel       | unknown                  |
| FAT1        | 4          | 187509780      | 187509780    | Missense_Mutation      | SNV          | G                | T                 | novel       | unknown                  |
| FAT1        | 4          | 187509781      | 187509781    | Missense_Mutation      | SNV          | G                | A                 | novel       | unknown                  |
| FAT1        | 4          | 187538242      | 187538242    | Missense_Mutation      | SNV          | C                | T                 | rs369004042 | unknown                  |
| FAT1        | 4          | 187538243      | 187538243    | Silent                 | SNV          | C                | T                 | rs138496810 | bycluster:by100genomes   |
| MLL2        | 12         | 49424489       | 49424489     | Silent                 | SNV          | G                | T                 | novel       | unknown                  |
| MLL2        | 12         | 49424490       | 49424490     | Missense_Mutation      | SNV          | G                | A                 | novel       | unknown                  |
| MLL2        | 12         | 49432396       | 49432396     | Nonsense_Mutation      | SNV          | G                | A                 | novel       | unknown                  |
| MLL2        | 12         | 49432397       | 49432397     | Silent                 | SNV          | G                | A                 | novel       | unknown                  |
| MLL2        | 12         | 49445988       | 49445988     | Missense_Mutation      | SNV          | G                | A                 | novel       | unknown                  |
| MLL2        | 12         | 49445989       | 49445989     | Missense_Mutation      | SNV          | G                | A                 | novel       | unknown                  |
| MLL3        | 7          | 151874737      | 151874737    | Missense_Mutation      | SNV          | C                | T                 | novel       | unknown                  |
| MLL3        | 7          | 151874738      | 151874738    | Silent                 | SNV          | C                | T                 | novel       | unknown                  |
| NEB         | 2          | 152468741      | 152468741    | Missense_Mutation      | SNV          | C                | T                 | novel       | unknown                  |
| NEB         | 2          | 152468742      | 152468742    | Silent                 | SNV          | C                | T                 | novel       | unknown                  |
| NEB         | 2          | 152477447      | 152477447    | Missense_Mutation      | SNV          | C                | T                 | novel       | unknown                  |
| NEB         | 2          | 152477448      | 152477448    | Silent                 | SNV          | C                | T                 | novel       | unknown                  |
| NEB         | 2          | 152522700      | 152522700    | Silent                 | SNV          | G                | A                 | novel       | unknown                  |
| NEB         | 2          | 152522701      | 152522701    | Missense_Mutation      | SNV          | G                | A                 | novel       | unknown                  |
| NOTCH1      | 9          | 139391980      | 139391980    | Missense_Mutation      | SNV          | C                | T                 | novel       | unknown                  |
| NOTCH1      | 9          | 139391981      | 139391981    | Silent                 | SNV          | C                | A                 | novel       | unknown                  |
| NOTCH1      | 9          | 139413074      | 139413074    | Silent                 | SNV          | G                | A                 | novel       | unknown                  |
| NOTCH1      | 9          | 139413075      | 139413075    | Missense_Mutation      | SNV          | G                | A                 | novel       | unknown                  |
| NOTCH2      | 1          | 120462204      | 120462204    | Nonsense_Mutation      | SNV          | G                | A                 | novel       | unknown                  |
| NOTCH2      | 1          | 120462205      | 120462205    | Silent                 | SNV          | G                | A                 | novel       | unknown                  |
| SPHKAP      | 2          | 22884203       | 22884203     | Missense_Mutation      | SNV          | G                | A                 | novel       | unknown                  |
| SPHKAP      | 2          | 22884204       | 22884204     | Missense_Mutation      | SNV          | G                | A                 | rs28934574  | bycluster                |
| TP53        | 17         | 7577094        | 7577094      | Missense_Mutation      | SNV          | G                | A                 | novel       | unknown                  |
| TP53        | 17         | 7577095        | 7577095      | Silent                 | SNV          | G                | A                 | novel       | unknown                  |
| TP53        | 17         | 7577105        | 7577105      | Missense_Mutation      | SNV          | G                | A                 | rs17849781  | unknown;alternate_allele |
| TP53        | 17         | 7577106        | 7577106      | Missense_Mutation      | SNV          | G                | A                 | novel       | unknown                  |
| TP53        | 17         | 7577537        | 7577537      | Silent                 | SNV          | C                | T                 | novel       | unknown                  |
| TP53        | 17         | 7577538        | 7577538      | Missense_Mutation      | SNV          | C                | T                 | rs11540652  | bycluster                |
| TP53        | 17         | 7577539        | 7577539      | Missense_Mutation      | SNV          | G                | A                 | rs121912651 | bycluster                |
| TP53        | 17         | 7577539        | 7577539      | Missense_Mutation      | SNV          | G                | A                 | rs121912651 | bycluster                |
| TP53        | 17         | 7577540        | 7577540      | Silent                 | SNV          | G                | A                 | novel       | unknown                  |
| TP53        | 17         | 7577540        | 7577540      | Silent                 | SNV          | G                | A                 | novel       | unknown                  |
| USH2A       | 1          | 215847651      | 215847651    | Silent                 | SNV          | C                | T                 | novel       | unknown                  |
| USH2A       | 1          | 215847652      | 215847652    | Missense_Mutation      | SNV          | C                | T                 | novel       | unknown                  |
| USH2A       | 1          | 216595517      | 216595517    | Silent                 | SNV          | G                | A                 | novel       | unknown                  |
| USH2A       | 1          | 216595518      | 216595518    | Missense_Mutation      | SNV          | G                | A                 | novel       | unknown                  |



| Tumor_Sample_Barcode | TToCov | TVarCov | NToCov | NVarCov | TVarRat   | NVarRat | dbSNV_AF        | dbSNV_PopFreq | dbSNV_Strength |
|----------------------|--------|---------|--------|---------|-----------|---------|-----------------|---------------|----------------|
| CSCC-TSAl-PT3-SCC1   | 129    | 29      | 113    | 0       | 0.224806  | 0       | .               | .             | none           |
| CSCC-TSAl-PT3-SCC1   | 129    | 29      | 115    | 0       | 0.224806  | 0       | .               | .             | none           |
| CSCC-TSAl-PT1-NS1    | 72     | 6       | 100    | 0       | 0.083333  | 0       | .               | .             | none           |
| CSCC-TSAl-PT1-NS1    | 73     | 6       | 99     | 0       | 0.0821918 | 0       | .               | .             | none           |
| CSCC-TSAl-PT5-AK1    | 199    | 15      | 126    | 0       | 0.0753769 | 0       | .               | .             | weak           |
| CSCC-TSAl-PT5-AK1    | 194    | 14      | 127    | 0       | 0.0721649 | 0       | C 0.999;T 0.001 | 0.001         | strong         |
| CSCC-TSAl-PT1-NS1    | 181    | 30      | 226    | 0       | 0.165746  | 0       | .               | .             | none           |
| CSCC-TSAl-PT1-NS1    | 182    | 30      | 230    | 0       | 0.164835  | 0       | .               | .             | none           |
| CSCC-TSAl-PT2-SCC1   | 38     | 20      | 32     | 0       | 0.526316  | 0       | .               | .             | none           |
| CSCC-TSAl-PT2-SCC1   | 38     | 20      | 29     | 0       | 0.526316  | 0       | .               | .             | none           |
| CSCC-TSAl-PT2-SCC1   | 62     | 33      | 42     | 0       | 0.532258  | 0       | .               | .             | none           |
| CSCC-TSAl-PT2-SCC1   | 62     | 32      | 43     | 0       | 0.516129  | 0       | .               | .             | none           |
| CSCC-TSAl-PT2-SCC1   | 281    | 70      | 254    | 0       | 0.24911   | 0       | .               | .             | none           |
| CSCC-TSAl-PT2-SCC1   | 282    | 70      | 260    | 0       | 0.248227  | 0       | .               | .             | none           |
| CSCC-TSAl-PT10-AK1   | 204    | 21      | 67     | 0       | 0.102941  | 0       | .               | .             | none           |
| CSCC-TSAl-PT10-AK1   | 206    | 22      | 67     | 0       | 0.106796  | 0       | .               | .             | none           |
| CSCC-TSAl-PT4-SCC2   | 226    | 13      | 197    | 0       | 0.0575221 | 0       | .               | .             | none           |
| CSCC-TSAl-PT4-SCC2   | 229    | 10      | 201    | 0       | 0.0436681 | 0       | .               | .             | none           |
| CSCC-TSAl-PT4-AK1    | 294    | 3       | 209    | 0       | 0.0102041 | 0       | .               | .             | none           |
| CSCC-TSAl-PT4-AK1    | 294    | 3       | 204    | 0       | 0.0102041 | 0       | .               | .             | none           |
| CSCC-TSAl-PT1-NS1    | 24     | 4       | 26     | 0       | 0.166667  | 0       | .               | .             | none           |
| CSCC-TSAl-PT1-NS1    | 24     | 4       | 26     | 0       | 0.166667  | 0       | .               | .             | none           |
| CSCC-TSAl-PT6-SCC1   | 80     | 21      | 4      | 0       | 0.2625    | 0       | .               | .             | none           |
| CSCC-TSAl-PT6-SCC1   | 82     | 21      | 4      | 0       | 0.256098  | 0       | .               | .             | none           |
| CSCC-TSAl-PT1-AK1    | 47     | 5       | 38     | 0       | 0.106383  | 0       | .               | .             | none           |
| CSCC-TSAl-PT1-AK1    | 46     | 5       | 36     | 0       | 0.108696  | 0       | .               | .             | none           |
| CSCC-TSAl-PT6-SCC1   | 127    | 7       | 79     | 0       | 0.0551181 | 0       | .               | .             | none           |
| CSCC-TSAl-PT6-SCC1   | 130    | 8       | 79     | 0       | 0.0615385 | 0       | .               | .             | none           |
| CSCC-TSAl-PT5-AK1    | 59     | 9       | 69     | 0       | 0.152542  | 0       | .               | .             | weak           |
| CSCC-TSAl-PT5-AK1    | 59     | 10      | 70     | 0       | 0.169492  | 0       | .               | .             | none           |
| CSCC-TSAl-PT1-NS1    | 53     | 10      | 86     | 0       | 0.188679  | 0       | .               | .             | none           |
| CSCC-TSAl-PT1-NS1    | 52     | 10      | 85     | 0       | 0.192308  | 0       | G 1.000; 0.000  | .             | alt            |
| CSCC-TSAl-PT8-SCC1   | 193    | 4       | 242    | 0       | 0.0207254 | 0       | .               | .             | none           |
| CSCC-TSAl-PT8-SCC1   | 194    | 4       | 241    | 0       | 0.0206186 | 0       | .               | .             | weak           |
| CSCC-TSAl-PT1-AK1    | 183    | 12      | 208    | 0       | 0.0655738 | 0       | .               | .             | weak           |
| CSCC-TSAl-PT4-AK1    | 150    | 5       | 200    | 0       | 0.0333333 | 0       | .               | .             | weak           |
| CSCC-TSAl-PT1-AK1    | 182    | 12      | 211    | 0       | 0.0659341 | 0       | .               | .             | none           |
| CSCC-TSAl-PT4-AK1    | 152    | 16      | 197    | 0       | 0.105263  | 0       | .               | .             | none           |
| CSCC-TSAl-PT8-NS1    | 93     | 2       | 118    | 0       | 0.0215054 | 0       | .               | .             | none           |
| CSCC-TSAl-PT8-NS1    | 92     | 2       | 117    | 0       | 0.0217391 | 0       | .               | .             | none           |
| CSCC-TSAl-PT6-SCC1   | 248    | 30      | 232    | 0       | 0.120968  | 0       | .               | .             | none           |
| CSCC-TSAl-PT6-SCC1   | 249    | 32      | 229    | 0       | 0.128514  | 0       | .               | .             | none           |



| COSMIC_Codon                                   | COSMIC_Gene | COSMIC_Gene_Freq | COSMIC_Site_Freq | Transcript_Id | Exon   | ChromChange | AACChange |
|--|-------------|------------------|------------------|---------------|--------|-------------|-----------|
| LOC51059,NS,carcinoma,-1,2                     | FAM135B     | 423              | 2                | NM_015912     | exon9  | C.A866G     | p.E289G   |
| LOC51059,NS,carcinoma,0,2                      | FAM135B     | 423              | 2                | NM_015912     | exon9  | C.G865A     | p.E289K   |
| .  | FAT1        | 500              | .                | NM_005245     | exon27 | C.C13733A   | p.P4578Q  |
| .  | FAT1        | 500              | .                | NM_005245     | exon27 | C.C13732T   | p.P4578S  |
| .  | FAT1        | 500              | .                | NM_005245     | exon11 | C.G8992A    | p.A2998T  |
| .  | FAT1        | 500              | .                | NM_005245     | exon11 | C.G8991A    | p.T2997T  |
| .  | MLL2        | 1173             | .                | NM_003482     | exon41 | C.C13734A   | p.P4578P  |
| .  | MLL2        | 1173             | .                | NM_003482     | exon41 | C.C13733T   | p.P4578L  |
| .  | MLL2        | 1173             | .                | NM_003482     | exon34 | C.C8743T    | p.R2915X  |
| .  | MLL2        | 1173             | .                | NM_003482     | exon34 | C.C8742T    | p.H2914H  |
| MLL2_ENST00000301067,NS,carcinoma,0,2          | MLL2        | 1173             | 2                | NM_003482     | exon10 | C.C1478T    | p.P493L   |
| .  | MLL2        | 1173             | .                | NM_003482     | exon10 | C.C1477T    | p.P493S   |
| .  | MLL3        | 1564             | .                | NM_170606     | exon38 | C.G7801A    | p.G2601S  |
| .  | MLL3        | 1564             | .                | NM_170606     | exon38 | C.G7800A    | p.P2600P  |
| .  | MLL3        | 1564             | .                | NM_170606     | exon78 | C.G11764A   | p.E3922K  |
| .  | NEB         | 1697             | .                | NM_001271208  | exon78 | C.G11763A   | p.P3921P  |
| .  | NEB         | 1697             | .                | NM_001271208  | exon72 | C.G10546A   | p.D3516N  |
| NEB_ENST00000427231,colon,carcinoma,-2,3       | NEB         | 1697             | 3                | NM_001271208  | exon72 | C.G10545A   | p.R3515R  |
| NEB,NS,carcinoma,0,1                           | NEB         | 1697             | 1                | NM_004543     | exon41 | C.C4935T    | p.T1645T  |
| NEB,NS,carcinoma,+1,1                          | NEB         | 1697             | 1                | NM_004543     | exon41 | C.C4934T    | p.T1645I  |
| .  | NOTCH1      | 1980             | .                | NM_017617     | exon34 | C.G6211A    | p.E2071K  |
| NOTCH1_ENST00000277541,NS,carcinoma,-1,2       | NOTCH1      | 1980             | 2                | NM_017617     | exon34 | C.G6210T    | p.R2070R  |
| .  | NOTCH1      | 1980             | .                | NM_017617     | exon6  | C.C1068T    | p.S356S   |
| .  | NOTCH1      | 1980             | .                | NM_017617     | exon6  | C.C1067T    | p.S356F   |
| NOTCH2,scalp,carcinoma,0,1                     | NOTCH2      | 348              | 1                | NM_024408     | exon31 | C.C5512T    | p.R1838X  |
| .  | NOTCH2      | 348              | .                | NM_024408     | exon31 | C.C5511T    | p.L1837L  |
| .  | SPHKAP      | 750              | .                | NM_030623     | exon7  | C.C1367T    | p.P456L   |
| .  | SPHKAP      | 750              | .                | NM_030623     | exon7  | C.C1366T    | p.P456S   |
| TP53_ENST00000455263,NS,adenocarcinoma,0,524   | TP53        | 33396            | 524              | NM_000546     | exon8  | C.C844T     | p.R282W   |
| TP53_ENST00000455263,NS,adenocarcinoma,-1,130  | TP53        | 33396            | 130              | NM_000546     | exon8  | C.C843T     | p.D281D   |
| TP53_ENST00000455263,NS,carcinoma,0,237        | TP53        | 33396            | 237              | NM_000546     | exon8  | C.C833T     | p.P278S   |
| TP53_ENST00000455263,NS,carcinoma,+1,237       | TP53        | 33396            | 237              | NM_000546     | exon8  | C.C832T     | p.P278S   |
| TP53_ENST00000545858,NS,adenocarcinoma,-1,1635 | TP53        | 33396            | 1635             | NM_000546     | exon7  | C.G744A     | p.R248R   |
| TP53_ENST00000545858,NS,adenocarcinoma,0,1635  | TP53        | 33396            | 1635             | NM_000546     | exon7  | C.G743A     | p.R248Q   |
| TP53_ENST00000545858,NS,adenocarcinoma,+1,1635 | TP53        | 33396            | 1635             | NM_000546     | exon7  | C.C742T     | p.R248W   |
| TP53_ENST00000545858,NS,carcinoma,-1,46        | TP53        | 33396            | 46               | NM_000546     | exon7  | C.C742T     | p.R248W   |
| TP53_ENST00000545858,NS,carcinoma,-1,46        | TP53        | 33396            | 46               | NM_000546     | exon7  | C.C741T     | p.N247N   |
| USH2A,NS,carcinoma,-2,1                        | USH2A       | 1168             | 1                | NM_206933     | exon63 | C.G13602A   | p.G4534G  |
| USH2A,NS,carcinoma,-1,1                        | USH2A       | 1168             | 1                | NM_206933     | exon63 | C.G13601A   | p.G4534E  |
| .  | USH2A       | 1168             | .                | NM_007123     | exon2  | C.C162T     | p.T54T    |
| .  | USH2A       | 1168             | .                | NM_007123     | exon2  | C.C161T     | p.T54I    |



| Genome_Plus_Minus_10_Bp | Drug_Target | Confidence  | Algorithm                 | Germline_Matches | C_G_Census      | Cohort_Subset         |
|-------------------------|-------------|-------------|---------------------------|------------------|-----------------|-----------------------|
| TGTAGCTCTGAGC           | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-scc       |
| GTAGCTCTGAGCA           | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-scc       |
| AGGGGCGGGATCG           | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-skin-vs-saliva |
| GGGGCGGGATCGT           | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-skin-vs-saliva |
| CAGTTGCCGTGATPASS       | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-ak        |
| AGTTGCCGTGATA           | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-ak        |
| GCCAAAGGGGGCA           | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-skin-vs-saliva |
| CCAAAGGGGGCAA           | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-skin-vs-saliva |
| CCAGTCGGTGGGG           | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-scc       |
| CAGTGGGTGGGGG           | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-scc       |
| GAGAGGGGCGATT           | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-scc       |
| AGAGGGGCGATTTC          | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-scc       |
| TAGGGCCCCGAAA           | .           | PASS        | Atlas-SNV 0               | .                | cgc-som         | nonagg-best-scc       |
| AGGGCCCCGAAAG           | .           | PASS        | Atlas-SNV 0               | .                | cgc-som         | nonagg-best-scc       |
| CAATTCCGGAGT            | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-ak        |
| AATTTCGGAGTG            | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-ak        |
| CAATATCCCGAGA           | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-scc       |
| AATATCCCGAGAG           | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-scc       |
| GGCGTTGGTGCA            | .           | scavenged   | Atlas-SNV 0               | .                | .               | nonagg-best-ak        |
| GC GTTGGTGGCA           | scavenged   | Atlas-SNV 0 | .                         | .                | .               | nonagg-best-ak        |
| GCCTTCCCGGGC            | .           | PASS        | Atlas-SNV 0               | .                | cgc-som         | nonagg-skin-vs-saliva |
| GCCCTCCCGGGCG           | .           | PASS        | Atlas-SNV 0               | .                | cgc-som         | nonagg-skin-vs-saliva |
| GTAGAAGGAGGCC           | .           | PASS        | Atlas-SNV 0               | .                | cgc-som         | nonagg-best-scc       |
| TAGAAGGAGGCCA           | .           | PASS        | Atlas-SNV 0               | .                | cgc-som         | nonagg-best-scc       |
| CTCCTCGGAGAGA           | .           | PASS        | Atlas-SNV 0               | .                | cgc-som         | nonagg-best-ak        |
| TCCTCGGAGAGAA           | .           | PASS        | Atlas-SNV 0               | .                | cgc-som         | nonagg-best-ak        |
| CCATCTGGA CTCT          | .           | PASS        | Atlas-SNV 0               | .                | .               | nonagg-best-scc       |
| CATCTGGA CTCTG          | .           | PASS        | Atlas-SNV 0               | .                | cgc-both        | nonagg-best-scc       |
| TGCGCCGCTCTCT           | .           | PASS        | Atlas-SNV 0               | .                | cgc-both        | nonagg-best-ak        |
| GC GCGGCTCTCTC          | .           | PASS        | Atlas-SNV 0               | .                | cgc-both        | nonagg-best-ak        |
| CTCCAGGACAGG            | .           | PASS        | Atlas-SNV 0               | .                | cgc-both        | nonagg-skin-vs-saliva |
| TCCAGGACAGGC            | .           | PASS        | Atlas-SNV 0               | .                | cgc-both        | nonagg-skin-vs-saliva |
| GGGCTTCGGTTC            | .           | scavenged   | Atlas-SNV 0               | .                | cgc-both        | nonagg-best-scc       |
| GGGCTTCGGTTCA           | .           | scavenged   | Atlas-SNV 0               | .                | cgc-both        | nonagg-best-scc       |
| GCGCTCCGGTTTCAT         | .           | PASS        | Atlas-SNV 0               | .                | cgc-both        | nonagg-best-ak        |
| GCGCTCCGGTTTCAT         | .           | scavenged   | Atlas-SNV 0               | .                | cgc-both        | nonagg-best-ak        |
| CCTCCGGTTTCATG          | .           | PASS        | Atlas-SNV cgc-both        | .                | nonagg-best-ak  | nonagg-best-ak        |
| CCTCCGGTTTCATG          | .           | PASS        | Atlas-SNV cgc-both        | .                | nonagg-best-ak  | nonagg-best-ak        |
| TTCCATCCCTGAG           | .           | scavenged   | Atlas-SNV 0               | .                | .               | nonagg-skin-vs-saliva |
| TTCCATCCCTGAG           | .           | scavenged   | Atlas-SNV 0               | .                | .               | nonagg-skin-vs-saliva |
| TGCTTGGGTTGGC           | .           | PASS        | Atlas-SNV 0               | .                | nonagg-best-scc | nonagg-skin-vs-saliva |
| GCTTGGGTTGGCA           | .           | PASS        | Atlas-SNV nonagg-best-scc | .                | nonagg-best-scc | nonagg-skin-vs-saliva |



| Sample | NOTCH1                          | NOTCH2                             |
|--------|---------------------------------|------------------------------------|
| 1-AK   |                                 | p.R1838*                           |
| 1-NS   | p.E2071K                        | p.E1148X                           |
| 2-AK   |                                 |                                    |
| 2-SCC  |                                 |                                    |
| 3-AK   | p.W745X                         |                                    |
| 3-SCC  |                                 | p.L2116F,<br>p.P939S               |
| 4-AK   |                                 |                                    |
| 4-NS   |                                 |                                    |
| 4-SCC1 |                                 | p.L1709F                           |
| 4-SCC2 |                                 |                                    |
| 5-AK   |                                 |                                    |
| 5-SCC  | p.G384C                         | p.G676fs,<br>p.S1468F,<br>p.W1529X |
| 6-NS   | p.S458L,<br>p.W1497X            |                                    |
| 6-SCC  | p.D464N,<br>p.F930I,<br>p.S356F | p.C1292S,<br>p.S104X               |
| 8-NS   |                                 |                                    |
| 8-SCC  | p.G472W                         |                                    |
| 10-AK  | p.S385F                         | p.P578S                            |
| 12-AK  | p.C762X                         |                                    |



## Appendix 2.

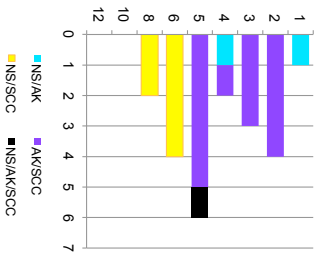
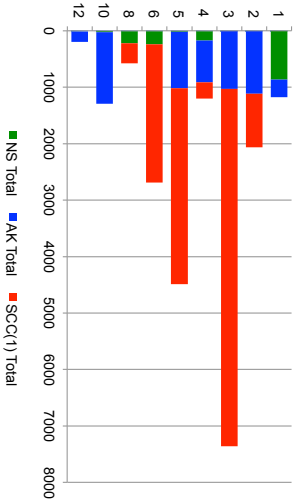
Table of overlapping mutated genes  
and positions within them



OverlapCharts

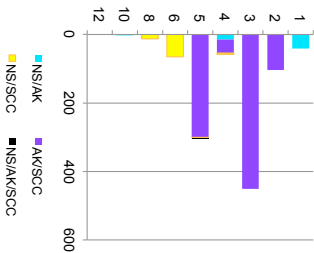
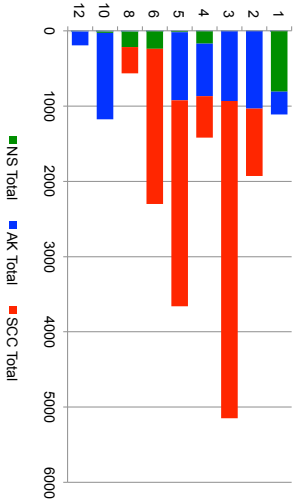
By Position

| PT | NS Total | NS/AK | AK Total | AK/SCC | SCC(1) Total | NS/SCC | NS/AK/SCC |
|----|----------|-------|----------|--------|--------------|--------|-----------|
| 12 | 17       | 0     | 187      |        |              |        |           |
| 10 | 17       |       | 1267     |        |              |        |           |
| 8  | 212      |       |          |        | 354          | 2      |           |
| 6  | 235      |       |          |        | 2445         | 4      |           |
| 5  | 15       | 0     | 999      | 5      | 3467         | 0      | 1         |
| 4  | 171      | 1     | 738      | 1      | 285          | 0      | 0         |
| 3  |          |       | 1027     | 3      | 6327         |        |           |
| 2  |          |       | 1113     | 4      | 950          |        |           |
| 1  | 865      | 1     | 311      |        |              |        |           |



By Gene

| PT | NS Total | NS/AK | AK Total | AK/SCC | SCC Total | NS/SCC | NS/AK/SCC |
|----|----------|-------|----------|--------|-----------|--------|-----------|
| 12 | 17       |       | 183      |        |           |        |           |
| 10 | 17       | 3     | 1148     |        |           |        |           |
| 8  | 210      |       |          |        | 347       | 13     |           |
| 6  | 234      |       |          |        | 2060      | 65     |           |
| 5  | 15       | 0     | 993      | 300    | 2735      | 2      | 1         |
| 4  | 167      | 15    | 698      | 39     | 549       | 4      | 3         |
| 3  |          |       | 930      | 451    | 4211      |        |           |
| 2  |          |       | 1030     | 104    | 894       |        |           |
| 1  | 806      | 41    | 303      |        |           |        |           |





## GenePatientRepetition

These are numbers of *patients* in which the given gene appears repeatedly in a patient. It's based on nonsilent mutations only.

| Gene        | Number of patients | Patients        |
|-------------|--------------------|-----------------|
| GPR98       | 4                  | PT1,PT2,PT3,PT4 |
| MYO7B       | 4                  | PT1,PT3,PT4,PT5 |
| RELN        | 4                  | PT1,PT3,PT4,PT5 |
| TP53        | 4                  | PT1,PT3,PT4,PT5 |
| CRB1        | 3                  | PT2,PT3,PT6     |
| FAT1        | 3                  | PT3,PT4,PT5     |
| FSIP2       | 3                  | PT2,PT3,PT5     |
| IGFN1       | 3                  | PT2,PT3,PT5     |
| MLL3        | 3                  | PT2,PT5,PT6     |
| RYR1        | 3                  | PT2,PT4,PT5     |
| VWDE        | 3                  | PT2,PT3,PT5     |
| ADAM29      | 2                  | PT3,PT4         |
| ADGB        | 2                  | PT2,PT3         |
| ANKRD31     | 2                  | PT3,PT6         |
| ATP8A1      | 2                  | PT3,PT5         |
| BTBD9       | 2                  | PT3,PT5         |
| C16orf62    | 2                  | PT3,PT4         |
| C2orf16     | 2                  | PT4,PT5         |
| CCDC168     | 2                  | PT3,PT5         |
| CHD8        | 2                  | PT1,PT4         |
| CLTCL1      | 2                  | PT3,PT6         |
| CMYA5       | 2                  | PT4,PT5         |
| COL11A1     | 2                  | PT4,PT5         |
| COL1A2      | 2                  | PT3,PT5         |
| COL24A1     | 2                  | PT3,PT5         |
| COL27A1     | 2                  | PT4,PT5         |
| COL4A2      | 2                  | PT2,PT3         |
| COL4A3      | 2                  | PT3,PT4         |
| COL6A5      | 2                  | PT3,PT5         |
| COL6A6      | 2                  | PT2,PT5         |
| CSF3R       | 2                  | PT3,PT5         |
| Ckorf22     | 2                  | PT3,PT4         |
| DDX60L      | 2                  | PT3,PT4         |
| DENND4A     | 2                  | PT4,PT5         |
| DGKH        | 2                  | PT4,PT5         |
| DNHD1       | 2                  | PT2,PT5         |
| DPP3        | 2                  | PT5,PT6         |
| DYNC11      | 2                  | PT3,PT5         |
| ENPP3       | 2                  | PT2,PT5         |
| FAM135A     | 2                  | PT5,PT8         |
| FER1L6      | 2                  | PT3,PT5         |
| FGA         | 2                  | PT3,PT5         |
| FREM3       | 2                  | PT3,PT5         |
| FRY         | 2                  | PT3,PT5         |
| GLDN        | 2                  | PT5,PT6         |
| HMCN1       | 2                  | PT3,PT5         |
| KIAA1324L   | 2                  | PT3,PT5         |
| KIAA1549    | 2                  | PT2,PT3         |
| LAMA1       | 2                  | PT3,PT4         |
| LAMC3       | 2                  | PT3,PT6         |
| LGI1        | 2                  | PT1,PT3         |
| LRP2        | 2                  | PT3,PT5         |
| MLL2        | 2                  | PT2,PT5         |
| MYH2        | 2                  | PT3,PT5         |
| MYH4        | 2                  | PT3,PT5         |
| MYO18B      | 2                  | PT3,PT4         |
| NAV3        | 2                  | PT2,PT5         |
| NHSL2       | 2                  | PT3,PT5         |
| NPAP1       | 2                  | PT3,PT5         |
| PALM2-AKAP2 | 2                  | PT2,PT3         |
| PAPPA2      | 2                  | PT3,PT5         |
| POLR3A      | 2                  | PT4,PT5         |
| PRB4        | 2                  | PT1,PT5         |
| PRDM9       | 2                  | PT4,PT5         |
| PREX1       | 2                  | PT2,PT4         |
| PRKD1       | 2                  | PT3,PT4         |
| PRR16       | 2                  | PT3,PT5         |
| PRRC2A      | 2                  | PT5,PT6         |
| PRUNE2      | 2                  | PT2,PT3         |
| PTPRQ       | 2                  | PT3,PT5         |
| ROS1        | 2                  | PT3,PT5         |
| RP1         | 2                  | PT3,PT5         |
| SCAND3      | 2                  | PT3,PT6         |
| SLC12A3     | 2                  | PT2,PT5         |
| SLC26A7     | 2                  | PT4,PT6         |
| SPAG17      | 2                  | PT3,PT5         |
| STARD9      | 2                  | PT1,PT3         |
| TCF20       | 2                  | PT5,PT6         |
| THSD7A      | 2                  | PT2,PT4         |
| TMEM131     | 2                  | PT2,PT5         |
| TRDN        | 2                  | PT1,PT3         |
| TRIM58      | 2                  | PT3,PT4         |
| TRIM66      | 2                  | PT2,PT4         |
| TTC40       | 2                  | PT3,PT6         |
| USH2A       | 2                  | PT2,PT6         |
| VWF         | 2                  | PT3,PT5         |
| WBP2NL      | 2                  | PT3,PT4         |
| WBSCR17     | 2                  | PT3,PT5         |
| WDR87       | 2                  | PT3,PT4         |
| XIRP2       | 2                  | PT2,PT3         |
| ZFXH4       | 2                  | PT2,PT3         |

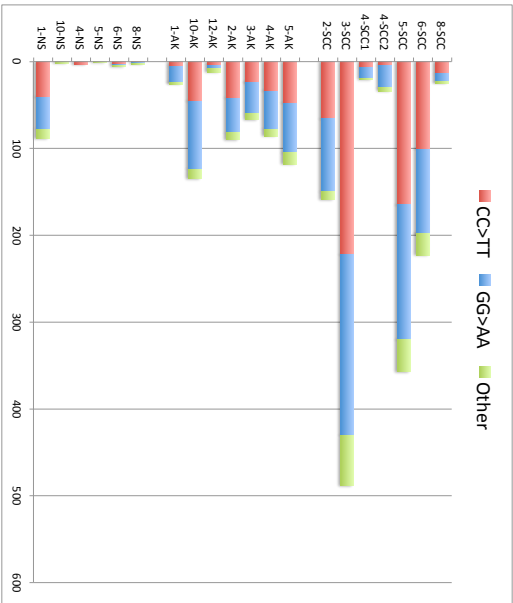
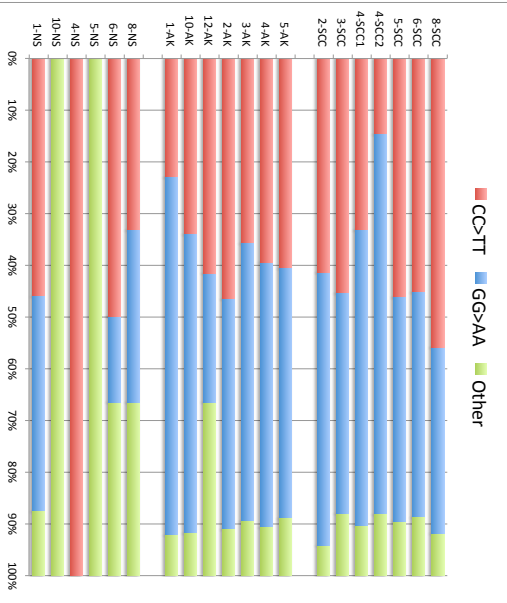
| Removed as common false positive genes: |                    |                             |
|---|--------------------|-----------------------------|
| Gene                                    | Number of patients | Patients                    |
| TTN                                     | 7                  | PT1,PT2,PT3,PT4,PT5,PT6,PT8 |
| MUC16                                   | 6                  | PT1,PT2,PT3,PT4,PT5,PT6     |
| CSMD3                                   | 3                  | PT2,PT3,PT5                 |
| DNAH6                                   | 3                  | PT2,PT3,PT6                 |
| DNAH7                                   | 3                  | PT3,PT5,PT6                 |
| HYDIN                                   | 3                  | PT3,PT5,PT6                 |
| LRP1B                                   | 3                  | PT1,PT3,PT5                 |
| MUC4                                    | 3                  | PT2,PT3,PT5                 |
| SYNE1                                   | 3                  | PT3,PT4,PT5                 |
| ADAMTS20                                | 2                  | PT2,PT4                     |
| CSMD1                                   | 2                  | PT3,PT5                     |
| CTTNBP2                                 | 2                  | PT5,PT6                     |
| DNAH10                                  | 2                  | PT1,PT5                     |
| DNAH14                                  | 2                  | PT3,PT5                     |
| DNAH5                                   | 2                  | PT2,PT4                     |
| DNAH8                                   | 2                  | PT3,PT5                     |
| KALRN                                   | 2                  | PT3,PT5                     |
| OR4K17                                  | 2                  | PT3,PT5                     |
| PCLO                                    | 2                  | PT1,PT5                     |



DNPSpectrum

| Change | 1-NS | 10-NS | 4-NS | 5-NS | 6-NS | 8-NS | 1-AK | 10-AK | 12-AK | 2-AK | 3-AK | 4-AK | 5-AK | 2-SCC | 3-SCC | 4-SCC1 | 4-SCC2 | 5-SCC | 6-SCC | 8-SCC | Total |
|--------|------|-------|------|------|------|------|------|-------|-------|------|------|------|------|-------|-------|--------|--------|-------|-------|-------|-------|
| GG>AA  | 37   | .     | .    | .    | 1    | 1    | 18   | 78    | 3     | 40   | 36   | 44   | 57   | 84    | 208   | 12     | 25     | 155   | 97    | 9     | 905   |
| CC>TT  | 41   | .     | 3    | .    | 3    | 1    | 6    | 46    | 5     | 42   | 24   | 34   | 48   | 66    | 222   | 7      | 5      | 165   | 101   | 14    | 833   |
| Other  | 11   | 2     | 0    | 1    | 2    | 1    | 2    | 11    | 4     | 8    | 7    | 8    | 13   | 9     | 58    | 2      | 4      | 37    | 25    | 2     | 207   |
| GG>TA  | 2    | .     | .    | .    | .    | .    | 1    | 1     | .     | 2    | 2    | .    | 2    | .     | 6     | 1      | .      | 3     | 1     | .     | 16    |
| AG>TA  | 2    | .     | .    | .    | .    | .    | .    | .     | 1     | 1    | 1    | .    | 1    | .     | 4     | .      | .      | 2     | 5     | .     | 15    |
| AC>TT  | .    | .     | .    | .    | 1    | 1    | .    | 1     | 1     | 1    | 1    | 1    | 1    | .     | 4     | .      | 2      | 2     | .     | .     | 12    |
| CT>TA  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 3     | .      | 2      | 2     | .     | .     | 12    |
| CC>TA  | 4    | .     | .    | .    | .    | .    | .    | .     | .     | 1    | 1    | 1    | 1    | .     | 4     | .      | .      | 2     | .     | .     | 12    |
| CC>AT  | .    | .     | .    | .    | .    | .    | 2    | .     | .     | .    | .    | .    | .    | .     | 1     | 4      | .      | 2     | 2     | 1     | 12    |
| GG>AT  | 1    | .     | .    | .    | .    | 1    | .    | .     | .     | .    | .    | .    | 1    | 2     | 3     | .      | .      | 2     | 2     | .     | 10    |
| GT>AA  | .    | .     | .    | .    | .    | .    | 1    | .     | .     | .    | 1    | 1    | 1    | .     | 5     | .      | .      | 1     | 2     | .     | 8     |
| GA>AT  | .    | .     | .    | .    | .    | .    | .    | 1     | .     | 1    | 1    | 1    | 1    | .     | 2     | .      | .      | 4     | 2     | .     | 8     |
| AG>GA  | .    | .     | .    | .    | .    | .    | .    | 1     | .     | 1    | 1    | 1    | 1    | .     | 2     | .      | .      | 1     | 1     | .     | 7     |
| CT>TC  | .    | .     | .    | .    | .    | .    | 1    | 1     | 1     | .    | .    | 2    | 2    | 1     | 1     | .      | 1      | 2     | .     | .     | 6     |
| GT>AG  | 1    | .     | .    | .    | .    | .    | .    | 1     | .     | .    | .    | .    | 1    | .     | 1     | .      | 1      | 1     | 1     | .     | 4     |
| CA>AT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | 1    | .    | 1    | .     | 2     | .      | .      | 1     | .     | .     | 4     |
| CA>AC  | .    | .     | .    | .    | .    | .    | .    | .     | .     | 1    | .    | .    | .    | .     | 2     | .      | .      | 1     | .     | .     | 4     |
| GG>CA  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 2     | .      | .      | 1     | 1     | .     | 4     |
| GA>AC  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | 1      | 1      | 1     | .     | .     | 4     |
| TC>AT  | .    | .     | .    | .    | .    | .    | .    | .     | 1     | .    | .    | .    | .    | .     | 1     | .      | 1      | 1     | .     | .     | 3     |
| CC>GT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | 1    | .    | 1    | .    | .     | 1     | .      | .      | 1     | .     | .     | 3     |
| TA>AT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | 1    | 1    | .     | 1     | .      | .      | 1     | .     | .     | 3     |
| CT>TG  | 1    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | 1    | .     | 1     | .      | .      | .     | .     | .     | 2     |
| GA>AG  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | 1    | 1    | .    | .     | 1     | .      | .      | .     | .     | .     | 2     |
| CA>AG  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | 1    | 1    | .     | 1     | .      | .      | 1     | .     | .     | 2     |
| AC>GT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | 1     | .     | .     | 2     |
| AG>CA  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | .     | 2      | .      | 1     | 1     | .     | 2     |
| CG>TA  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | .     | 2      | .      | 1     | .     | .     | 2     |
| CC>GG  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | .     | 1      | .      | 1     | .     | .     | 2     |
| GG>AC  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | 1    | .     | 1     | .      | .      | .     | .     | .     | 2     |
| GC>AA  | .    | .     | .    | .    | .    | .    | .    | 1     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | 1     | .     | .     | 2     |
| CA>TT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | 1    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | .     | 2     |
| CT>AA  | .    | 1     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | 1      | .      | .     | .     | .     | 2     |
| TC>CT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | 1     | .     | .     | 2     |
| TG>AA  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 2     |
| TG>AT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | 1     | .     | 2     |
| TC>AG  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| TG>CT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| TC>AA  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| CC>AG  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| AG>GT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | 1     | .     | .     | 1     |
| AT>TC  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| AT>TA  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| AT>TG  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| GC>AG  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| CC>AG  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| CC>GA  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| CG>AA  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| TT>CC  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| AC>CT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | 1    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| CG>TC  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| AG>TC  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| TA>GT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | 1    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| AC>TA  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| GC>AT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| CA>GG  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| AA>TT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | 1    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| TG>GT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| CA>TG  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| GC>TT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | 1    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |
| GC>CT  | .    | .     | .    | .    | .    | .    | .    | .     | .     | .    | .    | .    | .    | .     | 1     | .      | .      | .     | .     | 1     | 1     |

| Change | CC>TT | GG>AA | Other |
|--------|-------|-------|-------|
| NS     | 48    | 39    | 17    |
| AK     | 205   | 276   | 53    |
| SCC    | 580   | 590   | 137   |





## Appendix 3.

### Differentially-expressed genes in human samples



200



1



02



202



204



5



ENSG000001.12212703 -0.224532 -0.221313 0.4546354 2.870388 1.7133807 1.7861822 -0.730137 -0.690309 0.6389307 -0.452889 -0.333285 0.8795547 0.6858175 -0.815405 -0.535783 0.0085177 -0.724532 -0.372636 -0.735384 -0.379314 -0.708196 -0.513576 -1.084465 -1.10175 -0.635172  
ENSG000001 -0.718587 -0.63559 -0.658134 -0.738008 -0.786648 -0.782938 -1.093558 2.0430672 -0.648429 -0.5846 -0.496914 1.737986 0.6782812 -1.252941 -0.868446 0.3913291 1.6207333 -0.721067 0.1487989 -0.247829 0.5292786 0.8623579 1.8823766 -0.93983 0.7701398 0.5091704  
ENSG000001 0.865582 -0.627056 -0.772107 -0.857713 -0.876993 -1.084121 -0.186504 1.3040392 0.4301229 1.7853469 -0.208537 -0.831832 -0.625354 -0.492175 1.947409 0.1474948 -0.086989 -0.120917 3.0297923 -0.610312 -0.367908 0.2696888 0.1321641 -0.075362 -0.636435 0.2792476  
ENSG000001 -0.242114 -0.242114 2.2299365 0.1971683 -0.242114 4.085354 0.7177604 -0.242114 -0.242114 -0.242114 -0.242114 -0.242114 -0.546505 -0.171904 -0.546505 -0.313028 -0.242114 -0.242114 -0.242114 -0.242114 -0.546505 -0.546505 -0.318774 -0.546505  
ENSG000001 -0.29279 -0.484857 0.732831 0.8448145 -0.483268 3.6651756 1.9994004 -0.301568 -0.434376 1.1608412 -0.08585 -0.440965 -0.538915 -0.294257 -0.448944 -0.667557 -0.698401 -0.432345 -0.456596 0.3223778 -0.496691 -0.04254 -0.657132 -0.938397 -0.598247 0.0682559  
ENSG000001 1.8249669 1.2672735 -0.126771 0.1750525 0.5389314 1.1064394 0.6189396 0.9883581 -0.200134 -0.074751 -1.326073 -1.129577 -1.064162 1.016107 -1.381761 -0.611561 0.4791888 1.2980178 0.2703271 -1.544668 -0.936846 -0.806994 -0.469722 1.2905711 0.1423578 -1.34351  
ENSG000001 1.2135993 0.8397206 0.2618602 1.2211376 0.3183574 1.8893897 1.82943 -0.041012 -0.505148 0.145664 -1.307377 -0.94213 0.0281412 1.3260779 -1.639981 -0.070816 -0.731542 -0.103183 0.9278708 -0.546609 -1.306161 -0.77961 -0.598854 -1.559113 0.2868135 -0.156526  
ENSG000001 2.6174826 0.642452 0.2757336 -0.67965 1.6585994 0.9489106 0.2070991 -1.286034 -0.04033 -0.454454 -1.262373 -0.624191 0.2328514 -0.231633 -0.592165 2.099277 -0.623395 -0.423739 -1.075973 0.0196834 0.7147126 -0.426155 -1.037028 -0.827708 0.6316131 -0.463585  
ENSG000001 0.2158296 -0.447361 0.3273715 3.1498484 0.5110572 0.1923326 2.8958498 -0.619589 -0.585365 0.468996 -0.497773 -0.32414 0.0021211 -0.339805 -0.89041 -0.230103 0.971539 -0.578047 -0.641765 -0.307213 -0.641765 -0.472197 -0.665466 -0.550472 -0.763128 -0.180348



## NS-AK gene signature

| Gene       | p-value  | AK/NS fold change |
|------------|----------|-------------------|
| MS4A1      | 3.77E-02 | 13.88             |
| ADH7       | 6.99E-03 | 9.90              |
| AIM2       | 2.43E-02 | 7.28              |
| ERC2       | 2.17E-02 | 6.78              |
| ADAMDEC1   | 6.96E-03 | 6.32              |
| FABP5      | 1.98E-02 | 6.16              |
| RPTN       | 4.28E-02 | 6.10              |
| CXCL10     | 1.29E-02 | 5.80              |
| PLAC8      | 1.29E-02 | 5.66              |
| NAT1       | 1.18E-02 | 5.66              |
| AKR1B10    | 2.38E-02 | 5.57              |
| BANK1      | 1.64E-02 | 5.04              |
| IFIT2      | 3.97E-02 | 4.94              |
| OAS2       | 4.46E-02 | 4.76              |
| RBM44      | 3.46E-02 | 4.72              |
| HIST1H2BO  | 2.23E-03 | 4.43              |
| FAM133B    | 3.13E-02 | 4.38              |
| GBP6       | 4.86E-02 | 4.36              |
| S100A9     | 2.33E-02 | 4.29              |
| LCE3E      | 6.07E-03 | 4.27              |
| DSC2       | 2.04E-02 | 4.26              |
| CLEC4C     | 8.36E-03 | 3.89              |
| RP13-512J5 | 7.33E-03 | 3.86              |
| GZMA       | 1.78E-02 | 3.85              |
| KRT16      | 1.15E-02 | 3.79              |
| SPRR2A     | 4.08E-02 | 3.65              |
| FAM25A     | 3.72E-02 | 3.64              |
| PRKCQ      | 3.93E-02 | 3.63              |
| TFEC       | 2.52E-02 | 3.62              |
| HIST1H2AM  | 4.26E-02 | 3.59              |
| KRT6A      | 4.86E-03 | 3.53              |
| HIST1H2BJ  | 4.55E-02 | 3.53              |
| WFDC12     | 2.45E-02 | 3.49              |
| SLC7A11    | 3.92E-02 | 3.49              |
| S100A8     | 3.98E-02 | 3.47              |
| KLRD1      | 4.21E-03 | 3.44              |
| C10orf99   | 2.98E-02 | 3.38              |
| SLC16A1    | 3.50E-02 | 3.37              |
| CEP55      | 1.34E-03 | 3.37              |
| GZMK       | 4.62E-02 | 3.37              |
| E2F7       | 2.18E-02 | 3.34              |
| EPSTI1     | 1.87E-02 | 3.31              |
| GGH        | 2.50E-02 | 3.27              |
| CYP24A1    | 2.53E-02 | 3.27              |
| LCE3D      | 1.52E-02 | 3.26              |
| GPR1       | 8.66E-03 | 3.14              |
| SLAMF6     | 4.89E-02 | 3.11              |
| NREP       | 1.89E-02 | 3.10              |
| HMMR       | 1.20E-02 | 3.07              |
| SERPINB13  | 6.22E-03 | 3.02              |
| DLEU1      | 8.00E-03 | 3.01              |
| DSG3       | 2.69E-02 | 2.99              |
| ADAM23     | 2.86E-02 | 2.97              |
| DLGAP5     | 1.06E-02 | 2.96              |
| SIDT1      | 9.37E-03 | 2.95              |
| HIST1H3C   | 3.10E-02 | 2.93              |
| PARP15     | 2.31E-02 | 2.93              |
| ARNTL2     | 1.35E-02 | 2.90              |
| CMPK2      | 1.43E-02 | 2.89              |
| NEIL3      | 1.08E-02 | 2.89              |
| THAP5      | 3.11E-02 | 2.87              |
| KCTD7      | 1.45E-02 | 2.86              |
| GDAP1      | 2.58E-02 | 2.86              |
| CSTA       | 8.90E-03 | 2.81              |
| FLT3       | 1.66E-02 | 2.81              |
| LYZ        | 3.88E-02 | 2.80              |
| HOXA7      | 2.91E-02 | 2.79              |
| RNASE7     | 2.36E-02 | 2.75              |
| TXK        | 4.32E-02 | 2.74              |
| CENPO      | 6.03E-04 | 2.73              |
| CDKN2A     | 3.15E-02 | 2.72              |
| KLRK1      | 1.25E-02 | 2.71              |
| TP53INP1   | 2.20E-03 | 2.71              |
| CDKN3      | 1.35E-02 | 2.70              |
| HSD17B6    | 4.93E-02 | 2.70              |
| TPX2       | 8.86E-03 | 2.69              |
| GJB6       | 3.88E-02 | 2.69              |



|          |          |      |
|----------|----------|------|
| NMU      | 2.99E-02 | 2.68 |
| SP140L   | 1.61E-02 | 2.68 |
| ASPM     | 1.12E-02 | 2.66 |
| NDC80    | 1.67E-03 | 2.64 |
| LPGAT1   | 2.64E-02 | 2.64 |
| LRRC20   | 4.77E-02 | 2.62 |
| GORAB    | 8.10E-03 | 2.61 |
| MCM10    | 9.47E-03 | 2.57 |
| CCNB1    | 6.79E-03 | 2.57 |
| KIF18A   | 4.88E-02 | 2.56 |
| FANCM    | 2.06E-02 | 2.54 |
| EAF2     | 4.24E-02 | 2.51 |
| ARG1     | 1.86E-02 | 2.50 |
| KIF11    | 2.64E-02 | 2.49 |
| CCL5     | 3.63E-02 | 2.48 |
| GPR132   | 2.15E-02 | 2.47 |
| IRF8     | 1.61E-02 | 2.46 |
| HELLS    | 4.43E-02 | 2.45 |
| ARHGAP15 | 4.91E-02 | 2.45 |
| RUNX2    | 3.72E-02 | 2.45 |
| CKAP2L   | 1.50E-02 | 2.44 |
| C12orf56 | 5.41E-03 | 2.44 |
| POC5     | 1.92E-02 | 2.44 |
| ZNF286A  | 4.01E-02 | 2.43 |
| TOP2A    | 5.30E-03 | 2.42 |
| ZNF624   | 3.68E-02 | 2.41 |
| WNT5A    | 2.23E-02 | 2.40 |
| KRT6B    | 3.81E-02 | 2.38 |
| GBP5     | 1.03E-02 | 2.37 |
| HENMT1   | 2.48E-02 | 2.36 |
| SLAMF7   | 3.88E-02 | 2.35 |
| C12orf75 | 3.82E-02 | 2.32 |
| HELB     | 2.61E-02 | 2.32 |
| MAP3K9   | 4.05E-02 | 2.32 |
| PLBD1    | 9.32E-03 | 2.31 |
| RNASEH2B | 1.73E-02 | 2.30 |
| C12orf35 | 4.23E-02 | 2.30 |
| BUB1     | 1.21E-02 | 2.29 |
| RALGPS2  | 9.42E-03 | 2.29 |
| LCE2D    | 2.32E-02 | 2.28 |
| CCNA2    | 5.81E-03 | 2.26 |
| CENPE    | 1.41E-02 | 2.26 |
| ARHGAP11 | 1.67E-02 | 2.24 |
| LRRC8D   | 8.68E-03 | 2.24 |
| PARP14   | 2.12E-02 | 2.22 |
| KIF23    | 1.93E-02 | 2.22 |
| CCNB2    | 1.36E-02 | 2.22 |
| ZNF101   | 4.67E-02 | 2.22 |
| SKA3     | 3.30E-02 | 2.21 |
| TTC39A   | 1.05E-02 | 2.20 |
| MYO1B    | 2.66E-02 | 2.20 |
| APOBEC3G | 1.97E-02 | 2.20 |
| CLCA2    | 2.81E-03 | 2.19 |
| PLEKHF2  | 1.19E-03 | 2.19 |
| SPRR1A   | 2.76E-02 | 2.18 |
| CKS2     | 2.37E-02 | 2.17 |
| BORA     | 2.86E-02 | 2.16 |
| DTX3L    | 4.42E-03 | 2.16 |
| SRP9     | 4.89E-04 | 2.15 |
| BPGM     | 9.04E-04 | 2.14 |
| SPAG5    | 2.23E-02 | 2.13 |
| SLC36A1  | 5.97E-03 | 2.13 |
| ZNF772   | 4.16E-02 | 2.13 |
| HJURP    | 4.59E-02 | 2.12 |
| ECT2     | 2.23E-02 | 2.11 |
| AOAH     | 3.32E-02 | 2.11 |
| ZNF641   | 5.37E-03 | 2.11 |
| TMEM117  | 2.28E-02 | 2.10 |
| SSX2IP   | 4.33E-02 | 2.09 |
| LIN9     | 4.48E-03 | 2.08 |
| FAM105A  | 3.88E-02 | 2.07 |
| 4.13E+04 | 7.56E-03 | 2.07 |
| CDC42SE2 | 1.19E-02 | 2.06 |
| ORC1     | 2.69E-02 | 2.06 |
| P2RY1    | 2.34E-02 | 2.06 |
| KIAA1524 | 8.22E-03 | 2.05 |
| CKAP2    | 9.75E-03 | 2.04 |
| ERP27    | 3.04E-02 | 2.04 |
| GALNT6   | 1.04E-02 | 2.01 |
| POLQ     | 4.27E-02 | 1.99 |
| KLK8     | 4.90E-02 | 1.99 |



|          |          |      |
|----------|----------|------|
| CENPF    | 3.77E-02 | 1.98 |
| LCP1     | 2.82E-02 | 1.98 |
| GPR155   | 2.50E-04 | 1.97 |
| GIN51    | 3.74E-02 | 1.97 |
| ORC6     | 2.42E-02 | 1.97 |
| IFIT5    | 8.53E-03 | 1.97 |
| DMXL2    | 8.42E-03 | 1.96 |
| ARHGAP25 | 4.17E-02 | 1.96 |
| DIAPH3   | 3.07E-02 | 1.96 |
| ARPC3    | 4.45E-02 | 1.95 |
| MELK     | 1.16E-02 | 1.94 |
| YOD1     | 4.37E-02 | 1.93 |
| CDC7     | 8.12E-03 | 1.93 |
| FAM83D   | 3.12E-02 | 1.92 |
| GTF2E1   | 1.23E-02 | 1.92 |
| DDX58    | 8.41E-03 | 1.92 |
| AP1S3    | 1.23E-02 | 1.92 |
| NUSAP1   | 4.67E-02 | 1.91 |
| C20orf94 | 4.94E-02 | 1.90 |
| BIRC5    | 2.94E-02 | 1.90 |
| PRSS3    | 1.07E-02 | 1.90 |
| ENTPD7   | 4.24E-02 | 1.89 |
| PA2G4    | 4.69E-02 | 1.89 |
| RRM2     | 3.74E-02 | 1.89 |
| PDE7A    | 4.72E-02 | 1.89 |
| FBXO45   | 6.00E-03 | 1.88 |
| SASS6    | 2.59E-02 | 1.87 |
| ZNF770   | 2.21E-02 | 1.86 |
| PLK1     | 3.07E-02 | 1.86 |
| PRC1     | 2.89E-02 | 1.86 |
| MPEG1    | 2.14E-02 | 1.86 |
| RNF138   | 2.10E-02 | 1.86 |
| EIF5A2   | 1.11E-02 | 1.85 |
| NVL      | 4.17E-02 | 1.85 |
| CPSF3    | 9.62E-03 | 1.85 |
| CSNK1A1L | 4.00E-02 | 1.85 |
| SLAMF8   | 2.74E-02 | 1.85 |
| IL36RN   | 2.81E-02 | 1.84 |
| RAD51AP1 | 2.92E-02 | 1.84 |
| CCDC132  | 1.14E-02 | 1.84 |
| RALA     | 6.05E-03 | 1.84 |
| ATP10B   | 2.99E-02 | 1.84 |
| SNX10    | 1.51E-02 | 1.83 |
| RACGAP1  | 1.03E-02 | 1.83 |
| CALML4   | 1.71E-02 | 1.83 |
| FTSJ1    | 4.33E-02 | 1.82 |
| WDHD1    | 3.48E-02 | 1.82 |
| CALM1    | 1.44E-02 | 1.82 |
| SKP2     | 2.74E-04 | 1.82 |
| PARP9    | 2.64E-03 | 1.82 |
| FERMT1   | 2.95E-02 | 1.81 |
| CCDC112  | 4.22E-02 | 1.81 |
| GTF2A1   | 9.37E-03 | 1.81 |
| ANKRD32  | 4.06E-02 | 1.80 |
| HPSE     | 2.91E-02 | 1.80 |
| HMG2     | 3.73E-03 | 1.79 |
| ERCC6    | 3.72E-02 | 1.79 |
| USP1     | 2.60E-02 | 1.79 |
| ATM      | 2.85E-02 | 1.78 |
| KIAA1033 | 2.91E-02 | 1.78 |
| ZWINT    | 3.63E-02 | 1.78 |
| APOL6    | 4.73E-02 | 1.77 |
| STAT1    | 1.64E-02 | 1.77 |
| RFC3     | 2.41E-02 | 1.76 |
| CAPZA1   | 4.89E-02 | 1.76 |
| RB1      | 1.77E-02 | 1.75 |
| MCM2     | 4.64E-03 | 1.75 |
| ARHGEF3  | 1.79E-02 | 1.75 |
| CBWD1    | 4.65E-02 | 1.74 |
| PARP11   | 4.85E-02 | 1.74 |
| TTC13    | 2.98E-02 | 1.74 |
| NCAPH    | 3.52E-02 | 1.73 |
| CALML5   | 3.69E-02 | 1.73 |
| S100BP   | 2.50E-02 | 1.73 |
| ZWILCH   | 2.56E-02 | 1.72 |
| EIF2AK2  | 3.36E-02 | 1.72 |
| GIMAP7   | 1.77E-02 | 1.72 |
| ZNF518B  | 1.77E-02 | 1.72 |
| MS4A6A   | 3.12E-02 | 1.72 |
| TRIM14   | 3.29E-02 | 1.72 |
| R3HCC1L  | 5.06E-03 | 1.71 |



|          |          |      |
|----------|----------|------|
| LPAR3    | 3.18E-02 | 1.71 |
| SMC6     | 8.03E-03 | 1.71 |
| TPBG     | 8.49E-03 | 1.70 |
| AP4B1    | 1.36E-02 | 1.70 |
| KLK5     | 4.88E-02 | 1.69 |
| C12orf65 | 2.47E-02 | 1.69 |
| TMEM14A  | 1.16E-02 | 1.69 |
| MCM4     | 7.64E-03 | 1.69 |
| RPP40    | 4.68E-02 | 1.69 |
| TFDP1    | 1.76E-02 | 1.68 |
| DYRK2    | 1.08E-02 | 1.68 |
| RAB10    | 6.29E-03 | 1.68 |
| 4.13E+04 | 4.18E-02 | 1.67 |
| ODF2L    | 4.97E-02 | 1.67 |
| ANKRD5   | 1.90E-02 | 1.66 |
| PIK3CD   | 3.06E-02 | 1.66 |
| RAET1E   | 4.89E-02 | 1.66 |
| STAM     | 3.29E-02 | 1.66 |
| PTER     | 2.39E-02 | 1.66 |
| RIOK1    | 1.58E-02 | 1.66 |
| UBL3     | 1.96E-02 | 1.66 |
| ADAR     | 1.78E-02 | 1.65 |
| CASP3    | 4.47E-02 | 1.64 |
| WDR53    | 2.23E-03 | 1.64 |
| CTSC     | 1.08E-02 | 1.63 |
| TMEM241  | 4.31E-03 | 1.63 |
| DCP1B    | 4.66E-02 | 1.63 |
| ATAD3A   | 2.49E-02 | 1.63 |
| MFSD9    | 2.44E-02 | 1.63 |
| MCM3     | 1.17E-02 | 1.63 |
| TMEM194E | 1.29E-02 | 1.63 |
| PI4K2B   | 6.59E-03 | 1.62 |
| PDCD2L   | 1.72E-02 | 1.62 |
| CAB39    | 2.81E-02 | 1.62 |
| RAVER2   | 3.75E-02 | 1.62 |
| PLK4     | 2.87E-03 | 1.62 |
| AP4E1    | 2.74E-02 | 1.62 |
| ZFAT     | 4.23E-02 | 1.62 |
| XRCC4    | 6.25E-04 | 1.61 |
| CDC45    | 4.34E-02 | 1.61 |
| SLK      | 3.59E-02 | 1.60 |
| CPVL     | 1.67E-02 | 1.60 |
| ERCC4    | 2.41E-02 | 1.60 |
| TNFRSF21 | 9.51E-03 | 1.60 |
| 4.13E+04 | 3.06E-02 | 1.60 |
| RBM45    | 1.38E-02 | 1.60 |
| HSPA8    | 4.58E-02 | 1.60 |
| VRK2     | 2.37E-03 | 1.59 |
| NUP107   | 1.10E-02 | 1.59 |
| POLR3B   | 3.40E-02 | 1.59 |
| TDP1     | 3.42E-02 | 1.59 |
| PSMC2    | 1.12E-02 | 1.58 |
| NBN      | 3.43E-03 | 1.58 |
| ARHGDIB  | 1.71E-02 | 1.58 |
| CEP135   | 3.04E-02 | 1.58 |
| MAPK14   | 2.95E-02 | 1.58 |
| SMC2     | 3.35E-02 | 1.58 |
| TTC26    | 2.08E-02 | 1.57 |
| SUPT16H  | 3.52E-02 | 1.57 |
| SP100    | 1.83E-02 | 1.57 |
| PSAT1    | 3.61E-02 | 1.57 |
| MND1     | 4.67E-02 | 1.57 |
| TRMT13   | 3.98E-02 | 1.56 |
| LPIN2    | 3.18E-02 | 1.56 |
| FASTKD3  | 1.55E-02 | 1.56 |
| FAM49B   | 3.38E-02 | 1.56 |
| PKM      | 8.16E-03 | 1.56 |
| FKBP15   | 4.53E-02 | 1.54 |
| SPAST    | 2.55E-02 | 1.54 |
| RAP2A    | 8.51E-03 | 1.54 |
| NMI      | 1.06E-02 | 1.53 |
| CCDC109B | 1.43E-02 | 1.53 |
| UPF3A    | 4.94E-02 | 1.53 |
| TMEM65   | 1.21E-02 | 1.53 |
| DHTKD1   | 2.32E-02 | 1.53 |
| TMX1     | 1.27E-02 | 1.53 |
| CDK19    | 4.54E-02 | 1.53 |
| PRDX1    | 1.55E-02 | 1.53 |
| LIN54    | 3.23E-02 | 1.53 |
| IDNK     | 3.82E-02 | 1.53 |
| FBXO38   | 1.68E-02 | 1.53 |



|           |          |      |
|-----------|----------|------|
| LSP1      | 4.99E-02 | 1.52 |
| ZNF434    | 4.69E-02 | 1.52 |
| ERCC8     | 2.18E-02 | 1.52 |
| CLCN3     | 3.82E-02 | 1.52 |
| PUS7      | 4.30E-02 | 1.52 |
| KIAA1430  | 1.32E-02 | 1.52 |
| C9orf85   | 5.00E-02 | 1.52 |
| LMNB1     | 2.41E-02 | 1.52 |
| GPSM2     | 3.55E-02 | 1.52 |
| ARHGAP30  | 3.97E-02 | 1.52 |
| SELR1     | 3.25E-02 | 1.52 |
| ZNF212    | 4.88E-02 | 1.52 |
| RFC4      | 1.24E-02 | 1.52 |
| PKNOX1    | 1.88E-02 | 1.51 |
| SEPSECS   | 1.02E-03 | 1.51 |
| SEL1L     | 4.59E-02 | 1.51 |
| C17orf80  | 3.89E-02 | 1.51 |
| CDCA7     | 3.39E-02 | 1.50 |
| FZD6      | 2.10E-02 | 1.50 |
| PRMT5     | 9.58E-03 | 1.50 |
| GTF3C3    | 3.39E-02 | 1.50 |
| NEIL1     | 3.55E-02 | 0.67 |
| OSGIN2    | 8.55E-03 | 0.67 |
| MEPCE     | 2.44E-02 | 0.66 |
| ZNF577    | 9.12E-03 | 0.66 |
| BRP44L    | 4.03E-02 | 0.66 |
| NDRG2     | 2.20E-03 | 0.66 |
| ARHGAP10  | 9.11E-03 | 0.66 |
| PRICKLE4  | 4.71E-02 | 0.66 |
| NXN       | 2.00E-02 | 0.66 |
| PPP1R13B  | 1.21E-02 | 0.65 |
| GSDMB     | 1.64E-02 | 0.65 |
| LRP5      | 4.41E-02 | 0.65 |
| PDE2A     | 3.07E-02 | 0.65 |
| ICA1      | 3.47E-02 | 0.65 |
| TACC2     | 2.07E-02 | 0.65 |
| ARHGAP40  | 3.72E-02 | 0.65 |
| TINAGL1   | 2.30E-02 | 0.65 |
| SIK2      | 7.12E-03 | 0.65 |
| PLA2G6    | 4.36E-03 | 0.65 |
| COBL      | 1.42E-02 | 0.64 |
| PLEKHA4   | 3.59E-02 | 0.64 |
| ACTN1     | 1.64E-02 | 0.64 |
| CA13      | 3.63E-02 | 0.64 |
| TNFRSF10B | 3.01E-02 | 0.64 |
| PLEKHG6   | 4.66E-02 | 0.64 |
| NFIX      | 4.35E-02 | 0.64 |
| B4GALT3   | 2.87E-03 | 0.64 |
| STK40     | 7.85E-03 | 0.64 |
| NEK8      | 2.81E-02 | 0.64 |
| AIF1L     | 3.14E-02 | 0.63 |
| USP36     | 1.58E-02 | 0.63 |
| ACSF2     | 4.51E-02 | 0.63 |
| TENC1     | 3.70E-02 | 0.63 |
| CD34      | 3.20E-02 | 0.63 |
| PHLDB1    | 3.69E-02 | 0.63 |
| VPS37B    | 3.66E-02 | 0.63 |
| KANK2     | 2.65E-02 | 0.63 |
| SH3BGR12  | 2.80E-02 | 0.63 |
| SCARB1    | 4.92E-02 | 0.63 |
| FGFRL1    | 4.92E-02 | 0.63 |
| ECHDC2    | 3.58E-02 | 0.63 |
| AKAP1     | 1.23E-02 | 0.63 |
| CACNB1    | 2.31E-02 | 0.63 |
| HDAC5     | 2.79E-02 | 0.63 |
| PHF1      | 2.67E-02 | 0.63 |
| CDAN1     | 6.21E-03 | 0.63 |
| SLC12A7   | 3.99E-02 | 0.63 |
| DNAJA1    | 4.56E-02 | 0.63 |
| BCAR3     | 5.83E-03 | 0.62 |
| SYTL3     | 2.66E-02 | 0.62 |
| ECSCR     | 4.88E-02 | 0.62 |
| IMMP2L    | 1.06E-02 | 0.62 |
| CHKA      | 4.31E-03 | 0.62 |
| FAHD2A    | 3.11E-02 | 0.62 |
| PKIG      | 8.66E-03 | 0.62 |
| ACLY      | 3.08E-02 | 0.62 |
| PTPRU     | 2.25E-02 | 0.62 |
| JAM2      | 3.55E-02 | 0.62 |
| CNKS3     | 2.62E-02 | 0.62 |
| SLC9A1    | 3.36E-02 | 0.62 |



|            |          |      |
|------------|----------|------|
| KLK1       | 3.67E-02 | 0.61 |
| CHPT1      | 1.24E-02 | 0.61 |
| OBSN       | 1.95E-02 | 0.61 |
| DNAJB4     | 1.38E-02 | 0.61 |
| STK39      | 9.36E-03 | 0.61 |
| RTN4       | 4.11E-02 | 0.61 |
| DNAJA4     | 1.52E-02 | 0.61 |
| SREBF1     | 2.85E-02 | 0.61 |
| GALT       | 1.98E-02 | 0.61 |
| CAP2       | 7.22E-03 | 0.61 |
| ADCY6      | 5.91E-03 | 0.61 |
| NMNAT3     | 1.52E-02 | 0.61 |
| NAALADL1   | 2.25E-02 | 0.61 |
| CDK3       | 1.03E-02 | 0.61 |
| TLE1       | 2.21E-02 | 0.61 |
| SPG20      | 1.78E-03 | 0.61 |
| MMRN1      | 3.73E-02 | 0.61 |
| CTB-96E2.3 | 4.46E-02 | 0.61 |
| MAT2A      | 3.36E-02 | 0.61 |
| CDADC1     | 1.16E-02 | 0.61 |
| SPTBN1     | 1.79E-02 | 0.61 |
| PARVA      | 1.60E-02 | 0.61 |
| LRIG1      | 3.25E-04 | 0.61 |
| RETSAT     | 7.55E-03 | 0.61 |
| MTERFD3    | 1.28E-02 | 0.61 |
| BARX2      | 2.93E-02 | 0.61 |
| IL34       | 2.84E-02 | 0.60 |
| RPH3AL     | 4.90E-02 | 0.60 |
| ME3        | 2.31E-02 | 0.60 |
| KANK1      | 8.52E-03 | 0.60 |
| NDE1       | 1.08E-02 | 0.60 |
| FREM1      | 2.89E-02 | 0.60 |
| NEDD4L     | 8.02E-03 | 0.60 |
| MSRB3      | 5.63E-03 | 0.59 |
| BOC        | 2.27E-02 | 0.59 |
| ACADVL     | 1.59E-02 | 0.59 |
| ERG        | 6.90E-03 | 0.59 |
| CCDC24     | 1.59E-02 | 0.59 |
| TRPV4      | 3.33E-03 | 0.59 |
| CLDN1      | 5.83E-03 | 0.58 |
| BCAM       | 1.90E-02 | 0.58 |
| BBS1       | 3.35E-03 | 0.58 |
| GSTM2      | 2.22E-02 | 0.58 |
| BCL7A      | 2.52E-02 | 0.58 |
| METTL7A    | 4.39E-03 | 0.58 |
| FBXO32     | 5.97E-03 | 0.58 |
| MYH14      | 8.14E-03 | 0.58 |
| CTH        | 3.66E-02 | 0.58 |
| NTN4       | 1.95E-03 | 0.58 |
| MCF2L      | 1.04E-02 | 0.58 |
| SMARCD3    | 2.44E-02 | 0.58 |
| IRS2       | 4.92E-02 | 0.58 |
| ANGPTL1    | 2.98E-02 | 0.58 |
| CBX7       | 4.26E-02 | 0.57 |
| C8orf42    | 4.21E-02 | 0.57 |
| TRIB1      | 7.36E-03 | 0.57 |
| IL17RE     | 4.98E-03 | 0.57 |
| CPNE7      | 3.38E-02 | 0.57 |
| RP11-286N  | 1.67E-02 | 0.57 |
| SPRY1      | 4.85E-02 | 0.57 |
| CBX8       | 4.10E-02 | 0.57 |
| FGFR1      | 3.09E-02 | 0.57 |
| CFL2       | 9.19E-03 | 0.57 |
| POU2F3     | 1.70E-03 | 0.57 |
| CAB39L     | 3.65E-02 | 0.56 |
| BAIAP3     | 4.32E-02 | 0.56 |
| CNRIP1     | 6.57E-03 | 0.56 |
| SULT1E1    | 2.25E-02 | 0.56 |
| TGIF1      | 3.77E-02 | 0.56 |
| HDC        | 1.67E-02 | 0.56 |
| SOX13      | 2.71E-03 | 0.55 |
| EDNRB      | 6.62E-03 | 0.55 |
| CD55       | 1.60E-02 | 0.55 |
| ISYNA1     | 3.96E-02 | 0.55 |
| SLC41A1    | 4.84E-02 | 0.55 |
| SH3BGR     | 3.25E-02 | 0.55 |
| HMGCR      | 1.05E-02 | 0.55 |
| BNC2       | 4.20E-02 | 0.55 |
| LGI3       | 4.02E-02 | 0.55 |
| SDC4       | 2.06E-03 | 0.54 |
| AC006276.  | 3.70E-02 | 0.54 |



|          |          |      |
|----------|----------|------|
| GABARAPL | 5.40E-03 | 0.54 |
| TNS1     | 1.49E-02 | 0.54 |
| ARHGEF25 | 4.31E-02 | 0.54 |
| AXL      | 1.83E-02 | 0.54 |
| ENPP3    | 3.99E-02 | 0.54 |
| VEGFA    | 3.94E-02 | 0.54 |
| SEMA3G   | 4.48E-02 | 0.53 |
| SLC25A4  | 2.84E-02 | 0.53 |
| C5orf4   | 3.79E-02 | 0.53 |
| SPRY2    | 3.26E-02 | 0.52 |
| SRF      | 4.13E-02 | 0.52 |
| FOXP4    | 1.53E-02 | 0.52 |
| SELENBP1 | 1.84E-02 | 0.52 |
| DTX1     | 4.01E-02 | 0.52 |
| FBLN5    | 2.42E-02 | 0.52 |
| CABLES1  | 2.98E-02 | 0.52 |
| TMEM8B   | 2.07E-02 | 0.52 |
| RFX2     | 4.54E-02 | 0.51 |
| ADCK1    | 4.87E-02 | 0.51 |
| FAM149B1 | 7.19E-03 | 0.51 |
| NGFR     | 2.58E-02 | 0.51 |
| SH3BP5   | 3.28E-03 | 0.51 |
| SYBU     | 3.23E-02 | 0.51 |
| TOB1     | 1.02E-02 | 0.51 |
| SHROOM3  | 2.65E-02 | 0.51 |
| APOE     | 1.07E-02 | 0.51 |
| GKAP1    | 1.24E-02 | 0.51 |
| ZSCAN18  | 8.31E-03 | 0.50 |
| SLC44A3  | 2.02E-02 | 0.50 |
| PTCH1    | 1.81E-02 | 0.50 |
| GSN      | 1.67E-02 | 0.50 |
| CREM     | 4.54E-02 | 0.50 |
| SNCG     | 3.47E-03 | 0.49 |
| PNPLA7   | 2.14E-02 | 0.49 |
| PLA2R1   | 2.94E-02 | 0.49 |
| FRZB     | 3.20E-03 | 0.49 |
| NFIL3    | 9.18E-03 | 0.49 |
| 4.13E+04 | 2.09E-02 | 0.49 |
| LDLR     | 1.51E-02 | 0.49 |
| TM4SF1   | 1.87E-02 | 0.49 |
| SLIT2    | 3.23E-02 | 0.49 |
| FXVD6    | 2.23E-02 | 0.49 |
| FLT1     | 1.87E-02 | 0.49 |
| DLL1     | 1.92E-02 | 0.49 |
| NRG2     | 1.20E-02 | 0.49 |
| ACACB    | 6.44E-03 | 0.49 |
| SEMA3D   | 3.94E-02 | 0.49 |
| GPX3     | 2.03E-02 | 0.49 |
| NFIB     | 4.26E-02 | 0.48 |
| RCAN2    | 1.02E-02 | 0.48 |
| SYT17    | 3.90E-02 | 0.48 |
| RORC     | 1.06E-02 | 0.48 |
| PXDC1    | 2.69E-02 | 0.48 |
| PYROXD2  | 1.53E-02 | 0.48 |
| CYP4X1   | 2.76E-02 | 0.48 |
| SCHIP1   | 4.38E-02 | 0.48 |
| TIMP3    | 5.49E-03 | 0.48 |
| ADCYAP1R | 3.92E-02 | 0.48 |
| ACTA2    | 3.46E-02 | 0.47 |
| CRYAB    | 2.76E-03 | 0.47 |
| TMEM97   | 4.60E-02 | 0.47 |
| DENND2A  | 3.47E-02 | 0.47 |
| LHX2     | 2.95E-02 | 0.47 |
| ADAMTS1  | 3.97E-02 | 0.47 |
| VEGFC    | 1.20E-02 | 0.47 |
| MYADM    | 2.98E-02 | 0.47 |
| TLE2     | 1.15E-02 | 0.47 |
| ANKS1B   | 6.01E-03 | 0.46 |
| TFPI     | 1.83E-02 | 0.46 |
| CCL14    | 6.20E-04 | 0.46 |
| ABCA9    | 3.76E-02 | 0.46 |
| SUSD2    | 4.21E-03 | 0.46 |
| PID1     | 2.23E-03 | 0.46 |
| TGM2     | 3.95E-02 | 0.46 |
| TAGLN    | 1.91E-02 | 0.46 |
| PGM5     | 4.94E-02 | 0.46 |
| SLC25A25 | 9.67E-03 | 0.46 |
| C15orf59 | 4.41E-02 | 0.46 |
| HMGCS1   | 3.70E-02 | 0.46 |
| PALM     | 1.15E-02 | 0.46 |
| MYL9     | 3.05E-03 | 0.45 |



|           |          |      |
|-----------|----------|------|
| ID4       | 1.35E-02 | 0.45 |
| PRELP     | 1.81E-02 | 0.45 |
| MRAS      | 4.40E-03 | 0.45 |
| RNF152    | 4.27E-03 | 0.45 |
| DCLK1     | 1.34E-02 | 0.45 |
| RNASE4    | 1.72E-03 | 0.45 |
| LPL       | 2.84E-02 | 0.45 |
| TPM2      | 1.73E-03 | 0.45 |
| GLI2      | 9.06E-03 | 0.45 |
| CNGA1     | 3.23E-02 | 0.44 |
| TPM1      | 2.54E-03 | 0.44 |
| CFH       | 2.66E-02 | 0.44 |
| EGR2      | 2.68E-02 | 0.44 |
| SFRP1     | 3.39E-02 | 0.44 |
| INSIG1    | 2.28E-02 | 0.43 |
| FXYD1     | 2.15E-02 | 0.43 |
| GSTM5     | 4.87E-03 | 0.43 |
| EGR3      | 7.89E-03 | 0.43 |
| LIPE      | 3.27E-02 | 0.43 |
| PAMR1     | 2.04E-02 | 0.42 |
| PDZRN3    | 4.59E-03 | 0.42 |
| QRICH2    | 3.93E-03 | 0.42 |
| RELN      | 7.82E-03 | 0.42 |
| WNK2      | 1.42E-02 | 0.42 |
| SOX9      | 8.98E-04 | 0.42 |
| TMEM125   | 3.27E-02 | 0.42 |
| PLIN4     | 4.34E-02 | 0.41 |
| CAMK2N1   | 1.59E-02 | 0.41 |
| TESC      | 5.37E-03 | 0.41 |
| NTRK3     | 2.78E-02 | 0.41 |
| RAB17     | 9.18E-03 | 0.41 |
| SLC27A6   | 5.93E-03 | 0.40 |
| KRT77     | 3.76E-03 | 0.40 |
| RGMA      | 3.77E-04 | 0.40 |
| CSRP1     | 1.01E-04 | 0.40 |
| ZNF385D   | 2.51E-02 | 0.40 |
| GHR       | 4.80E-02 | 0.40 |
| CGNL1     | 1.41E-02 | 0.39 |
| FAM180B   | 1.05E-02 | 0.39 |
| INMT      | 1.32E-02 | 0.39 |
| PPARGC1A  | 1.41E-02 | 0.39 |
| FOXC1     | 8.37E-03 | 0.39 |
| PLEKHB1   | 4.27E-02 | 0.39 |
| CCL27     | 3.46E-02 | 0.39 |
| KRT15     | 2.88E-03 | 0.39 |
| FST       | 7.88E-03 | 0.39 |
| HSD11B1   | 1.53E-02 | 0.38 |
| GRIA4     | 1.63E-02 | 0.38 |
| AKAP12    | 1.59E-02 | 0.38 |
| KCNN4     | 3.12E-03 | 0.38 |
| C8orf46   | 2.35E-02 | 0.38 |
| NPAS3     | 4.40E-02 | 0.38 |
| ATP6V0A4  | 1.19E-02 | 0.38 |
| SOCS2     | 2.07E-03 | 0.38 |
| LVRN      | 3.83E-02 | 0.37 |
| TRIM55    | 3.18E-02 | 0.37 |
| VIT       | 2.16E-03 | 0.37 |
| C7        | 2.26E-03 | 0.37 |
| NCALD     | 1.42E-02 | 0.37 |
| AADACL3   | 4.08E-02 | 0.37 |
| SLC26A2   | 2.04E-02 | 0.37 |
| ACOX2     | 1.96E-02 | 0.37 |
| ABCA8     | 3.83E-03 | 0.36 |
| CTC-360G5 | 3.01E-02 | 0.36 |
| SEMA3A    | 4.93E-02 | 0.36 |
| FAM189A2  | 4.65E-03 | 0.36 |
| GLRB      | 3.10E-03 | 0.36 |
| SORBS2    | 5.01E-04 | 0.35 |
| PDE9A     | 4.20E-03 | 0.35 |
| SORBS1    | 2.16E-02 | 0.35 |
| CAPN12    | 3.99E-02 | 0.35 |
| FADS2     | 2.40E-02 | 0.34 |
| SLC26A7   | 2.81E-02 | 0.34 |
| SAMD4A    | 4.06E-02 | 0.34 |
| APOLD1    | 7.50E-03 | 0.34 |
| C3orf15   | 3.22E-02 | 0.34 |
| TTYH1     | 3.98E-03 | 0.34 |
| PDE6A     | 2.38E-02 | 0.34 |
| SAMD11    | 1.61E-02 | 0.34 |
| PYGM      | 7.64E-03 | 0.33 |
| PDLIM3    | 1.02E-02 | 0.33 |



|           |          |      |
|-----------|----------|------|
| LMOD1     | 1.82E-02 | 0.33 |
| ITIH3     | 1.88E-02 | 0.33 |
| ACTG2     | 4.65E-03 | 0.33 |
| KCNAB1    | 3.50E-02 | 0.33 |
| ZG16B     | 7.87E-03 | 0.33 |
| MLXIPL    | 1.79E-02 | 0.32 |
| CNTFR     | 6.93E-03 | 0.32 |
| PLCB4     | 3.35E-03 | 0.32 |
| AQP5      | 1.64E-03 | 0.32 |
| RP11-190A | 4.63E-02 | 0.31 |
| SEMA3B    | 1.30E-04 | 0.31 |
| ADH1B     | 7.40E-03 | 0.31 |
| CDH19     | 8.06E-03 | 0.31 |
| CDO1      | 1.36E-02 | 0.31 |
| ATF3      | 4.90E-02 | 0.31 |
| CYP4B1    | 5.62E-03 | 0.30 |
| C2orf82   | 1.13E-02 | 0.30 |
| SGCG      | 2.03E-03 | 0.30 |
| FNDC5     | 1.05E-03 | 0.30 |
| RBP4      | 2.12E-02 | 0.29 |
| ATP6V1B1  | 4.33E-03 | 0.29 |
| MRAP      | 3.90E-02 | 0.28 |
| SOX10     | 2.69E-02 | 0.28 |
| KIAA1324  | 1.04E-03 | 0.28 |
| PADI3     | 1.93E-02 | 0.28 |
| CNTN4     | 1.74E-02 | 0.27 |
| DNER      | 9.14E-04 | 0.27 |
| OGN       | 4.11E-05 | 0.27 |
| STK32A    | 3.45E-04 | 0.27 |
| GABRP     | 2.76E-03 | 0.27 |
| OXGR1     | 9.49E-03 | 0.26 |
| SCARA5    | 3.74E-02 | 0.26 |
| KRT7      | 1.97E-03 | 0.26 |
| SYNM      | 9.07E-04 | 0.26 |
| STAC2     | 1.46E-04 | 0.25 |
| MPZ       | 1.78E-03 | 0.25 |
| PCK1      | 2.02E-02 | 0.25 |
| SLC12A2   | 1.13E-02 | 0.25 |
| ESRRG     | 1.92E-02 | 0.25 |
| C13orf33  | 2.72E-02 | 0.25 |
| SCN7A     | 1.41E-02 | 0.24 |
| STC1      | 2.24E-02 | 0.24 |
| APOD      | 4.27E-04 | 0.24 |
| MUCL1     | 1.50E-03 | 0.24 |
| SLC14A1   | 2.74E-03 | 0.23 |
| GLYATL1   | 3.62E-02 | 0.23 |
| HSPB7     | 8.02E-03 | 0.23 |
| CFTR      | 7.19E-03 | 0.23 |
| EFHD1     | 2.73E-03 | 0.23 |
| CNN1      | 1.47E-03 | 0.22 |
| MF12      | 1.58E-02 | 0.21 |
| DES       | 4.61E-03 | 0.21 |
| CIDEC     | 6.64E-03 | 0.20 |
| S100A1    | 2.59E-03 | 0.20 |
| PPP1R1B   | 6.21E-04 | 0.20 |
| ADAMTS4   | 3.71E-02 | 0.20 |
| MYH11     | 6.87E-04 | 0.20 |
| MT4       | 4.23E-02 | 0.20 |
| PADI2     | 1.69E-03 | 0.20 |
| FAM150B   | 1.48E-02 | 0.19 |
| LYG2      | 1.52E-02 | 0.19 |
| SLC34A2   | 2.88E-02 | 0.19 |
| WFDC3     | 1.50E-02 | 0.19 |
| MYBPC1    | 5.85E-03 | 0.19 |
| ATP1A2    | 6.63E-03 | 0.19 |
| PLIN1     | 6.58E-03 | 0.18 |
| ASIP      | 4.63E-02 | 0.18 |
| S100A3    | 1.12E-02 | 0.18 |
| TCHH      | 1.32E-02 | 0.18 |
| GRB14     | 1.29E-04 | 0.18 |
| CASQ2     | 2.33E-03 | 0.17 |
| ADIPOQ    | 1.79E-03 | 0.17 |
| CCDC129   | 2.70E-03 | 0.17 |
| PPP1R1A   | 2.14E-03 | 0.17 |
| PHYHIP    | 1.53E-04 | 0.15 |
| PCP4      | 2.37E-03 | 0.15 |
| RIMS1     | 1.05E-02 | 0.15 |
| KRTAP17-1 | 2.78E-02 | 0.15 |
| CTNND2    | 2.44E-03 | 0.15 |
| TMPRSS2   | 3.71E-04 | 0.15 |
| KRTAP5-10 | 3.34E-02 | 0.14 |



|           |          |      |
|-----------|----------|------|
| FABP9     | 4.31E-03 | 0.13 |
| TMEM213   | 7.26E-04 | 0.13 |
| CLDN10    | 9.49E-05 | 0.12 |
| CGA       | 5.42E-03 | 0.12 |
| KRTAP12-3 | 2.09E-02 | 0.12 |
| DCD       | 4.09E-03 | 0.11 |
| SCGB2A2   | 2.94E-03 | 0.11 |
| PIP       | 8.99E-04 | 0.11 |
| KRT28     | 5.52E-03 | 0.10 |
| KRT27     | 2.72E-03 | 0.10 |
| KRTAP16-1 | 1.67E-02 | 0.10 |
| KRT25     | 4.56E-03 | 0.10 |
| HOXB-AS3  | 4.75E-02 | 0.10 |
| KRTAP19-1 | 4.73E-02 | 0.10 |
| RP11-176H | 3.01E-02 | 0.09 |
| KRTAP9-4  | 4.20E-02 | 0.09 |
| KRTAP26-1 | 2.74E-02 | 0.09 |
| GPRC5D    | 2.05E-02 | 0.09 |
| KRT71     | 2.88E-03 | 0.09 |
| KRT26     | 5.32E-03 | 0.08 |
| KRTAP9-3  | 4.32E-02 | 0.08 |
| ANGPTL7   | 5.34E-03 | 0.08 |
| MUC7      | 3.68E-02 | 0.08 |
| SCGB1D2   | 1.20E-02 | 0.08 |
| KRT82     | 1.04E-02 | 0.08 |
| KRTAP19-5 | 3.97E-02 | 0.07 |
| KRT32     | 6.61E-03 | 0.07 |
| KRTAP19-3 | 2.76E-02 | 0.07 |
| KRT85     | 1.88E-02 | 0.06 |
| KRT35     | 1.67E-02 | 0.06 |
| KRTAP12-2 | 2.50E-02 | 0.05 |
| KRTAP11-1 | 2.80E-02 | 0.04 |



## NS-SCC gene signature

| Gene       | p-value  | SCC/NS fold change |
|------------|----------|--------------------|
| IGF2BP3    | 4.16E-02 | 3391.26            |
| MMP1       | 1.96E-02 | 23.39              |
| MMP3       | 3.34E-02 | 20.97              |
| TDO2       | 3.17E-04 | 18.58              |
| PTHLH      | 2.52E-03 | 17.45              |
| TMPRSS11F  | 4.71E-02 | 13.48              |
| AIM2       | 1.03E-02 | 12.57              |
| HMGA2      | 1.07E-02 | 10.67              |
| KRT6C      | 2.55E-03 | 10.56              |
| ADH7       | 3.24E-02 | 10.14              |
| COL10A1    | 3.12E-02 | 9.98               |
| S100A12    | 1.50E-02 | 8.60               |
| AKR1B10    | 3.66E-03 | 8.09               |
| CD38       | 3.05E-02 | 7.67               |
| FABP5      | 2.00E-03 | 7.61               |
| MS4A1      | 3.44E-02 | 7.27               |
| RPTN       | 1.06E-02 | 6.85               |
| S100A7A    | 4.20E-02 | 6.73               |
| S100A9     | 1.24E-03 | 6.54               |
| AL136218.1 | 1.07E-02 | 6.38               |
| KRT6A      | 5.35E-04 | 6.35               |
| AKR1B15    | 1.03E-02 | 6.23               |
| CXCL9      | 3.22E-03 | 6.09               |
| NAT1       | 2.84E-03 | 6.07               |
| KRT16      | 2.28E-04 | 6.01               |
| IL12RB2    | 1.57E-03 | 5.96               |
| CXCL10     | 7.49E-03 | 5.82               |
| CXCL13     | 3.36E-02 | 5.79               |
| LAMC2      | 2.69E-02 | 5.75               |
| GBP6       | 4.32E-03 | 5.66               |
| CNGB1      | 1.91E-02 | 5.65               |
| FAM40B     | 1.70E-02 | 5.61               |
| PLAC8      | 2.75E-02 | 5.53               |
| C12orf70   | 4.56E-02 | 5.49               |
| S100A8     | 3.55E-03 | 5.49               |
| LAMP5      | 5.38E-03 | 5.30               |
| KLRD1      | 4.78E-03 | 5.24               |
| GPR1       | 2.25E-02 | 5.22               |
| DSC2       | 1.15E-03 | 5.22               |
| FBN2       | 4.79E-02 | 4.97               |
| CEP55      | 8.56E-04 | 4.88               |
| DFNA5      | 1.95E-02 | 4.83               |
| SLC16A1    | 4.20E-02 | 4.82               |
| C10orf99   | 4.06E-03 | 4.73               |
| EPGN       | 4.45E-02 | 4.73               |
| HIST1H2BO  | 2.53E-02 | 4.69               |
| HSD17B6    | 2.55E-02 | 4.68               |
| SULF1      | 4.31E-03 | 4.64               |
| CCL18      | 4.83E-02 | 4.58               |
| PPP1R14B   | 1.27E-02 | 4.51               |
| IGFL1      | 6.98E-03 | 4.47               |
| GZMA       | 4.41E-03 | 4.47               |
| CXCL11     | 6.75E-03 | 4.45               |
| GJB6       | 4.60E-03 | 4.45               |
| ADAMDEC1   | 8.50E-03 | 4.41               |
| GDAP1      | 2.85E-02 | 4.41               |
| SCG5       | 3.36E-02 | 4.40               |
| ARNTL2     | 5.68E-03 | 4.34               |
| EPSTI1     | 5.53E-04 | 4.28               |
| CYP24A1    | 4.55E-02 | 4.25               |
| DLGAP5     | 2.50E-02 | 4.23               |
| LCE3E      | 1.81E-02 | 4.22               |
| ADAM23     | 1.36E-02 | 4.21               |
| TH         | 3.02E-02 | 4.19               |
| SLC6A11    | 5.14E-03 | 4.19               |
| ARTN       | 1.56E-02 | 4.19               |
| MME        | 2.62E-02 | 4.11               |
| UBE2C      | 4.16E-03 | 4.09               |
| IGFBP2     | 2.16E-03 | 4.07               |
| ITGB6      | 1.76E-02 | 4.06               |
| NREP       | 3.63E-03 | 3.94               |
| TPX2       | 1.38E-02 | 3.94               |
| RUNX2      | 8.82E-03 | 3.92               |
| SAMD3      | 5.47E-03 | 3.85               |
| SPRR2A     | 5.96E-03 | 3.78               |
| PRKCQ      | 4.25E-03 | 3.78               |
| MCM10      | 1.78E-02 | 3.75               |
| OAS2       | 1.94E-03 | 3.74               |



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| KRT6B     | 3.10E-03 | 3.73 |
| S100A7    | 3.96E-02 | 3.71 |
| HMMR      | 2.91E-03 | 3.70 |
| CDKN2A    | 1.87E-02 | 3.68 |
| TBCA      | 9.59E-03 | 3.66 |
| IFI6      | 3.28E-02 | 3.65 |
| WNT5A     | 1.62E-02 | 3.60 |
| KRT3      | 3.66E-03 | 3.60 |
| ORC6      | 1.35E-02 | 3.59 |
| CKAP2L    | 9.06E-03 | 3.57 |
| KIF20A    | 3.34E-03 | 3.54 |
| EFR3B     | 3.70E-02 | 3.54 |
| COL5A2    | 1.55E-02 | 3.49 |
| CENPA     | 2.04E-05 | 3.49 |
| TM4SF19   | 4.69E-02 | 3.46 |
| MYO1B     | 2.12E-02 | 3.46 |
| CLEC4C    | 4.20E-02 | 3.45 |
| KIF18A    | 4.08E-02 | 3.43 |
| CCNB1     | 3.10E-04 | 3.32 |
| RSAD2     | 3.18E-02 | 3.31 |
| WFD12     | 3.54E-02 | 3.31 |
| GJB2      | 3.23E-03 | 3.26 |
| SLC7A11   | 3.78E-02 | 3.24 |
| COL3A1    | 3.76E-02 | 3.23 |
| TTK       | 4.32E-02 | 3.22 |
| CDKN3     | 1.88E-03 | 3.21 |
| DSG3      | 2.26E-03 | 3.21 |
| SERPINB13 | 6.58E-03 | 3.21 |
| LRRC8D    | 3.21E-05 | 3.16 |
| BUB1      | 9.82E-03 | 3.16 |
| SPAG5     | 7.11E-03 | 3.16 |
| NETO2     | 1.54E-02 | 3.14 |
| CCNA2     | 1.23E-03 | 3.14 |
| HIST1H2BK | 6.22E-03 | 3.12 |
| SLPI      | 4.64E-02 | 3.12 |
| GGH       | 2.01E-03 | 3.12 |
| CENPE     | 1.31E-03 | 3.09 |
| CDCA3     | 8.18E-03 | 3.08 |
| GALNT6    | 2.80E-03 | 3.04 |
| NRIP3     | 4.33E-02 | 3.01 |
| NDC80     | 3.63E-03 | 3.00 |
| PLK1      | 8.31E-04 | 3.00 |
| HIST1H3I  | 2.62E-03 | 2.99 |
| TNFRSF21  | 3.74E-04 | 2.98 |
| ODZ3      | 3.76E-02 | 2.97 |
| BPGM      | 2.58E-03 | 2.96 |
| TUBB3     | 2.70E-02 | 2.95 |
| BIRC5     | 1.15E-02 | 2.95 |
| ENAH      | 2.03E-03 | 2.94 |
| TRPM2     | 2.15E-03 | 2.93 |
| HENMT1    | 1.54E-02 | 2.92 |
| CLCA2     | 2.19E-02 | 2.91 |
| SPRR1A    | 2.80E-02 | 2.90 |
| HJURP     | 6.34E-03 | 2.90 |
| RNASE7    | 1.80E-02 | 2.90 |
| KIAA1609  | 2.64E-02 | 2.89 |
| CDH3      | 9.46E-03 | 2.89 |
| UPP1      | 2.01E-02 | 2.87 |
| NID1      | 1.46E-02 | 2.87 |
| RAB31     | 1.59E-02 | 2.86 |
| GZMB      | 4.29E-02 | 2.86 |
| PARP15    | 2.54E-02 | 2.84 |
| FAP       | 4.45E-02 | 2.84 |
| OASL      | 1.83E-04 | 2.83 |
| CDCA2     | 1.45E-03 | 2.83 |
| CORO6     | 6.30E-03 | 2.81 |
| KLRK1     | 1.26E-02 | 2.79 |
| GTSE1     | 2.70E-02 | 2.77 |
| TNNT1     | 2.72E-02 | 2.77 |
| CENPO     | 2.12E-02 | 2.77 |
| CSTA      | 4.64E-03 | 2.77 |
| LCE3D     | 8.52E-03 | 2.76 |
| BEND6     | 3.05E-02 | 2.76 |
| SLAMF8    | 3.85E-03 | 2.76 |
| ZNF323    | 4.72E-03 | 2.72 |
| CMPK2     | 8.94E-03 | 2.72 |
| BORA      | 9.90E-03 | 2.71 |
| SPRR1B    | 3.01E-02 | 2.71 |
| SKA3      | 6.85E-03 | 2.71 |
| FAM83D    | 4.76E-04 | 2.71 |
| BAIAP2L2  | 1.92E-02 | 2.71 |



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|-----------|----------|------|
| WISP1     | 1.93E-02 | 2.71 |
| MDF1      | 2.30E-03 | 2.70 |
| APOBEC3G  | 1.17E-03 | 2.69 |
| ITGA4     | 3.64E-02 | 2.68 |
| TOP2A     | 7.00E-03 | 2.67 |
| ASPM      | 1.51E-03 | 2.66 |
| THAP5     | 1.16E-02 | 2.65 |
| KIF2C     | 4.36E-02 | 2.65 |
| DLEU1     | 3.38E-03 | 2.65 |
| C1QTNF6   | 1.70E-02 | 2.65 |
| KCTD7     | 4.32E-02 | 2.65 |
| C8orf44   | 4.19E-02 | 2.65 |
| ARHGAP11L | 1.85E-02 | 2.64 |
| STX1A     | 1.68E-02 | 2.64 |
| SLAMF7    | 5.84E-03 | 2.64 |
| HIST1H3C  | 1.80E-02 | 2.64 |
| COL5A1    | 2.29E-02 | 2.63 |
| KIF23     | 1.86E-02 | 2.63 |
| PCGF6     | 4.72E-02 | 2.62 |
| PTTG1     | 1.10E-02 | 2.62 |
| ECT2      | 2.43E-02 | 2.62 |
| FN1       | 4.75E-02 | 2.61 |
| C12orf56  | 2.35E-02 | 2.60 |
| IFIT3     | 3.40E-02 | 2.60 |
| TMED7-TIC | 3.28E-02 | 2.59 |
| MFAP2     | 3.28E-03 | 2.59 |
| PRR11     | 1.06E-02 | 2.59 |
| HN1       | 3.10E-04 | 2.59 |
| RELL2     | 3.74E-03 | 2.59 |
| CDC45     | 8.26E-04 | 2.58 |
| MYBL2     | 8.86E-03 | 2.58 |
| CKAP2     | 7.64E-03 | 2.57 |
| CDCA8     | 1.23E-02 | 2.57 |
| TRIP13    | 2.33E-03 | 2.56 |
| C6orf141  | 1.30E-02 | 2.56 |
| CDC7      | 9.26E-04 | 2.56 |
| PTPLA     | 4.80E-02 | 2.55 |
| COL4A1    | 3.75E-02 | 2.54 |
| TIGIT     | 2.58E-02 | 2.53 |
| ZNF641    | 1.30E-02 | 2.53 |
| CCNB2     | 6.25E-03 | 2.52 |
| KIAA1524  | 3.50E-02 | 2.51 |
| PPP2R2C   | 3.25E-03 | 2.51 |
| PYGL      | 2.99E-02 | 2.50 |
| CCL5      | 4.44E-03 | 2.50 |
| DTX3L     | 2.01E-02 | 2.49 |
| HES2      | 1.90E-03 | 2.49 |
| GIN51     | 3.66E-02 | 2.48 |
| PRKAR1B   | 9.20E-03 | 2.47 |
| SLC47A2   | 4.65E-03 | 2.47 |
| MELK      | 6.39E-03 | 2.47 |
| F12       | 4.34E-02 | 2.46 |
| CENPF     | 4.24E-02 | 2.42 |
| GORAB     | 3.84E-04 | 2.41 |
| ANKRD5    | 1.35E-02 | 2.41 |
| CDC6      | 3.11E-02 | 2.41 |
| CLEC12A   | 4.04E-02 | 2.41 |
| PLBD1     | 3.90E-03 | 2.41 |
| CCDC142   | 3.71E-02 | 2.40 |
| TP53I3    | 2.15E-04 | 2.39 |
| SERPINB1  | 3.03E-02 | 2.39 |
| ORC1      | 2.34E-03 | 2.39 |
| CKS2      | 2.65E-02 | 2.38 |
| SELL      | 4.63E-02 | 2.37 |
| NKG7      | 6.37E-03 | 2.35 |
| TP53INP1  | 5.88E-03 | 2.35 |
| GBP5      | 1.51E-03 | 2.34 |
| STIL      | 1.18E-02 | 2.34 |
| DCBLD1    | 1.02E-02 | 2.34 |
| GBP4      | 1.74E-02 | 2.34 |
| RACGAP1   | 5.30E-03 | 2.34 |
| C11orf82  | 3.23E-02 | 2.32 |
| CDCA5     | 4.37E-03 | 2.32 |
| FAM109B   | 2.27E-03 | 2.32 |
| RALA      | 3.39E-02 | 2.30 |
| 41334     | 1.00E-02 | 2.30 |
| SNX10     | 5.81E-03 | 2.30 |
| COL6A3    | 2.83E-02 | 2.29 |
| PIK3CD    | 6.26E-04 | 2.27 |
| FAM26F    | 2.29E-02 | 2.26 |
| SCRN1     | 4.54E-02 | 2.25 |



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| MCM2       | 2.83E-02 | 2.25 |
| SP140L     | 2.00E-02 | 2.25 |
| LRIF1      | 4.07E-02 | 2.24 |
| TFEC       | 2.73E-02 | 2.24 |
| TPBG       | 1.87E-04 | 2.24 |
| CA2        | 2.11E-02 | 2.24 |
| AURKB      | 2.35E-03 | 2.23 |
| EIF4EBP1   | 2.26E-03 | 2.23 |
| CHST11     | 3.01E-03 | 2.23 |
| S100A11    | 3.68E-03 | 2.23 |
| KIAA0101   | 1.97E-02 | 2.23 |
| HIST2H2AC  | 1.43E-02 | 2.23 |
| OCIAD2     | 9.93E-04 | 2.22 |
| ARPC1B     | 1.93E-02 | 2.22 |
| CCNE2      | 6.36E-04 | 2.22 |
| CARHSP1    | 5.56E-03 | 2.21 |
| RGS20      | 1.15E-02 | 2.20 |
| OIP5       | 7.33E-03 | 2.20 |
| DMXL2      | 8.12E-04 | 2.20 |
| PTPN7      | 3.21E-04 | 2.20 |
| KLK8       | 3.06E-03 | 2.20 |
| KIF11      | 9.49E-03 | 2.19 |
| ITGA1      | 3.72E-02 | 2.19 |
| MMP14      | 1.32E-02 | 2.19 |
| NCAPH      | 4.10E-02 | 2.17 |
| PRELID1    | 1.53E-02 | 2.17 |
| PTPRC      | 3.79E-02 | 2.17 |
| SIDT1      | 2.17E-02 | 2.17 |
| PKM        | 3.89E-03 | 2.16 |
| TROAP      | 2.54E-02 | 2.16 |
| DIAPH3     | 2.23E-02 | 2.15 |
| FERMT1     | 1.79E-02 | 2.15 |
| PRSS23     | 2.00E-02 | 2.14 |
| DYRK2      | 3.80E-03 | 2.14 |
| ADAMTS2    | 8.62E-03 | 2.14 |
| ZNF75A     | 3.44E-02 | 2.13 |
| RRM2       | 4.94E-02 | 2.13 |
| MPZL2      | 8.14E-03 | 2.12 |
| RPS6KA4    | 3.93E-03 | 2.12 |
| RUVBL1     | 1.34E-02 | 2.12 |
| PPAPDC1A   | 3.86E-02 | 2.12 |
| PPP2R2B    | 3.85E-02 | 2.12 |
| TMEM14A    | 1.65E-02 | 2.11 |
| NUF2       | 3.19E-02 | 2.11 |
| TMSB10     | 4.33E-03 | 2.10 |
| C19orf33   | 1.03E-02 | 2.10 |
| KRT76      | 3.87E-02 | 2.10 |
| SLC2A9     | 2.33E-02 | 2.10 |
| EIF5A2     | 3.86E-04 | 2.09 |
| CYBA       | 9.51E-03 | 2.09 |
| AFAP1L2    | 1.71E-02 | 2.09 |
| HIST1H2AE  | 4.02E-02 | 2.08 |
| EML1       | 4.50E-02 | 2.08 |
| CCM2       | 6.57E-03 | 2.08 |
| IL21R      | 1.53E-02 | 2.08 |
| RRS1       | 1.36E-03 | 2.07 |
| SNX20      | 6.86E-03 | 2.07 |
| ZWINT      | 1.80E-03 | 2.07 |
| LOXL2      | 7.07E-03 | 2.07 |
| IQGAP3     | 1.93E-02 | 2.06 |
| TTC39A     | 1.24E-02 | 2.06 |
| IFI35      | 2.03E-02 | 2.06 |
| PKMYT1     | 1.32E-02 | 2.06 |
| FAM89A     | 3.47E-02 | 2.06 |
| LPAR3      | 3.29E-02 | 2.05 |
| CTSC       | 2.69E-03 | 2.05 |
| RP11-371E8 | 2.49E-02 | 2.05 |
| RNF138     | 5.66E-03 | 2.04 |
| KDELR3     | 1.49E-02 | 2.04 |
| SLC2A6     | 1.76E-02 | 2.04 |
| FAIM3      | 1.62E-02 | 2.03 |
| SULF2      | 8.57E-03 | 2.03 |
| HIST1H2AH  | 2.54E-02 | 2.03 |
| WDR91      | 1.60E-02 | 2.03 |
| CDC25B     | 2.05E-02 | 2.02 |
| MX1        | 1.89E-02 | 2.02 |
| JAK3       | 1.44E-03 | 2.02 |
| CDC25C     | 3.60E-02 | 2.01 |
| TYMP       | 1.19E-02 | 2.01 |
| ZNF23      | 3.54E-02 | 2.01 |
| PLD4       | 1.96E-02 | 2.01 |



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| PPIL1    | 5.93E-03 | 2.01 |
| RB1      | 2.62E-03 | 2.01 |
| CCNE1    | 1.38E-02 | 2.01 |
| EMR2     | 2.91E-02 | 2.00 |
| SPC24    | 1.79E-02 | 2.00 |
| LARP6    | 4.02E-02 | 2.00 |
| FANCM    | 9.00E-03 | 1.99 |
| POC1A    | 5.91E-03 | 1.99 |
| EHHADH   | 9.94E-03 | 1.99 |
| DEPDC1B  | 6.67E-03 | 1.99 |
| PAIP1    | 3.10E-02 | 1.98 |
| NEURL2   | 2.44E-02 | 1.98 |
| NAV1     | 2.30E-02 | 1.98 |
| FSCN1    | 2.07E-03 | 1.98 |
| GAPDH    | 1.08E-02 | 1.97 |
| CCDC109B | 3.55E-03 | 1.97 |
| DCAF4    | 2.61E-03 | 1.96 |
| CPXM1    | 4.76E-02 | 1.96 |
| MSANTD3  | 2.21E-02 | 1.96 |
| DTL      | 2.09E-02 | 1.96 |
| SEMA4B   | 1.12E-03 | 1.95 |
| VSNL1    | 1.80E-02 | 1.95 |
| SKP2     | 2.52E-02 | 1.95 |
| PARP9    | 3.06E-03 | 1.95 |
| RNF145   | 7.49E-04 | 1.95 |
| GPX2     | 1.11E-02 | 1.95 |
| SLC36A1  | 4.31E-02 | 1.95 |
| TUBA1C   | 8.71E-03 | 1.95 |
| CDK1     | 2.62E-02 | 1.94 |
| FAT2     | 2.04E-02 | 1.94 |
| FAM83A   | 4.10E-02 | 1.94 |
| SGTB     | 3.51E-02 | 1.94 |
| IDO1     | 4.97E-02 | 1.94 |
| MAZ      | 1.68E-03 | 1.94 |
| FUT2     | 1.04E-02 | 1.93 |
| RPP38    | 1.37E-02 | 1.93 |
| CTSW     | 7.25E-03 | 1.93 |
| CD300A   | 3.00E-02 | 1.93 |
| SH2D2A   | 2.44E-02 | 1.93 |
| FAM20A   | 3.37E-02 | 1.93 |
| ABCC4    | 9.31E-03 | 1.93 |
| BMP1     | 2.37E-02 | 1.92 |
| B3GALT1  | 8.53E-03 | 1.92 |
| MRPS17   | 1.02E-02 | 1.92 |
| RNASEH2B | 7.95E-03 | 1.92 |
| GTF2E1   | 1.86E-02 | 1.92 |
| RPE      | 2.94E-02 | 1.92 |
| IFI30    | 6.24E-04 | 1.91 |
| MB21D1   | 3.02E-02 | 1.91 |
| LIPA     | 2.69E-02 | 1.91 |
| EHBP1L1  | 1.43E-02 | 1.91 |
| PXDN     | 3.85E-02 | 1.91 |
| BANF1    | 1.02E-03 | 1.91 |
| ATAD3A   | 2.41E-02 | 1.90 |
| RGS3     | 1.70E-02 | 1.90 |
| CALM1    | 9.37E-04 | 1.90 |
| GSDMC    | 2.04E-02 | 1.90 |
| STAT1    | 9.59E-04 | 1.89 |
| RNF144A  | 1.61E-02 | 1.89 |
| BASP1    | 1.64E-02 | 1.89 |
| HOMER3   | 4.56E-02 | 1.88 |
| ITGA3    | 2.98E-02 | 1.88 |
| RAC2     | 1.06E-03 | 1.88 |
| CAPG     | 4.24E-04 | 1.88 |
| HDAC1    | 9.17E-05 | 1.88 |
| AKIP1    | 7.14E-04 | 1.88 |
| PARP14   | 8.47E-03 | 1.87 |
| HK3      | 3.21E-02 | 1.87 |
| CDC20    | 2.53E-02 | 1.87 |
| COTL1    | 2.62E-04 | 1.87 |
| HERC6    | 3.47E-02 | 1.87 |
| SEC61G   | 2.00E-02 | 1.86 |
| ENPEP    | 3.32E-02 | 1.86 |
| SFN      | 7.00E-03 | 1.86 |
| DOK2     | 2.70E-02 | 1.85 |
| PRDM4    | 6.22E-04 | 1.85 |
| LILRB4   | 1.06E-02 | 1.85 |
| YKT6     | 7.11E-03 | 1.85 |
| LPGAT1   | 4.91E-02 | 1.85 |
| CAP1     | 1.15E-02 | 1.85 |
| RAB10    | 1.13E-03 | 1.85 |



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| ZNF200   | 2.00E-02 | 1.85 |
| SRP9     | 3.59E-02 | 1.85 |
| TMEM117  | 7.38E-03 | 1.85 |
| C16orf55 | 2.22E-02 | 1.85 |
| CAPZA1   | 3.01E-02 | 1.85 |
| PLAU     | 1.57E-02 | 1.84 |
| GIMAP7   | 1.83E-02 | 1.84 |
| OAS3     | 1.78E-02 | 1.84 |
| FGF11    | 2.40E-02 | 1.84 |
| STAU2    | 2.63E-02 | 1.84 |
| ACTL6A   | 3.64E-02 | 1.83 |
| PMEPA1   | 2.61E-02 | 1.83 |
| LEPRE1   | 7.75E-04 | 1.83 |
| RPP40    | 1.42E-02 | 1.83 |
| GLO1     | 3.49E-02 | 1.83 |
| MAPK9    | 6.59E-03 | 1.83 |
| BTBD3    | 5.07E-03 | 1.83 |
| LIN9     | 4.29E-03 | 1.83 |
| FBLIM1   | 2.26E-02 | 1.82 |
| CLEC4A   | 2.85E-02 | 1.82 |
| GLRX3    | 2.43E-03 | 1.82 |
| ZAP70    | 4.30E-02 | 1.82 |
| CALU     | 4.11E-02 | 1.82 |
| PRKCDBP  | 2.99E-02 | 1.81 |
| KIAA1033 | 2.14E-02 | 1.81 |
| NMI      | 1.70E-02 | 1.81 |
| CCDC112  | 1.82E-02 | 1.81 |
| CSNK1A1L | 4.22E-02 | 1.81 |
| CMAS     | 4.11E-02 | 1.81 |
| NOP56    | 3.33E-03 | 1.81 |
| TMEM44   | 5.28E-03 | 1.81 |
| TXNDC17  | 2.76E-03 | 1.81 |
| MAPK12   | 4.68E-02 | 1.80 |
| ENO1     | 1.91E-02 | 1.80 |
| PDCD10   | 1.75E-02 | 1.80 |
| PRMT5    | 1.76E-03 | 1.80 |
| C1QC     | 8.91E-03 | 1.80 |
| NUSAP1   | 2.33E-02 | 1.80 |
| JAG1     | 1.15E-02 | 1.80 |
| LY6D     | 9.98E-03 | 1.80 |
| XDH      | 2.27E-02 | 1.80 |
| TMEM194B | 4.61E-02 | 1.80 |
| CDC27    | 1.55E-02 | 1.80 |
| MTSS1    | 2.11E-02 | 1.79 |
| ARL2BP   | 3.38E-04 | 1.79 |
| MAFB     | 1.64E-02 | 1.79 |
| MS4A6A   | 3.61E-02 | 1.79 |
| TGFB1    | 2.49E-02 | 1.79 |
| PDCD1LG2 | 3.42E-02 | 1.79 |
| TMEM42   | 3.97E-03 | 1.78 |
| FAM49B   | 2.04E-02 | 1.78 |
| S100A16  | 3.81E-03 | 1.77 |
| IFITM1   | 6.46E-03 | 1.77 |
| PWP1     | 3.75E-02 | 1.77 |
| ALG3     | 4.63E-02 | 1.77 |
| PDLM7    | 1.06E-02 | 1.77 |
| PKNOX1   | 2.71E-02 | 1.77 |
| EIF2AK2  | 1.08E-02 | 1.77 |
| MAGEF1   | 2.68E-02 | 1.77 |
| CASP8    | 1.94E-03 | 1.77 |
| KMO      | 1.59E-02 | 1.77 |
| MEI1     | 2.71E-02 | 1.76 |
| DUSP14   | 3.31E-02 | 1.76 |
| YAE1D1   | 1.86E-02 | 1.76 |
| AP2M1    | 2.16E-02 | 1.76 |
| RNA5EH2A | 3.92E-03 | 1.76 |
| CD47     | 4.95E-02 | 1.76 |
| SOX15    | 1.66E-02 | 1.76 |
| PARP12   | 1.80E-02 | 1.76 |
| TDP1     | 8.87E-03 | 1.76 |
| HEATR2   | 5.00E-03 | 1.76 |
| PGF      | 5.49E-03 | 1.76 |
| ITGAL    | 3.18E-02 | 1.76 |
| AGPS     | 5.68E-03 | 1.76 |
| SQLE     | 1.90E-02 | 1.76 |
| GSTP1    | 9.78E-04 | 1.75 |
| TBX2     | 2.57E-02 | 1.75 |
| FUCA2    | 3.01E-03 | 1.75 |
| AVIL     | 3.25E-02 | 1.75 |
| CAPRIN2  | 2.86E-03 | 1.75 |
| LTB4R2   | 3.33E-02 | 1.75 |



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| FZD6     | 1.51E-02 | 1.75 |
| GPR68    | 3.63E-02 | 1.75 |
| CDK18    | 1.14E-02 | 1.75 |
| CPSF3    | 3.66E-03 | 1.75 |
| ZNF562   | 7.76E-03 | 1.75 |
| ZNF101   | 2.29E-02 | 1.75 |
| HSPA8    | 3.13E-02 | 1.75 |
| EDEM2    | 1.54E-03 | 1.75 |
| UBE2F    | 2.18E-02 | 1.75 |
| TTC26    | 3.61E-02 | 1.75 |
| RFC4     | 2.31E-02 | 1.74 |
| C12orf35 | 2.40E-02 | 1.74 |
| MRPL51   | 3.57E-02 | 1.74 |
| SPHK1    | 1.82E-02 | 1.74 |
| PSMB10   | 2.22E-03 | 1.74 |
| YWHAZ    | 3.28E-03 | 1.74 |
| GTF2A1   | 1.58E-02 | 1.74 |
| PRKACB   | 4.10E-02 | 1.74 |
| RAD51    | 2.75E-02 | 1.74 |
| C15orf41 | 5.46E-03 | 1.74 |
| COL5A3   | 4.43E-02 | 1.74 |
| RANBP1   | 2.89E-02 | 1.74 |
| FGD3     | 7.07E-04 | 1.73 |
| POC5     | 2.51E-02 | 1.73 |
| OVCA2    | 4.72E-02 | 1.73 |
| WDHD1    | 3.96E-03 | 1.73 |
| SLC16A3  | 7.13E-03 | 1.73 |
| OSBPL7   | 1.69E-02 | 1.73 |
| GUCY1B3  | 4.51E-02 | 1.72 |
| GEMIN6   | 1.06E-02 | 1.72 |
| RFC3     | 3.12E-02 | 1.72 |
| HSBP1    | 1.34E-02 | 1.72 |
| CENPQ    | 1.10E-03 | 1.72 |
| MRPL17   | 9.69E-04 | 1.72 |
| C17orf80 | 2.62E-02 | 1.72 |
| TBRG4    | 8.76E-03 | 1.72 |
| RPL6     | 7.76E-03 | 1.71 |
| PTK7     | 2.23E-03 | 1.71 |
| CLEC11A  | 1.39E-02 | 1.71 |
| CD276    | 4.12E-02 | 1.71 |
| TFAP4    | 1.03E-02 | 1.71 |
| IFITM3   | 1.25E-02 | 1.71 |
| CEP41    | 1.21E-02 | 1.71 |
| TSEN15   | 9.59E-03 | 1.71 |
| TWISTNB  | 4.35E-02 | 1.70 |
| CCDC88C  | 1.24E-03 | 1.70 |
| ODF2L    | 1.43E-03 | 1.70 |
| DOK3     | 5.91E-03 | 1.70 |
| SNRPF    | 4.65E-02 | 1.70 |
| HSPB11   | 5.92E-05 | 1.70 |
| SNRPD1   | 2.90E-02 | 1.70 |
| PRC1     | 3.89E-02 | 1.70 |
| SLC1A4   | 1.73E-02 | 1.70 |
| CELSR1   | 2.72E-02 | 1.70 |
| PLK4     | 1.07E-02 | 1.70 |
| CD163L1  | 2.79E-02 | 1.70 |
| POP1     | 2.43E-02 | 1.69 |
| SLC38A1  | 4.33E-02 | 1.69 |
| WDR77    | 1.88E-02 | 1.69 |
| CCT5     | 1.01E-02 | 1.69 |
| CENPN    | 4.03E-02 | 1.69 |
| MAF      | 1.02E-02 | 1.69 |
| SLC35B4  | 4.26E-02 | 1.69 |
| LCP2     | 1.03E-02 | 1.68 |
| TMEM199  | 2.42E-02 | 1.68 |
| TXNDC5   | 4.66E-03 | 1.68 |
| SEC23A   | 2.48E-02 | 1.68 |
| CPSF2    | 1.54E-02 | 1.68 |
| ANO7L1   | 2.03E-02 | 1.68 |
| GLT25D1  | 1.89E-04 | 1.68 |
| MCM4     | 4.20E-03 | 1.67 |
| IL12RB1  | 2.86E-02 | 1.67 |
| CD247    | 4.31E-02 | 1.67 |
| TAX1BP3  | 1.55E-02 | 1.67 |
| LSM5     | 8.06E-03 | 1.67 |
| METTL5   | 4.90E-02 | 1.67 |
| FAR1     | 1.06E-02 | 1.67 |
| BTBD11   | 1.34E-02 | 1.67 |
| ZNF434   | 1.73E-02 | 1.67 |
| S100A10  | 2.68E-02 | 1.67 |
| CHEK2    | 4.11E-02 | 1.67 |



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| INVS     | 2.22E-02 | 1.67 |
| BCL11B   | 2.63E-02 | 1.67 |
| TK1      | 1.34E-02 | 1.67 |
| LIMK1    | 6.07E-03 | 1.67 |
| RAB22A   | 1.29E-02 | 1.67 |
| ARHGEF17 | 6.84E-03 | 1.66 |
| LCLAT1   | 4.55E-02 | 1.66 |
| SAMHD1   | 4.70E-02 | 1.66 |
| CTPS1    | 8.34E-03 | 1.66 |
| METTL1   | 3.17E-02 | 1.66 |
| CSE1L    | 7.60E-04 | 1.66 |
| NUDT15   | 3.94E-04 | 1.66 |
| LAT2     | 1.08E-02 | 1.66 |
| LMNB2    | 1.83E-03 | 1.66 |
| CCDC51   | 1.14E-02 | 1.66 |
| SAC3D1   | 1.01E-02 | 1.66 |
| RGS10    | 4.29E-02 | 1.66 |
| GSTO1    | 2.46E-02 | 1.65 |
| MYO1G    | 1.73E-02 | 1.65 |
| DHX37    | 2.25E-04 | 1.65 |
| PDIA5    | 6.60E-03 | 1.65 |
| EIF5A    | 4.46E-03 | 1.65 |
| PBK      | 2.95E-02 | 1.65 |
| CYTH4    | 4.58E-02 | 1.65 |
| FAM176A  | 3.95E-02 | 1.65 |
| DHRS7    | 1.83E-02 | 1.65 |
| SLC35C1  | 1.15E-02 | 1.64 |
| ARHGAP25 | 1.28E-02 | 1.64 |
| COMMD8   | 9.68E-03 | 1.64 |
| MPLKIP   | 1.40E-02 | 1.64 |
| NUP37    | 9.60E-03 | 1.64 |
| FTL      | 1.86E-02 | 1.64 |
| CCT6A    | 1.03E-02 | 1.64 |
| SAAL1    | 5.47E-03 | 1.64 |
| PI4K2B   | 1.05E-02 | 1.64 |
| SLC35B3  | 4.27E-04 | 1.64 |
| TRIM37   | 3.02E-02 | 1.64 |
| LCK      | 4.72E-02 | 1.64 |
| TAF1A    | 2.06E-02 | 1.63 |
| CCDC132  | 3.49E-03 | 1.63 |
| COPB2    | 9.93E-03 | 1.63 |
| CD53     | 8.79E-03 | 1.63 |
| RAP2B    | 6.91E-03 | 1.63 |
| LYN      | 1.13E-02 | 1.63 |
| LY96     | 4.94E-02 | 1.63 |
| PRDX1    | 7.00E-04 | 1.63 |
| RBM45    | 1.92E-02 | 1.63 |
| ZWILCH   | 1.67E-02 | 1.63 |
| LIMD2    | 1.02E-02 | 1.62 |
| WDR67    | 1.30E-02 | 1.62 |
| C17orf62 | 1.69E-02 | 1.62 |
| TAGLN2   | 9.97E-03 | 1.62 |
| CENPJ    | 9.67E-03 | 1.62 |
| TFDP1    | 1.10E-02 | 1.62 |
| CLEC7A   | 2.90E-02 | 1.62 |
| HIRA     | 2.21E-02 | 1.62 |
| CDK4     | 5.51E-03 | 1.61 |
| FXVD3    | 3.14E-02 | 1.61 |
| IMPDH1   | 1.54E-02 | 1.61 |
| RIC8A    | 2.81E-03 | 1.61 |
| ACP2     | 6.77E-03 | 1.61 |
| VRK2     | 1.61E-04 | 1.61 |
| CCDC92   | 4.15E-03 | 1.61 |
| HRAS     | 2.68E-03 | 1.61 |
| ZNF337   | 1.35E-02 | 1.61 |
| HPS3     | 1.39E-03 | 1.60 |
| ZNF205   | 8.30E-03 | 1.60 |
| PUS7     | 1.88E-02 | 1.60 |
| SLC38A7  | 2.44E-02 | 1.60 |
| 41341    | 3.67E-02 | 1.60 |
| CORO1A   | 3.00E-02 | 1.60 |
| STAM     | 2.66E-02 | 1.60 |
| CHN1     | 4.90E-02 | 1.60 |
| THUMPD2  | 3.71E-02 | 1.60 |
| LYAR     | 1.78E-02 | 1.60 |
| BLVRA    | 1.99E-02 | 1.60 |
| SCO2     | 2.58E-02 | 1.60 |
| LSM7     | 1.50E-02 | 1.60 |
| CEP135   | 1.42E-02 | 1.60 |
| PSMD4    | 6.19E-03 | 1.60 |
| HIST1H1E | 3.45E-02 | 1.60 |



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| CASP3     | 4.32E-02 | 1.59 |
| ZNF146    | 5.54E-03 | 1.59 |
| PRDX5     | 1.40E-02 | 1.59 |
| TAF5L     | 3.02E-02 | 1.59 |
| DUS2L     | 5.75E-04 | 1.59 |
| THAP1     | 4.98E-03 | 1.59 |
| MRPS23    | 4.50E-04 | 1.59 |
| ITM2C     | 6.75E-04 | 1.59 |
| FKBP15    | 3.57E-04 | 1.59 |
| TXN       | 6.65E-03 | 1.59 |
| RGS14     | 2.68E-03 | 1.59 |
| LAD1      | 1.46E-02 | 1.59 |
| SDCCAG3   | 4.56E-02 | 1.59 |
| RASAL3    | 1.49E-02 | 1.59 |
| DCUN1D5   | 3.00E-02 | 1.59 |
| STK32C    | 4.15E-02 | 1.59 |
| UBLCP1    | 6.64E-05 | 1.59 |
| UCLH3     | 5.11E-04 | 1.59 |
| CRELD2    | 7.71E-03 | 1.59 |
| FBXO45    | 2.43E-02 | 1.59 |
| MCM7      | 2.93E-02 | 1.58 |
| ZMPSTE24  | 1.59E-04 | 1.58 |
| GTPBP4    | 1.77E-02 | 1.58 |
| TNFSF10   | 3.66E-02 | 1.58 |
| SNRPC     | 5.98E-03 | 1.58 |
| B4GALT7   | 1.61E-03 | 1.58 |
| EVI2B     | 2.03E-02 | 1.58 |
| DUOXA1    | 4.01E-02 | 1.58 |
| CDCA7     | 3.92E-02 | 1.58 |
| ADAM10    | 2.73E-02 | 1.58 |
| FAM98A    | 9.36E-03 | 1.58 |
| WDR81     | 4.42E-03 | 1.58 |
| BUB3      | 2.84E-05 | 1.58 |
| DSCC1     | 3.96E-02 | 1.58 |
| LSP1      | 2.26E-02 | 1.58 |
| R3HCC1L   | 3.20E-03 | 1.58 |
| PCGF1     | 3.58E-02 | 1.58 |
| CCNT2     | 3.14E-03 | 1.58 |
| C20orf196 | 1.07E-02 | 1.58 |
| LYRM2     | 1.63E-02 | 1.58 |
| FAM48A    | 3.73E-02 | 1.58 |
| NHP2      | 3.78E-02 | 1.58 |
| RP9       | 1.10E-02 | 1.57 |
| C20orf27  | 2.17E-02 | 1.57 |
| H2AFX     | 1.77E-02 | 1.57 |
| FXYD5     | 1.19E-02 | 1.57 |
| RFC5      | 2.77E-02 | 1.57 |
| SMC6      | 2.93E-03 | 1.57 |
| CD68      | 4.87E-02 | 1.57 |
| CHPF2     | 1.67E-03 | 1.57 |
| SMARCE1   | 2.25E-02 | 1.57 |
| LRRC45    | 2.14E-03 | 1.57 |
| SASS6     | 3.13E-02 | 1.57 |
| PSMD2     | 1.37E-02 | 1.57 |
| AIMP2     | 3.06E-02 | 1.57 |
| EIF4H     | 4.24E-02 | 1.57 |
| FHOD1     | 6.22E-03 | 1.56 |
| RBX1      | 4.45E-02 | 1.56 |
| NSG1      | 8.97E-03 | 1.56 |
| CCDC23    | 8.58E-04 | 1.56 |
| RCC2      | 1.32E-02 | 1.56 |
| ANGEL1    | 2.42E-02 | 1.56 |
| LRRC59    | 2.71E-02 | 1.56 |
| DOK4      | 7.06E-03 | 1.56 |
| POLR2H    | 2.28E-02 | 1.56 |
| TMEM65    | 2.69E-03 | 1.56 |
| WDR76     | 4.40E-02 | 1.56 |
| ARHGAP22  | 4.28E-02 | 1.56 |
| LTBR      | 8.22E-03 | 1.56 |
| SLC7A7    | 2.33E-02 | 1.55 |
| C19orf66  | 1.73E-02 | 1.55 |
| DUT       | 1.32E-02 | 1.55 |
| PKP1      | 3.84E-02 | 1.55 |
| PPIH      | 1.03E-02 | 1.55 |
| PANK2     | 1.59E-04 | 1.55 |
| SRI       | 3.40E-03 | 1.55 |
| TPI1      | 3.50E-02 | 1.55 |
| IMPA1     | 1.38E-02 | 1.55 |
| UNC13D    | 6.23E-03 | 1.55 |
| RNF141    | 2.29E-02 | 1.55 |
| IL17RA    | 1.86E-03 | 1.55 |



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| CTTN      | 4.23E-02 | 1.55 |
| FHL3      | 1.72E-02 | 1.54 |
| NCBP2     | 1.04E-02 | 1.54 |
| MTHFD1L   | 1.12E-02 | 1.54 |
| BAX       | 2.27E-02 | 1.54 |
| RHOG      | 2.99E-04 | 1.54 |
| SELR1     | 1.16E-02 | 1.54 |
| GRN       | 2.00E-03 | 1.54 |
| ADAT1     | 4.46E-02 | 1.54 |
| HEATR3    | 1.07E-02 | 1.54 |
| SP110     | 1.86E-02 | 1.54 |
| FAM84A    | 3.19E-02 | 1.54 |
| PES1      | 1.74E-02 | 1.54 |
| ME2       | 8.52E-03 | 1.54 |
| DCAF13    | 2.56E-03 | 1.53 |
| TBCB      | 6.84E-04 | 1.53 |
| DDX39A    | 4.59E-02 | 1.53 |
| TTC13     | 2.42E-02 | 1.53 |
| TRIM21    | 3.14E-02 | 1.53 |
| ASF1B     | 1.97E-02 | 1.53 |
| NAA20     | 2.78E-03 | 1.53 |
| MTPN      | 4.33E-02 | 1.53 |
| PPP2R5C   | 1.25E-03 | 1.53 |
| SCNM1     | 4.09E-04 | 1.53 |
| TMEM87B   | 5.21E-03 | 1.52 |
| KDELR2    | 1.11E-02 | 1.52 |
| CCDC167   | 3.92E-03 | 1.52 |
| FASTKD3   | 1.97E-02 | 1.52 |
| NME1      | 4.73E-02 | 1.52 |
| IFRD2     | 2.53E-02 | 1.52 |
| CHD1L     | 3.11E-02 | 1.52 |
| SMYD2     | 5.65E-03 | 1.52 |
| PSPH      | 2.63E-02 | 1.52 |
| NEDD1     | 2.90E-02 | 1.52 |
| STAT2     | 3.55E-03 | 1.52 |
| SLC25A24  | 1.26E-02 | 1.52 |
| HTATIP2   | 1.64E-02 | 1.52 |
| TRIM44    | 3.74E-02 | 1.52 |
| PPIB      | 2.17E-03 | 1.51 |
| NT5C      | 9.02E-03 | 1.51 |
| C1QB      | 2.79E-02 | 1.51 |
| PRSS27    | 3.03E-02 | 1.51 |
| KIAA1430  | 5.05E-03 | 1.51 |
| NCDN      | 6.58E-03 | 1.51 |
| ZC3H8     | 1.11E-02 | 1.51 |
| DERA      | 1.65E-02 | 1.51 |
| NME2      | 4.74E-02 | 1.51 |
| CCDC88B   | 1.99E-02 | 1.51 |
| TMEM209   | 2.36E-03 | 1.51 |
| B4GALT2   | 9.81E-03 | 1.51 |
| ZHHHC12   | 4.19E-02 | 1.51 |
| GTF2H3    | 7.25E-03 | 1.51 |
| PIAS3     | 1.44E-02 | 1.51 |
| ARPC2     | 1.43E-02 | 1.50 |
| BRMS1     | 2.61E-03 | 1.50 |
| DRG1      | 2.38E-02 | 1.50 |
| PCED1A    | 2.10E-02 | 1.50 |
| TMEM54    | 2.55E-02 | 1.50 |
| PIGB      | 6.93E-03 | 1.50 |
| ATG2A     | 4.65E-03 | 0.67 |
| QPCT      | 3.69E-02 | 0.67 |
| SPTSSA    | 2.41E-02 | 0.66 |
| JAM2      | 4.95E-02 | 0.66 |
| INPP5A    | 2.04E-03 | 0.66 |
| RUSC2     | 1.18E-02 | 0.66 |
| PHF1      | 1.21E-02 | 0.66 |
| SCAF4     | 4.41E-02 | 0.66 |
| CDC37L1   | 1.14E-02 | 0.66 |
| KCTD12    | 2.19E-02 | 0.66 |
| IL22RA1   | 3.69E-02 | 0.66 |
| RUFY3     | 3.88E-02 | 0.66 |
| CD46      | 6.94E-03 | 0.66 |
| ZFAND5    | 4.83E-02 | 0.66 |
| DDX5      | 2.21E-02 | 0.66 |
| RTN3      | 2.73E-02 | 0.66 |
| CRB3      | 5.25E-03 | 0.66 |
| MRPL49    | 2.38E-02 | 0.66 |
| NINJ1     | 1.48E-02 | 0.66 |
| GTPBP1    | 8.50E-03 | 0.66 |
| AMT       | 1.87E-02 | 0.66 |
| RP11-162P | 3.36E-02 | 0.66 |



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| FOSL2     | 2.03E-02 | 0.66 |
| CADPS2    | 3.40E-02 | 0.66 |
| SOX13     | 9.65E-03 | 0.66 |
| PHYH      | 2.15E-03 | 0.66 |
| CYB561D1  | 4.71E-02 | 0.66 |
| IRX2      | 9.18E-03 | 0.66 |
| TAF6L     | 6.89E-04 | 0.66 |
| ALDH2     | 2.18E-02 | 0.65 |
| RHOT1     | 6.92E-03 | 0.65 |
| ACLY      | 1.74E-02 | 0.65 |
| GRAMD3    | 1.39E-02 | 0.65 |
| RPS6      | 1.25E-02 | 0.65 |
| HMBBOX1   | 7.32E-03 | 0.65 |
| MMAA      | 4.11E-03 | 0.65 |
| KRT23     | 4.79E-02 | 0.65 |
| CPE       | 2.92E-02 | 0.65 |
| COQ9      | 1.56E-03 | 0.65 |
| ANKH      | 2.51E-03 | 0.65 |
| TRIP11    | 2.00E-02 | 0.65 |
| ANK3      | 3.56E-02 | 0.65 |
| LMNA      | 1.01E-03 | 0.65 |
| NEO1      | 4.43E-02 | 0.65 |
| MFSD12    | 4.20E-02 | 0.65 |
| CDKN1B    | 5.28E-03 | 0.65 |
| CDAN1     | 1.50E-02 | 0.65 |
| N4BP2L1   | 1.66E-02 | 0.65 |
| TST       | 3.23E-02 | 0.65 |
| ARNTL     | 3.50E-02 | 0.65 |
| PCDH1     | 3.74E-02 | 0.65 |
| CTSF      | 2.54E-02 | 0.65 |
| SCNN1A    | 3.87E-02 | 0.65 |
| MLLT4     | 3.81E-02 | 0.65 |
| ERBB3     | 3.98E-02 | 0.65 |
| TANC1     | 1.69E-02 | 0.65 |
| ACAA1     | 2.96E-02 | 0.65 |
| RAPGEF5   | 3.45E-02 | 0.65 |
| SLC27A1   | 3.22E-04 | 0.65 |
| AMOTL2    | 3.42E-02 | 0.64 |
| UBE2B     | 1.05E-02 | 0.64 |
| AUH       | 1.20E-02 | 0.64 |
| MRPS25    | 1.82E-02 | 0.64 |
| SIDT2     | 6.56E-03 | 0.64 |
| GRB7      | 4.52E-02 | 0.64 |
| SNX30     | 4.90E-02 | 0.64 |
| HSD11B2   | 3.35E-02 | 0.64 |
| CALCOCO1  | 1.40E-02 | 0.64 |
| PEX19     | 3.06E-03 | 0.64 |
| PCCA      | 1.18E-03 | 0.64 |
| PPAP2A    | 4.64E-02 | 0.64 |
| ARHGEF10L | 1.60E-02 | 0.64 |
| MIDN      | 1.04E-02 | 0.64 |
| HERPUD1   | 8.69E-03 | 0.64 |
| PNPLA2    | 3.33E-02 | 0.64 |
| KIF13B    | 2.92E-02 | 0.64 |
| C2CD3     | 1.34E-02 | 0.64 |
| FGL2      | 4.45E-02 | 0.64 |
| DAAM1     | 4.34E-02 | 0.64 |
| MKL2      | 3.77E-02 | 0.63 |
| PEX3      | 5.52E-03 | 0.63 |
| STK39     | 7.16E-03 | 0.63 |
| FAM82A2   | 5.90E-03 | 0.63 |
| CAPN3     | 1.67E-02 | 0.63 |
| STXBP6    | 4.98E-02 | 0.63 |
| KDSR      | 2.31E-03 | 0.63 |
| RERE      | 5.90E-03 | 0.63 |
| H6PD      | 2.98E-03 | 0.63 |
| EEPD1     | 2.89E-02 | 0.63 |
| EPHX1     | 1.75E-03 | 0.63 |
| PLK3      | 2.71E-02 | 0.63 |
| CAT       | 2.65E-04 | 0.63 |
| SYTL1     | 5.94E-03 | 0.63 |
| NDEL1     | 4.45E-02 | 0.63 |
| NEDD9     | 2.78E-02 | 0.63 |
| ACYP2     | 1.77E-02 | 0.63 |
| DNAJA4    | 3.20E-02 | 0.63 |
| MAP1LC3B  | 1.19E-02 | 0.63 |
| PLEKHA4   | 2.19E-03 | 0.63 |
| C2orf55   | 4.36E-02 | 0.63 |
| SNX25     | 1.36E-03 | 0.62 |
| BIRC3     | 3.67E-02 | 0.62 |
| THRA      | 6.74E-03 | 0.62 |



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| GCFC1      | 3.94E-02 | 0.62 |
| ITPKB      | 6.05E-03 | 0.62 |
| SCNN1B     | 3.88E-02 | 0.62 |
| JMJD1C     | 2.19E-03 | 0.62 |
| GNE        | 3.04E-02 | 0.62 |
| ERBB2      | 2.02E-04 | 0.62 |
| ECI1       | 3.29E-02 | 0.62 |
| UNCSB      | 3.16E-02 | 0.62 |
| PCK2       | 2.65E-02 | 0.62 |
| LPCAT3     | 4.42E-02 | 0.62 |
| RALGAPA2   | 1.54E-02 | 0.62 |
| SCARB1     | 4.90E-03 | 0.62 |
| ABL1       | 1.83E-02 | 0.62 |
| MANSC1     | 1.43E-02 | 0.62 |
| TTC18      | 1.78E-02 | 0.62 |
| ANKHD1     | 3.70E-04 | 0.62 |
| PDE2A      | 1.42E-02 | 0.62 |
| PKP2       | 3.75E-02 | 0.62 |
| CENPV      | 5.67E-03 | 0.62 |
| MAP2K3     | 4.04E-02 | 0.61 |
| NAF1       | 4.30E-02 | 0.61 |
| MYL9       | 1.57E-02 | 0.61 |
| PIGV       | 2.54E-02 | 0.61 |
| EHBP1      | 1.97E-02 | 0.61 |
| CRELD1     | 3.08E-03 | 0.61 |
| GPHN       | 5.89E-03 | 0.61 |
| KANK1      | 1.95E-02 | 0.61 |
| ARSG       | 1.15E-02 | 0.61 |
| ADCY9      | 1.23E-02 | 0.61 |
| HIBADH     | 2.75E-03 | 0.61 |
| PTPRU      | 1.47E-02 | 0.61 |
| CKB        | 1.86E-02 | 0.61 |
| PRKCE      | 3.07E-02 | 0.61 |
| CXXC5      | 8.87E-03 | 0.61 |
| CPQ        | 1.90E-02 | 0.61 |
| IL17RE     | 1.51E-02 | 0.61 |
| NFIC       | 1.89E-02 | 0.61 |
| ST3GAL5    | 3.40E-02 | 0.61 |
| LRRFIP2    | 3.53E-03 | 0.61 |
| FAM160A1   | 2.38E-02 | 0.61 |
| PLA2G2F    | 4.88E-02 | 0.61 |
| TACSTD2    | 1.66E-03 | 0.61 |
| KALRN      | 2.92E-02 | 0.61 |
| SPARCL1    | 3.98E-02 | 0.61 |
| ANKRD36    | 8.30E-03 | 0.61 |
| CAMKMT     | 7.12E-03 | 0.61 |
| MEF2D      | 1.76E-02 | 0.61 |
| CMTM4      | 2.07E-02 | 0.61 |
| RP11-286N  | 4.58E-02 | 0.61 |
| PCM1       | 2.28E-02 | 0.61 |
| C14orf43   | 8.40E-03 | 0.61 |
| ATP2C2     | 3.04E-02 | 0.61 |
| SH3YL1     | 7.71E-03 | 0.61 |
| SHMT1      | 2.25E-02 | 0.60 |
| SESTD1     | 1.02E-02 | 0.60 |
| CBFA2T2    | 1.36E-02 | 0.60 |
| MAMDC4     | 8.97E-03 | 0.60 |
| EFNA3      | 2.27E-03 | 0.60 |
| CSF1       | 9.13E-03 | 0.60 |
| MEIS2      | 6.52E-03 | 0.60 |
| FAM131A    | 2.19E-02 | 0.60 |
| FAM59A     | 1.37E-02 | 0.60 |
| IL11RA     | 1.01E-02 | 0.60 |
| SLC37A1    | 5.08E-03 | 0.60 |
| IMMP2L     | 2.31E-03 | 0.60 |
| ZNF430     | 3.70E-02 | 0.60 |
| ZBTB44     | 7.05E-03 | 0.60 |
| NFAT5      | 2.00E-02 | 0.60 |
| SCEL       | 3.68E-02 | 0.60 |
| PRMT10     | 9.28E-03 | 0.60 |
| TOB2       | 3.98E-02 | 0.60 |
| PRSS8      | 1.49E-02 | 0.60 |
| RASAL1     | 2.18E-02 | 0.60 |
| IER2       | 8.21E-04 | 0.60 |
| ANO10      | 2.06E-02 | 0.60 |
| LGR4       | 3.18E-02 | 0.60 |
| GALNT11    | 1.40E-04 | 0.60 |
| RILP       | 1.10E-02 | 0.59 |
| SLC4A11    | 1.39E-02 | 0.59 |
| TIPARP     | 3.10E-02 | 0.59 |
| CTB-96E2.3 | 2.07E-02 | 0.59 |



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| PDCD4     | 1.24E-04 | 0.59 |
| ATF7IP2   | 3.24E-02 | 0.59 |
| PLEKHA7   | 7.83E-03 | 0.59 |
| KAZALD1   | 2.96E-02 | 0.59 |
| NOS3      | 2.65E-02 | 0.59 |
| DNAJB14   | 2.88E-02 | 0.59 |
| ALDH5A1   | 4.57E-02 | 0.59 |
| TEX264    | 2.97E-03 | 0.59 |
| PARVA     | 1.71E-02 | 0.59 |
| C3orf52   | 1.48E-02 | 0.59 |
| HHAT      | 3.48E-02 | 0.59 |
| TMEM45A   | 2.14E-02 | 0.59 |
| PPP1R15B  | 1.98E-03 | 0.59 |
| C17orf108 | 4.12E-02 | 0.59 |
| SNRPN     | 3.09E-02 | 0.59 |
| KLHDC8B   | 1.75E-02 | 0.59 |
| CNIH3     | 4.76E-02 | 0.59 |
| CCNG2     | 1.67E-02 | 0.59 |
| ELOVL1    | 3.08E-02 | 0.59 |
| RCL1      | 9.51E-03 | 0.59 |
| MYLIP     | 1.41E-05 | 0.59 |
| RHOJ      | 1.74E-02 | 0.59 |
| TESK2     | 9.10E-03 | 0.59 |
| C1orf210  | 3.83E-02 | 0.59 |
| PLA2G7    | 2.32E-02 | 0.58 |
| FEM1B     | 4.16E-02 | 0.58 |
| SAMD8     | 5.24E-03 | 0.58 |
| ZNF107    | 3.04E-02 | 0.58 |
| ITGA7     | 1.93E-02 | 0.58 |
| MPDZ      | 2.19E-02 | 0.58 |
| CHP1      | 2.49E-03 | 0.58 |
| PPTC7     | 2.89E-02 | 0.58 |
| 41336     | 1.82E-02 | 0.58 |
| HDC       | 4.45E-02 | 0.58 |
| MAT2A     | 3.10E-02 | 0.58 |
| MARCO     | 4.89E-02 | 0.58 |
| GSTM2     | 1.65E-02 | 0.58 |
| SLC25A20  | 2.04E-02 | 0.58 |
| C2CD2     | 2.25E-02 | 0.58 |
| ZCCHC2    | 5.82E-03 | 0.58 |
| NR1H3     | 7.03E-03 | 0.58 |
| SOX7      | 7.58E-03 | 0.58 |
| SLC31A1   | 8.89E-03 | 0.58 |
| ECH1      | 1.75E-02 | 0.58 |
| HADH      | 2.62E-02 | 0.58 |
| DBT       | 5.73E-04 | 0.58 |
| ALAS1     | 1.92E-02 | 0.58 |
| ADHFE1    | 2.14E-02 | 0.58 |
| TGM5      | 2.96E-02 | 0.58 |
| LGI4      | 1.06E-02 | 0.58 |
| SYTL3     | 2.28E-02 | 0.58 |
| GALT      | 4.01E-03 | 0.57 |
| CCDC3     | 3.25E-02 | 0.57 |
| ARHGAP24  | 4.39E-02 | 0.57 |
| ITPKC     | 6.25E-03 | 0.57 |
| PYROXD2   | 4.38E-02 | 0.57 |
| ENPP1     | 4.32E-02 | 0.57 |
| PGM1      | 2.48E-03 | 0.57 |
| HDAC5     | 6.43E-03 | 0.57 |
| CMBL      | 3.35E-02 | 0.57 |
| USP2      | 4.05E-02 | 0.57 |
| PCCB      | 1.46E-02 | 0.57 |
| ANGPTL4   | 3.45E-02 | 0.57 |
| SLC10A6   | 2.13E-02 | 0.57 |
| SNCG      | 5.66E-03 | 0.57 |
| RNF125    | 4.31E-02 | 0.57 |
| AKAP1     | 5.23E-05 | 0.57 |
| NEIL1     | 2.12E-03 | 0.57 |
| GAMT      | 7.06E-03 | 0.57 |
| CCDC146   | 4.53E-03 | 0.57 |
| FAM13A    | 2.68E-02 | 0.57 |
| ZMIZ1     | 4.44E-02 | 0.57 |
| DHRS3     | 4.13E-04 | 0.57 |
| EPHB6     | 1.88E-02 | 0.57 |
| ERLIN2    | 2.46E-02 | 0.57 |
| HES1      | 1.16E-02 | 0.57 |
| KANK2     | 5.27E-03 | 0.57 |
| WEE1      | 1.13E-02 | 0.57 |
| SULT1E1   | 4.02E-02 | 0.57 |
| IL17RC    | 3.13E-04 | 0.57 |
| ANKRD22   | 3.46E-02 | 0.56 |



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| LPAR1     | 2.00E-02 | 0.56 |
| DUSP16    | 2.08E-03 | 0.56 |
| RAB11FIP4 | 1.78E-02 | 0.56 |
| PTP4A1    | 3.85E-03 | 0.56 |
| SLC12A7   | 2.32E-03 | 0.56 |
| VDR       | 1.02E-03 | 0.56 |
| SCAP      | 4.99E-03 | 0.56 |
| SYNGR1    | 8.37E-03 | 0.56 |
| EPPK1     | 5.19E-03 | 0.56 |
| ASPH      | 5.54E-03 | 0.56 |
| PLEKHG1   | 1.52E-02 | 0.56 |
| PMAIP1    | 2.04E-02 | 0.56 |
| OVOL1     | 1.93E-02 | 0.56 |
| GLS2      | 1.08E-02 | 0.56 |
| NFKBIA    | 3.82E-02 | 0.56 |
| ETFDH     | 3.95E-03 | 0.56 |
| FAHD2A    | 1.14E-02 | 0.56 |
| TGIF1     | 1.02E-02 | 0.56 |
| USP36     | 3.50E-04 | 0.55 |
| CCDC171   | 3.25E-02 | 0.55 |
| USP54     | 2.81E-02 | 0.55 |
| EMP2      | 2.81E-02 | 0.55 |
| PFKFB3    | 4.80E-02 | 0.55 |
| C9orf72   | 1.32E-02 | 0.55 |
| KBTBD3    | 7.02E-04 | 0.55 |
| TTC38     | 2.38E-02 | 0.55 |
| PLSCR4    | 5.70E-03 | 0.55 |
| RCAN2     | 4.13E-02 | 0.55 |
| PC        | 4.34E-02 | 0.55 |
| NFIA      | 1.31E-02 | 0.55 |
| WISP2     | 1.59E-02 | 0.55 |
| LETMD1    | 6.69E-04 | 0.55 |
| TLE1      | 5.46E-03 | 0.55 |
| KIAA1456  | 3.98E-02 | 0.55 |
| SMARCD3   | 1.06E-02 | 0.55 |
| KLF9      | 1.40E-02 | 0.55 |
| DCXR      | 2.16E-02 | 0.55 |
| FAM73B    | 9.50E-04 | 0.55 |
| PTCH1     | 1.99E-02 | 0.55 |
| GOT1      | 6.38E-03 | 0.55 |
| ABCC3     | 6.53E-03 | 0.55 |
| CACNB1    | 1.43E-02 | 0.55 |
| CATSPERG  | 4.82E-02 | 0.55 |
| CLN8      | 6.62E-03 | 0.55 |
| TCEA3     | 6.71E-03 | 0.55 |
| EXOC8     | 3.60E-02 | 0.55 |
| ATP2A3    | 2.29E-02 | 0.55 |
| NDE1      | 4.21E-03 | 0.54 |
| ICA1      | 4.75E-03 | 0.54 |
| TRIB1     | 1.19E-02 | 0.54 |
| ACSL3     | 1.33E-02 | 0.54 |
| NMNAT3    | 2.89E-02 | 0.54 |
| MITF      | 4.80E-02 | 0.54 |
| ALCAM     | 2.10E-02 | 0.54 |
| GOLGA4    | 6.53E-03 | 0.54 |
| SNED1     | 1.31E-02 | 0.54 |
| FRY       | 3.87E-03 | 0.54 |
| MEGF9     | 6.46E-03 | 0.54 |
| JUN       | 3.31E-02 | 0.54 |
| DENND4C   | 1.83E-03 | 0.54 |
| LRIG1     | 4.59E-04 | 0.54 |
| C21orf33  | 9.92E-03 | 0.54 |
| CLDN4     | 5.10E-03 | 0.54 |
| PLCH2     | 1.33E-03 | 0.54 |
| BDH1      | 1.15E-02 | 0.54 |
| PEBP1     | 1.80E-03 | 0.54 |
| AGPAT9    | 1.36E-02 | 0.54 |
| CPD       | 7.76E-03 | 0.54 |
| GLUL      | 1.16E-02 | 0.54 |
| CRY2      | 7.31E-03 | 0.54 |
| GLI2      | 1.97E-02 | 0.54 |
| STK40     | 1.75E-03 | 0.54 |
| NCAM1     | 1.26E-02 | 0.54 |
| GULP1     | 1.11E-04 | 0.53 |
| BOC       | 1.38E-02 | 0.53 |
| CFL2      | 2.21E-03 | 0.53 |
| LDB2      | 1.14E-02 | 0.53 |
| FGFR2     | 2.58E-02 | 0.53 |
| PRICKLE2  | 1.59E-02 | 0.53 |
| SREBF1    | 3.22E-03 | 0.53 |
| RNF103    | 1.21E-02 | 0.53 |



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| PID1       | 1.41E-02 | 0.53 |
| BRP44      | 9.90E-03 | 0.53 |
| FAM190A    | 1.38E-02 | 0.53 |
| FGFRL1     | 8.23E-03 | 0.53 |
| NFATC1     | 1.05E-02 | 0.53 |
| ZFP36L1    | 6.70E-03 | 0.53 |
| HMGCL      | 8.11E-03 | 0.53 |
| PRUNE2     | 4.03E-02 | 0.53 |
| TRIM2      | 1.63E-02 | 0.53 |
| PDE1B      | 1.54E-02 | 0.53 |
| PPM1K      | 4.98E-02 | 0.53 |
| CLYBL      | 1.71E-02 | 0.53 |
| PDE4D      | 3.23E-02 | 0.53 |
| SLC5A1     | 2.50E-03 | 0.53 |
| IL1R2      | 3.18E-02 | 0.53 |
| TACC2      | 4.47E-03 | 0.53 |
| MTERFD3    | 1.29E-03 | 0.53 |
| ALDH9A1    | 2.72E-04 | 0.52 |
| NTAN1      | 1.90E-02 | 0.52 |
| NUDT13     | 3.37E-03 | 0.52 |
| SPG20      | 7.41E-05 | 0.52 |
| C10orf10   | 2.36E-02 | 0.52 |
| ACSL5      | 3.31E-02 | 0.52 |
| MYLK       | 2.37E-02 | 0.52 |
| LMO1       | 1.53E-02 | 0.52 |
| SOD3       | 2.36E-02 | 0.52 |
| SCARA3     | 7.80E-03 | 0.52 |
| GPD1L      | 1.57E-02 | 0.52 |
| RALGPS1    | 4.59E-03 | 0.52 |
| ITIH5      | 5.77E-03 | 0.52 |
| DOPEY2     | 3.27E-03 | 0.52 |
| PTPN14     | 4.51E-03 | 0.52 |
| RBP5       | 4.17E-02 | 0.52 |
| LONRF1     | 3.75E-02 | 0.52 |
| ACAT1      | 5.53E-03 | 0.52 |
| COBL       | 4.21E-04 | 0.52 |
| TEC        | 2.57E-02 | 0.52 |
| CBX4       | 9.89E-03 | 0.52 |
| ZSCAN18    | 9.39E-03 | 0.52 |
| ARHGAP10   | 4.70E-04 | 0.52 |
| ABHD6      | 3.55E-02 | 0.52 |
| PIM3       | 4.59E-03 | 0.52 |
| ITPR1      | 1.76E-02 | 0.52 |
| PALMD      | 1.06E-03 | 0.52 |
| TM7SF2     | 1.28E-02 | 0.52 |
| CCL28      | 1.14E-02 | 0.52 |
| DUSP4      | 5.18E-03 | 0.51 |
| ADAP1      | 1.56E-02 | 0.51 |
| ATP6V1C2   | 6.62E-03 | 0.51 |
| ESPN       | 8.79E-03 | 0.51 |
| ZFP36L2    | 4.06E-04 | 0.51 |
| IL20RA     | 1.00E-03 | 0.51 |
| SMARCA2    | 1.62E-04 | 0.51 |
| TACC1      | 1.95E-02 | 0.51 |
| CD207      | 1.82E-02 | 0.51 |
| ASRGL1     | 4.63E-02 | 0.51 |
| AP001055.7 | 2.16E-02 | 0.51 |
| ME3        | 1.35E-03 | 0.51 |
| SUSD4      | 8.72E-03 | 0.51 |
| ZNF295     | 1.02E-02 | 0.51 |
| TBC1D24    | 4.27E-02 | 0.51 |
| ZBTB20     | 1.90E-02 | 0.51 |
| ARHGAP40   | 4.86E-03 | 0.51 |
| CREM       | 4.21E-02 | 0.51 |
| RAB15      | 1.61E-02 | 0.51 |
| FBLN5      | 4.75E-03 | 0.51 |
| RFX3       | 1.90E-03 | 0.51 |
| CNKSR3     | 4.74E-03 | 0.51 |
| GCH1       | 9.41E-03 | 0.51 |
| CTSL2      | 2.29E-02 | 0.51 |
| PPP1R32    | 1.44E-02 | 0.51 |
| ADAMTS17   | 5.39E-03 | 0.51 |
| BHLHE40    | 1.24E-02 | 0.51 |
| ZNF577     | 5.82E-05 | 0.51 |
| NFIX       | 4.49E-03 | 0.51 |
| INSR       | 1.49E-03 | 0.51 |
| PPP1R12B   | 1.63E-02 | 0.50 |
| FNDC4      | 1.38E-02 | 0.50 |
| SUOX       | 2.45E-02 | 0.50 |
| PDGFRL     | 1.58E-02 | 0.50 |
| CERS4      | 7.26E-03 | 0.50 |



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| CBX7      | 9.97E-03 | 0.50 |
| GPR183    | 8.90E-03 | 0.50 |
| AVP11     | 9.10E-03 | 0.50 |
| MACROD1   | 6.81E-03 | 0.50 |
| ATP1B1    | 3.88E-03 | 0.50 |
| ACSF2     | 8.32E-04 | 0.50 |
| VASN      | 9.93E-03 | 0.50 |
| AACS      | 2.85E-04 | 0.50 |
| DTX1      | 1.76E-02 | 0.50 |
| CXCL12    | 4.02E-03 | 0.50 |
| OSR2      | 3.07E-02 | 0.50 |
| PRDX2     | 4.61E-03 | 0.50 |
| FDFT1     | 2.04E-03 | 0.50 |
| TSC22D1   | 2.77E-02 | 0.50 |
| CHPT1     | 9.46E-04 | 0.50 |
| SECISBP2L | 2.14E-03 | 0.49 |
| GJB4      | 3.61E-02 | 0.49 |
| PXDC1     | 2.47E-02 | 0.49 |
| MCCC1     | 3.51E-03 | 0.49 |
| MOCS1     | 2.95E-03 | 0.49 |
| USP53     | 1.31E-03 | 0.49 |
| SDC4      | 1.37E-03 | 0.49 |
| KIAA0040  | 3.84E-02 | 0.49 |
| CCDC64    | 2.38E-04 | 0.49 |
| PLAC9     | 5.04E-03 | 0.49 |
| AXL       | 5.16E-03 | 0.49 |
| DDAH1     | 1.28E-02 | 0.49 |
| ARNT2     | 3.50E-03 | 0.49 |
| CDC42EP4  | 1.12E-03 | 0.49 |
| PHYHD1    | 3.78E-03 | 0.49 |
| NTN4      | 1.36E-04 | 0.49 |
| ECHDC2    | 1.90E-04 | 0.49 |
| CLDN1     | 7.48E-04 | 0.48 |
| PGRMC2    | 2.40E-04 | 0.48 |
| BCHE      | 2.30E-02 | 0.48 |
| JUND      | 2.56E-03 | 0.48 |
| CHMP1B    | 6.20E-04 | 0.48 |
| SIK2      | 4.24E-04 | 0.48 |
| FAM149A   | 9.63E-03 | 0.48 |
| TCP11L2   | 1.72E-02 | 0.48 |
| NOTCH2    | 8.79E-03 | 0.48 |
| OSGIN2    | 4.47E-05 | 0.48 |
| PRKAR2B   | 2.58E-02 | 0.48 |
| NOSTRIN   | 1.69E-02 | 0.48 |
| SLC25A23  | 2.36E-03 | 0.48 |
| C16orf45  | 2.21E-03 | 0.48 |
| TTC39B    | 1.02E-02 | 0.48 |
| SEMA6A    | 9.73E-04 | 0.47 |
| PDE9A     | 1.07E-02 | 0.47 |
| NXPH4     | 2.56E-02 | 0.47 |
| CDKN1A    | 2.08E-02 | 0.47 |
| BRP44L    | 2.29E-04 | 0.47 |
| KIT       | 4.34E-02 | 0.47 |
| PI16      | 2.10E-02 | 0.47 |
| TM4SF1    | 1.48E-02 | 0.47 |
| CDON      | 2.73E-02 | 0.47 |
| SEMA7A    | 6.04E-04 | 0.47 |
| EPHA2     | 4.38E-02 | 0.47 |
| MECR      | 1.97E-02 | 0.47 |
| FGFR1     | 5.64E-03 | 0.46 |
| TPM1      | 4.74E-03 | 0.46 |
| ARHGEF26  | 4.67E-03 | 0.46 |
| PDZD2     | 1.49E-03 | 0.46 |
| DLL1      | 1.18E-02 | 0.46 |
| PPARGC1B  | 1.78E-02 | 0.46 |
| MFAP3L    | 4.10E-02 | 0.46 |
| NOV       | 1.07E-02 | 0.46 |
| DLG2      | 1.24E-02 | 0.46 |
| SPTBN1    | 2.92E-05 | 0.46 |
| BCL6      | 5.86E-06 | 0.46 |
| TRMT44    | 2.17E-03 | 0.46 |
| DHRS11    | 5.23E-04 | 0.46 |
| KLK1      | 1.06E-03 | 0.46 |
| IVD       | 1.78E-03 | 0.46 |
| DNASE1L2  | 4.44E-02 | 0.46 |
| ENTPD2    | 1.48E-02 | 0.46 |
| ZNF273    | 3.35E-03 | 0.46 |
| RDH11     | 2.25E-02 | 0.45 |
| FHIT      | 2.58E-02 | 0.45 |
| ZNF675    | 1.09E-02 | 0.45 |
| PPARA     | 8.40E-03 | 0.45 |



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| C19orf71  | 6.38E-03 | 0.45 |
| MAP3K8    | 5.61E-04 | 0.45 |
| SGPP2     | 3.27E-03 | 0.45 |
| TMEM99    | 2.49E-02 | 0.45 |
| C17orf28  | 1.87E-02 | 0.45 |
| ZNF91     | 3.34E-02 | 0.45 |
| ACADVL    | 1.27E-05 | 0.45 |
| IDH1      | 1.07E-02 | 0.45 |
| MLPH      | 2.46E-04 | 0.45 |
| LRTOMT    | 9.60E-03 | 0.45 |
| ENDOU     | 7.58E-03 | 0.45 |
| PCP4L1    | 1.30E-02 | 0.44 |
| RETSAT    | 3.87E-04 | 0.44 |
| CH25H     | 3.38E-02 | 0.44 |
| FRZB      | 9.19E-04 | 0.44 |
| MSRB1     | 1.12E-02 | 0.44 |
| BNC2      | 1.19E-02 | 0.44 |
| RDH5      | 3.28E-02 | 0.44 |
| GCNT2     | 4.41E-02 | 0.44 |
| MVD       | 1.09E-02 | 0.44 |
| CABLES1   | 1.61E-02 | 0.44 |
| SLIT3     | 1.95E-02 | 0.44 |
| EDNRB     | 4.11E-03 | 0.44 |
| CTC-435M1 | 1.14E-02 | 0.44 |
| F10       | 1.58E-03 | 0.44 |
| TNFAIP3   | 3.48E-03 | 0.44 |
| BCL7A     | 3.17E-03 | 0.44 |
| PIK3C2G   | 1.29E-02 | 0.44 |
| SLC4A5    | 3.88E-02 | 0.44 |
| TFF3      | 1.47E-02 | 0.44 |
| ERV3-1    | 1.73E-02 | 0.44 |
| MFAP4     | 1.66E-03 | 0.44 |
| PDE4B     | 1.29E-02 | 0.44 |
| ABHD12B   | 2.60E-02 | 0.44 |
| POU2F3    | 1.13E-04 | 0.43 |
| PLEKHH1   | 2.64E-02 | 0.43 |
| LPL       | 3.18E-02 | 0.43 |
| MATN2     | 5.37E-04 | 0.43 |
| MMRN1     | 9.99E-04 | 0.43 |
| C5AR1     | 1.14E-02 | 0.43 |
| DARC      | 1.99E-02 | 0.43 |
| L3MBTL4   | 8.99E-04 | 0.43 |
| NDRG2     | 3.20E-06 | 0.43 |
| RNF152    | 2.74E-03 | 0.43 |
| SLC16A7   | 3.96E-03 | 0.43 |
| PHLPP1    | 3.69E-03 | 0.43 |
| RNASE4    | 9.97E-04 | 0.43 |
| IQGAP2    | 8.51E-05 | 0.43 |
| PODN      | 3.86E-03 | 0.43 |
| TLE2      | 2.12E-03 | 0.43 |
| LIFR      | 1.10E-02 | 0.43 |
| ACAD8     | 2.61E-03 | 0.42 |
| MERTK     | 1.27E-02 | 0.42 |
| LRP4      | 1.01E-02 | 0.42 |
| GATM      | 4.85E-04 | 0.42 |
| FLT1      | 8.03E-03 | 0.42 |
| RGS22     | 2.45E-02 | 0.42 |
| HLCS      | 4.96E-03 | 0.42 |
| MYH14     | 7.34E-04 | 0.42 |
| CASP9     | 4.15E-03 | 0.42 |
| SYNE4     | 5.48E-03 | 0.42 |
| DPEP1     | 3.57E-02 | 0.42 |
| RPH3AL    | 2.75E-03 | 0.42 |
| NGFR      | 8.74E-03 | 0.42 |
| CORIN     | 1.98E-02 | 0.42 |
| RPSAP58   | 2.79E-02 | 0.42 |
| RTN4      | 9.63E-04 | 0.42 |
| SH3BGR2   | 7.69E-04 | 0.42 |
| PNPLA7    | 2.94E-03 | 0.42 |
| DENND2A   | 2.05E-02 | 0.42 |
| GABARAPL1 | 1.20E-03 | 0.42 |
| ANKS1B    | 4.75E-03 | 0.42 |
| FAM167A   | 4.20E-04 | 0.42 |
| SC5DL     | 2.17E-02 | 0.42 |
| PNPLA3    | 8.04E-03 | 0.42 |
| CREG1     | 1.48E-03 | 0.42 |
| MUC1      | 4.36E-02 | 0.41 |
| PTGFR     | 4.05E-02 | 0.41 |
| CITED2    | 8.13E-05 | 0.41 |
| ANG       | 1.79E-02 | 0.41 |
| LDLR      | 4.88E-03 | 0.41 |



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| C10orf57   | 3.16E-04 | 0.41 |
| DPT        | 1.68E-04 | 0.41 |
| ABCA3      | 3.06E-03 | 0.41 |
| FAM3D      | 7.56E-03 | 0.41 |
| ICOSLG     | 6.18E-04 | 0.41 |
| GLDN       | 3.63E-02 | 0.41 |
| DHCR24     | 1.35E-03 | 0.41 |
| GPT2       | 7.29E-04 | 0.41 |
| CRYAB      | 3.94E-04 | 0.41 |
| SPRY1      | 1.04E-04 | 0.41 |
| HACL1      | 8.75E-04 | 0.41 |
| PER1       | 3.72E-03 | 0.41 |
| DTX4       | 5.67E-03 | 0.41 |
| KLF2       | 4.60E-03 | 0.41 |
| FBLN1      | 9.71E-03 | 0.40 |
| FAM134B    | 4.86E-02 | 0.40 |
| C15orf48   | 1.96E-03 | 0.40 |
| CA13       | 2.59E-05 | 0.40 |
| PXMP4      | 6.93E-04 | 0.40 |
| SLC46A3    | 5.10E-03 | 0.40 |
| SYNE3      | 6.37E-03 | 0.40 |
| ZNF254     | 1.39E-02 | 0.40 |
| PHF17      | 2.22E-03 | 0.40 |
| FMO5       | 3.34E-03 | 0.40 |
| FAM132A    | 1.20E-02 | 0.40 |
| FITM2      | 3.66E-03 | 0.40 |
| ACSS3      | 5.46E-04 | 0.40 |
| PER2       | 1.36E-02 | 0.40 |
| CECR2      | 1.05E-02 | 0.40 |
| CCL14      | 2.43E-03 | 0.40 |
| TFAP2B     | 1.57E-03 | 0.40 |
| TTLL4      | 3.83E-04 | 0.40 |
| NAMPT      | 1.02E-02 | 0.40 |
| SYNPO2     | 3.22E-02 | 0.40 |
| GNPAT      | 9.15E-04 | 0.40 |
| METTL7A    | 2.97E-05 | 0.40 |
| SELENBP1   | 2.46E-03 | 0.40 |
| CASZ1      | 1.05E-04 | 0.40 |
| KLF4       | 5.81E-03 | 0.40 |
| CSRP1      | 1.32E-04 | 0.39 |
| JUNB       | 6.38E-04 | 0.39 |
| MUC20      | 1.46E-02 | 0.39 |
| GKAP1      | 4.77E-03 | 0.39 |
| RBP7       | 2.88E-03 | 0.39 |
| ITGA8      | 2.65E-02 | 0.39 |
| SOX9       | 2.10E-04 | 0.39 |
| XYLB       | 1.11E-02 | 0.39 |
| TESC       | 6.22E-03 | 0.39 |
| ADCK1      | 2.98E-03 | 0.39 |
| TNS1       | 3.51E-04 | 0.39 |
| CMTM8      | 8.74E-03 | 0.39 |
| KRT15      | 4.78E-03 | 0.39 |
| DPP6       | 2.98E-02 | 0.38 |
| CD69       | 8.36E-03 | 0.38 |
| CNTN3      | 4.20E-02 | 0.38 |
| SORD       | 2.37E-03 | 0.38 |
| FBXO32     | 3.37E-06 | 0.38 |
| PLA2G2A    | 1.20E-02 | 0.38 |
| ZC3H12A    | 1.53E-02 | 0.38 |
| HSPB6      | 1.05E-03 | 0.38 |
| SH3BP5     | 3.43E-04 | 0.38 |
| MIA        | 4.47E-02 | 0.38 |
| RGMA       | 5.76E-04 | 0.38 |
| TFPI       | 8.42E-03 | 0.38 |
| LPIN1      | 2.74E-02 | 0.38 |
| CD55       | 1.47E-03 | 0.38 |
| TMPRSS5    | 4.58E-02 | 0.38 |
| EPHX2      | 4.48E-02 | 0.38 |
| BTNL9      | 7.00E-03 | 0.38 |
| DUSP5      | 2.29E-03 | 0.38 |
| GFPT2      | 3.84E-02 | 0.38 |
| BTC        | 3.23E-02 | 0.37 |
| GGT6       | 2.23E-04 | 0.37 |
| TLCD1      | 1.43E-02 | 0.37 |
| NRARP      | 1.74E-03 | 0.37 |
| AL591845.1 | 2.86E-03 | 0.37 |
| ALDH6A1    | 3.34E-04 | 0.37 |
| PXMP2      | 4.51E-03 | 0.37 |
| ZDHHC2     | 3.64E-03 | 0.37 |
| ABCA6      | 7.97E-03 | 0.37 |
| SLC25A34   | 1.08E-02 | 0.37 |



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| SLC26A9  | 4.29E-03 | 0.37 |
| GEM      | 2.84E-03 | 0.37 |
| SFRP1    | 1.29E-02 | 0.37 |
| ADCY5    | 1.59E-03 | 0.37 |
| CYP27A1  | 1.44E-03 | 0.37 |
| GSN      | 1.03E-03 | 0.37 |
| SLC25A4  | 7.48E-03 | 0.37 |
| PPP1R15A | 8.70E-04 | 0.37 |
| SEMA3B   | 5.40E-04 | 0.37 |
| PALM     | 2.22E-04 | 0.37 |
| ZNF726   | 8.66E-04 | 0.37 |
| IRS2     | 4.84E-03 | 0.36 |
| RNF122   | 9.58E-03 | 0.36 |
| ISOC1    | 3.87E-04 | 0.36 |
| PLEKHB1  | 3.21E-02 | 0.36 |
| GK5      | 4.40E-03 | 0.36 |
| TIMP3    | 3.57E-05 | 0.36 |
| CEACAM1  | 6.87E-03 | 0.36 |
| HMGCR    | 6.62E-04 | 0.36 |
| MSMB     | 5.70E-03 | 0.36 |
| ADAMTS1  | 9.61E-03 | 0.36 |
| DHRS9    | 7.30E-03 | 0.36 |
| MPP2     | 1.64E-02 | 0.36 |
| FDPS     | 9.99E-03 | 0.36 |
| SUSD2    | 2.69E-04 | 0.35 |
| CP       | 3.95E-02 | 0.35 |
| CREB5    | 1.89E-02 | 0.35 |
| RELN     | 9.86E-04 | 0.35 |
| PYGM     | 6.19E-03 | 0.35 |
| KCNN4    | 3.16E-04 | 0.35 |
| CAB39L   | 1.61E-04 | 0.35 |
| CARD18   | 1.85E-02 | 0.35 |
| IDI1     | 1.03E-02 | 0.35 |
| ELF5     | 3.66E-03 | 0.35 |
| AGPAT3   | 1.79E-03 | 0.35 |
| PCTP     | 1.40E-02 | 0.35 |
| PNLIPRP3 | 1.83E-02 | 0.35 |
| ADAMTSL3 | 2.91E-02 | 0.35 |
| FXYD6    | 4.72E-03 | 0.35 |
| GLDC     | 1.73E-02 | 0.35 |
| PADI3    | 4.19E-02 | 0.35 |
| KRT7     | 1.05E-02 | 0.35 |
| APOE     | 4.46E-04 | 0.35 |
| GCHFR    | 6.78E-04 | 0.35 |
| FADS6    | 2.08E-03 | 0.35 |
| CD200    | 9.68E-03 | 0.35 |
| FAM176C  | 6.74E-05 | 0.35 |
| DAPK2    | 2.49E-04 | 0.35 |
| ISM1     | 2.70E-03 | 0.35 |
| DNER     | 7.83E-03 | 0.35 |
| BTG2     | 3.54E-03 | 0.34 |
| SLC15A1  | 8.52E-03 | 0.34 |
| IL34     | 3.10E-04 | 0.34 |
| ATP2A1   | 3.21E-02 | 0.34 |
| GLRB     | 5.86E-03 | 0.34 |
| UBIAD1   | 9.94E-03 | 0.34 |
| LVRN     | 2.73E-02 | 0.34 |
| RGS16    | 4.36E-02 | 0.34 |
| BHMT2    | 4.65E-02 | 0.33 |
| TTYH1    | 3.94E-03 | 0.33 |
| ABTB2    | 1.79E-04 | 0.33 |
| FREM1    | 1.74E-04 | 0.33 |
| MGST1    | 4.39E-03 | 0.33 |
| ANKRD37  | 1.19E-02 | 0.33 |
| GABRP    | 1.55E-02 | 0.33 |
| CNTN4    | 2.59E-02 | 0.33 |
| SRD5A1   | 3.46E-03 | 0.33 |
| MFSD4    | 6.60E-03 | 0.33 |
| ABCA9    | 1.43E-02 | 0.33 |
| ATP12A   | 1.37E-02 | 0.33 |
| ABHD5    | 2.59E-03 | 0.33 |
| NFIL3    | 1.06E-03 | 0.33 |
| ME1      | 2.10E-03 | 0.33 |
| SLC47A1  | 2.64E-03 | 0.33 |
| BRI3BP   | 1.40E-02 | 0.33 |
| EGF      | 1.70E-02 | 0.33 |
| SPIRE2   | 7.73E-03 | 0.33 |
| DHCR7    | 2.49E-03 | 0.33 |
| 41334    | 6.94E-04 | 0.33 |
| PRELP    | 5.42E-03 | 0.33 |
| ELOVL4   | 4.41E-03 | 0.33 |



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| SYN2    | 2.06E-02 | 0.33 |
| GRASP   | 1.33E-03 | 0.33 |
| LRG1    | 4.04E-03 | 0.33 |
| RASD1   | 7.16E-03 | 0.33 |
| CLMP    | 3.36E-02 | 0.32 |
| NOVA1   | 2.64E-02 | 0.32 |
| SLC7A2  | 7.84E-04 | 0.32 |
| SLC26A7 | 2.97E-02 | 0.32 |
| RGS2    | 7.71E-03 | 0.32 |
| CHI3L2  | 2.20E-04 | 0.32 |
| LIPK    | 1.94E-03 | 0.32 |
| ZNF681  | 3.01E-02 | 0.32 |
| TOB1    | 3.53E-04 | 0.32 |
| BCAT2   | 9.64E-03 | 0.32 |
| C20orf3 | 6.09E-04 | 0.32 |
| ANKDD1A | 1.27E-02 | 0.32 |
| F5      | 3.25E-02 | 0.32 |
| FAM166B | 1.49E-02 | 0.32 |
| ACAT2   | 3.57E-03 | 0.32 |
| SLIT2   | 1.73E-03 | 0.32 |
| DCN     | 3.51E-02 | 0.32 |
| LHX2    | 1.05E-02 | 0.32 |
| FXYD1   | 4.68E-03 | 0.32 |
| DCLK1   | 1.66E-03 | 0.32 |
| GADD45B | 1.23E-03 | 0.31 |
| SEMA3D  | 3.01E-03 | 0.31 |
| NCALD   | 8.07E-03 | 0.31 |
| SEMA3G  | 6.86E-04 | 0.31 |
| HSD17B2 | 2.95E-02 | 0.31 |
| GAL     | 2.99E-02 | 0.31 |
| ACADM   | 5.77E-03 | 0.31 |
| VSIG8   | 4.17E-02 | 0.31 |
| BCKDHB  | 1.73E-03 | 0.31 |
| MOGAT2  | 1.61E-02 | 0.31 |
| SLC44A3 | 2.42E-04 | 0.31 |
| CYP4X1  | 5.42E-03 | 0.31 |
| PKLR    | 2.02E-02 | 0.30 |
| NRG2    | 8.56E-04 | 0.30 |
| MCF2L   | 7.59E-05 | 0.30 |
| ANGPTL1 | 2.35E-04 | 0.30 |
| TMEM91  | 1.15E-02 | 0.30 |
| PLA2R1  | 6.98E-04 | 0.30 |
| STC1    | 4.43E-02 | 0.30 |
| PDLIM3  | 9.57E-03 | 0.30 |
| GFRA1   | 1.81E-06 | 0.30 |
| CILP    | 3.21E-03 | 0.30 |
| ACAA2   | 4.98E-03 | 0.30 |
| SEMA3A  | 2.89E-02 | 0.30 |
| PDZRN3  | 1.60E-03 | 0.30 |
| PANK1   | 6.58E-04 | 0.30 |
| ADTRP   | 6.29E-03 | 0.30 |
| FBP1    | 7.48E-03 | 0.30 |
| IRX6    | 8.43E-04 | 0.30 |
| SVEP1   | 1.31E-02 | 0.30 |
| EFHD1   | 4.60E-03 | 0.29 |
| DGAT2   | 1.44E-02 | 0.29 |
| GRIA4   | 9.71E-03 | 0.29 |
| LDHD    | 9.80E-03 | 0.29 |
| ACO1    | 1.42E-03 | 0.29 |
| LMOD1   | 1.95E-02 | 0.29 |
| CIDEA   | 1.11E-02 | 0.29 |
| CYR61   | 1.56E-03 | 0.29 |
| CCDC80  | 2.97E-03 | 0.29 |
| SCNN1D  | 9.93E-03 | 0.29 |
| MAMDC2  | 4.59E-05 | 0.29 |
| MSMO1   | 2.39E-03 | 0.29 |
| AQP5    | 2.61E-03 | 0.29 |
| PGM5    | 1.74E-02 | 0.29 |
| NTRK2   | 3.47E-03 | 0.29 |
| CTGF    | 4.69E-03 | 0.29 |
| EFCAB4A | 4.17E-03 | 0.28 |
| DES     | 2.22E-02 | 0.28 |
| SHROOM3 | 9.13E-04 | 0.28 |
| ACSS2   | 4.93E-04 | 0.28 |
| ID4     | 1.16E-03 | 0.28 |
| ANK2    | 3.57E-03 | 0.28 |
| CFD     | 1.53E-03 | 0.28 |
| MAFF    | 2.59E-03 | 0.28 |
| KRT77   | 6.93E-04 | 0.28 |
| PNLDC1  | 1.21E-02 | 0.28 |
| PAMR1   | 7.39E-04 | 0.28 |



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| TGFB3     | 6.19E-03 | 0.28 |
| GPR133    | 1.16E-02 | 0.28 |
| FA2H      | 1.25E-02 | 0.28 |
| IL20      | 3.69E-02 | 0.28 |
| SOCS3     | 1.89E-03 | 0.28 |
| SH3BGR    | 7.52E-04 | 0.27 |
| C3        | 6.80E-04 | 0.27 |
| SOX10     | 3.49E-02 | 0.27 |
| ZP1       | 1.82E-02 | 0.27 |
| PKD1L2    | 1.88E-02 | 0.27 |
| S100P     | 2.37E-03 | 0.27 |
| SLC41A1   | 1.18E-03 | 0.27 |
| ARC       | 2.81E-02 | 0.27 |
| CAMK2B    | 5.72E-03 | 0.27 |
| S100A3    | 2.87E-02 | 0.27 |
| RORC      | 1.37E-04 | 0.27 |
| SHF       | 1.67E-04 | 0.27 |
| LIPE      | 3.94E-03 | 0.27 |
| SEPP1     | 1.15E-03 | 0.26 |
| HSPB7     | 1.83E-02 | 0.26 |
| HBEGF     | 2.70E-03 | 0.26 |
| CST6      | 3.14E-03 | 0.26 |
| RP11-190A | 3.76E-02 | 0.26 |
| TMEM88    | 3.82E-02 | 0.26 |
| ZFP36     | 1.01E-03 | 0.26 |
| C2orf82   | 4.41E-03 | 0.26 |
| PEX11A    | 9.74E-03 | 0.26 |
| PON3      | 4.18E-04 | 0.26 |
| NFIB      | 2.50E-03 | 0.26 |
| SLC25A25  | 1.03E-03 | 0.25 |
| APOC1     | 3.70E-03 | 0.25 |
| CXCL2     | 9.86E-03 | 0.25 |
| FAM107A   | 1.10E-03 | 0.25 |
| C3orf15   | 1.54E-02 | 0.25 |
| TMEM97    | 2.84E-04 | 0.25 |
| LYVE1     | 3.90E-03 | 0.25 |
| ABCA4     | 4.08E-03 | 0.25 |
| CFH       | 3.08E-03 | 0.25 |
| RP11-324D | 2.57E-02 | 0.25 |
| SORBS1    | 5.17E-03 | 0.25 |
| GSTM5     | 1.21E-04 | 0.25 |
| EGR3      | 3.63E-04 | 0.25 |
| SLC26A2   | 8.97E-03 | 0.25 |
| HEATR4    | 2.75E-02 | 0.25 |
| ZG16B     | 3.01E-03 | 0.24 |
| PNPLA5    | 6.67E-03 | 0.24 |
| CYB5A     | 5.45E-04 | 0.24 |
| CLU       | 5.90E-03 | 0.24 |
| C2orf40   | 3.85E-03 | 0.24 |
| EGR2      | 8.91E-04 | 0.24 |
| SLC2A14   | 2.33E-03 | 0.24 |
| CGNL1     | 3.84E-03 | 0.24 |
| CDO1      | 6.82E-03 | 0.24 |
| PSAPL1    | 7.64E-04 | 0.24 |
| SGK2      | 7.82E-03 | 0.24 |
| SAA2      | 1.08E-02 | 0.24 |
| PK4       | 1.36E-02 | 0.24 |
| HMGCS1    | 1.65E-03 | 0.24 |
| TCHH      | 3.23E-02 | 0.24 |
| TMPRSS11E | 1.33E-03 | 0.23 |
| PLIN2     | 1.65E-03 | 0.23 |
| PRLR      | 1.71E-03 | 0.23 |
| WNK2      | 1.33E-03 | 0.23 |
| CRAT      | 6.40E-03 | 0.23 |
| LGI3      | 4.87E-04 | 0.23 |
| ADCY2     | 1.27E-03 | 0.23 |
| GALNTL1   | 1.74E-03 | 0.23 |
| AKAP12    | 3.38E-03 | 0.23 |
| CASQ2     | 8.89E-03 | 0.23 |
| SORBS2    | 6.80E-05 | 0.23 |
| CDH19     | 4.21E-03 | 0.23 |
| C5orf4    | 5.16E-05 | 0.22 |
| CCL27     | 7.74E-03 | 0.22 |
| HILPDA    | 9.26E-04 | 0.22 |
| CHI3L1    | 9.36E-03 | 0.22 |
| PCP4      | 9.10E-03 | 0.22 |
| VIT       | 2.29E-04 | 0.22 |
| ROS1      | 3.39E-03 | 0.22 |
| GPT       | 1.93E-03 | 0.22 |
| CKMT2     | 1.40E-03 | 0.22 |
| OLAH      | 6.20E-03 | 0.22 |



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| CLEC3B    | 5.93E-04 | 0.22 |
| FASN      | 1.45E-03 | 0.22 |
| DUSP1     | 8.95E-04 | 0.22 |
| C5orf27   | 4.08E-04 | 0.22 |
| MF12      | 2.07E-02 | 0.22 |
| PLIN5     | 7.83E-03 | 0.21 |
| PPARGC1A  | 2.15E-03 | 0.21 |
| KRT79     | 2.50E-03 | 0.21 |
| ACACB     | 3.94E-05 | 0.21 |
| ARHGEF38  | 4.80E-02 | 0.21 |
| KCNIP2    | 5.34E-03 | 0.21 |
| PLCB4     | 4.19E-04 | 0.21 |
| MYBPC1    | 1.09E-02 | 0.21 |
| ACOT2     | 1.93E-03 | 0.21 |
| SEC14L4   | 1.49E-02 | 0.21 |
| ZNF385D   | 6.01E-04 | 0.21 |
| TSPAN8    | 1.20E-04 | 0.21 |
| SPRR4     | 1.65E-03 | 0.21 |
| MLXIPL    | 2.19E-03 | 0.20 |
| SIK1      | 1.81E-03 | 0.20 |
| CNN1      | 1.67E-03 | 0.20 |
| STAC2     | 1.96E-04 | 0.20 |
| SOAT1     | 1.30E-02 | 0.20 |
| ABCA10    | 1.04E-02 | 0.20 |
| GRB14     | 2.55E-04 | 0.20 |
| IL6       | 1.83E-02 | 0.20 |
| CA6       | 2.54E-03 | 0.20 |
| ELOVL5    | 1.78E-03 | 0.20 |
| CSRNP1    | 1.20E-03 | 0.20 |
| UPB1      | 9.36E-04 | 0.20 |
| ABCA8     | 4.63E-04 | 0.20 |
| DUSP2     | 4.23E-03 | 0.20 |
| MRAP      | 2.18E-02 | 0.19 |
| LPHN3     | 1.01E-02 | 0.19 |
| CYP4F2    | 6.26E-04 | 0.19 |
| PPARG     | 2.13E-05 | 0.19 |
| EGR1      | 1.46E-03 | 0.19 |
| KCNAB1    | 1.30E-02 | 0.19 |
| CNTFR     | 1.35E-03 | 0.19 |
| ZC2HC1B   | 1.45E-03 | 0.19 |
| TRHDE     | 2.37E-02 | 0.19 |
| CDKL2     | 2.46E-02 | 0.19 |
| TF        | 3.30E-03 | 0.19 |
| CFTR      | 4.67E-03 | 0.19 |
| CCDC129   | 3.50E-03 | 0.19 |
| C10orf129 | 2.67E-03 | 0.19 |
| PM20D1    | 2.46E-03 | 0.18 |
| CTC-360G5 | 6.84E-03 | 0.18 |
| APOLD1    | 3.31E-04 | 0.18 |
| FOXC1     | 4.93E-05 | 0.18 |
| ALDH1L1   | 7.68E-03 | 0.18 |
| ATP6V1B1  | 7.12E-04 | 0.18 |
| TMEFF2    | 3.08E-02 | 0.18 |
| FOS       | 2.82E-03 | 0.18 |
| CAPN8     | 1.98E-04 | 0.18 |
| SYNM      | 5.03E-04 | 0.18 |
| LIPH      | 6.44E-04 | 0.18 |
| C1QTNF7   | 1.38E-02 | 0.18 |
| ACOX2     | 1.33E-03 | 0.18 |
| HBA2      | 4.59E-04 | 0.18 |
| FAM189A2  | 6.38E-04 | 0.18 |
| SLC27A6   | 1.32E-04 | 0.18 |
| C13orf33  | 2.11E-02 | 0.17 |
| ACSL1     | 9.05E-03 | 0.17 |
| FAR2      | 3.47E-03 | 0.17 |
| CYP4B1    | 1.18E-03 | 0.17 |
| ACSBG1    | 1.41E-03 | 0.17 |
| ELOVL3    | 4.04E-03 | 0.17 |
| OXGR1     | 6.76E-03 | 0.17 |
| G0S2      | 5.74E-03 | 0.17 |
| SLC9A2    | 6.94E-03 | 0.17 |
| CLPSL2    | 1.56E-03 | 0.17 |
| SLC2A3    | 3.44E-03 | 0.17 |
| KIAA1324  | 5.72E-05 | 0.16 |
| C11orf96  | 9.79E-03 | 0.16 |
| SLC12A2   | 4.77E-03 | 0.16 |
| MYEOV     | 4.21E-03 | 0.16 |
| TMEM56    | 1.88E-02 | 0.16 |
| INSIG1    | 1.01E-04 | 0.16 |
| PADI2     | 1.26E-03 | 0.16 |
| FADS1     | 3.15E-03 | 0.16 |



|           |          |      |
|-----------|----------|------|
| SEC14L6   | 1.20E-03 | 0.16 |
| ACSM3     | 1.27E-03 | 0.15 |
| MYH11     | 4.50E-04 | 0.15 |
| PLIN4     | 5.15E-04 | 0.15 |
| HSD3B1    | 1.45E-02 | 0.15 |
| HBB       | 3.70E-05 | 0.15 |
| PHYHIP    | 2.44E-04 | 0.15 |
| ALOX15B   | 5.22E-04 | 0.15 |
| NTRK3     | 5.73E-05 | 0.15 |
| UGT2A1    | 2.87E-02 | 0.15 |
| MUCL1     | 6.14E-04 | 0.14 |
| SLC34A2   | 2.97E-02 | 0.14 |
| AADACL3   | 3.38E-03 | 0.14 |
| NR4A1     | 9.30E-03 | 0.14 |
| SLC27A2   | 5.85E-03 | 0.14 |
| PECR      | 9.21E-04 | 0.14 |
| STK32A    | 5.54E-05 | 0.14 |
| ATP1A2    | 7.00E-03 | 0.14 |
| THRSP     | 2.04E-03 | 0.14 |
| RERGL     | 1.42E-02 | 0.14 |
| FNDC5     | 1.92E-04 | 0.14 |
| CYP4F8    | 4.29E-04 | 0.14 |
| SLC14A1   | 7.66E-04 | 0.14 |
| PADI4     | 1.18E-03 | 0.13 |
| TMPRSS2   | 7.21E-04 | 0.13 |
| SAA1      | 1.53E-04 | 0.13 |
| ZNF331    | 2.11E-03 | 0.13 |
| ZBTB16    | 7.16E-06 | 0.13 |
| AHSP      | 1.11E-02 | 0.13 |
| LYG2      | 1.25E-02 | 0.13 |
| ATP6V0A4  | 2.85E-04 | 0.12 |
| MOGAT1    | 8.49E-03 | 0.12 |
| C7        | 7.03E-06 | 0.12 |
| SLC25A18  | 1.78E-03 | 0.12 |
| WFDC3     | 9.78E-03 | 0.12 |
| KRTAP16-1 | 2.46E-02 | 0.12 |
| HPSE2     | 1.03E-02 | 0.12 |
| GPD1      | 2.42E-03 | 0.12 |
| HAO2      | 3.65E-04 | 0.12 |
| SCARA5    | 1.78E-02 | 0.12 |
| PDZK1     | 1.51E-03 | 0.12 |
| KRTAP26-1 | 4.05E-02 | 0.12 |
| FAM180B   | 1.39E-04 | 0.12 |
| OGN       | 1.43E-05 | 0.12 |
| HMGCS2    | 2.39E-05 | 0.12 |
| INMT      | 4.60E-04 | 0.11 |
| SGCG      | 2.51E-04 | 0.11 |
| S100A1    | 1.55E-03 | 0.11 |
| ADAMTS4   | 2.62E-02 | 0.11 |
| MT1A      | 4.13E-02 | 0.11 |
| KRTAP5-10 | 4.07E-02 | 0.11 |
| TRIM55    | 2.07E-04 | 0.11 |
| FADS2     | 7.41E-04 | 0.11 |
| HSD11B1   | 1.02E-04 | 0.11 |
| KRTAP17-1 | 2.96E-02 | 0.11 |
| PDE6A     | 9.84E-04 | 0.11 |
| MPZ       | 1.19E-04 | 0.10 |
| SPINK8    | 2.39E-02 | 0.10 |
| TMEM213   | 8.75E-04 | 0.10 |
| ASIP      | 3.62E-02 | 0.10 |
| KRTAP12-3 | 2.58E-02 | 0.10 |
| RIMS1     | 9.48E-03 | 0.10 |
| ATF3      | 7.88E-03 | 0.10 |
| ANGPTL5   | 1.05E-02 | 0.10 |
| APOD      | 3.22E-05 | 0.10 |
| NR4A3     | 1.11E-02 | 0.09 |
| CGA       | 6.56E-03 | 0.09 |
| C1orf158  | 2.13E-02 | 0.09 |
| FOSB      | 8.18E-04 | 0.09 |
| SCN7A     | 4.87E-03 | 0.09 |
| FAM150B   | 8.50E-03 | 0.09 |
| KRTAP12-2 | 3.99E-02 | 0.08 |
| CLDN10    | 4.28E-05 | 0.08 |
| PPP1R1B   | 6.90E-05 | 0.08 |
| MT4       | 2.61E-02 | 0.07 |
| KRT32     | 1.03E-02 | 0.07 |
| NR4A2     | 6.43E-04 | 0.07 |
| GPRC5D    | 2.48E-02 | 0.07 |
| MUC7      | 4.51E-02 | 0.07 |
| SCGB1D2   | 1.56E-02 | 0.06 |
| ANGPTL7   | 7.12E-03 | 0.06 |



|           |          |      |
|-----------|----------|------|
| PPP1R1A   | 7.35E-04 | 0.06 |
| ADH1B     | 4.36E-04 | 0.06 |
| KRT82     | 1.34E-02 | 0.06 |
| KRTAP19-5 | 4.78E-02 | 0.06 |
| CIDEC     | 8.92E-04 | 0.06 |
| KRTAP19-1 | 4.94E-02 | 0.06 |
| PCK1      | 1.29E-03 | 0.06 |
| KRT85     | 2.51E-02 | 0.05 |
| ADIPOQ    | 3.62E-04 | 0.05 |
| KRTAP19-3 | 3.46E-02 | 0.05 |
| PLIN1     | 2.26E-03 | 0.05 |
| SCGB2A2   | 2.68E-03 | 0.05 |
| PIP       | 7.19E-04 | 0.05 |
| KRT35     | 2.17E-02 | 0.04 |
| KRT27     | 2.74E-03 | 0.04 |
| KRT71     | 3.11E-03 | 0.04 |
| KRT28     | 5.20E-03 | 0.04 |
| KRTAP11-1 | 3.65E-02 | 0.04 |
| FABP9     | 2.96E-03 | 0.03 |
| KRT25     | 4.25E-03 | 0.03 |
| KRT26     | 5.48E-03 | 0.03 |
| DCD       | 2.28E-03 | 0.03 |



# AK-SCC gene signature

| Gene          | p-value   | SCC/AK fold change |
|---------------|-----------|--------------------|
| RP11-571M6.15 | 3.947E-02 | 13.70              |
| PTHLH         | 1.641E-03 | 6.10               |
| ARTN          | 2.767E-03 | 5.25               |
| MMP1          | 2.172E-02 | 5.20               |
| SH2D5         | 2.933E-02 | 5.04               |
| ZIC1          | 2.759E-02 | 4.17               |
| RASGEF1A      | 2.619E-02 | 3.69               |
| LAMC2         | 2.104E-02 | 3.59               |
| SEZ6L2        | 3.876E-02 | 3.21               |
| APOC2         | 4.809E-02 | 3.17               |
| TREM2         | 1.593E-02 | 3.09               |
| RGS4          | 3.909E-02 | 3.09               |
| AL136218.1    | 2.293E-02 | 3.03               |
| SULF1         | 6.816E-03 | 2.92               |
| PITX2         | 2.912E-02 | 2.89               |
| TDO2          | 1.088E-02 | 2.86               |
| MME           | 2.715E-02 | 2.82               |
| IGFL1         | 1.375E-02 | 2.71               |
| LAMB3         | 4.846E-02 | 2.67               |
| DFNA5         | 2.898E-02 | 2.58               |
| SERPINE1      | 2.299E-02 | 2.54               |
| ITGB6         | 3.088E-02 | 2.46               |
| FAM176A       | 1.408E-03 | 2.45               |
| IGFBP2        | 7.055E-03 | 2.45               |
| PPP1R14B      | 2.894E-02 | 2.42               |
| LAMP5         | 3.151E-02 | 2.40               |
| C6orf141      | 6.685E-03 | 2.40               |
| RRAS2         | 3.534E-02 | 2.36               |
| SOCS2         | 1.699E-03 | 2.35               |
| TH            | 4.241E-02 | 2.35               |
| TUBB3         | 2.352E-02 | 2.33               |
| GREM1         | 3.074E-02 | 2.29               |
| STX1A         | 1.113E-02 | 2.29               |
| TBCA          | 3.865E-02 | 2.26               |
| FGF11         | 4.801E-03 | 2.25               |
| BAIAP2L2      | 1.728E-02 | 2.24               |
| UBE2C         | 1.224E-02 | 2.20               |
| CYTL1         | 4.344E-02 | 2.19               |
| PPAPDC1A      | 2.145E-02 | 2.18               |
| KMO           | 1.751E-03 | 2.14               |
| INHBA         | 1.426E-02 | 2.12               |
| C3orf55       | 4.415E-02 | 2.12               |
| ENPEP         | 5.176E-03 | 2.11               |
| LARP6         | 2.583E-02 | 2.11               |
| GTSE1         | 3.143E-02 | 2.11               |



|          |           |      |
|----------|-----------|------|
| PDLIM7   | 2.735E-03 | 2.07 |
| PDGFB    | 6.759E-03 | 2.06 |
| HN1      | 4.920E-04 | 2.06 |
| HSPH1    | 1.227E-02 | 2.05 |
| SLC26A10 | 1.331E-02 | 2.03 |
| FAM109B  | 4.192E-03 | 2.03 |
| C12orf5  | 9.810E-03 | 2.02 |
| PYGL     | 3.441E-02 | 2.00 |
| GPR176   | 3.207E-02 | 2.00 |
| UPP1     | 4.263E-02 | 1.99 |
| MDFI     | 1.411E-02 | 1.98 |
| RTN2     | 3.458E-03 | 1.97 |
| MFAP2    | 1.213E-02 | 1.97 |
| MAPK12   | 1.960E-02 | 1.97 |
| SLC4A3   | 2.897E-03 | 1.97 |
| TM4SF18  | 1.291E-02 | 1.96 |
| TEAD2    | 1.212E-02 | 1.95 |
| SMTN     | 2.997E-02 | 1.94 |
| ARHGEF17 | 9.121E-03 | 1.93 |
| SHANK2   | 4.766E-02 | 1.92 |
| RELL2    | 8.015E-03 | 1.92 |
| CDCA3    | 4.426E-02 | 1.92 |
| CSRP2    | 2.673E-02 | 1.91 |
| GUCY1B3  | 1.667E-02 | 1.91 |
| SPHK1    | 4.693E-03 | 1.91 |
| TMEM206  | 4.902E-02 | 1.91 |
| S100A11  | 6.893E-03 | 1.90 |
| TPM2     | 1.536E-02 | 1.89 |
| PRELID1  | 1.238E-02 | 1.89 |
| PPP2R2B  | 2.399E-02 | 1.88 |
| CDK18    | 3.831E-03 | 1.87 |
| SYNPO    | 2.737E-02 | 1.87 |
| TNFRSF21 | 2.141E-03 | 1.87 |
| GJB2     | 2.563E-02 | 1.85 |
| FSCN1    | 2.616E-03 | 1.84 |
| SLC2A9   | 1.911E-02 | 1.84 |
| LMAN2L   | 4.528E-04 | 1.84 |
| SLC16A3  | 8.789E-03 | 1.83 |
| ITGA3    | 1.943E-02 | 1.83 |
| BAI2     | 2.658E-02 | 1.82 |
| DCBLD1   | 1.263E-02 | 1.81 |
| LRWD1    | 1.021E-02 | 1.81 |
| RIN1     | 3.459E-02 | 1.80 |
| KRT6A    | 2.995E-02 | 1.80 |
| AVIL     | 4.892E-02 | 1.79 |
| NCS1     | 3.578E-02 | 1.77 |
| C16orf55 | 2.401E-02 | 1.77 |
| PRKAR1B  | 2.610E-02 | 1.76 |
| WDR91    | 1.691E-02 | 1.76 |



|              |           |      |
|--------------|-----------|------|
| TGM2         | 4.834E-02 | 1.76 |
| PCBP3        | 8.449E-03 | 1.76 |
| MARCKSL1     | 3.744E-02 | 1.75 |
| PLOD1        | 3.558E-02 | 1.75 |
| CENPN        | 1.572E-02 | 1.75 |
| SLC35C1      | 8.905E-03 | 1.75 |
| PGF          | 7.111E-03 | 1.75 |
| ITGA5        | 5.410E-03 | 1.74 |
| CTD-2228K2.5 | 1.888E-02 | 1.74 |
| PTK7         | 1.780E-03 | 1.74 |
| IPO13        | 8.635E-03 | 1.74 |
| C19orf55     | 1.946E-02 | 1.73 |
| CELSR1       | 8.922E-03 | 1.73 |
| PMEPA1       | 3.625E-02 | 1.73 |
| MMP14        | 3.587E-02 | 1.72 |
| RASIP1       | 2.310E-02 | 1.72 |
| NRSN2        | 2.299E-02 | 1.71 |
| OCIAD2       | 1.271E-02 | 1.71 |
| RRS1         | 5.056E-03 | 1.71 |
| ETV1         | 2.323E-02 | 1.70 |
| TEAD4        | 3.881E-02 | 1.70 |
| THAP1        | 5.697E-04 | 1.70 |
| RIC8A        | 3.087E-03 | 1.69 |
| RTKN         | 8.398E-03 | 1.69 |
| FHL3         | 2.046E-02 | 1.69 |
| STARD3NL     | 2.325E-03 | 1.68 |
| ADAMTS2      | 4.148E-02 | 1.67 |
| ARAP3        | 3.819E-02 | 1.67 |
| C10orf125    | 1.149E-02 | 1.67 |
| TP53I3       | 1.022E-02 | 1.67 |
| CD276        | 3.826E-02 | 1.66 |
| ARPC1B       | 4.850E-02 | 1.66 |
| PVR          | 1.171E-02 | 1.66 |
| SAC3D1       | 1.711E-02 | 1.65 |
| TRPM2        | 3.535E-02 | 1.65 |
| KRT17        | 4.805E-02 | 1.65 |
| GAPDH        | 2.004E-02 | 1.65 |
| CCM2         | 1.725E-02 | 1.64 |
| ZNF323       | 3.561E-02 | 1.64 |
| COX6A1       | 4.390E-02 | 1.64 |
| GPX7         | 5.105E-03 | 1.63 |
| FBLIM1       | 3.773E-02 | 1.63 |
| SLC25A15     | 3.109E-02 | 1.63 |
| TYMP         | 3.623E-02 | 1.63 |
| WDR77        | 2.256E-02 | 1.62 |
| SRM          | 2.311E-02 | 1.62 |
| C20orf27     | 2.490E-02 | 1.62 |
| SERINC2      | 2.723E-02 | 1.62 |
| GALNT2       | 2.153E-02 | 1.62 |



|          |           |      |
|----------|-----------|------|
| MFSD10   | 3.597E-02 | 1.62 |
| TMEM44   | 3.036E-02 | 1.62 |
| RUSC1    | 2.806E-02 | 1.62 |
| LRRC59   | 6.386E-03 | 1.62 |
| MRPL17   | 1.324E-03 | 1.62 |
| PLK1     | 3.507E-02 | 1.61 |
| POLR3K   | 1.992E-02 | 1.61 |
| WRAP53   | 2.878E-02 | 1.61 |
| S100A10  | 3.574E-02 | 1.61 |
| POLR2H   | 9.048E-03 | 1.60 |
| CDC45    | 2.007E-02 | 1.60 |
| RUVBL1   | 2.792E-02 | 1.60 |
| LTBR     | 4.877E-03 | 1.60 |
| PFDN2    | 3.661E-02 | 1.60 |
| CENPA    | 3.642E-02 | 1.60 |
| CHPF     | 2.996E-02 | 1.59 |
| ANKRD13B | 1.787E-02 | 1.59 |
| FLT4     | 4.232E-02 | 1.59 |
| FHOD1    | 9.387E-03 | 1.59 |
| PYCR2    | 6.796E-03 | 1.59 |
| VASH1    | 2.472E-03 | 1.59 |
| PKMYT1   | 4.904E-02 | 1.59 |
| CARHSP1  | 4.724E-02 | 1.58 |
| FAM213B  | 1.372E-02 | 1.58 |
| RAP1B    | 4.966E-02 | 1.58 |
| TIMM9    | 1.282E-02 | 1.58 |
| TP53I13  | 2.124E-02 | 1.58 |
| GALE     | 2.476E-02 | 1.58 |
| AKR1B1   | 3.887E-02 | 1.57 |
| LEPRE1   | 1.658E-02 | 1.57 |
| JAG1     | 2.743E-02 | 1.57 |
| TBRG4    | 1.198E-02 | 1.57 |
| ZNF692   | 4.104E-02 | 1.56 |
| CDK2AP1  | 1.151E-03 | 1.55 |
| ENTPD6   | 1.888E-04 | 1.55 |
| NHP2     | 1.557E-02 | 1.55 |
| HSCB     | 5.120E-03 | 1.54 |
| AKIP1    | 1.389E-02 | 1.54 |
| MAPK9    | 1.131E-02 | 1.54 |
| ZNF746   | 4.276E-02 | 1.54 |
| GSTP1    | 2.974E-02 | 1.54 |
| TUBA1A   | 4.591E-02 | 1.54 |
| DNLZ     | 3.307E-02 | 1.54 |
| GRB10    | 4.395E-02 | 1.53 |
| ACYP1    | 3.952E-02 | 1.53 |
| CUL7     | 1.653E-02 | 1.53 |
| MRPL55   | 2.493E-02 | 1.53 |
| BOP1     | 4.850E-02 | 1.52 |
| POLD2    | 1.013E-02 | 1.52 |



|           |           |      |
|-----------|-----------|------|
| DUT       | 1.226E-02 | 1.52 |
| STK32C    | 3.900E-02 | 1.52 |
| PLSCR3    | 3.336E-02 | 1.52 |
| LIMK1     | 1.277E-02 | 1.52 |
| PIEZO1    | 2.834E-02 | 1.51 |
| PRDX5     | 2.299E-02 | 1.51 |
| CDK4      | 1.001E-02 | 1.51 |
| PLXNB2    | 7.907E-03 | 1.51 |
| C7orf60   | 1.831E-02 | 1.51 |
| ADSL      | 5.397E-03 | 1.51 |
| KIAA0895L | 2.823E-02 | 1.51 |
| C10orf88  | 3.342E-02 | 1.50 |
| DHX37     | 7.518E-03 | 1.50 |
| LPCAT1    | 1.639E-02 | 1.50 |
| CPEB4     | 4.299E-02 | 0.67 |
| MFSD9     | 2.920E-02 | 0.67 |
| CEP350    | 3.903E-02 | 0.66 |
| DENND4C   | 4.546E-02 | 0.66 |
| MFSD6     | 4.033E-02 | 0.66 |
| CBWD1     | 3.449E-02 | 0.65 |
| NDRG2     | 1.292E-02 | 0.65 |
| TBC1D12   | 2.439E-02 | 0.65 |
| PTPN3     | 4.834E-02 | 0.65 |
| FRRS1     | 4.288E-02 | 0.65 |
| TCEA3     | 4.995E-02 | 0.65 |
| ADD3      | 4.567E-02 | 0.65 |
| FAM160A1  | 3.910E-02 | 0.65 |
| ZBTB44    | 3.585E-02 | 0.65 |
| ANKHD1    | 8.365E-03 | 0.65 |
| FAM214A   | 3.256E-04 | 0.64 |
| GPHN      | 6.877E-03 | 0.64 |
| NIPAL2    | 4.867E-02 | 0.64 |
| ZNF273    | 3.296E-02 | 0.64 |
| MLPH      | 3.959E-02 | 0.64 |
| TANC1     | 2.244E-02 | 0.64 |
| CADM1     | 2.248E-02 | 0.64 |
| C14orf142 | 4.095E-02 | 0.63 |
| MAP3K8    | 4.882E-02 | 0.63 |
| RALGPS2   | 4.358E-02 | 0.63 |
| EIF4E3    | 2.005E-02 | 0.63 |
| SMARCA2   | 4.445E-03 | 0.63 |
| RFX3      | 1.587E-02 | 0.63 |
| PLEKHA7   | 4.865E-02 | 0.62 |
| CBFA2T2   | 3.564E-02 | 0.62 |
| YTHDC2    | 1.669E-02 | 0.62 |
| IQGAP2    | 4.941E-02 | 0.62 |
| FNBP1     | 3.739E-02 | 0.61 |
| DTWD2     | 3.628E-03 | 0.61 |
| ZNF407    | 1.401E-03 | 0.61 |



|            |           |      |
|------------|-----------|------|
| EPHX2      | 1.573E-02 | 0.61 |
| ZFP106     | 9.493E-03 | 0.60 |
| CNTLN      | 4.802E-02 | 0.60 |
| SNX30      | 3.575E-02 | 0.60 |
| TTC21B     | 3.467E-02 | 0.60 |
| CDC14A     | 2.254E-02 | 0.60 |
| ACAT1      | 3.328E-02 | 0.60 |
| PCDH1      | 2.812E-02 | 0.60 |
| PLEKHM3    | 1.727E-02 | 0.60 |
| TAF6L      | 7.661E-04 | 0.60 |
| OTUB2      | 4.774E-02 | 0.59 |
| RDH5       | 2.520E-02 | 0.59 |
| PER2       | 2.260E-02 | 0.59 |
| RASGEF1B   | 2.840E-02 | 0.59 |
| PSAT1      | 1.359E-02 | 0.59 |
| AC090186.1 | 5.318E-03 | 0.58 |
| SECISBP2L  | 2.291E-02 | 0.58 |
| RALGPS1    | 3.938E-02 | 0.58 |
| DAAM1      | 2.250E-02 | 0.58 |
| SPATA6     | 1.419E-02 | 0.58 |
| ERBB3      | 1.530E-02 | 0.58 |
| JAK2       | 4.895E-02 | 0.58 |
| PRDM1      | 3.592E-02 | 0.58 |
| GATM       | 2.507E-02 | 0.57 |
| CASZ1      | 5.199E-03 | 0.57 |
| ABCA12     | 4.138E-02 | 0.57 |
| ANKRD36    | 1.271E-02 | 0.57 |
| RALGAPA2   | 1.975E-02 | 0.57 |
| CD200      | 4.795E-02 | 0.57 |
| ARSG       | 4.000E-02 | 0.57 |
| FAM167A    | 4.591E-02 | 0.57 |
| PLEKHG1    | 1.310E-02 | 0.56 |
| ASRGL1     | 2.909E-02 | 0.56 |
| L3MBTL4    | 4.097E-02 | 0.56 |
| CPEB2      | 3.639E-02 | 0.55 |
| ZDHHC2     | 4.978E-02 | 0.55 |
| NOTCH2     | 2.823E-02 | 0.54 |
| SERTAD4    | 1.568E-02 | 0.53 |
| DAPK2      | 1.795E-02 | 0.53 |
| ZNF684     | 9.055E-03 | 0.53 |
| MCF2L      | 5.492E-03 | 0.53 |
| RPS6KA5    | 3.673E-02 | 0.53 |
| PHLPP1     | 1.095E-02 | 0.52 |
| ICOSLG     | 2.290E-02 | 0.52 |
| CCDC64     | 5.041E-03 | 0.52 |
| PHF17      | 2.141E-02 | 0.52 |
| TTC39B     | 2.787E-02 | 0.52 |
| ZNF286A    | 4.129E-02 | 0.51 |
| AFF3       | 4.498E-02 | 0.51 |



|           |           |      |
|-----------|-----------|------|
| FAM59A    | 2.106E-02 | 0.51 |
| FAM176C   | 4.826E-02 | 0.51 |
| SH3BGR    | 3.169E-02 | 0.50 |
| SNRPA1    | 2.449E-02 | 0.50 |
| AGPAT9    | 2.587E-02 | 0.49 |
| GRAMD1C   | 1.316E-02 | 0.49 |
| XYLB      | 3.269E-02 | 0.49 |
| IQCH      | 4.168E-02 | 0.48 |
| GFRA1     | 3.405E-02 | 0.48 |
| SLC47A1   | 2.501E-03 | 0.47 |
| ATP10B    | 4.478E-03 | 0.46 |
| CLU       | 3.211E-02 | 0.46 |
| GCH1      | 4.006E-02 | 0.45 |
| C10orf131 | 4.942E-02 | 0.45 |
| SPRR2E    | 2.203E-02 | 0.44 |
| PIK3C2G   | 4.386E-02 | 0.44 |
| ACACB     | 1.933E-02 | 0.44 |
| ALDH1A3   | 1.739E-02 | 0.43 |
| ENDOU     | 2.305E-02 | 0.43 |
| KCTD9     | 1.261E-02 | 0.43 |
| OGN       | 3.024E-02 | 0.43 |
| MLIP      | 1.530E-02 | 0.43 |
| LGI3      | 4.752E-02 | 0.42 |
| DHRS9     | 4.449E-02 | 0.42 |
| ADCY2     | 4.492E-02 | 0.41 |
| MAMDC2    | 3.101E-02 | 0.41 |
| SLC4A5    | 4.507E-03 | 0.41 |
| BCKDHB    | 1.283E-02 | 0.41 |
| CHI3L2    | 2.995E-03 | 0.38 |
| HIST1H4F  | 4.169E-02 | 0.37 |
| FAM174B   | 3.044E-02 | 0.34 |
| CD69      | 3.932E-02 | 0.34 |
| LIPH      | 4.990E-02 | 0.33 |
| ATP12A    | 1.577E-02 | 0.33 |
| KRT25     | 3.881E-02 | 0.31 |
| ANGPTL5   | 4.521E-02 | 0.28 |
| SLC2A14   | 3.294E-02 | 0.26 |
| CDKL2     | 2.779E-02 | 0.25 |
| FABP9     | 1.521E-02 | 0.25 |
| ZBTB16    | 7.766E-03 | 0.19 |
| ADH1B     | 2.802E-02 | 0.19 |



## Appendix 4.

### Differentially-expressed genes in mouse samples



| Mouse correlation |           | CHR       | CHR       | CHR       | CHR       | CHR       | CHR       | CHR       | PAP       | PAP       | PAP       | PAP       | PAP       | PAP       | PAP        | PAP       | SCC        | SCC       | SCC       | SCC       | SCC       | SCC       | SCC     |
|-------------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|------------|-----------|-----------|-----------|-----------|-----------|---------|
| Groups            | Sample    | HR10_CHR  | HR2_CHR   | HR3_CHR   | HR7_CHR   | HR8_CHR   | HR9_CHR   | HR10_PAP  | HR2_PAP   | HR3_PAP   | HR7_PAP   | HR8_PAP   | HR9_PAP   | HR10_SCC  | HR2_SCC    | HR3_SCC   | HR7_SCC    | HR8_SCC   | HR9_SCC   | HR10_SCC  | HR2_SCC   | HR3_SCC   | HR7_SCC |
| HR10_CHR          | 1         | 0.5978755 | 0.5138051 | 0.6620747 | 0.6398536 | 0.6674473 | -0.531347 | -0.483692 | -0.477299 | -0.48706  | -0.426777 | -0.405224 | -0.497395 | -0.208292 | -0.38137   | -0.033626 | -0.174142  | -0.458068 |           |           |           |           |         |
| HR2_CHR           | 0.5978755 | 1         | 0.4788741 | 0.498839  | 0.6437714 | 0.5751609 | -0.522017 | -0.34729  | -0.434039 | -0.419873 | -0.374445 | -0.335618 | -0.437581 | -0.05591  | -0.449511  | -0.169033 | -0.268092  | -0.457079 |           |           |           |           |         |
| HR3_CHR           | 0.5138051 | 0.4788741 | 1         | 0.7207821 | 0.7150483 | 0.6738375 | -0.60638  | -0.586359 | -0.447801 | -0.511745 | -0.453775 | -0.437092 | -0.546985 | -0.23993  | -0.316514  | 0.1193178 | 0.0030709  | -0.002395 | -0.409708 |           |           |           |         |
| HR7_CHR           | 0.6620747 | 0.498839  | 0.7207821 | 1         | 0.698006  | 0.7692729 | -0.647267 | -0.544692 | -0.544739 | -0.635942 | -0.582019 | -0.494645 | -0.630554 | -0.202903 | -0.321025  | 0.028713  | 0.2243906  | 0.0030709 | -0.424937 |           |           |           |         |
| HR8_CHR           | 0.6398536 | 0.6437714 | 0.7150483 | 0.698006  | 1         | 0.7543285 | -0.654001 | -0.606662 | -0.512086 | -0.527275 | -0.640159 | -0.580975 | -0.450315 | -0.410579 | -0.568162  | -0.626405 | 0.5780945  | 0.3476275 | 0.4920854 | 0.5438897 | 0.5149499 | 0.0047226 |         |
| HR9_CHR           | 0.6674473 | 0.5751609 | 0.6738375 | 0.7692729 | 0.7543285 | 1         | -0.67056  | -0.560768 | -0.563832 | -0.640159 | -0.580975 | -0.456741 | -0.626405 | -0.183103 | -0.285817  | 0.1238561 | 0.2103606  | 0.0884813 | 0.0128678 | -0.002298 | 0.0909002 | 0.0683448 |         |
| HR10_PAP          | -0.531347 | -0.522017 | -0.60638  | -0.647267 | -0.654001 | -0.67056  | 1         | 0.4123514 | 0.4494555 | 0.5485079 | 0.4666013 | 0.2799437 | 0.5780945 | 0.0112668 | 0.1238561  | -0.28507  | -0.153058  | -0.275173 | -0.361451 | -0.376567 | -0.109454 | -0.331716 |         |
| HR2_PAP           | -0.483692 | -0.34729  | -0.586359 | -0.544692 | -0.606662 | -0.560768 | 0.4123514 | 1         | 0.301911  | 0.2797269 | 0.2509849 | 0.2222892 | 0.3476275 | 0.1413368 | 0.2103606  | -0.153058 | -0.06076   | 0.2800933 |           |           |           |           |         |
| HR3_PAP           | -0.477299 | -0.434039 | -0.447801 | -0.544739 | -0.512086 | -0.563832 | 0.4494555 | 0.301911  | 1         | 0.4758994 | 0.4854885 | 0.2425242 | 0.4920854 | -0.02005  | 0.0884813  | -0.275173 | -0.129454  | 0.1086206 |           |           |           |           |         |
| HR7_PAP           | -0.48706  | -0.419873 | -0.511745 | -0.635942 | -0.527275 | -0.640159 | 0.5485079 | 0.2797269 | 0.4758994 | 1         | 0.6200181 | 0.3854529 | 0.5438897 | -0.013448 | 0.0128678  | -0.361451 | -0.127034  | 0.189842  |           |           |           |           |         |
| HR8_PAP           | -0.426777 | -0.374445 | -0.453775 | -0.582019 | -0.450315 | -0.580975 | 0.4666013 | 0.2509849 | 0.4854885 | 0.6200181 | 1         | 0.2899391 | 0.5149499 | 0.0047226 | -0.0002298 | -0.376567 | -0.133103  | 0.0662236 |           |           |           |           |         |
| HR9_PAP           | -0.405224 | -0.335618 | -0.437092 | -0.494645 | -0.410579 | -0.456741 | 0.2799437 | 0.2222892 | 0.2425242 | 0.3854529 | 0.2899391 | 1         | 0.3341871 | 0.0415988 | 0.0909002  | -0.109454 | -0.125138  | 0.2654756 |           |           |           |           |         |
| HR10_SCC          | -0.497395 | -0.437581 | -0.546985 | -0.630554 | -0.568162 | -0.626405 | 0.5780945 | 0.3476275 | 0.4920854 | 0.5438897 | 0.5149499 | 0.0047226 | -0.002298 | 0.0909002 | 0.0683448  | -0.014331 | -0.0944417 | -0.015716 | 0.0554668 | -0.003096 |           |           |         |
| HR2_SCC           | -0.208292 | -0.05591  | -0.23993  | -0.202903 | -0.189711 | -0.183103 | 0.0112668 | 0.1413368 | -0.02005  | -0.013448 | 0.0047226 | 0.0415988 | -0.014331 | 1         | 0.0944417  | -0.015716 | 0.0554668  | -0.003096 |           |           |           |           |         |
| HR3_SCC           | -0.38137  | -0.449511 | -0.316514 | -0.321025 | -0.387752 | -0.285817 | 0.1238561 | 0.2103606 | 0.0884813 | 0.0128678 | -0.002298 | 0.0909002 | 0.0683448 | 0.0944417 | 1          | 0.2480362 | 0.2990135  | 0.2981709 |           |           |           |           |         |
| HR7_SCC           | -0.033626 | -0.169033 | 0.1193178 | 0.2243906 | 0.028713  | 0.1732363 | -0.28507  | -0.153058 | -0.275173 | -0.361451 | -0.376567 | -0.109454 | -0.331716 | -0.015716 | 0.2480362  | 1         | 0.3000441  | 0.1487618 |           |           |           |           |         |
| HR8_SCC           | -0.174142 | -0.268092 | -0.002395 | 0.0030709 | -0.071885 | -0.027733 | -0.105778 | -0.06076  | -0.129454 | -0.127034 | -0.133103 | -0.125138 | -0.14917  | 0.0554668 | 0.2990135  | 0.3000441 | 1          | 0.1053476 |           |           |           |           |         |
| HR9_SCC           | -0.458068 | -0.457079 | -0.409708 | -0.424937 | -0.482795 | -0.444777 | 0.2700685 | 0.2800933 | 0.1086206 | 0.189842  | 0.0662236 | 0.2654756 | 0.1962674 | -0.003096 | 0.2981709  | 0.1487618 | 0.1053476  | 1         |           |           |           |           |         |



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|         |           |           |           |           |           |           |           |           |           |            |           |           |           |           |           |            |           |           |
|---------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|
| Plin4   | 0.5882256 | 1.7850923 | 1.5766658 | 1.2993224 | 1.1977818 | 1.5253652 | -0.766021 | -0.638958 | -0.737742 | -0.728998  | -0.749744 | -0.779989 | -0.757713 | -0.45914  | -0.551751 | -0.738894  | -0.319861 | -0.743642 |
| Chaf1a  | -1.332082 | -1.107822 | -0.869921 | -1.50989  | -1.274313 | -1.350862 | 0.5809968 | 1.6005447 | 0.975465  | 0.9108912  | 0.858992  | 0.6753346 | 0.0989945 | -0.119729 | 1.144073  | -0.024825  | 0.4839597 | 0.2581105 |
| Mcm2    | -1.246918 | -1.225414 | -0.757839 | -1.377254 | -1.184434 | -1.225414 | 1.9365086 | 0.5676248 | 0.2416473 | 0.4539799  | 0.5883311 | 0.2835682 | -0.009757 | -0.320041 | 1.3693098 | 0.231502   | 0.404377  | 1.2685133 |
| Tcpa1   | 1.6405845 | 1.1491894 | 1.3041267 | 1.3181404 | 0.9441439 | 1.1423348 | -0.635208 | -0.586967 | -0.354612 | -0.859274  | -0.169643 | -0.453229 | -0.815699 | 0.4433144 | -1.310308 | -0.547686  | -0.798099 | -1.411111 |
| Nab1    | -1.796706 | -0.231399 | -0.966531 | -1.42117  | -1.224456 | -1.130394 | 0.0994402 | 1.7502639 | 0.1836347 | 0.9689777  | 1.05925   | 0.5158808 | -0.110991 | 0.8242854 | -0.356791 | 0.1630538  | 0.4450259 | 1.2286225 |
| Cd97    | 1.5931872 | 0.2690169 | 0.8611397 | 2.2413356 | 0.2184621 | 1.579496  | -0.822231 | -0.697111 | -0.888141 | -0.112692  | -0.766696 | -0.955507 | -0.761797 | -0.32641  | -0.454773 | 0.5878305  | 0.0515581 | -0.666742 |
| Cd36    | 1.673798  | 0.4679553 | 1.0377033 | 2.3247781 | 0.2723446 | 1.6335482 | -0.707719 | -0.66532  | -0.701901 | -0.702974  | -0.707441 | -0.679784 | -0.702833 | -0.605329 | -0.55459  | -0.310308  | -0.431101 | -0.641727 |
| Apoe    | 1.8132224 | 1.4377715 | 0.4533182 | 1.5755406 | 0.9865139 | 1.3613934 | -1.124483 | -0.911797 | -0.694358 | -0.822929  | -0.453847 | -0.556688 | -0.756605 | -0.529104 | -0.576185 | 0.1784222  | -0.381169 | -0.999018 |
| Elf3    | -0.92037  | -0.887748 | -0.589122 | -0.981241 | -0.775852 | -0.932728 | 1.5616516 | -0.642305 | -0.062476 | 0.6418453  | -0.458926 | 2.8104354 | 0.4848373 | -0.030603 | -0.511464 | 0.1795079  | 0.3903737 | 0.7241838 |
| Lipe    | -0.418902 | 1.7741432 | 2.3729707 | 0.7244262 | 1.510913  | 0.8084204 | -0.218104 | -1.099742 | -1.037496 | -0.286349  | -0.525466 | -0.553308 | -0.502601 | -0.409098 | -0.408015 | -0.59388   | -0.585267 | -0.552644 |
| Mical3  | -0.322031 | -0.543272 | -0.473201 | -0.663033 | -0.649462 | -1.187315 | 1.6705622 | 1.501735  | 1.706399  | 1.0304905  | 1.2323803 | -0.877818 | 0.2103228 | -0.092482 | -0.489544 | -0.957431  | 0.1543557 | -1.250656 |
| Ebi3    | 0.4307951 | 0.9049946 | 1.4666118 | 1.6503139 | 1.2378147 | 0.5722504 | -0.946069 | -0.345209 | -1.018712 | -0.94552   | -1.17716  | -0.094167 | -1.326047 | -0.814507 | -0.94552  | 1.2594571  | -0.039848 | 0.1305222 |
| Fkbp11  | -0.510821 | -0.994815 | -1.424614 | -0.430796 | -0.723857 | -0.386038 | -1.03694  | 0.691467  | -0.161362 | -0.366876  | 0.1116543 | 0.7513838 | -1.023117 | 1.086125  | 1.7346915 | 0.4916736  | -0.06361  | 2.255852  |
| Pld3    | 0.992196  | 0.5259594 | 1.5285033 | 2.2180441 | 0.5702052 | 1.5999515 | -1.311688 | -0.995275 | -0.614306 | -0.60395   | -0.392002 | -0.543008 | -0.77714  | -0.291691 | -0.474134 | -0.187198  | -0.418531 | -1.005936 |
| Etv3    | 2.2351501 | 0.4417335 | 0.2490802 | 1.558319  | 1.4519419 | 0.6069773 | -1.081233 | 0.1572696 | -0.776319 | -0.565567  | -0.498287 | -1.107988 | -0.906849 | -0.53264  | -1.058903 | -0.730424  | -0.129386 | 0.6871247 |
| St8sia6 | 2.6671839 | 0.5905215 | 0.0834484 | 1.4753469 | 0.7859422 | 0.9758727 | -1.183252 | -0.412869 | -0.755921 | -0.841187  | -0.304379 | -1.04059  | -0.05267  | -1.027494 | -0.535482 | 0.0394503  | 0.1581091 | -0.62203  |
| Fcgrt   | 0.9425854 | 0.6887273 | 0.9175509 | 0.998845  | 1.509071  | 1.7541136 | -1.103653 | -0.737781 | -0.985975 | -1.067192  | -0.98846  | -0.770958 | -1.033954 | -1.424818 | -0.209947 | 1.1461295  | -0.199293 | 0.716137  |
| Phyhip  | 3.6159363 | 0.295429  | -0.055314 | 0.5479033 | 0.6200731 | 0.1489824 | -0.391072 | -0.338863 | -0.412478 | -1.107021  | -0.060485 | -0.015296 | -0.649236 | -0.640267 | -0.60794  | -0.916447  | -0.216183 | -0.754607 |
| Imnt    | -0.316848 | -0.271166 | 2.9233841 | 0.2985414 | 1.6331911 | 1.6210172 | -0.497749 | -0.497749 | -0.412885 | -0.497749  | -0.497749 | -0.497749 | -0.497749 | -0.497749 | -0.497749 | -0.497749  | -0.497749 | -0.497749 |
| Dusp3   | 1.5865824 | -0.094141 | 0.6035069 | 2.3274273 | 0.01722   | 1.4558579 | -0.698898 | -0.612737 | -1.166581 | -1.107738  | -0.846202 | -0.612031 | -0.780527 | -0.338559 | 0.2375187 | 0.993443   | -0.233105 | -0.766787 |
| Dgcr14  | -0.959619 | 1.430647  | -1.3509   | -0.926907 | -0.945682 | -1.637386 | 1.3304508 | 1.2516771 | 0.7391408 | 0.9634983  | 0.3851546 | 0.5942629 | 0.9918514 | 0.5663279 | -0.190626 | -0.483122  | 0.1784508 | 0.9240745 |
| Ier3    | -0.70093  | -0.884156 | -0.883075 | -0.898939 | -0.843782 | -0.756072 | 0.9013766 | 0.3249987 | -0.240469 | 0.2812724  | -0.154653 | 0.0734808 | -0.161304 | -0.094971 | 0.4029121 | 1.0431934  | -0.284779 | -0.052204 |
| Ercr1   | -0.659741 | -0.844245 | -0.933714 | -1.103051 | -1.177682 | -1.199385 | 0.2839346 | 0.8989166 | -0.218679 | 1.5807097  | 1.2359739 | 0.1040378 | -0.369526 | 0.9316321 | 1.3452747 | 0.6315548  | 0.8736199 | -0.683681 |
| Cyp11a  | 2.149992  | 2.1318855 | 0.3042816 | 0.1990221 | 1.056295  | 1.202471  | -0.812736 | -0.691868 | -0.425885 | -1.00546   | -0.04201  | -0.758636 | -0.716569 | -0.689941 | -0.60214  | -0.852127  | -0.520537 | -0.880287 |
| Home1   | -1.138705 | -1.277678 | -0.737163 | -0.968246 | -1.059254 | -1.152633 | 2.3631469 | 0.8215006 | -0.143475 | 1.3423547  | 0.2463261 | -0.472043 | 0.677971  | 0.3237397 | 0.2421715 | -0.261198  | 0.9840026 | 0.2451818 |
| Cp      | 0.2667871 | 1.3278478 | 1.5136873 | 0.8547217 | 1.1729385 | 1.6900402 | -1.00035  | -0.607598 | -1.084139 | -1.048306  | -1.063409 | -1.062514 | -1.032178 | -0.609771 | -0.312911 | 0.3852098  | 0.0420523 | 0.5678181 |
| Crot    | 2.6470591 | 1.7432509 | -0.017849 | 0.6719998 | 0.8447066 | 0.8320404 | -0.588399 | -0.298266 | -0.731305 | -0.221566  | -1.822729 | -0.297598 | -0.106486 | -0.507846 | -0.969017 | -0.881843  | -1.18563  | -0.750972 |
| Insig2  | 2.537879  | 1.3675759 | -0.060134 | 1.5181988 | 0.8443578 | 0.9424023 | -0.213372 | -0.782827 | -0.606084 | -0.363848  | -0.675817 | -0.748044 | -0.31404  | -0.4438   | -0.633928 | -0.865107  | -0.631389 | -0.872024 |
| Kif20a  | -1.303145 | -0.871444 | -1.225998 | -1.321038 | -1.163176 | -1.109168 | 0.7201682 | 2.0666182 | 1.0269947 | 0.9387018  | 0.1077032 | 0.7828031 | 0.1398332 | 0.5581757 | 0.5283412 | 0.313701   | -0.158242 | -0.17083  |
| Dnase2a | 1.3554924 | 1.6812765 | 0.2458975 | 1.2791689 | 0.9149434 | 1.3717012 | -0.65882  | -0.020842 | 0.5008655 | -0.207403  | 0.3188537 | -1.459165 | -0.384597 | -0.135356 | -0.842957 | -0.976313  | -0.684579 | -1.623166 |
| Syce2   | -0.925813 | -0.875109 | -0.887228 | -0.957186 | -0.930548 | -0.886883 | 2.6944827 | 0.3595109 | -0.100674 | 0.577784   | 0.0440708 | -0.33471  | 0.6641962 | -0.27295  | 1.4206313 | -0.340968  | -0.412235 | 1.1634892 |
| Nob3    | -0.787723 | -0.834066 | -0.95342  | -1.071672 | -0.819602 | -1.014639 | 2.8541352 | 0.7663277 | 0.4593489 | 0.2770758  | 0.2770758 | -0.659151 | 0.4215083 | -0.152358 | 0.5803025 | -0.480833  | -0.129982 | 1.2676731 |
| Ruvbl2  | -0.890364 | -1.02784  | -0.945535 | -0.893789 | -1.055255 | -1.0422   | 0.368397  | 1.3873122 | 0.3268062 | -0.113015  | 0.0487717 | 1.1016239 | 0.1351679 | -0.348505 | 0.2027497 | 0.0685516  | -0.092048 | 2.7691645 |
| Ilr7    | 1.5057274 | 0.185137  | 1.1833466 | 2.7033963 | 0.2012357 | 1.0799495 | -0.851526 | -0.788328 | -0.652975 | -0.767725  | -0.771225 | -0.552703 | -0.660358 | -0.766886 | -0.612123 | 0.289932   | -0.374603 | -0.571814 |
| Zfp81   | -0.635665 | -0.495187 | -1.511254 | -0.96248  | -1.193975 | -0.90399  | 1.2991092 | 2.2628872 | 0.5517306 | -0.193599  | 0.2074044 | 0.432722  | 0.907848  | -0.454771 | 1.4684569 | -0.52465   | -0.23255  | -0.022038 |
| Mmd     | 0.8409594 | 2.2198724 | 0.9331086 | 0.7845537 | 0.7104575 | 1.2279095 | -1.182028 | -0.127667 | -0.420621 | -0.27882   | 0.0141233 | -1.416753 | -0.808228 | -0.802927 | 0.7726898 | -1.065684  | -0.401555 | -0.999393 |
| Fam162a | -1.4197   | -0.690459 | 0.911768  | -1.2826   | -0.84177  | -1.262421 | 1.1585745 | -1.47153  | 0.8143119 | 1.0173034  | 1.0408836 | 0.1281744 | 1.3737991 | -0.224611 | 0.5894054 | -1.059704  | 0.0522258 | 0.0522258 |
| Gstm5   | 2.674521  | 1.1546729 | -0.616837 | 1.1949618 | 0.4619466 | 0.996251  | -1.284894 | -0.422    | -0.397829 | -0.73466   | -0.567817 | 0.1282919 | -0.517023 | 0.5125837 | -0.222468 | -0.477994  | -0.800821 | -1.08449  |
| Stat5a  | 0.6266364 | 2.2041806 | 0.6803628 | 1.6109921 | 1.320289  | 0.6872895 | -0.600865 | -0.955969 | -0.888442 | -0.24767   | -0.57799  | -0.551783 | -0.897408 | 0.2992432 | -1.347828 | -0.088789  | -0.33417  | -0.93808  |
| Ppan    | -0.90066  | -1.206891 | -1.093133 | -1.190493 | -1.253898 | -1.149108 | 0.0212784 | 0.9006982 | 0.8867833 | 0.3948621  | 0.4512944 | 1.6397763 | 1.0267116 | -0.097282 | 0.6171856 | -0.14031   | -0.57576  | 1.668711  |
| Trmt10a | -0.179131 | -1.052602 | -1.683928 | -1.125534 | -1.144659 | -1.307473 | 1.0416687 | 0.3290218 | -0.135763 | 0.9345495  | -0.043565 | 1.0517674 | 0.365237  | 1.8667283 | 0.2433145 | 0.3155233  | -0.573716 | 0.7285601 |
| Psap    | 0.8255299 | 0.5032265 | 1.4331149 | 2.646759  | 0.2113418 | 1.1453861 | -1.021761 | -0.68338  | -0.491338 | -0.858395  | -0.764047 | -0.800076 | -0.692153 | -0.30294  | -0.482907 | 0.52152912 | -0.29757  | -0.880973 |
| Atn1    | -0.060648 | -1.627306 | -0.860752 | -0.089576 | -1.244974 | -1.598816 | 1.7942806 | 0.5279595 | 0.5545319 | 1.6851277  | 1.1151888 | -0.943096 | -0.079117 | 0.5282939 | -0.20641  | -0.199106  | 0.1300043 | 0.5746877 |
| Ptpn6   | 0.5076871 | 0.7120838 | 1.6703667 | 1.7621715 | 1.1790319 | 1.358223  | -1.300892 | -0.900985 | -0.723817 | -0.844669  | -0.897336 | -0.620391 | -0.893158 | -0.502394 | -0.773241 | 0.6659636  | -0.163301 | -0.235285 |
| Il11    | -1.23873  | 0.1352337 | -0.878422 | -1.280209 | -1.275658 | -0.721807 | 2.4220078 | 0.8094265 | 0.0308854 | 1.6335011  | 0.3597899 | -0.886214 | 0.0430552 | 0.5379772 | 0.0412034 | 0.298133   | 0.092798  | -0.482971 |
| Ralb    | -1.057927 | -1.175397 | -0.752748 | -0.893332 | -0.969223 | -0.77307  | 2.7884427 | -0.097099 | -0.150645 | -0.2851803 | -0.768577 | 0.2001852 | 0.5832692 | 0.2609981 | 0.904809  | -0.232008  | 0.6761044 | 1.1226672 |
| Gab2    | 0.8785071 | 0.350743  | 1.3854022 | 1.9351119 | 0.5843183 | 1.2775753 | -1.377497 | -0.772498 | -0.950604 | -0.864538  | -0.955656 | -0.473468 | -1.056152 | -0.521923 | -0.416515 | 1.1533937  | 0.2844715 | -0.460672 |
| Ndr2    | 2.1250651 | 1.144571  | 0.7623717 | 1.7153795 | 1.078293  | 0.964003  | -0.883387 | -0.823041 | -0.938236 | -0.797489  | -0.607688 | -0.521301 | -0.773666 | -0.415941 | -0.654447 | -0.669295  | -0.50548  | -0.199713 |
| Sgce    | 0.6656157 | 0.6584033 | 0.480168  | 1.0303295 | 0.8232676 | 2.4471812 | -1.297396 | -0.692705 | -1.164143 | -1.309209  | -1.026442 | -0.309951 | -1.087517 | 0.5694793 | 0.3992240 | 0.2540983  | -0.102668 | -0.310639 |
| Aqp1    | 0.5653333 |           |           |           |           |           |           |           |           |            |           |           |           |           |           |            |           |           |



|         |           |           |           |            |           |           |           |           |           |           |           |           |           |           |           |           |           |             |
|---------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-------------|
| Cdc20   | -1.171198 | -0.946498 | -1.034441 | -1.237642  | -0.933762 | -1.083744 | 0.891937  | -0.294606 | 2.1269814 | 0.9348628 | 0.7004567 | 0.4459093 | 0.4269118 | 0.1372888 | 0.3150955 | -0.705837 | -0.090769 | 1.5190548   |
| Adams4  | -1.081061 | -0.949758 | -0.84137  | -1.013269  | -0.609077 | -0.832932 | -0.313916 | -0.266883 | 0.647167  | -0.322199 | 0.146555  | 0.4829975 | -0.311975 | 0.6762485 | 1.2173108 | 2.442498  | 1.9231268 | 0.00085     |
| Srm     | -0.722479 | -0.784568 | -0.839556 | -1.049175  | -0.969151 | -0.972094 | -0.228837 | -0.266832 | 1.6822145 | 0.844414  | 0.8217265 | 0.4759374 | 1.0445078 | -0.434623 | 0.3953118 | -1.005115 | -1.113835 | 2.2175528   |
| Epha2   | -1.1453   | -1.255313 | -0.644697 | -1.527745  | -1.117861 | -1.374202 | 0.7852058 | -0.743298 | 0.575201  | 1.5282217 | 0.529065  | 1.2048743 | 0.4523395 | -0.193734 | 0.4624292 | 0.9771384 | 0.4788562 | 1.0088191   |
| Actn3   | 0.234926  | 2.6385497 | 0.3021325 | -0.080575  | 1.3890333 | 1.9763269 | -0.717878 | 0.571445  | -0.720352 | -0.713174 | -0.719535 | -0.713665 | -0.71367  | -0.286136 | -0.443246 | -0.046115 | -0.282514 | -0.532664   |
| Pdk1    | -1.067586 | -0.558016 | -0.764296 | -0.844194  | -0.746138 | -0.816839 | 3.1633338 | 0.2911285 | 0.2743171 | 0.0537585 | -0.222959 | 0.4066806 | 0.9059333 | 0.6237422 | -0.523064 | -0.473559 | -0.518765 | 0.8165196   |
| Ptbp1   | -1.199205 | -0.611697 | -0.91883  | -1.271248  | -0.905766 | -1.175026 | 0.1210328 | 2.0395254 | 0.8713478 | 0.2650444 | 0.6050563 | -0.483618 | -0.207623 | 1.9375938 | 0.1865143 | -0.483618 | 0.8381852 | 0.3923301   |
| Rundc3a | -1.203599 | -0.496043 | -1.012581 | -1.105036  | -1.037497 | -0.432011 | 0.6671251 | 0.6334552 | -0.302056 | 0.8570556 | 0.0156544 | 0.6820638 | -0.340926 | 0.7685592 | 0.5030863 | -0.340926 | -0.700783 | 2.8444571   |
| Gtf2h1  | -0.814708 | -0.813295 | -1.175386 | -1.330444  | -1.320036 | -1.021453 | 1.1420756 | 2.6050056 | 0.5920291 | 0.0741527 | 0.1772012 | 0.3441827 | 0.472994  | -0.335514 | 0.3236545 | 0.3456182 | -0.027538 | 0.7614602   |
| Hfe     | 0.478547  | 0.8872043 | 0.7986257 | 0.9012435  | 1.2542589 | 1.8819354 | -1.315926 | -0.923697 | -0.668135 | -0.81401  | -0.971695 | -0.451906 | -0.896227 | -0.335793 | -0.511059 | 1.6853532 | -0.325621 | -0.673099   |
| Aplp1   | -0.60677  | -1.362463 | -1.246845 | -0.880885  | -1.009168 | -0.930735 | 1.6575959 | 0.2201645 | -0.57589  | -0.028401 | 1.4118577 | 0.0910454 | -0.131662 | 1.6187474 | 1.510791  | 0.6571915 | -0.206144 | -0.188429   |
| Pola1   | -1.163087 | -0.653912 | -1.113309 | -1.280814  | -1.218244 | -1.368967 | 0.8710975 | 1.26697   | 0.3393085 | 0.4935583 | 0.0766826 | 0.38449   | 0.646074  | -0.458626 | 0.8761984 | -0.004829 | 0.1419056 | 2.1655022   |
| Gmn     | -0.937374 | -0.862843 | -0.799721 | -0.913209  | -1.018277 | -0.942552 | 0.4054322 | 3.0219917 | 0.11781   | 0.4755901 | -0.124581 | -0.309023 | 0.1758687 | -0.141049 | 0.2983665 | 0.2553623 | -0.151651 | 1.4498586   |
| Mett11  | -0.695188 | -0.655804 | -1.089361 | -1.39362   | -1.371691 | -1.242365 | 0.4143638 | 1.0309214 | 0.4599598 | 0.5016975 | 0.3765371 | 1.1664373 | 0.5655446 | -0.179213 | -0.028107 | 1.0080038 | -0.923285 | 2.019134    |
| Saal1   | -1.370754 | -0.411454 | -1.13371  | -1.374793  | -1.043736 | -1.149702 | 1.4028943 | 1.9820249 | 1.4591543 | 0.1023318 | 0.0411335 | 0.3186355 | 0.0144734 | 0.0633045 | 0.3217721 | 0.0854835 | -0.133325 | 1.0062788   |
| Krt23   | 2.2943117 | 1.7937985 | 0.2781249 | 0.4605286  | 1.1216083 | 1.3139915 | -0.324613 | -0.913409 | -0.785276 | -0.572419 | -0.631017 | -0.233968 | -0.793829 | -0.843737 | -0.753236 | -0.009016 | -0.788621 | -0.613223   |
| Sulf2   | 0.5751043 | 0.581148  | 1.2661609 | 1.1479204  | 1.8532973 | 1.7061986 | -1.30576  | -0.936929 | 0.2727996 | -0.725235 | -0.375433 | -0.904326 | -0.193859 | 0.1057672 | -0.85349  | -0.244766 | -0.112514 | -0.956085   |
| Leprel4 | -1.078995 | -0.638481 | -0.572755 | -1.250902  | -0.697067 | -1.029451 | 0.8825467 | -0.692308 | 1.4468001 | 0.6784396 | 1.2918763 | 0.1032831 | -0.526978 | 1.3085843 | 1.8859743 | -0.876639 | -0.217069 | -0.232859   |
| Lsm2    | -0.107007 | -0.824795 | -1.044533 | -1.258132  | -1.305391 | -1.195904 | 0.9088261 | 1.8083543 | 1.1440355 | 1.1188482 | 0.2489272 | 0.9469876 | 0.7758762 | -0.505425 | 0.0500179 | 0.0696787 | -0.665083 | 0.7447177   |
| Pole    | -1.072701 | -1.108252 | -1.1637   | -1.395162  | -1.258191 | -1.21227  | 1.5180826 | 1.1852897 | 0.3113775 | 0.4331548 | 0.9701572 | 0.0429078 | 0.8336925 | 0.0855046 | 1.2433352 | 0.1151003 | -0.456239 | 0.9279126   |
| Atsp1a2 | 1.1895341 | 1.1152901 | 1.6787528 | 1.6592843  | 1.2357558 | 0.9975071 | -0.898426 | -0.799087 | -0.913244 | -0.915337 | -0.915728 | -0.90829  | -0.91156  | -0.103941 | -0.550353 | -0.413863 | -0.246262 | -0.300005   |
| Casq1   | 0.9939387 | 2.4904169 | 0.4555308 | 0.9851224  | 1.5074827 | 1.0276088 | -0.813035 | -0.650453 | -0.793062 | -0.813035 | -0.805993 | -0.787079 | -0.813035 | -0.053333 | -0.595885 | -0.414362 | -0.309357 | -0.611471   |
| Stx1a   | -1.123601 | -1.390386 | -1.038667 | -1.034272  | -1.116317 | -1.363762 | 1.5022714 | 1.7248713 | 0.4580774 | 0.7367774 | 0.4666339 | 0.3440476 | 0.882249  | -0.282812 | 0.995608  | 0.3440476 | -0.409846 | 0.3050797   |
| Scube2  | 0.7744514 | 2.6651495 | 0.3776376 | 1.3853849  | 0.2798765 | 1.1187728 | -1.086362 | -0.280007 | -0.726477 | 1.2619815 | -0.644342 | -0.584022 | 0.2858685 | -0.362532 | -0.806812 | -0.915507 | -0.681024 | -1.062074   |
| Dennd2c | -1.133772 | -0.611936 | -1.000003 | -1.465175  | -1.005777 | -1.419308 | 1.0275088 | 1.5645579 | -0.004487 | 0.6408331 | -0.064027 | 1.0439829 | 0.02372   | -0.042492 | 0.9509626 | 0.436909  | 0.790171  | -0.023515   |
| Mark3   | -1.112217 | -1.11932  | -0.90649  | -1.132468  | -1.141942 | -1.264394 | 2.0033942 | 0.9456147 | 0.8052452 | -0.03734  | 0.5011689 | 0.0496734 | 0.3732586 | 1.3492242 | 1.3380368 | 0.169669  | 0.0298113 | -0.400925   |
| Mc5r    | 2.2879167 | 2.6232304 | 0.238022  | 0.700689   | 0.7075299 | 1.0405497 | -0.607729 | -0.574548 | 0.681493  | -0.47508  | -0.590747 | -0.733018 | -0.668332 | -0.556652 | -0.357764 | -0.733018 | -0.526629 | -0.733018   |
| Tinf2   | -1.204958 | -0.765408 | -0.824911 | -1.167636  | -1.228882 | -0.977985 | 1.272114  | 0.4047903 | -1.052782 | 0.7274665 | 0.5269088 | 0.5858854 | 0.5892847 | -0.535816 | 0.7656291 | 1.0008249 | -0.141098 | 2.0376288   |
| Rad51c  | -1.284852 | -0.671703 | -0.992456 | -0.977165  | -1.036927 | -1.0395   | 2.076595  | 0.0690723 | 0.7553759 | 0.2826917 | 0.1785348 | 0.1804145 | 1.2394579 | 0.621065  | 1.6426826 | 0.0039913 | -1.063101 | -0.015242   |
| Ankr2d6 | -0.781863 | -0.996004 | -0.970455 | -0.821324  | -1.234008 | -0.958402 | 2.2606009 | 0.243179  | 0.8102147 | 0.4581013 | 0.0815584 | 0.1705735 | 0.6803825 | -0.30481  | 0.4922624 | -0.257531 | -0.511547 | -0.160928   |
| Ifit43  | -0.869213 | -0.368229 | -0.809874 | -1.540866  | -0.832131 | -1.324685 | 1.7646603 | 0.3888173 | -0.046051 | 0.3009323 | 1.172544  | 0.3140721 | 1.7201951 | 1.2679179 | -0.328834 | -1.034173 | 0.2369033 | -0.011356   |
| Tcap    | 1.2901356 | 2.2019399 | 1.4024937 | 1.1050474  | 1.0937324 | 0.7169631 | -0.682639 | -0.762754 | -0.821247 | -0.821453 | -0.824576 | -0.814394 | -0.824163 | -0.205019 | -0.460288 | -0.576813 | -0.358225 | -0.601491   |
| Ctsd    | 1.3592815 | 1.759646  | 0.7486075 | 1.8969967  | 0.1681288 | 1.3592815 | -1.15182  | -0.224184 | -0.927902 | -0.871083 | -0.847805 | -0.024809 | -0.866671 | -0.128802 | -0.300428 | -0.128802 | -0.603842 | -0.815395   |
| Hmgcl1  | -0.978246 | -0.868151 | -0.815066 | -0.915877  | -0.915277 | -0.93081  | 0.3233136 | 0.2839416 | 1.048204  | -0.19083  | -0.843182 | -0.396323 | -0.090218 | 0.337386  | 1.349439  | -0.202414 | 0.5489457 | 0.3451992   |
| Fhl2    | -1.16015  | -0.717452 | -0.883188 | -1.117275  | -0.964943 | -1.043436 | 0.9444378 | 2.6915834 | 0.2886065 | 0.631032  | 0.4618213 | -0.372048 | 0.4311171 | 0.4273648 | 1.1457808 | -0.469086 | 0.1501667 | -0.444333   |
| Clstn3  | 2.6037323 | 1.9744581 | 0.3077086 | -0.150537  | 0.8119376 | 1.3755175 | -0.612999 | -0.485538 | -0.567078 | -0.552588 | -0.568275 | -0.614138 | -0.621176 | -0.408786 | -0.473627 | -0.625477 | -0.49424  | -0.622594   |
| Lass4   | 2.3585104 | 2.1029922 | 0.2910442 | 0.3740518  | 0.9376492 | 1.1814298 | -0.713452 | -0.609136 | -0.429594 | -0.544222 | -0.597181 | -0.726779 | -0.694526 | -0.432162 | -0.545313 | -0.751524 | -0.150854 | -0.609933   |
| Elk3    | -1.374573 | -1.237799 | -0.780962 | -0.84345   | -0.92792  | -0.565124 | -0.598167 | 1.1184704 | 0.121852  | -0.24768  | -0.116057 | 1.0442511 | -0.444784 | 0.156648  | 1.4848213 | 2.3364021 | 0.354855  | 0.387645    |
| Nutf2   | -0.79466  | -0.610556 | -0.78092  | -0.996604  | -1.019623 | -0.762163 | 1.3512561 | 1.1192028 | 0.1753777 | -0.190533 | -0.147182 | -0.998351 | 0.371369  | -0.155118 | 0.2077545 | -0.211704 | -0.179433 | 1.9332363   |
| Mgst1   | 1.3518122 | 2.524702  | 0.5981341 | 1.0079543  | 0.7411085 | 1.1802657 | -0.729473 | 0.0269598 | -0.383449 | -0.982601 | -0.901687 | -0.778845 | -0.667944 | -0.387388 | -0.867255 | -0.586904 | -0.387388 | -0.758004   |
| Nfib    | 1.8420683 | 1.767921  | 0.098482  | 1.2193151  | 0.8779583 | 0.9684345 | -0.967563 | -0.262746 | 0.6667617 | -0.452548 | -0.47043  | -1.167462 | 0.1814402 | -0.548699 | -0.650901 | 1.073378  | -0.827571 | -1.201084   |
| Rbfox1  | 0.5840206 | 2.168943  | 0.6227952 | 0.9465499  | 0.5006452 | 1.41778   | -1.19501  | -0.646056 | -1.139963 | -0.105399 | -0.567367 | -1.19051  | -1.099916 | 0.0199673 | 0.1146829 | 0.1029407 | -0.248798 | -0.271179   |
| Cd163   | 1.1432681 | 0.6410045 | 0.8130595 | 0.7576006  | 1.756639  | 1.3589532 | -0.657026 | -0.702315 | -0.932334 | -0.805397 | -0.938949 | -0.146161 | -0.77141  | -0.293671 | -0.656904 | 1.6907423 | -0.547718 | -0.869351   |
| Hdac5   | 1.7408123 | 0.9235592 | 1.3868026 | 1.4527     | 1.1556243 | 0.795342  | -1.187236 | -0.731722 | -0.420695 | -0.378629 | -0.145969 | -1.030125 | -0.764944 | 0.282521  | -0.566374 | -0.166336 | -1.219518 | -1.25904    |
| Rarres2 | 1.011019  | 0.9289361 | 0.7268126 | 1.3568366  | 0.982466  | 1.4445223 | -0.999247 | -0.769316 | -0.998697 | -0.994223 | -0.989132 | -0.941803 | -0.998409 | -0.626092 | -0.273981 | 1.6265369 | -0.134473 | -0.348053   |
| Fgfs    | -1.219468 | -1.185307 | -1.131075 | -1.294985  | -1.164415 | -1.426636 | 0.2833599 | 0.801791  | 1.470667  | 1.544245  | 0.0545929 | 0.28567   | 0.065541  | 0.0403373 | 0.9701785 | 1.1244027 | -0.038072 | 1.272305    |
| Sardh   | 2.4029949 | 1.1304381 | -0.167259 | 1.2991334  | 0.8515379 | 1.1643577 | -1.000154 | -0.837023 | -0.865875 | -0.890328 | -0.947203 | -0.466376 | -0.881351 | -0.90479  | -0.202481 | 0.3903535 | -0.01125  | -0.064724   |
| Bcr     | -0.962891 | -1.393757 | -0.166318 | -1.013669  | -0.920333 | -1.631211 | 0.0069356 | 0.7397013 | 0.1829409 | 0.80616   | 2.2424722 | 0.5336958 | 0.0919455 | -0.77929  | 6.21E-06  | 0.1966429 | 1.3771249 | 0.6871536   |
| Wnt3a   | -1.193131 | -1.069495 | -0.84088  | -1.0130659 | -0.97755  | -1.224937 | 0.0494007 | 0.3435792 | 0.42135   | 0.4665441 | 0.2405286 | 1.4351372 | 0.0361398 | -0.558135 | 0.290616  | 0.460979  | -0.258419 | 1.4993826</ |



|         |           |           |           |           |           |            |           |            |           |            |            |           |           |           |           |            |            |           |
|---------|-----------|-----------|-----------|-----------|-----------|------------|-----------|------------|-----------|------------|------------|-----------|-----------|-----------|-----------|------------|------------|-----------|
| Hmgb3   | -1.01362  | -0.705178 | -1.303828 | -1.356852 | -1.131003 | -1.027926  | 0.58103   | 2.2665034  | 0.2299467 | -0.239235  | -0.122082  | 0.2526848 | 0.3268664 | 0.385784  | 0.567771  | 0.2595567  | 1.7990058  | 0.230574  |
| Mta2p   | 1.0664788 | 2.1462267 | 0.5927026 | 0.5445659 | 1.3452666 | 0.744145   | -0.280188 | -0.981098  | -0.669657 | -0.8562184 | 0.5197603  | -0.304809 | -0.101059 | -0.798028 | -0.775185 | -1.308454  | -1.066983  | -0.986304 |
| Abca1   | 0.7503535 | 0.7891317 | 0.7666973 | 1.6406765 | 0.9075145 | 1.8975695  | -1.258508 | -0.886525  | -0.548422 | -0.874377  | -0.534578  | -1.122654 | -0.610963 | -0.355051 | -0.605754 | 1.0870431  | -0.058639  | -1.103375 |
| Sash1   | 0.2689721 | 0.6644029 | 1.3541268 | 1.5907839 | 1.177986  | 1.7410866  | -1.370016 | -0.091992  | -1.195059 | -0.708635  | -0.711193  | -0.784264 | -0.914132 | 0.1111785 | -0.741897 | 0.5677117  | 0.06164    | -1.0207   |
| Cybb    | 0.3316186 | 0.1762219 | 1.660929  | 2.6509563 | 0.3113559 | 1.1751988  | -0.897728 | -0.753103  | -0.748025 | -0.846412  | -0.654693  | -0.595057 | -0.788342 | -0.562549 | -0.38365  | 0.7131053  | -0.087289  | -0.492537 |
| Pcolce2 | 2.0826483 | 1.2393039 | 0.334396  | 0.4175732 | 1.6787551 | 1.3367723  | -0.707728 | -0.810247  | -0.828784 | -0.495883  | -0.865319  | -0.472787 | -0.102881 | -0.267339 | -0.517335 | 0.5101313  | -0.471801  | -0.986698 |
| Cd48    | 0.9473226 | 0.9145262 | 1.1113046 | 1.8067054 | 1.1631045 | 1.6570208  | -1.14774  | -0.855112  | -0.733938 | -0.889076  | -0.947777  | -0.604565 | -0.854548 | -0.67789  | -0.563886 | 0.4567487  | -0.34216   | -0.440041 |
| Fam116b | -1.217428 | -0.126041 | -0.04102  | -0.957888 | -0.624374 | -1.230264  | 0.4579384 | -0.539346  | 0.2069706 | 1.2799324  | 0.1190636  | 2.7674732 | 0.7897381 | -0.359851 | -0.37823  | 0.1802739  | -0.302884  | 0.8759352 |
| Cd83    | 1.0482606 | 0.3851941 | 0.8551081 | 2.4261397 | 0.3767683 | 2.0344905  | -0.934083 | -0.698949  | -0.723668 | -0.631772  | -0.802748  | -0.322096 | -0.799951 | -0.561435 | -0.650634 | -0.108392  | -0.315658  | -0.576575 |
| C4a     | 0.5368289 | 2.7435411 | 1.2235746 | 0.4854349 | 1.3626083 | 0.6482467  | -0.426413 | -0.415597  | -0.883933 | -0.683621  | -0.849208  | -0.828049 | -0.813643 | 0.1720742 | -0.691553 | -0.26376   | -0.486542  | -0.82999  |
| Notch4  | -1.158351 | -1.627566 | -0.537917 | -0.629888 | -1.554858 | -1.308412  | 0.7417548 | 2.0105157  | 0.7210415 | -0.447087  | 0.5973066  | 0.1110775 | 0.4891711 | 0.888338  | 0.558036  | 1.0418443  | 0.2544249  | -0.149431 |
| Ppt2    | 1.0837797 | 0.4159092 | 1.1524647 | 2.0808827 | 0.5021923 | 1.0442955  | -0.252199 | -0.011798  | -1.168206 | -0.453635  | -0.251155  | -0.410254 | -0.930214 | -0.810287 | -0.135487 | 0.8318609  | -0.368944  | -0.519206 |
| Hivep2  | -1.389188 | -0.994229 | -0.597216 | -1.067277 | -0.820963 | -0.92101   | 0.0002223 | 0.3413524  | 1.4142371 | 0.5991828  | 1.0087254  | -0.377011 | -0.090139 | -0.013758 | 2.6506935 | -0.290498  | 0.5562708  | -0.009393 |
| Itga2   | -1.219146 | -0.866276 | -0.621486 | -1.097576 | -1.062491 | -0.071196  | -0.032426 | 2.2442944  | 1.0878811 | 0.8498781  | 0.1443985  | 0.3940895 | 0.1861257 | -0.505942 | 1.6642747 | 0.6578161  | -0.370153  | -0.382066 |
| Lpl     | 1.010198  | 0.70899   | 1.1312035 | 2.4790782 | 0.9228152 | 1.4200106  | -0.726419 | -0.765677  | -0.755375 | -0.765212  | -0.756491  | -0.72444  | -0.745174 | -0.548102 | -0.570835 | -0.276592  | -0.403226  | -0.724825 |
| Lama5   | -1.389481 | -1.309983 | -0.097399 | -1.216144 | -0.709197 | -1.270021  | 1.9294847 | -0.457743  | -0.297871 | 0.8245183  | 0.5198664  | 0.962242  | 0.8338494 | 1.4804127 | -0.564463 | -0.263177  | 0.3521077  | 0.6729977 |
| Steap1  | -0.637    | -0.679081 | -0.665824 | -0.652645 | -0.693057 | -0.516764  | 0.6915543 | -0.381702  | -0.570778 | 0.2588819  | -0.418781  | -0.084325 | -0.558805 | -0.188984 | 0.5162139 | 0.8430617  | 0.2870026  | 3.510532  |
| Steap2  | -0.863365 | -0.917065 | -0.808129 | -0.818196 | -0.873802 | -0.306012  | 0.1946687 | -0.057149  | -0.931819 | -0.026388  | -0.632547  | -0.030397 | -0.835718 | 0.4275325 | 1.1846986 | 1.7761513  | 0.7346999  | 2.3008036 |
| Anxa1   | 2.4335279 | 2.2522359 | 0.1641029 | 0.2115645 | 1.0358353 | 0.8726965  | -0.650331 | -0.568234  | -0.590242 | -0.524078  | -0.575723  | -0.651118 | -0.633045 | -0.510067 | -0.476718 | -0.650967  | -0.486766  | -0.652675 |
| Awat9   | 2.304881  | 1.7068462 | 0.3501407 | 0.7687512 | 1.2658948 | 0.7416312  | -0.940914 | -0.861648  | -0.759403 | -0.303402  | -0.371057  | 0.3872875 | -0.38649  | -0.466435 | -0.862864 | -0.885901  | -0.797057  | -0.885761 |
| Plekho1 | 0.954146  | 0.1985201 | 1.0801703 | 2.3276185 | 0.5657506 | 1.2705498  | -1.181299 | -0.888272  | -0.59634  | -1.006794  | -1.042708  | -0.500089 | -0.984247 | -0.561006 | -0.298678 | 1.0296739  | -0.073896  | -0.446287 |
| Eps8    | 1.6044767 | 0.3403667 | 0.5010975 | 1.4917615 | 0.1437125 | 2.0585524  | -1.092096 | -0.654038  | -0.461338 | -0.789569  | -0.1061471 | -1.188112 | -1.128077 | -0.268246 | -0.408657 | 1.0211945  | -0.158392  | 0.0444347 |
| Fcrls   | 1.4126346 | 1.1890086 | -0.418868 | 1.0495742 | 1.6851599 | 1.8235652  | -1.113549 | -0.793785  | -0.444305 | -0.90853   | -0.461374  | -0.989044 | -0.838919 | -0.182598 | 0.2836164 | 0.08243    | -0.303567  | -1.07145  |
| Ncagp   | -1.246498 | -0.992457 | -1.325966 | -1.337289 | -1.24447  | -1.229706  | 1.4024975 | 1.4710915  | 0.3554108 | 0.4510941  | 0.3798319  | 0.4134532 | 0.8555217 | 0.0302427 | 0.743878  | -0.036191  | -0.028145  | 1.3377013 |
| Gatsl2  | -1.161156 | -1.134276 | -0.70556  | -0.800854 | -1.158711 | -1.56916   | 0.3670713 | -0.072789  | -0.656406 | 1.5341269  | 1.4159584  | 0.4022112 | 1.2062382 | -0.409928 | 0.8589237 | 0.4913621  | 1.3084264  | 0.0391245 |
| Ncf1    | 1.7187302 | 0.0649939 | 0.6615783 | 2.530668  | 0.1494217 | 1.1350669  | -0.968993 | -0.723904  | -0.686812 | -0.819825  | -0.856017  | -0.537621 | -0.77013  | -0.556304 | -0.565022 | 0.9508019  | -0.236243  | -0.463389 |
| Lrrc27  | 1.0610172 | 0.586959  | -0.433216 | 2.1876532 | -0.130137 | 2.2115736  | 0.7257918 | -0.629588  | -1.309686 | -0.002286  | -1.172786  | -0.582718 | -0.884027 | -0.506082 | -0.320147 | -0.068449  | -0.52723   | -0.78378  |
| Lbp     | 0.9571576 | 0.4647867 | 1.3682856 | 1.2374029 | 0.8457165 | 1.8552381  | -1.026137 | -0.55669   | -0.912    | -1.026137  | -1.008511  | -0.642049 | -0.946015 | -0.478342 | -0.375419 | 1.3284245  | -0.466597  | -0.619113 |
| Fil1    | 0.462253  | 0.5351547 | 1.0336329 | 1.8612076 | 0.9674404 | 1.7385525  | -1.28859  | -0.696872  | -0.848257 | -1.091384  | -0.999499  | -0.917239 | -0.680003 | -0.442763 | -0.15746  | 0.9291676  | 0.1608881  | 0.294431  |
| Diexf   | -0.324291 | -0.310581 | -0.871409 | -1.039489 | -1.198999 | -1.27214   | 0.8486631 | 0.1245034  | -0.848631 | 0.9012253  | 0.2137388  | 0.4405244 | 0.5884777 | 2.0930085 | -0.545667 | -1.405348  | 0.593096   | 1.0370254 |
| Hsd11b1 | 0.5580973 | 0.6854415 | 1.5331081 | 1.4857735 | 0.7458346 | 0.9650719  | -1.054789 | -0.703334  | -0.968756 | -1.008131  | -0.899194  | -0.895685 | -0.989459 | -0.41184  | -0.432708 | 1.835504   | 0.090828   | -0.535762 |
| H2-M1   | -0.472528 | 0.200967  | 1.9851416 | 1.6688229 | 1.4801708 | 0.9955943  | -0.044987 | -1.290235  | -0.242051 | -0.75872   | -0.87904   | -0.358605 | -0.902555 | -0.107562 | -0.4519   | 0.4657394  | 0.4219248  | 0.217887  |
| Lcnf3   | 1.9710384 | 0.476825  | 0.4668494 | 2.2850369 | 0.0063997 | 1.5829798  | -0.936013 | -0.286787  | -0.750173 | -0.891602  | -0.584649  | -0.554    | -0.314842 | 0.0789799 | -0.932082 | -0.720205  | -0.56027   | -0.783325 |
| Ctsr    | 1.1159416 | 0.2657407 | 1.2106492 | 2.2736631 | 0.3574157 | 1.581296   | -0.997063 | -0.846175  | -0.812629 | -0.908574  | -0.9288013 | -0.574758 | -0.855061 | -0.510684 | -0.457018 | 0.80405636 | -0.237915  | -0.481741 |
| H2-M2   | -0.423043 | 1.4169042 | 0.9570671 | 0.9126719 | 1.0479627 | 2.0081104  | -1.42398  | -0.928557  | -0.856661 | -0.391307  | -0.989548  | 0.5712916 | -0.926782 | -0.662815 | -0.703099 | 0.828751   | 0.1532256  | -0.590191 |
| Eef1a2  | 1.208785  | 1.931524  | 1.1544195 | 1.8041779 | 0.645081  | 0.8330797  | -0.891225 | -0.747328  | -0.899218 | -0.896337  | -0.891163  | -0.899218 | 0.1623357 | -0.573432 | -0.267227 | -0.44702   | -0.328018  |           |
| Lnx2    | -1.267392 | -1.124472 | -0.932999 | -1.148055 | -0.86651  | -1.623333  | 1.7996127 | 0.1979324  | 0.7574585 | 1.2458476  | 0.7644821  | 0.2732788 | 1.0424015 | -0.353554 | 0.1189864 | -0.374546  | 0.276283   | 0.4927773 |
| Il19    | -0.865552 | -0.837815 | -0.720796 | -0.810475 | -0.524898 | -0.1970964 | -0.618851 | -0.5725867 | 1.506688  | -0.16471   | 1.0609799  | 0.6530366 | -0.424536 | -0.754599 | 0.5305076 | -0.070696  | 2.9847932  |           |
| Dyrk3   | -0.878597 | -1.178832 | -0.849463 | -0.611815 | -1.051231 | -0.688676  | 1.5598395 | -0.0089862 | 0.7313366 | 0.6185839  | 0.1315603  | -0.381711 | 0.7257548 | -0.112125 | 0.0992149 | -0.580375  | -0.0114666 | 2.7160665 |
| Foxred2 | 1.2816616 | 0.25821   | 0.5628106 | 0.8015274 | 1.715885  | 2.1142339  | 0.2112686 | -1.468533  | -0.144275 | -0.53308   | -0.088423  | -0.92494  | -0.213095 | -0.644912 | 0.0820094 | -0.903598  | -0.905146  | -1.201605 |
| Cmah    | -0.303123 | -1.093333 | -0.914587 | -0.723302 | -0.910365 | -1.037668  | 0.3389416 | 0.395659   | 0.293216  | -0.036366  | -0.041461  | -0.961899 | 1.8731692 | -0.9916   | 2.220854  | 0.646344   | 0.1056457  | 1.1414326 |
| Tll12   | -0.964842 | -1.243714 | -0.923222 | -1.306253 | -1.116634 | -1.204794  | 0.0071386 | 0.984379   | 1.7179662 | 0.798782   | 1.2938891  | 0.2662199 | 0.1721807 | 0.0753812 | 0.3441669 | -0.782756  | 0.486509   | 1.4045137 |
| Etaa1   | -0.905261 | -0.715117 | -1.146741 | -0.93933  | -1.198965 | -1.673191  | 0.9334759 | 1.0455271  | 1.269018  | 0.8612692  | 0.4813087  | 1.0778184 | 0.5322718 | -0.801749 | 0.031298  | 0.3933718  | -0.661194  | 1.4162072 |
| Mtn4    | 0.7478503 | 0.0518722 | 1.2359314 | 2.8151578 | 0.952684  | 1.0690543  | -0.050923 | -0.790355  | -0.619359 | -0.92439   | -0.347868  | -0.860751 | -0.872687 | -0.152298 | -0.462284 | -0.381838  | -0.51764   | -0.889456 |
| Brcs1   | -1.164454 | -0.906214 | -1.0928   | -1.200899 | -1.19474  | -0.978519  | 1.9160663 | 1.0684908  | -0.012641 | 0.62303    | -0.001222  | 0.757028  | 0.5840582 | -0.406899 | 1.5917924 | -1.177186  | -0.326219  | 0.912326  |
| Gsdma   | 2.3316364 | 1.7769922 | 0.3532864 | 0.7950411 | 1.3942502 | 0.5522329  | -0.835424 | -0.91648   | -0.897253 | -0.085448  | -0.196961  | -0.335157 | -0.410495 | -0.758772 | -0.341011 | -0.106586  | -0.8018    | -0.618052 |
| Tnnx2   | 0.7819768 | 0.656425  | 0.838843  | 1.0940097 | 1.1272103 | 0.1011096  | -0.783379 | -0.67023   | -0.788191 | -0.787254  | -0.789914  | -0.784869 | -0.789914 | -0.217315 | -0.528125 | -0.467427  | -0.355689  | -0.547254 |
| Cd300lg | 1.6233445 | 0.6823744 | 1.300723  | 1.6194798 | 0.5978322 | 0.6974236  | -0.674069 | -1.631966  | 0.1635264 | -0.687706  | -0.652754  | 0.0763492 | -1.275315 | -0.521924 | 0.0699203 | -1.620616  | 0.3563243  | -0.123257 |
| Vtn     | 0.7735865 | 1.3881426 | 0.997241  | 1.5968865 | 0.9598751 | 1.3001598  | -1.226    | -0.916848  | -1.226    | -1.131068  | -0.926023  | -0.241793 | -1.226    | 0.4179901 | 0.881692  | 0.0517404  | 0.0325794  | -0.760644 |
| Traf4   | -0.866363 | -0.924911 |           |           |           |            |           |            |           |            |            |           |           |           |           |            |            |           |



|           |           |           |           |           |           |            |            |           |           |            |           |            |           |           |           |            |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|------------|------------|-----------|-----------|------------|-----------|------------|-----------|-----------|-----------|------------|-----------|-----------|
| Mb        | 1.2585641 | 0.7458927 | 1.7789596 | 2.6522714 | 0.2681079 | -0.063465  | -0.730481  | -0.624203 | -0.757375 | -0.759086  | -0.771089 | -0.750385  | -0.750714 | 0.1981843 | -0.549337 | -0.300103  | -0.395732 | -0.450011 |
| P4ha2e    | -1.213637 | -1.368197 | -0.952604 | -1.122782 | -0.717702 | -0.831407  | -0.066422  | 0.4788329 | 2.2506697 | 0.503789   | 0.5691818 | 0.5221902  | 0.8144119 | 1.1031997 | 0.9431847 | 0.4191631  | -0.706317 | -0.772505 |
| Allox12e  | 2.8810822 | 1.2791528 | 0.2678192 | 1.3425861 | 0.685066  | 0.6700051  | -0.669848  | -0.507981 | -0.604242 | -0.550234  | -0.845156 | -0.661104  | -0.63701  | -0.566675 | -0.598186 | -0.625404  | -0.481509 | -0.647257 |
| Abrb1     | 1.1512306 | -0.353278 | 0.9820157 | 2.5360599 | 0.932423  | 0.7210976  | 0.8873822  | -0.633029 | -0.219111 | -0.545951  | -0.525724 | -0.101654  | -0.455432 | -0.543818 | -1.337488 | 0.0954733  | -0.508985 | -1.166327 |
| Sart3     | -1.188575 | -0.778032 | -0.792381 | -1.181638 | -1.117763 | -1.29668   | 1.548311   | 0.0231602 | -0.08328  | 0.2625046  | 1.1040158 | 0.3394124  | 0.9530315 | 0.0031452 | 0.235149  | -0.786057  | -0.133338 | 1.8906488 |
| Sifn3     | -0.935309 | -0.860689 | -0.374897 | -0.610748 | -0.68794  | -0.665224  | -0.404162  | -0.287852 | -0.787207 | 0.2966452  | -0.314349 | 1.5607123  | -0.260401 | -0.455688 | -0.026044 | 1.2318121  | 0.1025494 | 2.938147  |
| Nars2     | -0.750544 | -1.163357 | -0.728756 | -1.654396 | -0.799353 | -1.334041  | 0.1598134  | 1.9695524 | 0.9771525 | 1.3597089  | 0.4603895 | 0.1915241  | 0.7815329 | 0.7635556 | 0.2292689 | -0.922264  | 0.5741631 | -0.113952 |
| Mfsd3     | -1.22208  | -0.719117 | -1.142821 | -1.377888 | -1.005173 | -1.192678  | 1.277548   | 1.7051467 | 0.8171706 | 0.3862073  | 0.59727   | 0.2345176  | 1.1250079 | -0.110194 | -0.451908 | -0.1225751 | -0.222374 | 1.4270149 |
| Dnase11   | 1.2395405 | 0.5260326 | 1.0045273 | 1.6121771 | 0.4878657 | 1.2241673  | -0.87815   | -0.588642 | -0.817916 | -0.859841  | -0.833994 | -0.893317  | -0.829175 | 1.7044025 | -0.988494 | 0.1758609  | -0.197392 | -1.087653 |
| Alldh3a1  | 0.3128519 | 0.5373525 | -0.133002 | 0.6945623 | 0.703922  | 0.8304786  | -0.676008  | -0.146043 | -0.259376 | -0.597167  | -0.415355 | -0.621168  | -0.577593 | -0.376784 | -0.550047 | -0.67819   | -0.473486 | -0.674948 |
| Scrn1     | 0.7446547 | 0.3782289 | 0.7017897 | 0.7084719 | 1.9729134 | 2.4349493  | -1.202611  | -0.518252 | -0.987266 | -0.805517  | -0.724092 | -0.489184  | -0.573337 | -0.003017 | -0.551578 | -0.14793   | -0.104139 | -0.870486 |
| Scn1b     | 1.1479459 | 1.4355985 | 0.7809818 | 1.6333367 | 1.1288394 | 1.3164587  | -1.314082  | -0.619001 | -1.084324 | -1.1039835 | -0.749146 | -0.854299  | -1.105158 | 0.1231638 | -0.534219 | 0.0914008  | 0.0260218 | -0.383683 |
| Chtf18    | -1.285149 | -1.375349 | -0.903146 | -1.37105  | -1.258665 | -1.407309  | 0.8288904  | 1.013018  | 0.3852969 | 0.9399825  | 0.8260022 | 0.6502729  | 0.3504804 | 0.1003384 | 1.1302379 | 0.5555795  | -0.392989 | 1.2135593 |
| 2610027L1 | -0.626029 | -0.788738 | -1.292989 | -1.057397 | -1.122456 | -0.919293  | 1.0909576  | 0.0432023 | -0.921747 | 0.8216519  | 0.5497143 | 0.48413    | 0.4779277 | -0.292064 | 0.5858323 | -0.072104  | 0.3890764 | 2.6503241 |
| Atp6v0a1  | 1.8257858 | 0.8995591 | 0.8287998 | 1.8916342 | 0.3559081 | 1.2549282  | -0.414217  | -1.112208 | -0.898277 | -0.175176  | -0.417418 | -0.777204  | -0.618328 | 0.4235034 | -0.104108 | -0.049575  | -0.62457  | -1.352038 |
| Psmc3ip   | -0.779097 | -0.921593 | -0.924692 | -1.138851 | -0.969785 | -0.939589  | 2.8227218  | 0.6313964 | 0.1653689 | 0.3585352  | 0.1080396 | 0.1415894  | 0.3989058 | -0.136201 | 1.2393105 | -0.392133  | -0.570369 | 0.906442  |
| Aoc3      | 0.1770958 | 2.0581669 | 1.2361019 | 0.7079976 | 0.9779886 | 0.5988535  | -0.920993  | -0.781117 | -1.138675 | -1.032194  | -1.17754  | -0.712903  | -1.206995 | -0.068774 | 0.1188949 | 0.9544348  | -0.077353 | 0.1620158 |
| Sec14l4   | 2.0314019 | 2.5054761 | 0.1890511 | 0.2187281 | 1.1768406 | 0.9405232  | -0.6382    | -0.489871 | -0.597218 | -0.474341  | -0.553845 | -0.663033  | -0.643255 | -0.475806 | -0.545213 | -0.718156  | -0.540096 | -0.722926 |
| Tlcd1     | 1.5303486 | 1.9016405 | -0.085434 | 0.5185847 | 1.0768822 | 1.0723106  | -0.728488  | -0.515338 | -0.771739 | 0.3927099  | -0.033765 | -0.629162  | -0.375497 | 1.0934545 | -0.9856   | -1.492401  | -1.162358 | -0.79992  |
| Gyg       | 1.1449558 | 1.0041946 | 1.2906222 | 1.8720383 | 0.9455106 | 1.3930023  | -1.022214  | -0.690071 | -0.926301 | -1.06497   | -0.963655 | -0.707452  | -0.907057 | -0.384296 | -0.324475 | 0.2123898  | -1.130211 | -0.652601 |
| Sic6a8    | 1.8334817 | 1.0924536 | 0.926463  | 1.6275893 | 0.2901059 | 0.3230485  | -0.751662  | -0.833727 | -1.076295 | -0.038021  | -0.239408 | 0.0321304  | -0.440118 | 0.7689634 | -1.316589 | -0.467489  | 0.1434154 | -1.873432 |
| Pdk4      | 1.3078236 | 0.9143687 | 0.2799976 | 0.6739757 | -0.372069 | -0.039927  | -0.540603  | -0.440635 | -0.632622 | -0.636231  | -0.661812 | -0.521851  | -0.386632 | -0.042681 | -0.29381  | -0.55273   | -0.534651 | -0.519891 |
| Sema6a    | 2.3490261 | 0.9129127 | 0.4505028 | 1.4471771 | 1.0211765 | 1.5787511  | -0.713974  | -0.218947 | -0.703268 | -0.645082  | -0.774819 | -0.753758  | -0.904334 | -0.295933 | -0.366929 | -0.651035  | -0.536784 | -0.775683 |
| Lyst      | 1.7940611 | 1.4737588 | 0.9951711 | 1.4324062 | 0.631663  | 1.5775776  | -0.832314  | -0.579671 | -0.933873 | -0.973382  | -0.809578 | -0.097317  | -0.889141 | -0.669363 | -0.733242 | 0.2732997  | -0.351509 | -0.921445 |
| Syne1     | 1.4257541 | 0.6656178 | 0.1867356 | 1.8352814 | 0.6899315 | 1.7882337  | -1.526702  | -0.640207 | -0.517366 | -0.855586  | -1.00578  | -0.751181  | -0.951534 | 0.4036755 | -0.174968 | 0.5383299  | -0.305761 | -0.800656 |
| Fbxo5     | -1.297961 | -0.833208 | -0.136097 | -1.293945 | -1.376669 | -1.086357  | 0.9909457  | 1.7881218 | 0.8174037 | 1.116493   | 0.4558896 | 0.8050608  | 0.3625132 | -0.288544 | 0.360096  | -0.564122  | -0.008399 | 1.0936225 |
| Frk       | -0.981156 | -0.562896 | -1.245844 | -1.050712 | -0.89874  | -0.586449  | 0.0526745  | 1.3878306 | -1.038973 | -0.403341  | -0.712222 | 0.20772463 | -0.350676 | 0.0760953 | 1.0939686 | 0.0314556  | 0.6314502 | 1.5895874 |
| Trdn      | 1.045581  | 1.969464  | 1.0725772 | 1.3196564 | 1.3065976 | 0.9876257  | 0.934325   | -0.69759  | -0.947213 | -0.939919  | -0.942667 | -0.951545  | -0.951545 | 0.1446206 | -0.469619 | -0.477534  | -0.230517 | -0.304548 |
| Trmt11    | -0.821364 | -0.652479 | -1.304166 | -1.301567 | -1.404509 | -1.279072  | 0.846175   | 1.6503162 | 0.4596221 | -0.008084  | -0.23817  | 0.1828531  | 1.0418532 | 0.4499023 | 1.1033635 | -0.369824  | 0.061853  | 1.5848535 |
| Lrp1      | -0.622431 | -0.904507 | -0.761665 | -0.684291 | -0.885746 | -0.609027  | 3.3660722  | 0.7461648 | 0.5017646 | -0.114321  | -0.731487 | -0.274699  | 0.5144582 | -0.026759 | 0.8954    | 0.0242659  | -0.588476 | 0.2452857 |
| Adat2     | -1.049186 | -0.80655  | -1.222894 | -1.354628 | -1.355387 | -1.130017  | 1.443916   | 0.6314116 | 0.9659767 | 0.7395533  | 0.1457224 | 0.8160782  | 0.7307755 | 0.4770055 | 1.0682207 | -0.665574  | -0.619205 | 1.0207815 |
| Pex3      | 2.1836215 | 2.1647502 | -0.144051 | 0.1179791 | 0.8146729 | 0.10379005 | -0.774115  | -0.076274 | -0.458913 | -0.54465   | -0.907245 | -0.213576  | -0.782755 | -0.235074 | -0.827014 | -0.587881  | -0.718601 |           |
| Mical1    | 0.8039048 | 0.2591427 | 0.8522881 | 2.9341228 | 1.1013929 | 1.2486251  | -1.60909   | -0.308696 | -1.006613 | -1.023883  | -0.759597 | -0.744247  | -1.145615 | 0.0148632 | -0.210816 | 0.7263251  | -0.094892 | 0.520877  |
| Sic16a10  | 0.6579784 | 0.9221967 | 1.8935941 | 1.2322385 | 0.2163641 | 1.4034362  | -1.125367  | -1.088464 | 0.2329653 | -0.668074  | -0.509129 | -0.224373  | -0.338069 | -1.06252  | -0.66371  | 0.0956848  | -0.733114 | -0.939835 |
| Fyn       | 0.5014779 | 0.4670556 | 0.8601257 | 1.5188635 | 1.2831042 | 1.5599021  | -1.671092  | -0.401228 | -0.839504 | -1.090226  | -1.149884 | -0.391842  | -1.099612 | -0.119785 | -0.477011 | 1.1012497  | -0.48197  | 0.4303742 |
| Tube1     | -0.916861 | -0.778812 | -1.128384 | -1.136225 | -1.209878 | -1.217391  | 1.9366604  | 1.4821689 | 0.5838696 | 0.7732684  | 0.7204834 | 0.7874101  | 0.5604072 | -0.656916 | 0.5478108 | -0.394838  | -0.614578 | 0.6618037 |
| Prep      | -1.305202 | -1.201984 | -1.031805 | -1.354004 | -1.145276 | -1.351168  | 1.0709926  | 1.214604  | 0.8206592 | 1.3454855  | 0.9851806 | 0.0767006  | 0.407366  | -0.12256  | 0.4937059 | -0.230912  | 0.2318263 | 0.0963923 |
| D10Bwg13  | 2.8311732 | -0.120016 | -0.012304 | 1.2967579 | -0.303128 | 0.8376226  | -0.795486  | -0.280363 | -0.468815 | -0.505267  | -0.34398  | -0.633286  | -0.478544 | -0.67597  | -0.559669 | -0.444318  | -0.576908 | 0.3356003 |
| Hebp2     | 1.9971726 | 1.7876835 | -0.007613 | 0.4341504 | 1.0154299 | 0.5489732  | -0.201119  | -0.481342 | -1.027412 | -0.362656  | -0.404697 | 1.5097475  | -0.794873 | -0.698715 | -0.621507 | -0.874754  | -0.875281 | 0.0564122 |
| Smpd13a   | 0.7266513 | 1.5518654 | 0.9753931 | 0.7739677 | 1.2294628 | 1.0542687  | -1.214822  | -0.969604 | -0.599197 | -0.484109  | -0.520609 | 1.7330207  | -0.682061 | -0.832781 | -0.841591 | -0.078718  | -0.716893 | -1.102444 |
| Fabp7     | 0.8989746 | 0.6396798 | 0.6284867 | 1.7817573 | 0.254308  | 2.2377502  | -1.035027  | -0.747461 | -1.035027 | -0.592454  | 0.8631909 | 0.1460123  | -0.896906 | -0.922781 | -0.863029 | -0.249039  | -0.204226 | -0.905021 |
| Fabp2     | 2.0327589 | 0.8317894 | 0.8326859 | 1.123539  | 0.8168126 | 1.9352694  | -1.132661  | -0.869712 | -0.800286 | -0.253344  | -0.49564  | 0.0428418  | -0.697448 | -0.766299 | -0.726    | -0.462335  | -0.655506 | -0.756465 |
| Ecdcd1    | 1.7594735 | 2.813914  | 0.9004809 | 0.0863104 | 0.708597  | 1.1434235  | -0.5021281 | -0.490813 | -0.597139 | -0.453678  | -0.498805 | -0.353061  | -0.472185 | -0.371152 | -0.611744 | -1.028265  | -0.314775 | -0.901901 |
| Cdc59     | -0.844658 | -1.114559 | -1.096743 | -1.273905 | -0.918673 | -0.956406  | -0.364268  | -0.746537 | -0.046447 | 0.5285857  | -0.158172 | 2.8783312  | 0.0982158 | -0.056359 | 0.2978708 | -0.041602  | 0.0656634 | 0.8767217 |
| Lama2     | 1.1091285 | 0.2272351 | 0.6773507 | 1.8547962 | 1.1482613 | 1.9039386  | -1.108788  | -0.82268  | -1.021166 | -0.863218  | -0.923031 | -0.688652  | -0.994093 | 0.1890938 | -1.12785  | 0.0350507  | 0.2576378 | -0.877081 |
| P4ha1     | -0.953406 | -1.449369 | -0.761151 | -0.637724 | -1.13663  | -0.709582  | -0.256209  | 0.162472  | 2.5245893 | -0.010052  | -0.583417 | 1.2685417  | 0.0369758 | 0.6028593 | 1.126526  | 0.8940157  | -0.479616 | 0.3611786 |
| Dcn       | 1.287249  | 1.3299127 | 0.5438755 | 0.979242  | 1.4038825 | 2.1062678  | -0.890579  | -0.748081 | -0.865897 | -0.877718  | -0.841712 | -0.798962  | -0.882848 | -0.23872  | -0.515209 | 0.0606042  | -0.392127 | -0.66646  |
| 2310015B2 | 0.9404039 | 2.9238933 | 0.9957819 | 1.4774392 | -0.2107   | 0.408385   | -0.331573  | -0.71112  | -0.491605 | -0.423699  | -0.853487 | -0.605485  | -0.147547 | -0.749769 | -0.513161 | -0.54058   | -0.92177  | -0.245354 |
| Cdk1      | -1.165601 | -1.202269 | -1.142108 | -1.342121 | -1.17479  | -1.046001  | 0.3876203  | 1.814615  | 0.3342358 | 0.5477817  | -0.008889 | 0.6662223  | 0.3062815 | -0.232161 | 0.6729817 | 0.4296722  | 0.2991391 | 1.8553871 |
| Poc1b     |           |           |           |           |           |            |            |           |           |            |           |            |           |           |           |            |           |           |



|             |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Appl2       | 1.0256422 | 2.2673209 | 0.5573624 | 1.1082361 | 1.0895787 | 1.4645488 | -1.002532 | -1.018644 | -0.464508 | -0.08478  | -0.811624 | -1.033583 | -0.816853 | -0.478508 | -0.308703 | -0.776248 | -0.142959 | -0.573747 |
| Slk36a2     | 0.4807406 | 1.6527401 | 1.378713  | 1.8793794 | 1.5369669 | 0.4610104 | -1.003549 | -0.91875  | -0.629406 | -0.306526 | -0.396794 | -0.040104 | -0.989198 | -0.353252 | -0.936957 | -0.13181  | -0.624393 | -1.065174 |
| Stc10       | 0.6922728 | 0.164382  | 1.246778  | 1.9884277 | 0.8731623 | 0.8871785 | 1.4985812 | -0.885224 | -0.872871 | -0.705904 | -0.755257 | -1.116691 | -1.125192 | -1.074537 | -0.523113 | 0.5376046 | -0.310568 | -0.699031 |
| Pfkl        | -1.373637 | -1.188872 | -0.937022 | -1.44615  | -1.171353 | -1.406582 | 1.4692118 | 0.9654303 | 1.0601117 | 0.5711615 | 0.5531545 | 0.7754091 | 0.7250451 | 0.1673532 | 0.8740607 | -0.342987 | 0.0010099 | 0.7046561 |
| Pex13       | 0.6804425 | 3.1910393 | 0.870116  | 0.1680683 | 0.5048986 | 0.4432632 | -0.734149 | 0.908027  | -0.390062 | -0.221464 | -0.366962 | -0.695399 | -0.274599 | 0.3967838 | 0.7040709 | -1.229938 | -0.895462 | -0.839982 |
| Xpo1        | -1.154836 | -0.384663 | -0.757314 | -1.417291 | -1.357314 | -1.37297  | 0.8989132 | 1.2449082 | 0.5615682 | 0.4656204 | 0.0246374 | 0.310532  | 0.1526147 | 0.2627087 | 1.2497011 | -0.011265 | 0.0765898 | 1.8169491 |
| Cpeb4       | 1.948411  | 0.9198592 | 0.7331158 | 1.8230557 | 0.7647964 | 1.3961997 | -1.070254 | -0.941684 | -1.226002 | -0.330844 | -0.584402 | -0.201887 | -0.41648  | -0.475757 | -0.59127  | -0.738719 | -0.247201 | -0.760937 |
| Shc2        | 1.9110314 | 0.1056671 | 0.603602  | 1.1734996 | 0.6012187 | 1.559538  | -1.110363 | -0.96856  | -1.216955 | -0.993939 | -0.939752 | -0.601693 | -1.188898 | 0.2681228 | -0.04315  | 1.1651845 | -0.260013 | -0.064542 |
| Spnb2       | 1.3855704 | 0.9555344 | 0.5342268 | 1.3966524 | 0.8509592 | 1.4398936 | -1.365674 | 0.335001  | -0.952235 | -1.153214 | -0.80072  | -1.030698 | -1.272595 | 0.0065533 | 0.2168767 | 0.0845849 | 0.5042811 | -1.134999 |
| Fgf22       | 0.521454  | 2.6391274 | 1.4498681 | 0.1794202 | 1.2945339 | 0.6653851 | -0.803491 | -1.068216 | -0.451761 | -0.206665 | -0.371377 | -0.330827 | 0.0355801 | -0.440543 | -0.111889 | -0.968988 | -1.1129   | -0.918712 |
| Nudcd2      | -0.822729 | -0.840473 | -1.222416 | -0.820515 | -0.864124 | -0.726878 | -0.053114 | 2.6676807 | 0.3772251 | -0.221461 | -0.046011 | -0.034419 | 0.4117741 | -0.345538 | 0.6310965 | 0.0218668 | -0.149162 | 2.0371954 |
| Hmmr        | -1.292452 | -0.651624 | -1.440224 | -1.45891  | -1.290683 | -1.310695 | 1.0145073 | 1.6333757 | 0.7731753 | 0.8677431 | 0.2919923 | 0.5910075 | 0.4552506 | 0.1755096 | 0.0532071 | 0.2495125 | 0.0247603 | 1.2785444 |
| Cyflp2      | 0.8249577 | 1.4360027 | 1.6890366 | 1.4699258 | 0.901668  | 1.4830751 | -1.232712 | -0.983566 | -0.610307 | -0.253604 | -0.576399 | -0.403478 | -0.83811  | -0.873663 | -0.957366 | -0.189128 | -0.414289 | -0.472043 |
| Sgcd        | 0.6830569 | 1.3668415 | 0.8795951 | 1.377644  | 1.0489616 | 1.9609698 | -1.143427 | -0.857122 | -0.980492 | -0.989977 | -1.009993 | -0.815535 | -1.099715 | 0.0657337 | 0.0707541 | -0.06224  | -0.147766 | -0.363589 |
| Rnf130      | 0.7838435 | 0.7159808 | 0.6586646 | 1.6461079 | 1.0199873 | 1.5488687 | -0.707903 | -0.16847  | -0.556296 | -1.31942  | -1.254884 | -0.663773 | -1.045305 | -0.24091  | -0.992149 | 1.4544996 | -0.20851  | 0.707334  |
| Ltc4s       | 0.7302731 | 1.2331343 | 0.9150945 | 1.5675148 | 1.004523  | 1.381075  | -1.488071 | -0.729977 | -0.711497 | -0.067015 | -0.871779 | 0.3770438 | -0.867958 | -0.645348 | -1.148312 | 0.9079902 | -0.834315 | -0.752377 |
| Phf15       | 0.9565559 | -0.091564 | 0.2348603 | 1.7329426 | 0.3813345 | 1.1118774 | -0.31858  | -0.567056 | -0.741211 | -1.048863 | -0.76926  | -1.449528 | -1.286381 | -0.081564 | 0.1914182 | 0.0157623 | -0.449081 | 0.1783363 |
| Pdlim4      | 1.8597443 | 0.2830464 | 0.3291538 | 1.2183987 | 0.4548841 | 1.6860211 | -0.954546 | -0.744248 | -0.832982 | -0.827638 | -0.838778 | -0.741897 | -0.823847 | -0.425284 | -0.521433 | 0.5745751 | -0.17736  | -0.428711 |
| Cdk13       | -1.25514  | -1.414496 | -1.824425 | 0.1758434 | -0.670218 | -1.201055 | 1.0407638 | 0.6668803 | 1.0787825 | 0.433502  | 0.6570791 | -0.141496 | 0.3710679 | 0.9276154 | 0.7482973 | 0.479537  | -0.941206 | 1.0307676 |
| Cdkn2ai9npl | -0.930674 | -0.714357 | -1.472488 | -1.187486 | -1.384285 | -0.966028 | 0.7584212 | 1.1074891 | 0.6621389 | 0.9631972 | 0.7294495 | -0.53246  | 1.0866158 | -0.183385 | 1.6419823 | -0.193315 | -0.376855 | 1.0232985 |
| Itk         | 0.2936492 | 0.6915551 | 2.0274843 | 1.5057494 | 1.2085842 | 0.845468  | -1.300568 | -1.335398 | -0.192009 | -0.508528 | -0.568487 | -0.458794 | -0.585284 | -1.207241 | -1.062215 | 0.6379731 | -0.297974 | 0.3242342 |
| Upp1        | -0.713054 | -0.653469 | -0.629169 | -0.667388 | -0.67978  | -0.605378 | 0.2692253 | 0.2309199 | -0.389742 | -0.282082 | -0.528541 | -0.19837  | -0.558767 | -0.122958 | -0.217037 | 1.1979051 | 1.5688445 | 0.3668403 |
| Hus1        | -0.913124 | -0.811908 | -1.008485 | -1.098683 | -1.169814 | -1.280717 | 0.3130213 | 0.7267743 | 0.1351552 | 0.2417472 | -0.191313 | 0.6368365 | 0.1427988 | 0.0767787 | 0.5495149 | 0.2462189 | 0.489638  | 2.9155597 |
| Pttg1       | -1.312876 | -1.124975 | -1.349057 | -1.238462 | -0.992884 | -1.18328  | 0.8907742 | 1.1823192 | 1.289023  | 1.0088356 | -0.177643 | 0.819257  | 0.2422304 | -0.152854 | -0.068681 | 0.1519988 | 0.6691769 | 1.447205  |
| Tns3        | 0.5936272 | 0.1456743 | 1.0414219 | 1.9447586 | 0.8552025 | 1.1022009 | -1.043885 | 0.0607138 | -0.780933 | -1.140064 | -0.277787 | -1.03474  | -1.443217 | -0.163555 | 0.4912084 | 0.9592001 | 0.2396571 | -0.263783 |
| Gats13      | -1.332793 | -0.494539 | -0.82664  | -1.117062 | -0.680573 | -1.219596 | 0.6219364 | 0.624593  | -0.115393 | 0.8588579 | 2.0806131 | -0.688513 | 0.8724686 | 1.648087  | -0.08478  | -0.534341 | -0.484595 | 0.8724686 |
| Igfbp3      | -1.063875 | -0.869305 | -0.296285 | -0.946723 | -0.673985 | -0.834611 | -0.492257 | -0.576033 | -0.541851 | 0.3410956 | -0.31072  | 0.9873041 | 1.8743312 | 1.3631091 | 1.2189945 | 1.8348254 |           |           |
| Myo1g       | 1.1286843 | 0.4004082 | 1.2864362 | 2.5109509 | 0.7890014 | 1.0512001 | -1.021272 | -0.908527 | -0.728961 | -0.691959 | -0.797523 | -0.475051 | -0.771173 | -0.636299 | -0.725733 | 0.4545495 | -0.30724  | -0.557493 |
| Guk1        | 2.1048058 | 2.0240651 | 0.0722962 | 0.6535735 | 1.2611618 | 0.9710282 | -1.201808 | -0.621508 | -0.694213 | -0.313687 | -0.409526 | -0.261295 | -0.513557 | -0.1741   | -0.890351 | -0.869873 | -0.99883  | -0.138184 |
| Etfemp1     | 1.4591177 | 1.1421458 | 0.7250657 | 0.2047648 | 1.8274505 | 1.3993878 | -0.760839 | -0.46351  | -0.941059 | -1.05149  | -0.997382 | -0.729888 | -1.0512   | 0.1506009 | -0.816816 | 0.9621377 | -0.76106  | -0.294868 |
| Polod2      | -0.895232 | -0.862366 | -0.899189 | -0.965943 | -0.883097 | -0.65816  | 0.8611811 | 1.5326381 | -0.233173 | 0.2460442 | -0.121933 | 0.6845074 | -0.527962 | 0.0248683 | -0.144581 | 0.4419275 | -0.448194 | 2.8486631 |
| Pgam2       | 0.9384746 | 1.9245401 | 1.4336312 | 1.2979892 | 1.3002811 | 1.1050045 | -0.827764 | -0.721637 | -0.805445 | -0.846484 | -0.779663 | -0.797513 | -0.838276 | -0.257313 | -0.541465 | -0.61725  | -0.34628  | 0.620831  |
| Xbp1        | 1.665595  | 1.0214473 | 0.7842592 | 1.5625029 | 1.2036795 | 1.0360773 | -1.38184  | -1.264323 | -0.70532  | -0.275936 | -0.846003 | -0.857721 | -0.546717 | -0.217359 | -0.178466 | 0.2546956 | -0.27862  | 0.626952  |
| Ska2        | -0.851521 | 0.953966  | -1.506101 | -1.705093 | -1.156109 | -0.852835 | 1.3820498 | 1.7531259 | -1.808488 | 0.5186126 | -0.066473 | 0.7747571 | 0.8506486 | 0.9301722 | 1.126317  | -0.82482  | 0.158758  | 0.1788578 |
| Prr11       | -1.291603 | -0.817104 | -1.269991 | -1.385509 | -1.378762 | -1.301679 | 1.1121808 | 1.4347103 | 1.0313961 | 0.942203  | 1.1389049 | 0.3628969 | 0.0555013 | 0.172624  | 0.7733969 | 0.0307623 | -0.081128 | 0.471198  |
| Smg8        | -0.88182  | -1.315804 | -0.932868 | -1.290446 | -1.022485 | -1.028092 | 0.9506623 | 1.006391  | 0.4684982 | 0.5274661 | -0.344503 | 0.8940975 | 0.5088077 | -0.78734  | 1.795286  | -0.31488  | 0.2672934 | 1.4975806 |
| Tubd1       | -1.17223  | -0.176133 | -0.9522   | -1.385242 | -0.930766 | -1.542073 | 0.8806751 | 0.8679202 | 1.2877081 | 1.4132994 | -0.671888 | 1.0470365 | 1.2319177 | 0.0914313 | -0.179717 | -0.507503 | -0.931423 | 0.2946104 |
| Mrpl22      | -0.696217 | -0.893625 | -0.967427 | -1.342828 | -0.84547  | -0.736033 | 0.5401021 | 1.0122225 | 0.6478193 | 0.44855   | -0.266485 | 0.5769219 | 0.7940457 | -0.817497 | 0.307073  | -0.335118 | -0.225481 | 2.7965376 |
| Znhit3      | -1.003711 | -0.4515   | -1.07844  | -1.101197 | -1.311933 | -0.996329 | 0.4691344 | 1.2423568 | 0.1626673 | 0.679546  | -0.062657 | 0.8496387 | 0.6103452 | -0.335563 | 0.3585357 | -0.544349 | -0.180168 | 2.604299  |
| Shmt1       | -0.800492 | -0.701871 | -0.884818 | -1.412593 | -0.678795 | -1.252829 | -0.022341 | 1.0691345 | 1.8925971 | 0.5945623 | 1.018564  | 0.3670986 | 1.4524643 | -0.621535 | 0.0826751 | -0.72868  | -0.574374 | 1.201049  |
| Ela2        | -1.178842 | -0.840993 | -0.650903 | -1.281705 | -1.174647 | -1.737256 | 0.7059695 | 0.7149883 | 0.734227  | 0.6228985 | 0.8475365 | -0.061778 | 0.5181213 | 1.2552384 | -0.30627  | -0.466964 | 0.4508549 | 1.8495238 |
| Ptcat       | 2.7280722 | 1.2369981 | 0.296742  | 0.7229228 | 0.6687354 | 1.5798025 | -0.694845 | -0.690956 | -0.650818 | -0.702438 | -0.751091 | -0.733796 | -0.570985 | -0.679901 | -0.398299 | -0.456327 | -0.349389 | -0.49736  |
| Twistnb     | -0.693628 | -0.9229   | -1.612908 | -0.977349 | -1.256708 | -1.519722 | 1.3611334 | 0.5089991 | -0.160022 | 0.882451  | -0.172327 | 0.6857838 | 2.0072899 | 0.392669  | 0.2431637 | 0.5464907 | 0.2256295 | 0.4619549 |
| Atp6f1c2    | 2.667584  | 1.4334183 | 1.0446035 | 1.0517663 | 0.974034  | 0.8341046 | -0.827074 | -0.714269 | -0.655129 | -0.156939 | -0.44444  | 0.2167552 | -0.669791 | -0.622467 | 0.780459  | -0.76881  | -0.586396 | -0.736492 |
| Pik3cg      | 0.6364793 | 1.0174329 | 1.1380655 | 1.75818   | 0.7787952 | 1.6838451 | -1.314458 | -1.024761 | -0.84471  | -0.732489 | -0.89764  | -0.680775 | -1.027172 | -0.700973 | -0.29953  | 0.694571  | 0.2939485 | -0.478811 |
| Tspan13     | 1.1737075 | 0.6990172 | 1.575964  | 1.0506209 | 0.641586  | 1.6533367 | -1.527441 | -0.66576  | -0.130562 | -1.341959 | -1.134854 | -0.544486 | -0.943934 | -0.72921  | -0.45673  | 0.1752607 | -0.216002 | 0.1813898 |
| Fam49a      | 0.3607458 | 1.0328318 | 1.382428  | 1.63391   | 1.3949811 | 1.3616779 | -0.266604 | -0.258455 | -0.28618  | -0.744506 | -0.617276 | -0.589238 | -0.700194 | 0.1895672 | -0.474425 | -0.761297 | -0.325956 | -0.532071 |
| Lpin1       | 1.0700131 | 0.820642  | 1.4719305 | 1.2522879 | 1.4842336 | 1.8059383 | -0.521675 | -0.948615 | -0.722684 | -0.754793 | -0.649191 | -0.353866 | -0.84374  | -0.605753 | -0.896628 | -0.299652 | -0.317069 | -1.022798 |
| Nrcam       | 0.9714022 | 1.6636185 | 0.7423662 | 0.7101244 | 1.6270563 | 1.7956924 | -0.955252 | -0.619127 | -0.926467 | -0.915959 | -0.616132 | -0.827026 | -0.846394 | -0.515721 | -0.480694 | 0.4382094 | -0.27835  | -0.749523 |
| Fam84a      | 1.3815671 | 1.8534614 | 0.9672566 | 0         |           |           |           |           |           |           |           |           |           |           |           |           |           |           |



|           |           |           |           |           |           |           |           |            |           |           |           |            |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| Pole2     | -0.838695 | -0.864006 | -1.292312 | -1.144852 | -1.273601 | -1.053345 | 1.7224367 | 1.1400076  | 0.8745376 | 0.3538643 | 0.1576817 | 0.5390647  | 0.4551096 | -0.150697 | 1.0975245 | -0.675169 | -0.529263 | 1.4817122 |
| Galc      | 1.4969722 | 0.0563633 | 1.51011   | 1.9203765 | 0.3230092 | 1.6386265 | -0.940323 | -0.709159  | -0.986481 | -0.93624  | -0.411177 | -0.815515  | -0.690079 | -0.109832 | 0.4341236 | -0.235146 | -0.753609 |           |
| Pole2h    | 0.039045  | -0.855471 | -1.391204 | -0.947905 | -0.882399 | -1.030261 | 1.5936265 | 1.897377   | 0.0552856 | -0.199874 | -0.210287 | -0.265251  | 0.7558872 | -0.523045 | 0.427096  | -0.253392 | 0.254893  | 2.0352047 |
| Mbip      | -1.039919 | -0.553936 | -0.915392 | -1.268081 | -1.099706 | -1.296633 | 2.8534471 | 0.1745719  | 0.0337525 | 0.5841922 | -0.271788 | 0.5747971  | 0.428605  | 0.3750791 | -0.037787 | 0.0947097 | 0.8949708 | 0.4691161 |
| Gstz1     | 0.2168706 | 2.2356068 | 0.815273  | 0.5803344 | 1.2945241 | 1.0446876 | 0.8518964 | -0.554825  | -0.920738 | -0.822146 | -0.721104 | -0.807317  | 0.0757608 | 0.683085  | -0.824085 | -1.02546  | -1.027312 | -1.09502  |
| 270007361 | -0.316593 | -1.847203 | -1.163233 | -0.802141 | -0.755937 | -0.598211 | 2.5819728 | 0.555693   | 0.056721  | 0.8344437 | 0.2295582 | 0.8399806  | 1.2042423 | -0.047328 | 0.5834283 | -0.329557 | -0.291026 | 0.3776246 |
| Novat1    | 1.5350607 | 0.4752595 | 1.0721019 | 0.9370331 | 1.806417  | 1.6336756 | -0.958487 | -0.729308  | -0.934432 | -0.905521 | -0.882596 | -0.663695  | -0.923086 | -0.439681 | -0.411426 | 0.488318  | -0.413198 | -0.686435 |
| Mthdfl1   | -1.050194 | -1.14503  | -0.877655 | -1.364684 | -1.151508 | -1.641327 | 1.3132798 | 0.2500127  | 0.4158503 | 0.2934403 | 0.166181  | 0.9888204  | 0.5595029 | 0.3449721 | 0.8049705 | 0.7383704 | -0.403837 | 1.758835  |
| Sgpp1     | 1.0867186 | 2.1102843 | 0.8235756 | 0.4920769 | 1.3574434 | 1.1763777 | -0.959474 | -1.0278    | -0.710117 | -0.128192 | -0.150401 | 0.4698083  | -0.235527 | -0.172993 | -1.065295 | -0.967388 | -0.806027 | -1.293071 |
| Nin       | 0.4147271 | 0.4258798 | 1.2226936 | 1.7348964 | 0.6171353 | 2.0165569 | -1.226753 | -0.726834  | -0.817992 | -1.234522 | -0.75929  | -0.72054   | -1.206341 | -0.539373 | -0.32985  | 0.5435432 | 0.4514671 | 0.1345955 |
| Bdkrb2    | -1.190164 | -1.090479 | -0.885207 | -1.274424 | -1.003424 | -1.018955 | 2.2132615 | -0.245293  | 1.140626  | 0.988812  | 0.7553533 | 0.0996641  | 1.1892873 | 0.5245842 | 0.2386379 | -0.529455 | -0.171891 | 0.2590658 |
| Serpina3n | 1.2638442 | 0.8673594 | 1.1266419 | 1.62336   | 0.965145  | 1.4142561 | -0.973648 | -0.804162  | -0.970188 | -0.922125 | -0.981252 | -0.908139  | -0.934794 | -0.668989 | -0.101521 | 0.8196134 | -0.017556 | -0.797837 |
| Dhrs7     | 1.8063235 | 2.3254001 | 0.1093037 | 0.3863498 | 0.9351127 | 1.1636713 | -0.245631 | -1.071987  | -0.279885 | -0.640503 | -0.58814  | -0.317689  | -0.822718 | 0.5165118 | -1.057052 | -0.496536 | -0.817046 | -0.905485 |
| Hif1a     | -1.311585 | -0.684088 | -0.922479 | -1.226914 | -0.900674 | -1.206651 | 0.0174103 | -0.282959  | 2.2046933 | 0.8393005 | 0.6233792 | -0.063241  | 0.7315083 | 1.5055911 | 0.8727995 | -0.256189 | -0.539847 | -0.479469 |
| Snaptc1   | -1.062784 | -1.278662 | -1.242019 | -1.22346  | -0.947393 | -1.02714  | 2.1077485 | 0.1258322  | 1.1607193 | 0.5500573 | 0.0615867 | 0.3979862  | 1.0674088 | 1.1651809 | 0.4499419 | -0.282874 | -0.098091 | 0.1515361 |
| Eif2s1    | -1.122523 | -0.719811 | -1.236022 | -1.314982 | -1.313656 | -1.252761 | 1.5591069 | 0.6042505  | 0.3567776 | 0.1798461 | -0.256493 | 0.6816614  | 0.5157541 | 1.7267252 | 0.8244415 | -0.12789  | -0.199938 | 1.0955131 |
| Plrk      | -1.220817 | -0.673546 | -0.455759 | -1.235477 | -0.723746 | -0.993278 | 1.7897609 | -0.610052  | 1.1263763 | 0.9419982 | 1.4688028 | 0.2505159  | 1.0210989 | 1.0403197 | -0.199938 | -1.272926 | -0.24139  | -0.005574 |
| Ehe       | -1.156727 | -0.801394 | -1.234358 | -1.670805 | -1.308288 | -1.336284 | 1.1394541 | 0.990654   | 0.4696105 | 0.516849  | 0.1828859 | 0.0701434  | 0.8161777 | 1.3727444 | 0.4825417 | 0.2206602 | -0.006649 | 1.2524734 |
| Slc10a1   | -0.724773 | -1.599304 | -1.61391  | -0.665632 | -1.128701 | -0.242373 | 1.881022  | 0.1200945  | 0.3973228 | 0.8937877 | 0.3527849 | 1.3359733  | 1.4944171 | 0.3151981 | 0.2370265 | -0.374423 | -0.226983 | -0.622438 |
| Mta1      | -0.61936  | -1.011052 | -0.84091  | -0.951507 | -1.158707 | -1.446341 | 1.7872194 | 0.2288018  | 1.1125019 | 0.0184587 | 0.2010754 | -0.082996  | 2.3679106 | 0.3110459 | 0.1418613 | -0.45568  | 0.3886154 |           |
| Gtpbp4    | -0.63493  | -0.623759 | -1.070279 | -0.953408 | -1.142632 | -0.898433 | 0.3633566 | 1.097614   | -0.092558 | -0.164842 | -0.264753 | 0.369546   | 0.3574706 | 0.2809228 | 0.1128256 | 0.0214058 | -0.386176 | 2.616481  |
| Tdp1      | -1.548596 | -0.613471 | -1.184452 | -0.620589 | -1.116624 | -0.667457 | 2.1711665 | 0.8973529  | 0.6207924 | -0.010036 | 0.380807  | -0.506321  | 0.228314  | 1.9940252 | -0.087977 | 0.3849886 | -0.479547 | 0.1576256 |
| Lgmn      | 0.5661281 | 0.1871825 | 0.9240921 | 1.8807268 | 0.5697563 | 1.8198367 | -1.136994 | -1.032665  | 0.1744451 | -1.091848 | -1.029741 | -0.889671  | -0.879589 | -0.300803 | -0.175553 | 1.3748449 | 0.000636  | -0.860785 |
| Pitrm1    | -1.362093 | -0.847021 | -1.197251 | -1.161023 | -1.161464 | -1.007656 | 1.1095224 | 1.8881622  | 0.2400513 | 0.1268134 | 0.0426947 | 0.5874518  | 0.1819481 | 0.0817869 | 1.1829056 | 0.4196995 | -0.7351   | 1.3247238 |
| Chga      | 2.0221496 | -0.273717 | 0.464315  | -0.227933 | 0.5012757 | -0.96851  | -0.863412 | -0.773856  | -0.616612 | 0.1513067 | -0.874293 | -0.79359   | -0.687087 | -0.294083 | -0.58441  | -0.689438 | -0.290118 |           |
| Asb2      | 0.3448414 | 1.9709212 | 1.1196728 | 0.5106856 | 1.3399103 | 1.5070569 | -0.399483 | -1.132572  | -0.925693 | -0.458413 | -0.241552 | -0.122658  | -0.383308 | 0.8485713 | -1.009508 | -0.152068 | -0.916351 | -1.000054 |
| Akrk1c18  | 0.5737141 | 2.0336753 | 0.6405459 | 0.3692832 | 1.2826365 | 1.2770583 | -0.959209 | -0.838691  | -0.520028 | 1.0545624 | -0.390006 | 0.6099948  | -0.888825 | -0.860971 | -0.953781 | -0.978141 | -0.121652 | -1.330255 |
| Rgs6      | 3.1706887 | 0.3960537 | -0.154244 | 1.8173057 | 0.4505392 | 0.3501968 | -0.585659 | -0.557519  | -0.352237 | -0.585659 | -0.528406 | -0.585659  | -0.585659 | -0.469481 | -0.380354 | -0.585659 | -0.329069 | -0.485118 |
| Alcd2     | 1.8837518 | 1.937788  | 0.2621257 | 0.9482274 | 0.9282873 | 1.1728612 | -0.176003 | -0.998315  | -0.241331 | -0.633729 | -0.289744 | -0.87264   | -0.891847 | 0.4821573 | -0.998159 | -0.872856 | -0.705033 | -0.935541 |
| Alph6a1   | 1.0402327 | 1.5949047 | 0.9949349 | 0.9243375 | 1.1639681 | 1.1908115 | -0.307307 | -0.872899  | -0.426236 | -0.82125  | -0.693142 | -0.89085   | -0.178034 | 1.2076854 | -0.621656 | -0.105795 | -0.805515 | -1.493291 |
| Vash1     | -1.151439 | -1.367934 | -0.988877 | -0.582293 | -1.172483 | -0.89486  | -0.363729 | -0.1182403 | 0.1417962 | -0.097688 | 0.0914406 | 1.2676625  | 0.0162737 | 0.1046711 | 0.4021326 | 0.2480602 | 0.0036922 | 1.0567874 |
| Cvsk      | -0.698988 | -0.795431 | -0.741381 | -0.930056 | -0.962977 | -1.521389 | 2.2371455 | -0.182618  | 0.8843365 | 1.7872066 | 0.8653951 | -0.325589  | 0.1699847 | 1.0212053 | -0.392302 | -0.226456 | -0.035114 | -0.006973 |
| Hvhlp1    | -0.528491 | -1.224233 | -0.784812 | -0.583629 | -0.369275 | -0.421686 | -0.351811 | -0.620629  | -0.937187 | -0.293257 | -0.389125 | 0.5205791  | -1.024796 | 1.5174203 | 1.7668275 | 0.2400558 | 0.836472  | 0.8470919 |
| Eip1      | 0.6275362 | -0.003081 | 1.7908221 | 2.5041176 | 0.0803536 | 0.9918188 | -1.48557  | -0.076684  | -0.642291 | -0.399015 | -0.334579 | -0.709996  | -0.436847 | -0.686782 | 0.7841876 | -0.688478 | -0.574588 |           |
| Hsp90aa1  | -1.151078 | -1.036486 | -1.146177 | -1.044452 | -1.400831 | -0.811042 | 1.2689953 | 2.0054976  | 0.0620582 | -0.480288 | -0.241611 | 0.5204157  | -0.001965 | 0.5349288 | 0.5045904 | 0.5875746 | 0.274747  | 1.5551206 |
| Cinp      | -0.928941 | -0.754293 | -1.140117 | -1.103858 | -1.283974 | -1.479482 | 0.7624885 | 0.3419912  | 0.4946846 | 0.8934304 | 0.2358371 | 0.8482327  | 0.9947407 | 1.9831447 | 0.5720758 | -0.557599 | -0.769808 | 0.8261753 |
| Kif26a    | -1.205931 | -0.984653 | -0.376943 | -1.139042 | -1.026379 | -1.042211 | 0.8204435 | 2.5441665  | 0.5968362 | 1.0797151 | 0.5358898 | -0.267405  | 1.1125431 | 0.0844342 | 0.3329532 | -0.203771 | -0.039542 | -0.783952 |
| Gpr137b   | 1.5658238 | 0.4421571 | 0.5621556 | 2.2680455 | 0.5988145 | 1.770288  | -0.787664 | -0.530044  | -0.941153 | -0.86472  | -0.940201 | -0.707688  | -0.871606 | -0.048737 | -0.587595 | 0.4566946 | -1.380802 | -0.707688 |
| Glil3     | -1.206643 | -1.051749 | -0.805452 | -1.378145 | -1.054393 | -0.229376 | -0.40599  | 0.8035727  | 0.635539  | 0.1342094 | 0.9632083 | -0.136252  | -0.669887 | 0.7531099 | 2.4477361 | 0.0653932 | 0.9595267 | 1.4496906 |
| Soah      | -0.140891 | 0.6192759 | 1.4273268 | 0.9265462 | 1.659966  | 1.5200117 | -1.494469 | -1.055994  | -0.015848 | -1.118131 | -1.274548 | -0.743487  | -1.132093 | 0.0980324 | -0.382351 | 0.5111264 | 0.2785428 | 0.3106666 |
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| Gplm1     | 2.1674779 | 2.3294841 | 0.3369256 | -0.184735 | 0.7894646 | 0.6303282 | -0.68916  | -0.066051  | -0.421951 | -0.196381 | 0.2087822 | -1.117087  | -0.766507 | -0.49893  | -1.209144 | -1.040758 | -0.524046 | 0.2522876 |
| Irf4      | 0.572968  | 0.5552096 | 0.683369  | 1.7833077 | 0.8924228 | 1.2267913 | -1.271344 | -1.142152  | 0.4140153 | -0.005408 | -0.975087 | -0.774813  | -0.563373 | -0.946483 | -0.919397 | 1.6873849 | -0.359073 | -0.858332 |
| Trap2a    | -0.763874 | -0.818459 | -0.883078 | -1.101804 | -0.981128 | -1.286116 | 0.6596405 | 1.6083701  | 1.8043056 | 1.3630935 | 1.4398578 | -0.072023  | 0.3499785 | 0.2334392 | -0.109801 | -0.581301 | -0.600186 | -0.284979 |
| Tbcd1d7   | -0.865907 | -0.388391 | -1.13183  | -1.355697 | -0.979712 | -1.29378  | 1.7492255 | 1.7523858  | 0.3110784 | 0.5236342 | 0.2495101 | 0.2546066  | 0.6250742 | 1.6537763 | -0.72138  | -0.539954 | -0.473327 | 1.0406697 |
| Id4       | 1.2591037 | 2.2837106 | 0.299625  | 0.4094092 | 1.354787  | 1.588399  | -0.771951 | -0.752865  | -0.581543 | -0.429358 | -0.367802 | -0.4006064 | -0.759642 | -0.277222 | -0.726384 | -0.312898 | -0.777639 | -0.869219 |
| Susd3     | 0.1574058 | 1.263375  | 0.3909954 | 1.7069074 | 1.1711388 | 1.6097945 | -1.475902 | -0.870489  | -1.011706 | -0.380429 | -1.030556 | 0.1513063  | -0.758777 | -0.079498 | -1.028769 | 0.9673238 | -0.017939 | -0.764183 |
| Ogn       | 0.5327785 | 0.9731773 | 1.1673081 | 0.7286056 | 2.1907178 | 1.8357625 | -0.813816 | -0.645085  | -0.760909 | -0.86221  | -0.829469 | -0.771204  | -0.841128 | -0.088389 | -0.465451 | 0.1015987 | -0.612367 | -0.839921 |
| Cenpp     | -1.136029 | -0.810627 | -1.265981 | -1.551428 | -1.208738 | -1.25525  | 1.0250591 | 1.3699467  | 0.7037463 | 1.2441187 | 0.4910698 | 0.9510629  | 1.0987856 | -0.071472 | 0.5757529 | -0.052461 | -0.464355 | 0.3567359 |
| No18      | -1.110607 | -0.4      |           |           |           |           |           |            |           |           |           |            |           |           |           |           |           |           |



|           |            |            |           |           |           |           |           |            |           |            |            |           |           |           |           |           |           |           |
|-----------|------------|------------|-----------|-----------|-----------|-----------|-----------|------------|-----------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Oxnad1    | -1.02656   | -0.556204  | -0.614947 | -1.462806 | -1.343081 | -1.324526 | 0.6192244 | 1.9556646  | -1.135164 | 0.049016   | 0.3350468  | 0.4016944 | 0.9479892 | 0.0987974 | 0.8348796 | 0.5851836 | 0.3168383 | 1.3189544 |
| Ctsb      | 1.2759629  | 0.4416629  | 1.1608445 | 2.307019  | 0.4068653 | 1.6068566 | -1.000315 | -0.884143  | -0.833009 | -0.744262  | -0.625262  | -0.694302 | -0.703919 | -0.288157 | -0.573562 | 0.2352092 | -0.155092 | -0.932398 |
| Pkrkd     | 1.1021159  | 0.0415651  | 1.1103799 | 1.9950824 | 0.5431458 | 0.9674754 | -0.655498 | -0.805356  | -1.180684 | -0.724852  | -0.939236  | -0.939236 | -0.86481  | -0.754887 | -0.336379 | 1.5628109 | 0.1947957 | -0.956761 |
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| Wnt5a     | -1.076937  | -0.857095  | -0.762671 | -0.963416 | -0.823802 | -0.826268 | -0.922665 | -0.491312  | -0.117491 | 1.3369134  | 0.5826753  | 0.5101209 | -0.872433 | 0.6327864 | 1.6363971 | -0.058052 | 1.831494  | 1.242278  |
| Lcp1      | 0.9623296  | 0.2565177  | 1.0238137 | 2.4185866 | 0.5032041 | 1.3052459 | -0.076844 | -0.732113  | -0.755009 | -0.866957  | -0.582401  | -0.721401 | -0.8872   | -0.627615 | -0.563168 | 1.0820262 | -0.018385 | -0.430631 |
| Nufip1    | -0.650067  | -0.734695  | -0.951279 | -0.98484  | -0.829899 | -0.870314 | 1.3239848 | 0.3445842  | -0.735971 | 0.1291494  | -0.000862  | 0.49068   | 0.5781587 | -0.224761 | 0.0494363 | 0.0422591 | -0.082024 | 3.1064606 |
| Epst1     | -0.156256  | -0.1408331 | 1.8870519 | 1.3155216 | 1.4220832 | 1.59216   | -1.322492 | -1.06966   | -0.440007 | -0.751479  | -0.966898  | -0.645962 | -0.673264 | -0.754736 | -0.457811 | 0.9572759 | -0.073032 | -0.035328 |
| Tnfsf11   | -0.737289  | -0.61432   | -0.380209 | -0.197191 | -0.411979 | -0.364737 | -0.560912 | -0.176397  | -0.665353 | -0.609288  | -0.751896  | -0.278925 | -0.571191 | -0.378798 | 1.3833438 | 2.8313021 | 0.8252182 | 1.6496219 |
| 1190002H2 | 2.057557   | 0.9204358  | 0.137147  | 1.6005992 | 0.4142902 | 1.8208632 | -1.366996 | -0.295904  | -0.400414 | -0.982502  | -0.614714  | -0.172806 | -0.621175 | -0.408369 | -0.645121 | -0.018502 | -0.521083 | -0.003305 |
| Diap3     | -0.717095  | -1.195439  | -1.27337  | -1.304513 | -1.209479 | -0.932547 | 1.1587552 | 0.1053751  | -0.805518 | 0.9473051  | 0.6275998  | 0.7356369 | 0.292774  | -0.343636 | 1.4093459 | 0.5509263 | 0.2142185 | 1.7396602 |
| Scara5    | 1.5093477  | 0.2855917  | 1.2318369 | 0.7931228 | 1.8826153 | 1.8540989 | -0.761931 | -0.720682  | -0.761931 | -0.761931  | -0.751201  | -0.755581 | -0.75539  | -0.45914  | -0.665467 | 0.1462185 | -0.575523 | -0.734055 |
| Pbk       | -1.239128  | -0.928865  | -1.256705 | -1.312674 | -1.192058 | -1.085273 | 0.661903  | 0.7756113  | -0.448638 | 1.2741795  | 0.9771725  | 1.1698852 | 1.129095  | 0.3084392 | 0.3856771 | -0.606246 | 0.1178287 | 1.2697956 |
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| Clu       | 1.2682465  | 1.633312   | 0.3945044 | 1.3949084 | 1.3699753 | 0.6848473 | -1.396106 | 0.3689138  | -0.619083 | 1.38767    | 0.3005293  | -0.815477 | -0.333544 | -0.966539 | -0.832073 | -1.31658  | -0.024905 | -1.249696 |
| Ephx2     | 0.8023347  | 1.7468909  | 1.8468875 | 0.7635782 | 1.3156871 | 1.2889816 | -1.003579 | -0.906579  | -0.828443 | -0.385637  | -0.622858  | -0.078455 | -0.847319 | -0.489399 | -0.5      | -0.733858 | -0.385919 | -0.982315 |
| Pyxis2    | 1.3083963  | 0.0406182  | 1.0658996 | 2.2355298 | 0.895848  | 1.2638288 | -1.151642 | -0.893676  | -0.951585 | -0.858332  | -0.944247  | -0.586541 | -1.102376 | -0.302374 | -0.229849 | 0.8526465 | 0.0082882 | -0.344168 |
| Bora      | -1.364042  | -0.103181  | -1.221963 | -1.428402 | -1.166992 | -1.177705 | 1.0670703 | 0.669583   | 0.3725914 | 1.1810405  | 0.8219434  | 1.1019209 | 0.5982376 | 0.6305805 | -0.159541 | -0.291281 | -0.012156 | 1.3965946 |
| Pdlm2     | 1.4064426  | 1.2860397  | 0.2736262 | 0.0920295 | 1.013536  | 1.0491732 | -1.069634 | -1.524625  | -1.105761 | 0.0383375  | 0.1058477  | 0.3643282 | -0.75372  | 0.685335  | -0.807908 | -1.430842 | 0.932796  | 1.3078712 |
| Sorbs3    | 1.0801024  | 0.273389   | 1.104657  | 2.2483033 | 1.107378  | 0.9944089 | -0.105185 | -0.801858  | -1.034345 | -1.250534  | -1.193028  | -0.548335 | -1.043883 | 0.3360742 | -0.111002 | 0.264799  | -0.097203 | -0.413741 |
| Bmp1      | -0.628141  | -0.798708  | -0.494682 | -0.460965 | -0.429946 | -0.117616 | -1.281275 | -0.548595  | -0.714568 | -0.486937  | 8.89E-05   | -0.006671 | -0.789311 | 1.3351389 | 1.6806068 | 2.401687  | 1.2722055 | 0.0676886 |
| Dok2      | 1.5516012  | 0.8103563  | 0.6683979 | 2.2021242 | 0.6623271 | 0.7074361 | -0.908844 | -0.608024  | -0.724515 | -0.957987  | -0.794127  | -0.922574 | -0.640015 | -0.679542 | -0.761241 | 1.3080751 | -0.430891 | -0.482558 |
| EdnrB     | 1.4091999  | 0.7946382  | -0.528214 | 0.2142434 | 1.784683  | 2.1922945 | -0.599828 | -0.988337  | -0.683147 | -1.171443  | -0.106135  | -0.736514 | -0.795295 | 0.2407184 | -0.196561 | 0.6371778 | -0.150916 | -0.847515 |
| Scel      | 1.6919873  | 2.1823226  | 0.3507419 | 0.7873782 | 1.0688197 | 1.0101013 | -0.620622 | -1.122022  | -0.928754 | 0.0082669  | -0.50431   | 0.3731884 | -0.651038 | -0.21301  | -0.986132 | -1.062441 | -0.832549 | -0.552287 |
| Nup155    | -1.147458  | -0.917317  | -0.211117 | -1.140784 | -1.268235 | -1.038731 | 0.3071719 | 2.3516692  | 0.3624449 | 0.2942342  | 0.0732276  | 0.5613407 | 0.2967736 | -0.188057 | 0.4325979 | 0.7184231 | -0.038447 | 1.5476982 |
| Gdnf      | -1.107229  | -0.910688  | -0.672029 | -1.092574 | -0.926874 | -0.626658 | -1.050369 | -0.4672661 | 1.5332576 | 1.3651604  | -0.507276  | 0.4331672 | -0.52955  | 0.7643575 | 0.1426194 | 0.6227674 | -0.092811 | 2.1874602 |
| Fyb       | 0.000236   | 0.7370885  | 1.5590803 | 1.9042481 | 1.2853451 | 1.2182633 | -1.333224 | -0.893018  | -0.635462 | -1.040644  | -0.9269    | -0.856521 | -0.970134 | -0.124653 | -0.447756 | 0.5725187 | 0.2236609 | -0.721219 |
| Dab2      | 0.8662974  | 0.8662974  | 0.284155  | 1.4777041 | 1.5137949 | 1.4657299 | -1.175404 | -0.693118  | -0.722416 | -1.072598  | 0.119904   | -0.05537  | -0.950776 | -0.21847  | -0.218778 | 1.2498808 | 1.1295218 | -0.726548 |
| Rem2      | -0.966105  | -0.907756  | -0.806052 | -1.045298 | -0.751262 | -0.990841 | 0.7551263 | 0.2733851  | -0.550821 | 1.9178873  | 0.23114665 | -0.000553 | 0.7116362 | 0.1981228 | 1.2484036 | -0.517884 | -0.060524 | -0.638932 |
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| C6        | -0.425432  | -1.068808  | -0.729273 | -1.136123 | -0.942719 | -1.419244 | 0.2126668 | -1.353297  | -0.478376 | 0.8018088  | 1.0972572  | 0.4050842 | 0.4020912 | 0.2531168 | 1.3934536 | 0.0393743 | 0.5572712 | 0.5911468 |
| Jub       | -0.248244  | 1.431036   | 1.9338465 | -0.101041 | 2.1732501 | 1.3543003 | -0.785467 | -0.6214    | -0.735163 | -0.764355  | -0.785467  | -0.743157 | -0.750409 | -0.435932 | -0.365562 | 0.2494837 | -0.323072 | -0.482647 |
| Drosha    | -1.177707  | -0.726656  | -0.565775 | -1.407549 | -1.095587 | -1.174127 | 0.2752558 | 2.3411865  | 1.124859  | 0.5557288  | 0.2656662  | -0.23879  | -0.409059 | 0.1889055 | 0.3867552 | 0.2564498 | -0.179344 | 1.5797424 |
| Fitm1     | 1.6319342  | 1.974422   | 1.2422946 | 1.580404  | 0.8576649 | 0.5247464 | -0.88354  | -0.966507  | -0.779106 | -0.827319  | -0.88354   | -0.781725 | -0.83826  | -0.121949 | -0.437589 | 0.602036  | -0.398989 | -0.866926 |
| Ripk3     | -0.892193  | -0.87202   | -0.718832 | -0.762195 | -0.956794 | -0.483896 | 0.0795871 | -0.19533   | -0.921335 | 0.0672423  | 0.0631797  | 0.3964107 | -0.737179 | -0.42843  | 2.2033786 | 1.9897056 | 0.7344347 | 1.434265  |
| Cma1      | 0.6006547  | 1.2341872  | 1.3990409 | 0.6140629 | 1.6100706 | 2.2191757 | -0.880246 | -0.638755  | -0.838281 | -0.568889  | -0.775066  | -0.726815 | -0.678302 | -0.385281 | -0.538713 | -0.650644 | -0.265698 | -0.729962 |
| Mcp2      | -0.647212  | -0.637758  | -0.543748 | -0.644873 | -0.585261 | -0.633149 | -0.525503 | -0.504255  | -0.104086 | 0.0956322  | -0.504553  | 0.5913769 | 0.8328844 | 0.4221701 | -0.419269 | 0.0118404 | 0.267444  | 3.5278665 |
| Atp12a    | 3.5473296  | 0.3682228  | -0.273825 | 0.9490251 | 0.7654375 | 0.230106  | -0.522618 | -0.491056  | -0.472375 | -0.457431  | -0.411933  | -0.482905 | -0.486808 | -0.501063 | -0.481982 | -0.513459 | -0.240013 | -0.524653 |
| Cmb1      | 1.3631541  | 1.3044248  | 0.9827211 | 1.7052146 | 1.1806959 | 1.6015663 | -0.782468 | -0.636081  | -0.787808 | -0.74537   | -0.69159   | -0.730713 | -0.753924 | -0.697645 | -0.63622  | -0.62147  | -0.514255 | -0.540232 |
| Tars      | -1.068439  | -0.87577   | -1.2627   | -1.400932 | -1.179529 | -1.107325 | 0.1396483 | 1.09612    | 0.9579999 | 0.5495384  | 0.3543277  | 0.197934  | 0.9335995 | -0.617909 | 0.1806759 | 1.3795306 | -0.04326  | 1.7664895 |
| Brix1     | -0.555894  | -1.58374   | -0.952093 | -1.141433 | -1.173181 | -1.153013 | 0.8400495 | 1.8433602  | 0.4692357 | 0.555431   | -0.079419  | 0.3900521 | 0.3907118 | -0.699672 | -0.145913 | 0.5383656 | -0.129943 | 2.1617101 |
| Ank       | -2.0109114 | 1.5228516  | 0.3412837 | 1.1796866 | 0.9228956 | 1.6051047 | -0.605195 | -0.430071  | -0.700627 | -0.27725   | -0.47302   | -0.523945 | -0.822979 | -0.154649 | -0.190844 | -0.198223 | -0.65558  | -0.759075 |
| Fam134b   | 1.8618262  | 2.0649933  | 0.5361046 | 0.7178063 | 1.523268  | 1.0485872 | -1.407514 | -0.261826  | -0.69879  | -0.455789  | -0.587783  | -0.166291 | -0.530031 | -0.14501  | -0.974278 | -0.432136 | -0.859706 | -0.861396 |
| Grhl2     | -1.094778  | -0.339515  | -0.709091 | -1.431729 | -1.067975 | -1.507492 | 1.253043  | 1.2765118  | 1.291911  | 0.17088919 | 0.7247172  | 0.1604984 | 1.34788   | 0.7624423 | -0.322496 | -0.988054 | -0.394814 | 0.2678262 |
| Lrp12     | 1.4669731  | 0.1534814  | 1.2741033 | 2.5881019 | -0.111347 | 1.3562876 | -0.889902 | -0.035302  | -0.433189 | -0.890791  | -0.58178   | -0.687057 | -0.691741 | -0.736839 | -0.34726  | -0.243818 | -0.317822 | -0.873899 |
| Angpt1    | 0.5646565  | 1.132439   | 1.0398897 | 1.3980716 | 0.6653076 | 1.081422  | -1.334289 | -1.219278  | -1.147665 | -1.103231  | -1.352101  | -0.365716 | -1.157688 | 0.5770582 | 1.1270412 | 0.054449  | 0.1617828 | -0.12215  |
| Utp23     | -0.664198  | -0.318754  | -1.20792  | -0.601574 | -1.066819 | -0.733747 | 0.1949532 | 2.380208   | 0.3110465 | -0.067914  | -0.675599  | 0.4967286 | 0.2746784 | -0.147853 | 0.2724959 | -0.338185 | -0.532833 | 2.4252857 |
| Rad21     | -0.967919  | -0.84839   | -0.804591 | -1.070004 | -1.014576 | -0.716635 | 0.4196705 | 2.7544291  | 0.8383316 | 0.1961248  | 0.2563086  | 0.3093283 | -0.307072 | 0.0686592 | 0.433685  | -0.404979 | -0.694593 | 1.5524016 |
| Shcnp1    | -0.96435   | -0.796234  | -1.092395 | -1.160675 | -1.028562 | -0.932581 | 1.5226056 | 1.6327819  | -1.35317  | 0.17710339 | 0.1334859  | 0.8399748 | 0.2533998 | -0.251586 | 0.2866253 | 0.0901979 | 0.5164193 | 1.5329813 |



|           |            |           |           |            |           |           |           |            |           |           |           |           |           |           |           |           |           |           |
|-----------|------------|-----------|-----------|------------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Snai2     | -0.940545  | -1.14677  | -1.137843 | -1.299516  | -0.995231 | -1.255854 | 0.4250052 | 1.955346   | 1.5542412 | 1.1017639 | 0.3531749 | 0.2727828 | -0.186971 | 0.5728085 | 0.9871933 | -0.249808 | 0.0857763 | -0.095554 |
| Qtrtd1    | -0.5178    | -1.031568 | -0.569865 | -1.053114  | -1.469676 | -0.484368 | 0.9429991 | 1.1970372  | 1.4014109 | -0.74973  | 0.0848728 | 0.4369857 | 1.0214945 | -1.342946 | 1.3274658 | -0.379648 | -0.224077 | 1.410525  |
| Zbtb20    | 0.97773895 | 0.9211904 | 1.1783169 | 1.6182186  | 1.3638963 | 1.6786914 | -0.817667 | -0.709352  | -0.842694 | -1.205435 | -1.032422 | -0.701335 | -0.695857 | -0.180873 | -0.142346 | -0.04471  | -0.14163  | -0.954192 |
| Cmsm1     | -0.66271   | -0.830836 | -0.917807 | -1.24157   | -1.034447 | -0.937828 | 2.1140242 | 0.6319962  | 0.0202146 | 0.638245  | -0.16408  | 0.4107512 | 0.7019356 | -1.041648 | 0.4930372 | -0.187919 | -0.042502 | 2.0511431 |
| Temem45a  | 1.8168954  | 1.9760715 | 0.990977  | 0.6333016  | 1.0109846 | 0.8794329 | -0.46722  | -1.14796   | -0.273593 | -0.404842 | -0.223904 | 1.250318  | -0.579549 | -1.080115 | -1.005044 | -0.145421 | -0.939798 | 1.165248  |
| Fgd4      | 1.2157184  | 0.3262492 | 1.1056679 | 2.3716714  | 0.4539712 | 1.7127363 | -0.850499 | -0.143863  | -0.604868 | -1.002623 | -0.580833 | -0.697488 | -0.934768 | -0.705985 | -0.447653 | 0.0466336 | -0.366116 | -0.627952 |
| Yars2     | -0.746005  | -0.951346 | -1.142682 | -0.858436  | -1.294628 | -0.767091 | 1.0308381 | 2.3875921  | 0.2987425 | 0.2650398 | 0.124269  | 1.0504485 | 1.0602524 | -0.508473 | 0.1798074 | -0.281855 | -0.527062 | 1.5805866 |
| Arhgap31  | 1.2085022  | 0.120859  | 0.9971033 | 1.898275   | 1.0214753 | 1.5688214 | -1.348865 | -0.838035  | -0.869543 | -0.903063 | -0.75914  | -0.719395 | -1.115552 | -0.073383 | 0.0785193 | 0.5112983 | 0.0668419 | -0.844721 |
| Umps      | -0.844472  | -0.916039 | -1.186128 | -0.804245  | -1.183717 | -0.785492 | -0.244923 | 1.3008189  | 0.8615272 | 0.6294778 | 0.0887227 | 0.5778438 | 1.1260764 | -1.391766 | 2.0058664 | 0.1696189 | -0.296582 | 0.8934134 |
| Abcc5     | 0.7579272  | 0.8951727 | 1.2658491 | 2.2118254  | 0.6042805 | 1.1562551 | -1.418435 | -0.743718  | 0.5483149 | -0.342629 | 0.0834491 | -0.780467 | -0.810357 | -0.38658  | -0.630979 | -0.439822 | -0.490041 | -1.480046 |
| Hclsl     | 0.4311357  | 0.4574287 | 1.2715356 | 1.7130822  | 0.7953567 | 1.2530796 | -1.384642 | -0.867701  | -0.751228 | -1.033014 | -1.058408 | -0.508869 | -0.946414 | -0.503973 | -0.656176 | 1.6027437 | 0.1348589 | 0.0512045 |
| Cdccl4    | -0.115158  | -0.845995 | -1.129054 | -1.044992  | -1.284242 | -0.933908 | 1.6173329 | 1.1907363  | 0.9655467 | 0.8016291 | 0.2723169 | 0.4342262 | 1.5565098 | -1.093842 | 0.8226583 | -0.397503 | -0.109082 | 0.1891783 |
| Adipoq    | 0.1439059  | 2.1823369 | 1.6045325 | 1.2590546  | 1.39746   | 1.0521995 | -0.701311 | -0.579408  | -0.710236 | -0.706757 | -0.708071 | -0.710236 | -0.707489 | -0.516001 | -0.524488 | -0.684184 | -0.381073 | -0.710236 |
| Rfc4      | -0.168572  | -0.870651 | -1.287427 | -1.253486  | -1.118971 | -1.114468 | 1.6632242 | 1.4967638  | 0.2467448 | 0.2156368 | 0.2867204 | 0.2004957 | 0.8627413 | -0.014644 | 0.141282  | 0.097744  | -0.294277 | 1.811421  |
| Robo1     | -1.227107  | -0.536716 | -0.652821 | -1.702939  | -0.546212 | -1.191165 | -0.257805 | 0.6343828  | 1.7486931 | 0.7324646 | 1.5719758 | 1.0084873 | 0.9154642 | 0.1403624 | 0.0541812 | -1.207711 | -0.023378 | 0.5398421 |
| St6gal1   | 1.1343527  | 0.7141099 | 1.3140405 | 1.5138215  | 0.8708983 | 1.4778603 | -1.288254 | 0.2752581  | -0.864641 | -1.123198 | -0.946567 | -0.673484 | -0.930683 | -0.791417 | -0.786341 | 0.7606138 | 0.0207393 | -0.677108 |
| Adamts5   | 0.5441362  | 1.0922979 | 0.9557024 | 1.7882615  | 1.3391087 | 1.5357976 | -1.129167 | -0.50228   | -1.270021 | -0.558237 | -0.907379 | -0.388974 | -1.341764 | -0.3074   | -0.770042 | 0.2748779 | 0.1346395 | -0.489458 |
| Ildrl     | 3.0732014  | 0.328943  | -0.176493 | 1.5597109  | 1.1493406 | 0.1471552 | -0.166447 | 0.0027922  | -0.620246 | -0.53501  | -0.569699 | -0.632793 | -0.278213 | -0.804761 | -0.359333 | -0.793138 | -0.494923 | -0.398198 |
| Cd86      | -0.325578  | 1.0856072 | 1.1310736 | 0.6975156  | 1.2237883 | 1.1052473 | -1.807393 | -1.332885  | -0.34616  | -0.004532 | -0.713157 | 1.3072641 | -1.199118 | -0.682201 | -1.0239   | 0.9322618 | -0.14188  | 0.0940458 |
| Pros1     | 0.5918398  | 1.2641025 | 0.6419834 | 1.1964179  | 1.3825855 | 1.9875501 | -1.607662 | -1.100711  | -0.528419 | -0.972622 | -0.76438  | -0.445644 | -0.265411 | -0.451208 | -0.087972 | 0.4902518 | -0.405952 | -0.924749 |
| Chaf1b    | -0.622058  | -1.146423 | -0.834079 | -1.277743  | -1.297296 | -0.950079 | 1.0843848 | 1.4120267  | 0.1477417 | 0.7106765 | 0.6223308 | 0.800316  | 0.2381293 | -1.132964 | 1.0598399 | -0.573743 | 0.0671376 | 1.6925585 |
| Itsn1     | 1.2638836  | 0.9674631 | 0.834584  | 1.1562649  | 1.3598549 | 1.6516671 | -1.09567  | -0.511186  | -0.786704 | -0.83375  | -0.908212 | -1.055546 | -0.087421 | -0.509734 | -0.136166 | 0.845028  | -0.134903 | -0.995287 |
| Ifngr2    | 1.7362574  | 1.3926139 | 0.4735433 | 1.6545451  | 0.948019  | 0.8966269 | -1.310965 | -1.32405   | -0.918858 | -0.897632 | -0.441606 | -0.220921 | -0.948336 | -0.838624 | -0.720112 | 1.2126621 | -0.490607 | -0.831886 |
| Il10rb    | 1.1175346  | 0.5344728 | 1.034915  | 1.7703237  | 0.7720677 | 1.7524805 | -1.315993 | -0.753041  | -0.172943 | -0.794937 | -0.707799 | 0.0892759 | -1.037399 | -0.660219 | -0.725223 | 0.7309458 | -0.099608 | -0.574015 |
| Mis18a    | -0.737357  | -0.101137 | -1.296415 | -1.14199   | -1.172128 | -1.054461 | 0.814918  | 0.9197592  | 0.1704832 | 0.8599594 | 0.099928  | 0.7731856 | 0.1134997 | -1.074154 | 0.4990207 | 0.592075  | 0.3702877 | 2.2745312 |
| Enah      | -1.090963  | -0.633268 | -0.586688 | -1.008216  | -0.71029  | -0.97416  | 0.1280273 | -0.091004  | 0.3252345 | 0.5855243 | 0.5483923 | -0.210046 | 0.495893  | 2.6171212 | -0.200651 | -0.099986 | 1.9425268 | -0.245448 |
| Racgap1   | -1.239164  | -0.982775 | -1.217654 | -1.383557  | -1.202628 | -0.986323 | 0.8745451 | 0.1937001  | 0.9899188 | 0.7224299 | 0.692667  | 0.5029773 | 0.3066581 | 0.2961704 | 1.124683  | -0.626233 | 0.0887325 | 2.0012614 |
| Gpd1      | 0.9072942  | 1.2688546 | 1.1092691 | 0.5751366  | 1.5508979 | 1.4740566 | -0.75056  | -0.62693   | -0.745724 | -0.777341 | -0.772346 | -0.749366 | -0.749051 | -0.382174 | -0.553603 | -0.659457 | -0.296105 | -0.722852 |
| Lass5     | 1.201762   | 2.8493599 | -0.396848 | 0.70155    | 0.6106616 | 1.3426777 | -0.768692 | 0.3165013  | -0.506915 | -0.837124 | -0.768087 | -0.564182 | -0.944233 | -0.492575 | -0.206161 | -0.592543 | -0.672618 | -0.727534 |
| Slic11a2  | 1.9289499  | 1.2598883 | -0.008175 | 0.5267603  | 0.9275409 | 1.7398173 | -1.274907 | -0.1025431 | -1.166669 | -0.236463 | -0.489597 | -0.683513 | -0.873623 | -1.081497 | -0.584586 | -0.447044 | -0.278572 | 0.9091452 |
| Cela1     | 0.6327971  | 1.1879883 | -0.123091 | 1.5865476  | 0.8270732 | 2.3543264 | -1.259638 | -0.765917  | -0.905628 | -0.64571  | -0.637704 | -0.921062 | -0.467266 | -0.833609 | -0.316148 | 0.7872498 | -0.197361 | -0.302848 |
| Krt18     | -0.58951   | -0.848886 | -0.778211 | -0.853046  | -0.777946 | -0.735926 | 0.2559321 | 2.394749   | -0.397586 | -0.300012 | -0.51968  | 0.0248741 | -0.363176 | -0.670118 | 1.9005844 | 1.2862258 | 1.1328846 | -0.179153 |
| Igfbp6    | 0.926207   | 0.3343291 | 0.3679073 | 1.8760668  | 0.4506928 | 1.8498533 | -1.396629 | -1.201142  | 0.771215  | 0.0806478 | -0.570311 | -1.243789 | -0.960048 | 0.4310252 | -0.863308 | 0.4298172 | -0.536164 | -0.746782 |
| Calcolec1 | 0.993425   | 2.0209885 | 1.3945566 | 1.89016821 | 1.3594484 | 0.9805718 | -1.234132 | -0.789205  | -0.27266  | -0.615579 | -0.089256 | -0.345276 | -0.415972 | -0.690784 | -0.760706 | -0.101158 | -0.261229 | -1.154293 |
| Rttm      | -0.914313  | -0.698814 | -1.066988 | -0.880899  | -1.124804 | -0.883023 | 1.8323428 | 1.5371162  | 0.8154327 | 1.1116216 | -0.019594 | 0.2764699 | 0.5703175 | -0.66425  | 1.5542379 | -0.762934 | -0.236197 | -0.445723 |
| Rgn       | 2.011162   | 1.2203042 | 0.0817776 | 0.0158341  | 1.2424564 | 1.4277414 | -0.707463 | -0.696723  | -0.256483 | -0.306561 | 0.0455716 | -0.588245 | -0.408202 | -0.712994 | -0.74687  | -0.825352 | -0.806124 | -0.92074  |
| Mospd1    | 1.7190733  | 2.3676796 | 0.3361906 | 0.2463834  | 1.1031036 | 1.3325044 | -1.052314 | -0.480676  | -0.658425 | -0.403547 | -0.382429 | -0.512862 | -0.366706 | -0.29856  | -0.309711 | -0.86978  | -0.506604 | -1.263322 |
| Cxcl13    | -0.500041  | 0.4550303 | 1.9789008 | 1.0091838  | 2.2897866 | 0.7865022 | -0.907221 | -0.744608  | -0.785697 | -0.812779 | -0.723175 | -0.876871 | -0.822825 | -0.493796 | -0.227975 | -0.505282 | 0.1376709 | 0.7432125 |
| Fhl1      | 1.5629777  | 1.2347398 | 1.4710649 | 1.8015481  | 0.4281496 | 0.3489207 | -1.023984 | -0.774761  | -1.025383 | -1.034281 | -1.02474  | -0.933687 | -1.008077 | 0.6742021 | -0.283731 | -0.18147  | -0.029005 | -0.202484 |
| Rfc2      | -1.630132  | -1.254744 | -0.942134 | -1.276721  | -0.956838 | -1.150614 | 1.3271888 | -0.054109  | 0.550207  | 0.3486226 | 0.6805023 | 0.561339  | 0.8802063 | -0.413748 | 1.0471256 | 1.0202619 | -0.130674 | 1.3942602 |
| Prmt5     | -0.73161   | -0.974169 | -0.846558 | -0.842335  | -1.043167 | -0.646098 | 0.4532073 | 0.023936   | -0.670251 | 0.5550129 | 0.1448889 | 0.2830166 | 0.2968766 | 0.3538843 | 0.6571142 | 0.0128668 | -0.309656 | 2.3830404 |
| Temem52   | 1.1077104  | 1.4866628 | 1.224536  | 1.9019011  | 1.1305493 | 1.0126013 | -0.815564 | -0.757551  | -0.815564 | -0.815564 | -0.815564 | -0.704926 | -0.815564 | -0.510407 | -0.661497 | -0.455965 | -0.343497 | -0.518255 |
| Rpp14     | -0.878767  | -0.540331 | -1.246987 | -0.989228  | -1.210619 | -0.863223 | 0.5817428 | 0.9417799  | -0.905867 | 0.5717282 | 0.5995348 | 0.5372629 | 1.0668434 | 0.8311349 | 0.136674  | -0.406857 | -0.726551 | 2.3220883 |
| Vwa5a     | 0.7734725  | 1.0993889 | 1.4630447 | 1.6311108  | 1.0321458 | 1.36048   | -1.475311 | -1.220641  | 0.0447986 | -1.211831 | -0.944489 | 0.0299894 | -0.675536 | -0.177367 | -0.722181 | -0.709595 | -0.467324 | -0.460154 |
| Serping1  | 0.5743359  | 0.2328268 | 1.5913829 | 1.5037983  | 1.1963527 | 1.4255238 | -1.106446 | -0.903321  | -1.056962 | -0.993275 | -1.029747 | -0.825527 | -1.036406 | -0.545366 | -0.133691 | 0.9928881 | 0.2679548 | -0.156783 |
| Guca2a    | -0.115735  | 2.082255  | 0.29652   | -0.046689  | 0.3183596 | 0.8777089 | -0.260628 | -1.085307  | -0.389363 | 0.7795328 | 1.6612946 | 1.2233488 | 0.0249808 | -1.14168  | -1.07628  | -1.084889 | -0.967095 | -1.033307 |
| Acy1      | -1.266084  | -0.601546 | -1.200971 | -1.527376  | -1.230052 | -0.866528 | 0.9489111 | 1.4622297  | 0.4219336 | 1.2397694 | -0.096779 | 1.252641  | 0.2070468 | 0.6201263 | 0.0404942 | -0.353368 | -0.436055 | 1.385608  |
| Cd4       | -0.584055  | 0.7265919 | 0.9807172 | 1.7917755  | 1.7042126 | 1.6944678 | -0.850537 | -0.886469  | -0.757244 | -0.78343  | -0.765458 | -0.667118 | -0.843286 | -0.584816 | -0.663556 | 0.7009651 | 0.3658948 | -0.615056 |
| Dtdw1     | -0.732954  | -0.90914  | -0.986744 | -1.203215  | -0.843973 | -0.62313  | 2.7632085 | 0.98363    | 0.4826293 | 0.2191911 | -0.34457  | -0.03319  | 0.9269161 | -0.137405 | 0.2007231 | -0.264882 | -0.747484 | 1.2503265 |
| Wfdcl     | 1.16       |           |           |            |           |           |           |            |           |           |           |           |           |           |           |           |           |           |



|            |           |           |           |           |           |           |           |           |           |           |           |            |           |           |           |            |           |           |
|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|------------|-----------|-----------|
| Tmem178    | 1.2678421 | 0.1804312 | 1.9537583 | 2.3024232 | 0.184998  | 1.3376971 | -0.650083 | -0.674854 | -0.645409 | -0.647252 | -0.66111  | -0.506108  | -0.68381  | -0.630469 | -0.534288 | -0.437391  | -0.557703 | -0.598672 |
| Thumpd2    | -1.08076  | -0.496168 | -1.250068 | -1.061706 | -1.049074 | -1.174908 | 1.2180761 | 1.1945957 | 1.8115915 | -0.218952 | 1.0632588 | 0.0762328  | 0.0544654 | 1.1520266 | 0.6707466 | -0.588826  | 0.49544   | -0.815973 |
| Pkdcc      | 2.1170199 | 0.345685  | -0.007716 | 2.1535043 | 0.4713282 | 0.5880406 | -1.338135 | -0.101674 | -0.927292 | -0.129728 | -0.951797 | -0.508701  | -1.02964  | -0.422316 | -0.350408 | 0.9432004  | -0.141809 | 0.1904374 |
| Poir2d     | -1.313988 | -0.683649 | -1.006934 | -1.334055 | -1.350886 | -1.111697 | 1.1389192 | 1.8996545 | 0.9780042 | 0.7537596 | 0.7522647 | 0.4907109  | 1.0802537 | -0.06376  | 0.5449579 | -0.381502  | -0.30584  | -0.086213 |
| Celf4      | -1.060212 | -0.794188 | -0.973181 | -0.946527 | -0.897924 | -0.77861  | -0.242108 | 2.6614395 | 0.7986711 | 1.6901342 | 0.951561  | 0.2806857  | -0.0437   | 0.2835852 | 1.3535435 | -0.011671  | -0.750922 | -0.520577 |
| Slc39a6    | -1.27326  | -0.724684 | -0.715359 | -1.201796 | -0.890484 | -1.458214 | 1.1152998 | 1.530779  | 1.5004971 | 1.6896114 | 1.4640926 | 0.4217969  | 0.5340125 | 0.2764429 | 0.2999351 | -0.402564  | -0.426502 | -0.739604 |
| Adams10    | 0.5286469 | 0.2061728 | 0.9087645 | 1.635905  | 1.4313232 | 1.6373922 | -1.43315  | -0.357843 | -1.075337 | -1.189863 | -1.013568 | -0.346909  | -1.173303 | -0.066323 | 0.4390173 | 0.6252006  | 0.005325  | -0.761451 |
| Myo1f      | 1.1221864 | 0.3828911 | 1.852217  | 2.6035423 | 0.4908571 | 1.2187102 | -0.953965 | -0.743849 | -0.68992  | -0.790573 | -0.498914 | -0.634547  | -0.802206 | -0.590431 | -0.57117  | 0.4834621  | -0.238796 | -0.6216   |
| Kifc5b     | -1.079856 | -0.689553 | -1.075501 | -1.171518 | -1.274992 | -1.241623 | 0.9408658 | 2.498055  | 0.8245062 | 1.0919979 | 0.3007617 | 0.2053723  | 0.0675223 | 0.6435943 | 0.0964911 | -0.271848  | -0.03321  | 0.1689344 |
| Dtna       | 0.7685202 | 1.1955384 | 1.5142092 | 1.3766589 | 0.8836877 | 1.179094  | -1.181345 | -1.141852 | -1.232671 | -1.018412 | -0.810983 | -0.885487  | -1.15383  | 0.1020182 | -0.175658 | 0.714141   | -0.192396 | 0.0587674 |
| Dsc2       | -0.939865 | -1.011181 | -0.986835 | -1.020714 | -1.022002 | -1.061943 | 0.5875278 | 1.2855987 | -0.408879 | 0.9906856 | -0.614515 | 0.4342309  | -0.594469 | 2.2267053 | 1.1391517 | -0.018064  | 0.6932958 | 0.3212711 |
| Spata24    | -0.758266 | -0.060396 | -1.505441 | -1.111604 | -0.770538 | -1.14843  | 1.7345341 | 1.6932116 | -0.556202 | -0.172089 | 0.4741699 | 0.8458258  | -0.612543 | 0.0666663 | -0.195621 | 0.627179   | -0.272745 | 1.7222883 |
| 2010001M   | -0.74559  | 0.772412  | 2.2842814 | 0.8499645 | 1.6112112 | 1.2677048 | -0.949056 | -0.695266 | -0.578622 | -0.949056 | -0.715441 | -0.81095   | -0.83589  | -0.837749 | -0.010167 | -0.079163  | 0.6685225 | -0.247148 |
| C2         | -0.474449 | 0.2095059 | 2.2720148 | 0.9398528 | 1.5396535 | 1.0439176 | -1.164214 | -1.175848 | -1.013118 | -0.70059  | -0.806241 | 0.5050543  | -0.105637 | -0.538311 | -0.50753  | 0.5557361  | 0.4128112 | -0.082629 |
| Epb4.1l4a  | -0.9736   | -0.723463 | -0.874924 | -1.241285 | -0.808272 | -1.080874 | 1.6650294 | 0.700883  | 0.8094991 | 1.5437138 | 1.2189545 | 0.7245797  | 1.0723533 | 0.412461  | -0.759655 | -0.956138  | -0.291136 | -0.438146 |
| Tslp       | -0.971193 | -0.929512 | -0.43988  | -0.932477 | -0.879513 | -0.944858 | -0.100465 | 0.0740582 | 0.018848  | 0.4714073 | 1.5969951 | 0.9410669  | 1.7998232 | -0.797365 | 1.8716467 | 0.6263597  | -0.828672 | -0.576271 |
| Bin1       | 0.1725604 | 1.2462322 | 0.1712005 | 1.7405863 | 0.9718701 | 1.2810581 | -1.172667 | -0.57496  | -1.203356 | -1.122347 | -1.096201 | -0.736958  | -1.203191 | -0.070383 | 0.1003049 | 0.9782868  | -0.096634 | -0.471403 |
| Lims2      | 1.6352837 | 0.4156886 | 0.9431596 | 1.2225452 | 0.7381769 | 1.2609976 | -0.008415 | -0.50396  | -1.24476  | 0.0601431 | -0.104453 | -1.50257   | 0.0611621 | 0.7005689 | -1.253659 | -0.87945   | -0.992453 | -1.178005 |
| Zfp521     | 0.761834  | 0.8372729 | 0.751761  | 1.4680586 | 1.2798352 | 1.669952  | -1.459669 | -0.75463  | -1.130983 | -1.273903 | -0.687862 | -0.879718  | -1.128758 | 0.2315465 | -0.004544 | 0.352501   | 0.3629914 | -0.390551 |
| Lama3      | -1.208288 | -0.886663 | -0.604393 | -1.156642 | -0.943865 | -1.089031 | 0.1648334 | 0.6599099 | 1.7980843 | 2.1553608 | 0.3268337 | -0.09207   | 0.0739361 | -0.276928 | 0.6342399 | -0.07088   | 1.2311538 | -0.715592 |
| Hrps18b    | -0.900416 | -0.959904 | -0.941505 | -1.19438  | -1.230669 | -0.091838 | 0.9126442 | 1.7926999 | 1.6483019 | -0.06238  | 0.4106022 | 0.0705743  | 0.6064268 | 0.1074404 | 0.3906295 | -0.068408  | -0.892783 | 1.3963944 |
| M2-M5      | 1.2508373 | 2.4769526 | 0.3068233 | 1.4507454 | 1.1478448 | 0.6884803 | -0.819613 | -0.845282 | -0.246086 | -0.062646 | -0.516549 | -0.317121  | -0.587411 | -0.596987 | -0.813769 | -0.894734  | -0.713646 | -0.90424  |
| Gabbr1     | 0.8282211 | 0.2138322 | 1.1744749 | 1.7439575 | 1.1942254 | 1.5506476 | -1.270768 | -0.305856 | -0.826395 | -1.102887 | -0.313396 | -0.430151  | -1.575019 | -0.069052 | 0.802666  | -0.246281  | 0.0280897 | -0.676319 |
| Myot       | 1.3876796 | 1.2322417 | 1.6692167 | 1.7637864 | 1.0474872 | 0.9288609 | -0.899847 | -0.720675 | -0.896193 | -0.893348 | -0.899847 | -0.899847  | -0.899847 | -0.899847 | -0.899847 | -0.545657  | -0.279077 | -0.463088 |
| 4833403l15 | 0.4732035 | -0.328976 | 2.2915583 | 0.635476  | 1.872466  | 1.108892  | -0.458424 | -0.910826 | -0.980336 | -0.945044 | -0.447135 | -0.899925  | -0.32406  | 0.0137109 | 0.2958678 | 0.0695418  | -0.621898 |           |
| Hbeqf      | -0.894229 | -1.293862 | -0.105054 | -0.887934 | -1.135601 | -1.195891 | 1.1527477 | 1.7549476 | -0.673859 | 1.3396251 | 0.4204084 | 1.1527477  | 0.8991773 | -0.469695 | 0.238888  | 0.803305   | 0.0788349 | -0.246922 |
| Hsd17b4    | 1.5395737 | 2.0126436 | 0.5027223 | 1.1583121 | 0.795585  | 1.4948606 | -1.164228 | -1.10831  | -0.206642 | -0.778258 | -0.529046 | -0.484     | -0.481569 | -0.540734 | -0.486326 | -0.82137   | -0.635006 | -1.355327 |
| Pmaip1     | -0.934289 | -0.92084  | -0.754962 | -1.180333 | -0.876105 | -1.210499 | 1.006456  | 0.5764173 | -0.353496 | -0.261404 | 0.6823572 | -0.024748  | 1.3310258 | 1.2409172 | 1.8618864 | -0.829905  | 1.161158  | -0.514537 |
| Impa2      | -0.463043 | -0.638444 | -0.963937 | -1.14688  | -1.078973 | -1.485212 | 2.0981493 | 0.879906  | 0.7789960 | 1.431938  | 0.9788347 | 1.34693    | 0.5539348 | 0.186749  | 0.6538544 | -0.968317  | -0.658241 | -0.217412 |
| Cidea      | 2.8652555 | 1.7228566 | -0.173121 | 0.3995853 | 0.7276756 | 1.0157    | -0.726009 | -0.412862 | -0.736569 | -0.613187 | -0.552227 | -0.381514  | -0.415634 | -0.042602 | 0.537036  | -0.1795413 | -0.624168 | -0.720731 |
| Ppic       | -0.710576 | -0.997637 | -0.851098 | -0.744673 | -0.077012 | 1.0409829 | -1.705772 | 0.553544  | -0.263916 | -0.567194 | -0.561014 | 0.0464254  | -0.685059 | 1.8683001 | 1.834412  | 1.2050964  | 0.6545965 | -0.039219 |
| Cep192     | -1.211305 | -0.671893 | -0.881571 | -1.030503 | -1.113725 | -0.808979 | 0.8047473 | 0.7696781 | 0.7431124 | 0.543937  | 0.216886  | 0.3531235  | 0.1447859 | -0.13004  | 1.1341117 | -0.699427  | 0.2204307 | -0.383341 |
| Lmbn1      | -0.112066 | -0.744351 | -1.138397 | -1.428018 | -1.206664 | -1.431691 | 1.8095288 | 1.3300939 | 0.6474127 | 0.7065891 | 0.2986953 | 0.4960455  | -0.305425 | 0.4768655 | 0.2867627 | -0.445958  | 0.7270034 | 1.010934  |
| Sic27a6    | 2.0782629 | 0.6715544 | 0.6282321 | 1.5338877 | 0.6077432 | 0.4925388 | -1.015532 | 0.7013753 | -0.674424 | 0.204317  | 0.195308  | 0.1250677  | -1.040097 | -1.435142 | 0.0679817 | -0.56175   | -0.916269 | -1.587304 |
| Cd74       | -0.350226 | 1.1335003 | 2.0108997 | 1.5647084 | 1.4149364 | 0.7490018 | -1.264184 | -0.988254 | -0.61875  | -0.836846 | -0.902511 | -0.385107  | -0.988254 | -0.357301 | -0.711808 | 0.5413929  | 0.0734158 | -0.084614 |
| Camk2a     | 1.8737812 | 2.0207249 | 0.7407528 | 0.9462041 | 1.0658074 | 0.698632  | -1.038986 | -0.923339 | -0.942031 | -0.828787 | -0.984227 | -0.962777  | -0.826524 | -0.33677  | -0.178942 | -0.270832  | -0.15333  | 0.1006434 |
| Sf1r       | 0.6231279 | 0.5370263 | 0.8686868 | 1.7020348 | 1.3969473 | 1.6038784 | -1.125295 | -0.853858 | -0.866899 | -0.903331 | -0.938619 | -0.695929  | -0.96465  | -0.426887 | -0.504271 | 1.2082645  | -0.034515 | -0.625712 |
| Psat1      | -0.925389 | -0.497432 | -0.876029 | -1.341879 | -0.725651 | -1.133923 | 2.1588602 | 0.2097318 | -0.900097 | 0.6054329 | 0.1538471 | -0.10252   | 0.98509   | 1.0067483 | -0.465436 | 0.5264434  | -0.402003 | 1.7215066 |
| Cndp2      | 1.2213539 | 0.1274426 | 0.9230823 | 2.3945851 | 0.7227454 | 1.4254424 | -0.903521 | -0.540009 | -1.286916 | -0.59637  | -0.681346 | -0.52347   | -0.707996 | -0.672231 | -0.691222 | 0.5476914  | -0.104061 | -0.866724 |
| Cyb5       | 1.8448117 | 1.8982845 | 0.2495077 | 1.0670089 | 0.7111481 | 1.2366058 | -1.239187 | 0.3795135 | -0.281213 | -0.610743 | -0.457947 | -0.039201  | -0.514829 | -0.392302 | -0.587271 | -1.037138  | -0.895376 | -1.331673 |
| Incnp      | -1.42743  | -1.088478 | -0.911288 | -1.194059 | -1.094741 | -1.274677 | 0.2560639 | 1.774314  | -0.354196 | 0.9250285 | 1.0514772 | 0.4501907  | -0.005408 | -0.177207 | 0.3450266 | 0.3426652  | 1.0075596 | 1.3794987 |
| Fth1       | 0.9003345 | 0.479573  | 1.018285  | 2.5830188 | -0.133517 | 1.0367672 | -0.79346  | -0.240223 | -0.910952 | -0.944247 | -0.974279 | -0.78216   | -0.857008 | -0.523056 | -0.509673 | 1.3042119  | -0.211915 | -0.437045 |
| Rab3l1     | 0.8569231 | 0.4396553 | 0.5749347 | 1.8781971 | 1.4727006 | 1.425532  | -1.187497 | -0.846732 | -0.848399 | -1.061792 | -1.113011 | -0.76004   | -0.900081 | -0.270551 | -0.23834  | 1.3599251  | 0.0733227 | -0.529318 |
| Tmem138    | -0.803912 | -1.144461 | -1.418916 | -1.327497 | -1.480035 | -0.86964  | 1.3190765 | 1.5623639 | -0.380497 | 0.6229127 | 0.2018995 | 0.1128484  | 0.6340799 | 0.7052629 | 1.2271444 | -0.037751  | 0.0058939 | 1.0711573 |
| Ms4a4d     | 0.4506571 | 0.3936256 | 1.7306944 | 1.0466599 | 1.5080919 | 1.4931269 | -1.264075 | -0.897737 | -0.994975 | -1.114384 | -1.143478 | -0.682895  | -1.143716 | 0.3230255 | 0.3621844 | 0.0140467  | 0.1726354 | -0.253488 |
| Ms4a2      | 0.9974715 | 0.7860051 | 0.6126296 | -0.273349 | 1.7122312 | 2.076744  | -1.169698 | -1.207405 | -1.116499 | -0.121633 | -0.835511 | -0.104047  | 0.0235318 | -0.753939 | -0.615904 | -0.944768  | -0.38585  | 1.0952555 |
| Lpxn       | 1.4132527 | 0.7237009 | 1.3069544 | 1.8321274 | 0.6048855 | 1.6656764 | -0.945414 | -0.869875 | -0.776859 | -0.875744 | -0.886735 | -0.719106  | -0.816573 | -0.617364 | -0.680689 | 0.3939285  | -0.368215 | -0.383951 |
| Pcsk5      | -0.272296 | -0.442337 | -0.454498 | -0.282782 | -0.284789 | -0.197935 | -0.912639 | -0.472629 | -0.767295 | -0.72551  | -0.733135 | -2.800E-06 | -0.903074 | 1.4102169 | 1.5479365 | 2.845231   | 0.5575717 | 0.0877863 |
| Ms4a8a     | 0.6940888 | 0.9927399 | 1.6601883 | 0.644303  | 1.1656695 | 1.3306874 | -0.679312 | -1.038264 | -0.687647 | -1.098302 | -1.04259  | -0.80277   | -0.855301 | -0.464378 | -0.508496 | 1.621345   | -0.385766 | -0.546249 |
| Ccdc86     | -0.779792 | -1.0      |           |           |           |           |           |           |           |           |           |            |           |           |           |            |           |           |



|           |           |           |            |           |           |           |           |           |           |           |           |           |           |           |           |           |            |           |
|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|
| Myadm12   | 1.666762  | 1.1770968 | 1.2487231  | 0.6202875 | 1.6939325 | 0.7909734 | -0.997497 | -0.905563 | -0.997497 | -0.997497 | -0.997497 | -0.997497 | -0.997497 | 0.6064342 | -0.319881 | -0.209053 | -0.102795  | -0.282794 |
| Fasn      | 0.5929875 | 1.4446359 | 1.5955099  | 0.0068496 | 2.1123379 | 0.651433  | -0.850102 | -1.65959  | -0.588465 | -0.075755 | 0.4268669 | -0.70909  | -1.115951 | -0.361305 | 0.3351973 | -0.54488  | -0.496494  | -0.763738 |
| Arhgap19  | -1.254069 | -0.694092 | -0.875231  | -0.928584 | -0.886569 | -1.126689 | 0.9881865 | 1.3441059 | -0.489699 | 1.2481075 | 0.3267956 | 0.6977921 | 0.0234266 | -0.742172 | 0.1988529 | 0.1160379 | -0.293048  | 0.2384889 |
| Zdhc16    | -1.162008 | -0.886406 | -0.934515  | -1.257132 | -1.113249 | -1.192647 | 0.3650537 | 2.2070715 | -0.775146 | 0.5197017 | 0.6494156 | 0.85206   | 0.5885284 | -0.112346 | 0.6349755 | -0.203345 | 0.5454601  | 1.2745268 |
| Rfng      | -0.991417 | -0.859456 | -0.522024  | -1.122946 | -0.775338 | -1.171105 | 1.183722  | -0.354477 | 1.9249839 | 0.976499  | 1.0838826 | 0.865747  | 1.60685   | 0.1067766 | -0.430068 | -0.515796 | -0.739315  | -0.266519 |
| Sic16a3   | -1.109051 | -1.284922 | -0.88427   | -0.992616 | -1.202289 | -1.209167 | 1.2666236 | 0.8817483 | 0.765234  | 0.6770381 | 0.1797404 | 0.2832832 | 0.834355  | -0.58022  | 1.7832898 | 0.6169035 | -0.82278   | 0.7970914 |
| Cd7       | 3.3915044 | -0.173014 | 0.5999816  | -0.259783 | 1.2020083 | 0.6306638 | -0.644126 | -0.492899 | -0.374129 | 0.1737436 | -0.403671 | -0.441279 | -0.211486 | -0.70043  | -0.758066 | -0.749231 | -0.274827  | -0.51496  |
| Sectm1a   | 1.0766415 | 0.8944215 | 0.2309977  | 0.3079659 | 1.8387577 | -0.086017 | -1.14043  | -1.008363 | 0.7327477 | -0.286547 | -0.379097 | -0.039031 | -0.073287 | -0.96399  | -0.965764 | -0.923604 | -0.748405  | -0.466996 |
| Got1      | 1.0411926 | 1.3829523 | 1.1685172  | 1.5391312 | 1.0442407 | 1.4575884 | -0.508742 | -1.037722 | -1.058135 | -0.112379 | -0.191134 | -0.101747 | -0.952347 | -0.503734 | -0.79749  | 0.2804149 | -0.610071  | -1.131536 |
| Entpd7    | -0.949646 | -1.269709 | -0.694167  | -0.80916  | -1.309936 | -1.152249 | 0.6376962 | -0.426631 | -0.600647 | 1.8893398 | 1.8216596 | 0.9128974 | -0.270112 | 0.1402365 | 0.3932074 | 1.0038173 | 0.6123565  | 0.0710468 |
| Cpn1      | -0.938184 | -0.813149 | -0.587064  | -0.914026 | -0.828304 | -0.866994 | 1.1422762 | -0.42714  | -0.239873 | 2.89383   | -0.155066 | 0.3803724 | 0.1043239 | 0.0871621 | 1.1413249 | -0.349951 | -0.602422  | 0.9728832 |
| Cwf191    | -1.114144 | -1.139017 | -1.200631  | -1.094145 | -1.076087 | -0.881356 | 1.1768294 | 1.6553745 | -0.38968  | 0.8839827 | 0.3494758 | 0.597077  | 0.8756411 | -0.133109 | 0.4599365 | -0.322065 | -0.405065  | 1.756983  |
| Scd3      | -0.03285  | 3.3960797 | 1.2767048  | 0.0205107 | 0.6131591 | 0.5757668 | -0.530655 | -0.359805 | -0.606348 | -0.531407 | -0.526049 | -0.622202 | -0.522306 | -0.048876 | -0.439604 | -0.590814 | -0.458582  | -0.612288 |
| Sufu      | -0.5021   | -0.974075 | -0.645545  | -1.467664 | -0.774554 | -1.822403 | 0.2860036 | 0.9602616 | -0.374572 | 1.3870938 | 2.199455  | 0.4471278 | 0.5362925 | 0.5106884 | -0.572618 | 0.3002232 | 0.0220963  | 0.4842885 |
| Hexa      | 0.8810241 | 0.3537075 | 1.5349036  | 1.7557079 | 0.8524014 | 1.8285056 | -0.191919 | -0.862693 | -0.902554 | -0.974089 | -0.928355 | -0.621116 | -0.866978 | -0.240996 | -0.294756 | 0.513448  | -0.25259   | -0.756374 |
| Adpgk     | -0.968236 | -0.97     | -0.883044  | -1.02244  | -1.092717 | -1.542304 | -0.252738 | 0.3607882 | 1.0365338 | 1.53839   | 0.4566714 | -0.042839 | 1.2093968 | 0.8290311 | 0.7819368 | -0.330481 | -0.696298  | 1.5883497 |
| Fyco1     | 0.5996407 | 1.6725486 | 1.4468066  | 1.1858773 | 1.4068469 | 0.1919307 | -0.103655 | -0.834793 | -0.137556 | -0.67521  | 0.2626335 | -0.942842 | -0.923598 | -0.245659 | -0.792373 | -0.305029 | -0.282026  | -1.523538 |
| Ribc1     | -0.938278 | -1.041518 | -0.773826  | -0.884331 | -0.710098 | -0.760814 | 0.5451106 | -0.402965 | 1.5081506 | 0.1469166 | 0.1346647 | 0.2210599 | 0.2134581 | 0.2483427 | 0.4412174 | -0.39261  | -0.552372  | 2.9978549 |
| Fgd1      | -0.794532 | -1.011794 | -1.00102   | -0.670022 | -1.077074 | -0.733221 | 0.8385023 | 1.276739  | -1.088544 | 0.6782872 | 0.4021114 | 1.855226  | -0.440357 | 0.7585197 | 0.4493106 | -0.229349 | 2.635244   | -0.196403 |
| ltg8      | 2.4932417 | 1.666026  | 0.0852223  | 1.1315957 | 0.8148939 | 0.599747  | -0.591375 | -0.338362 | -0.064571 | -0.901269 | -0.929141 | -0.790077 | -0.630358 | -0.453995 | -0.944545 | -1.168103 | -0.362826  | -1.263101 |
| Gdf11     | -0.855812 | -0.717607 | -0.816207  | -0.52766  | -0.282444 | 0.1203432 | -1.465773 | -0.156839 | -1.044797 | -0.738024 | -0.307046 | 0.5055907 | -0.340518 | 0.6971301 | 1.7410692 | 1.5385054 | 0.6029868  | 0.2047106 |
| Cdk2      | -1.230759 | -1.146343 | -0.956161  | -1.349598 | -1.235734 | -1.275819 | 0.4474289 | 0.6718685 | 0.4667821 | 0.6247012 | 0.4009818 | 2.0998369 | 0.5944086 | -0.271798 | 0.9854605 | 0.7797195 | -0.088364  | 0.7889877 |
| Pa2g4     | -1.311763 | -0.223517 | -1.112618  | -1.348307 | -1.112618 | -1.306262 | 0.5128153 | 2.1319089 | 0.1254309 | 0.4357929 | 0.3365876 | 1.5676494 | 0.0493115 | 0.6140989 | 0.011264  | 0.2891255 | -0.578407  | 0.9204075 |
| Eys1      | 1.0079863 | 0.341737  | 1.1666705  | 2.3374352 | 0.8140007 | 1.0302032 | -1.252444 | -0.787125 | -0.728796 | -0.846417 | -0.926858 | -0.329922 | -0.982531 | -0.52443  | -0.554658 | 0.9862758 | -0.087551  | -0.636031 |
| Baiap2    | 2.7737346 | 1.1160083 | 0.3291823  | 1.195925  | 0.5168127 | 0.4992572 | -0.266582 | -0.951161 | -1.21184  | -0.254835 | -0.054957 | -0.607944 | -0.686779 | -0.371177 | 0.485298  | -0.51386  | -1.105739  | -0.889345 |
| Aatk      | 0.2696682 | -0.15913  | 2.0777013  | 2.627672  | 0.6283181 | 0.391357  | -0.891874 | -0.375125 | -1.022055 | -0.833448 | -0.92289  | -0.476363 | -0.648445 | -0.627636 | -0.420497 | 0.4287993 | 0.2950247  | -0.341074 |
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| Prim1     | -1.13957  | -0.827985 | -1.032273  | -1.466001 | -1.183097 | -1.167687 | 0.3332106 | 1.7691437 | 0.1324222 | 0.1179556 | 0.5159666 | 1.2425688 | 0.6166069 | -0.227696 | 1.0560064 | 1.1212509 | -0.660435  | 0.7083539 |
| Shmt2     | -1.430794 | -0.707218 | -0.694842  | -1.497787 | -1.018139 | -1.381824 | 0.357019  | 1.0686288 | 1.103013  | 0.4092211 | 0.7472032 | 1.6018328 | -0.18655  | -0.367993 | 0.5420952 | 0.5367507 | 0.0191968  | 1.265186  |
| Pstp1p2   | 3.0875468 | 0.757692  | 0.3043555  | 1.319947  | 0.5418982 | -0.225198 | -0.897248 | -0.204283 | -1.275186 | -0.23434  | -0.536239 | 0.2144255 | -0.446351 | -0.514952 | -0.986171 | -0.340918 | 0.06536    | -0.58434  |
| Xrcc6bp1  | -0.627256 | -1.129398 | -0.390704  | -1.054855 | -1.208668 | -0.944296 | 0.5493499 | 0.9694156 | 2.7212192 | -0.318169 | 0.0570061 | 1.525035  | 0.5779769 | -0.795957 | 0.8817774 | -0.536453 | -0.559095  | 0.7329824 |
| Zfp51     | -1.071077 | -0.536676 | -1.188641  | -1.071625 | -1.192209 | -1.280881 | 0.7579024 | 1.4336866 | 0.7212694 | -0.256369 | 0.338376  | 1.1813906 | 0.4825508 | 0.117377  | 0.2902218 | 0.4555178 | -0.829485  | 2.0412306 |
| Cyp2e1    | 0.5485956 | 0.9419454 | 3.1884953  | 0.8051605 | 1.0730666 | 0.1600887 | -0.560345 | -0.474858 | -0.615839 | -0.609487 | -0.556675 | -0.577639 | -0.580438 | -0.449994 | -0.584192 | -0.715712 | -0.495335  | -0.495198 |
| Xcb8      | 1.0208079 | 1.2308236 | 1.555139   | 1.971165  | 1.3934698 | 0.7809392 | -0.797894 | -0.667858 | -0.826413 | -0.826413 | -0.826413 | -0.809621 | -0.427843 | -0.499062 | -0.511074 | -0.429634 | -0.500235  |           |
| 1600016N2 | -1.010328 | -0.78043  | -0.869756  | -1.038691 | -0.743024 | -1.112621 | 1.3742196 | 2.5675625 | 0.6580565 | 0.531139  | 0.8800268 | 0.7188105 | 0.6179335 | -0.235756 | -0.062551 | -0.302551 | -0.680608  | -0.511432 |
| Lrdd      | -0.967912 | -0.191659 | -0.948431  | -0.887898 | -0.979991 | -1.261362 | 1.8343385 | 1.4314086 | 0.3305614 | 1.108033  | 0.91613   | 0.3381205 | 0.5953773 | -0.161626 | -0.859932 | -0.120174 | -0.604131  | 1.2575079 |
| Pnp1a2    | 1.0144193 | 0.8807122 | 2.4588968  | 1.3528509 | 0.9465437 | 1.0400257 | -0.747736 | -0.72794  | -0.79028  | -0.792729 | -0.792729 | -0.727508 | -0.939238 | -0.553406 | -0.658424 | -0.362808 | -0.327842  | -0.379706 |
| Gusb      | 1.507268  | -0.076252 | 1.583607   | 2.3258294 | 0.2888003 | 1.5883581 | -1.06606  | -0.635588 | -0.813579 | -0.774818 | -0.819991 | -0.489494 | -0.819125 | -0.606401 | -0.236429 | 0.3631715 | -0.346806  | -0.529244 |
| Sic15a1   | 2.9945213 | 0.991387  | -0.035266  | 1.685894  | 0.9525626 | 0.7178088 | -0.754212 | -0.697886 | -0.687059 | -0.404216 | -0.325801 | -0.025379 | -0.22625  | -0.550457 | -0.793374 | -0.599472 | -0.579364  | -0.746228 |
| Tk1       | -1.318299 | -1.225876 | -0.989876  | -1.19614  | -1.050207 | -1.244942 | 1.0498227 | 0.7029627 | 0.1269078 | 0.5056195 | 0.7385169 | -0.163516 | -0.015234 | 0.2394634 | 1.6274875 | 0.1007352 | 0.2398328  | 1.872955  |
| Cpeb1     | 2.1042534 | 0.4172185 | 1.1430627  | 1.3416867 | 0.5668912 | 1.5697469 | -0.077558 | -0.69649  | -1.03863  | -0.945314 | -0.924975 | -0.672617 | -1.023527 | -0.186093 | -0.056962 | 0.1675876 | -0.005886  | -0.682395 |
| Tma16     | -0.938346 | -0.933609 | -1.0209774 | 1.024741  | -1.175288 | -0.62989  | 0.942168  | 0.9858692 | 0.4083718 | -0.045442 | -0.959558 | 0.3389764 | -0.078897 | -1.126233 | 0.5420963 | -0.065395 | -0.2709957 | 2.9279059 |
| Phf6      | -1.1898   | -0.321355 | -1.391903  | -1.083436 | -1.422109 | -0.938605 | 0.942495  | 2.3907559 | 0.4743347 | 0.2785315 | 0.1375653 | 0.0557832 | 0.2244298 | -0.149408 | 1.4813442 | 0.4532173 | -0.207564  | -0.149408 |
| Ccdc51    | -1.181685 | -1.005893 | -1.227514  | -1.188033 | -1.133541 | -1.15316  | 0.7485281 | 0.8607724 | 0.8030323 | 0.5634988 | -0.031816 | 0.5065221 | 0.6667965 | 0.3341703 | 0.3734274 | 1.1252795 | -0.967943  | 1.9075664 |
| Ckl7a1    | -1.344157 | -0.978682 | -0.402772  | -1.25759  | -0.631589 | -0.810266 | -1.157435 | 1.0368794 | 0.6128411 | 0.55285   | 0.7157119 | 0.0789781 | -0.057404 | 1.6083778 | 1.7783108 | -0.287831 | 1.2306642  | -0.686887 |
| Rps6ka6   | 1.7996686 | 2.5958295 | 0.536214   | -0.058683 | 0.7816659 | 1.0325585 | -0.654714 | -0.434566 | -0.370188 | -0.156947 | -0.016641 | -0.346831 | -0.51766  | -0.765021 | -0.335836 | -0.972521 | -0.929324  | -1.175302 |
| Alox5     | 1.079165  | 1.2711341 | 0.8750001  | 0.7765061 | 2.0504853 | 1.1066337 | -1.261699 | -1.173808 | -0.892988 | -0.021052 | 0.2069627 | -0.050785 | -0.799235 | -0.776275 | -1.350419 | -0.007789 | -0.440097  | -0.59174  |
| 8-Mar     | 1.3248529 | 0.278852  | 0.6632312  | 1.0406515 | 1.1866615 | 1.4513841 | -0.727315 | 0.0112739 | -0.942329 | -0.716597 | -0.79928  | -0.851779 | -1.077596 | -0.48087  | -0.659005 | -0.4585   | -0.454387  | -0.589247 |
| Wdr73     | -0.986717 | -0.843169 | -0.936652  | -0.924688 | -1.357996 | -0.795479 | -0.058989 | 0.8372966 | 0.6850926 | 0.1240584 | 0.2235841 | 0.6827468 | 0.4109176 | 0.0435148 | 1.0492101 | -0.357725 | -0.662863  | 2.7498    |



|           |           |           |           |           |           |           |            |           |           |           |            |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Sp100     | -0.131064 | 0.0207924 | 2.7138065 | 1.5779948 | 1.2229041 | 0.6867444 | -1.176848  | -0.875182 | -0.231623 | -0.409328 | -0.65738   | 0.0686796 | -0.652526 | -0.98774  | -0.492781 | 0.2739608 | -0.174758 | -0.775653 |
| Ncl       | -1.227592 | -0.989906 | -1.170244 | -1.125435 | -1.183047 | -1.09793  | 1.2357612  | 0.3542186 | 0.1755504 | 0.524265  | -0.638549  | 0.5566049 | 0.4176291 | 0.4292076 | 1.2630059 | 0.1966183 | 0.1387522 | 2.1411363 |
| Farsb     | -0.962382 | -0.487447 | -1.01531  | -1.228209 | -1.302378 | -1.329755 | 1.1697375  | 1.0890589 | 0.29279   | 0.1096455 | -0.6081523 | 0.6462957 | 0.6995043 | 0.6634974 | 0.4408909 | -0.129068 | -0.881275 | 2.2162512 |
| Serpine2  | -0.450608 | -0.571871 | -0.669486 | 0.0767077 | -0.334889 | -0.396079 | -1.117047  | -0.079152 | -0.993223 | -0.349526 | -0.564878  | 0.3353625 | -1.012976 | 1.0561569 | 2.0840651 | 2.3486529 | 0.930708  | -0.29192  |
| Ngf       | -0.891395 | -0.934052 | -0.827909 | -1.030797 | -0.988438 | -0.918059 | 3.1161202  | -0.279216 | 0.1264085 | 0.6923035 | 0.0524877  | 0.0327001 | 0.97174   | 0.0361651 | 0.2834765 | 0.2760336 | -0.268582 | 0.5510123 |
| Gpr35     | -1.306791 | -1.149463 | -0.525487 | -0.70643  | -1.134109 | -1.189703 | 1.0901658  | 1.1803567 | 2.3149399 | 1.4830691 | 0.3112341  | 0.4728893 | -0.18434  | 0.0816563 | -0.33522  | 0.652627  | -0.629728 | 0.469833  |
| Inpp5d    | 0.508335  | -0.117668 | 1.6230452 | 1.3959608 | 1.4775217 | 1.6079584 | -1.369396  | -0.942482 | -0.846096 | -0.786665 | -0.877662  | -0.543342 | -0.755004 | -0.469807 | -0.567375 | 0.9692707 | 0.0980699 | -0.422664 |
| Serpinb8  | 1.0770096 | 2.3909328 | 7.4441474 | 0.1404584 | 0.631381  | 0.6882506 | -0.681709  | -0.961934 | -0.988886 | 0.6135652 | -0.362255  | 0.8880982 | -0.454909 | 0.0656021 | -0.481531 | 1.365793  | -0.957073 | -1.345356 |
| Cln8      | 2.0188537 | 1.3021536 | 0.8433069 | 1.130333  | 0.9667078 | 1.0966215 | -0.238182  | -1.234672 | -1.155579 | 0.207958  | -0.238881  | -0.163888 | -0.11916  | -0.647899 | -0.907933 | -0.745184 | -0.987508 | -1.127048 |
| Tnfrsf11a | 1.5834398 | 0.5609928 | 0.796159  | 2.1788089 | 0.6899908 | 1.6002812 | -1.201577  | -1.082188 | -0.502463 | -0.595247 | -0.549339  | -0.582252 | -0.890601 | -0.760649 | -0.377886 | -0.138531 | -0.164866 | -0.572165 |
| Gin1      | -0.838138 | -0.73945  | -1.315823 | -0.868053 | -1.248546 | -0.985796 | 1.373864   | 0.2457651 | 0.9408255 | 0.7662722 | -0.455757  | 0.2680632 | 1.5823493 | 0.7453424 | 1.1663987 | -1.488002 | 0.5659509 | 0.284732  |
| Mcm6      | -0.964445 | -0.718614 | -0.670388 | -1.029866 | -1.118992 | -1.088867 | 0.9637012  | -0.356419 | 0.1325092 | 0.7571629 | -0.125563  | 0.7500611 | 0.5918089 | -0.271977 | 2.1925069 | -0.999507 | 0.192426  | 1.76446   |
| Rgs18     | 1.8481556 | 1.1919555 | 0.0532814 | 1.4078117 | 1.2226524 | 1.8325924 | -1.005712  | -0.908411 | -0.442571 | -0.215868 | -0.802333  | -0.411562 | -0.473658 | -0.576705 | -0.738682 | -0.541822 | -0.747474 | -0.69165  |
| Rgs1      | 1.035519  | 0.4515398 | 1.2818353 | 2.0812633 | 1.367205  | 1.426118  | -0.708843  | -0.631092 | -0.545536 | -0.610038 | -0.701196  | -0.644766 | -0.644294 | -0.521424 | -0.630142 | -0.444804 | -0.48692  | -0.543941 |
| Rgs2      | 1.092915  | 1.1192457 | 0.9178463 | 2.0154425 | 0.4133498 | 1.4282836 | -1.486367  | -0.693404 | -0.655261 | -0.844244 | 0.8288288  | -0.809556 | -0.772409 | -0.775869 | -0.401957 | -0.384914 | -0.658526 |           |
| Cfh       | 0.4401743 | 0.8118079 | 1.041205  | 1.1385884 | 1.3589947 | 1.9347664 | -0.980326  | -0.790876 | -0.991665 | -0.969004 | -0.984825  | -0.838837 | -0.966728 | -0.52018  | -0.092898 | 1.1105558 | 0.0378714 | -0.738625 |
| Mki67ip   | -0.942701 | -0.717877 | -1.003942 | -1.138037 | -1.043266 | -1.014766 | 0.0945999  | 0.7217916 | 0.6068774 | 0.6736074 | 0.2162988  | 0.9142405 | 1.1675891 | 0.1740542 | 0.9543534 | -1.446141 | 0.0258274 | 2.2374907 |
| Dbi       | 1.0641918 | 2.6488162 | 0.1255271 | 0.6038022 | 0.6919635 | 0.5174872 | -0.598336  | -1.243138 | -0.13329  | -0.17621  | -0.491168  | -0.040412 | -0.211294 | 0.7301327 | -0.105094 | -1.509994 | -0.144379 | -0.282978 |
| Steap3    | 1.4599159 | -0.016789 | 1.2877959 | 1.822638  | 0.7839401 | 1.5906145 | -0.812986  | -1.034912 | -1.047757 | -0.918323 | -0.983822  | -0.739253 | -0.840395 | -0.094608 | -0.241851 | 0.4357022 | 0.1115554 | -0.761467 |
| Ptprc     | 0.7200023 | 0.5545798 | 1.0760391 | 1.9062791 | 0.8426683 | 1.5851758 | -1.264455  | -0.863478 | -0.755947 | -0.995044 | -1.014331  | -0.704855 | -0.963473 | -0.587403 | -0.541758 | 1.0722434 | 0.0339058 | -0.10015  |
| Cd55      | 1.1901561 | 0.733292  | 0.5759338 | 1.3116306 | 1.2066046 | 1.2432463 | -1.140072  | -0.975966 | -0.364329 | -0.673956 | -0.833942  | -0.515679 | -0.865771 | -0.645906 | -0.790129 | 1.8206466 | -0.269114 | -1.006646 |
| Ddx59     | -0.894389 | -0.376666 | -0.901116 | -1.00287  | -0.820198 | -0.751729 | -0.625586  | -0.120825 | 0.7635625 | 1.0986021 | -0.31826   | -0.259765 | 0.5741982 | 2.8186806 | -0.334192 | -1.239369 | 0.386108  | 0.7526421 |
| Cacna1s   | 0.9876326 | 2.1109396 | 0.9651388 | 1.1565725 | 1.572649  | 0.8557815 | -0.844333  | -0.773344 | -0.938579 | -0.927278 | -0.920991  | -0.867364 | -0.938579 | -0.036446 | -0.567079 | -0.320561 | -0.247347 | -0.280814 |
| Tnni2     | -0.868935 | -0.786057 | -0.888898 | -0.872182 | -0.953092 | -0.928803 | -0.244604  | 0.3022017 | -0.2509   | 2.3368913 | -0.199813  | -0.566729 | -0.007303 | 0.2528343 | 0.6889286 | 2.0354601 | 1.1894801 | -0.148538 |
| Il24      | -1.113416 | -1.086053 | -0.47024  | -1.062317 | -0.981368 | -1.050423 | 1.37825524 | 0.4094365 | 0.0838502 | 0.8238223 | -0.202109  | 0.4946726 | 0.0072803 | -0.868658 | 0.4574808 | 2.5278007 | -0.203287 | 0.8551801 |
| Ube2t     | -0.72496  | -1.041344 | -1.012063 | -1.303225 | -1.209283 | -1.195727 | 1.7318451  | -0.28896  | 0.7186288 | 1.095498  | -0.158892  | -0.041303 | 1.6522096 | -0.039995 | 0.7060111 | -0.787468 | 0.324147  | 0.9996613 |
| Scl45a3   | 2.7215445 | 0.7256683 | 0.2948269 | 1.2250655 | 1.5368543 | 0.6873644 | -0.826005  | -0.658187 | -0.572725 | -0.53681  | -0.732837  | -0.633998 | -0.665651 | -0.730372 | -0.491498 | -0.767291 | -0.297649 | -0.276499 |
| Cdk18     | 2.0652964 | -0.04465  | 1.2517387 | 2.5744761 | -0.16029  | 0.6107348 | -0.614422  | -0.796697 | -0.626564 | -0.578112 | -0.798332  | -0.601809 | -0.671    | -0.818661 | -0.150699 | -0.002717 | -0.486828 | -0.153445 |
| Atp2b4    | 1.2189501 | 0.9963625 | 0.7492284 | 0.9319079 | 1.0993355 | 1.0813407 | -0.963392  | -0.884842 | 0.0597615 | 0.6909733 | 0.5207197  | -1.150698 | -0.220707 | 0.0630463 | -1.230783 | -1.383445 | -0.524103 | -1.653674 |
| Glul      | 2.1302937 | 0.5447263 | 0.6651621 | 1.5361617 | 1.1243944 | 1.5147063 | -1.047374  | -0.692402 | -0.751911 | -0.902741 | -0.891631  | -0.748176 | -0.782568 | 0.0384853 | -0.649226 | -1.187315 | -0.386664 | -0.541922 |
| Lamc2     | -1.139074 | -0.8721   | -0.258601 | -1.021657 | -0.855748 | -0.972894 | -0.001133  | -0.42962  | 1.1566252 | 2.4971026 | 0.5790821  | -0.163866 | 0.0143467 | -0.370847 | 0.7551845 | -0.025125 | 1.7181085 | -0.609783 |
| Ncf2      | 1.0926544 | 0.2251191 | 0.7522772 | 2.228822  | 0.3284702 | 1.7117459 | -1.0437    | -0.721469 | -0.748783 | -0.909088 | -0.864774  | -0.629952 | -0.775158 | -0.66578  | -0.16078  | 1.1649402 | -0.080759 | -0.446127 |
| Rgl1      | 1.2233413 | 0.3696914 | 1.0265689 | 1.9495808 | 0.5734398 | 1.9573122 | -1.077089  | -0.636631 | -0.669864 | -0.956328 | -0.960866  | -0.358322 | -0.964138 | -0.398811 | -0.521156 | 0.2806081 | -0.40021  | -0.710097 |
| Acdk3     | 0.7832958 | 1.1898624 | 1.5412736 | 1.2157298 | 1.1536833 | 0.7747294 | -1.099435  | -0.958075 | -0.718586 | -0.906739 | -0.617426  | -0.785387 | -0.716134 | 0.3089295 | -0.737629 | -0.415481 | -0.395036 | -0.450972 |
| Mnda      | 0.5078236 | 0.3518995 | 2.2526369 | 0.801082  | 0.6936464 | 1.4089734 | -0.65696   | -1.325906 | -0.88585  | -0.753117 | -1.455415  | -0.122084 | -0.841679 | -1.018231 | -0.228384 | 0.7631842 | -0.100841 | 0.609222  |
| Uck2      | -1.293709 | -0.963719 | -1.055622 | -1.253871 | -0.662574 | -0.662574 | -0.2414785 | -0.981423 | -0.304642 | 1.6023179 | 0.1284755  | 0.7231652 | 0.8234071 | 1.6535871 | -0.526549 | -0.166134 | 0.9281935 | 1.1901918 |
| Mplz1     | -0.167125 | -1.017375 | -1.413949 | -0.923265 | -1.109128 | -0.783612 | 2.3440385  | 0.5656953 | -0.651495 | 0.8771854 | 0.5845937  | -0.47597  | -0.437191 | 1.0853984 | 0.0301744 | 0.2401225 | 0.2307982 | 1.0409606 |
| Dpt       | 1.4739573 | 1.781888  | 0.4071343 | 0.9408796 | 0.7079115 | 1.1588432 | -0.776281  | -1.144392 | -0.46114  | -0.216681 | -1.044134  | -0.580204 | -0.654441 | 1.3200436 | -1.202194 | -0.914494 | 0.0425695 | -0.839264 |
| Mpc2      | 0.8861202 | 1.0810803 | 0.5720502 | 0.993277  | 1.7397151 | 2.1019564 | -0.956151  | -0.685583 | -0.863364 | -0.833782 | -0.803852  | -0.804423 | -0.882254 | 0.6436129 | -0.567559 | -0.201612 | -0.399765 | -0.819466 |
| Nme7      | -1.084734 | -0.60609  | -0.81727  | -1.119124 | -0.907784 | -1.002254 | 0.988778   | -0.49075  | 1.3625028 | 0.2692435 | -0.18246   | 1.0005702 | 1.23064   | 0.7396176 | -0.305959 | -1.306534 | 0.3496961 | 1.8816392 |
| Atp1b1    | 2.8816905 | 0.9624536 | 0.4218297 | 1.108442  | 0.8939618 | 0.6452622 | -0.931183  | -0.800803 | -0.648172 | -0.680004 | -0.706063  | 0.3290092 | -0.76449  | -0.522197 | -0.762387 | -0.599778 | -0.51231  | -0.311664 |
| F5        | 0.9147211 | 1.0194734 | 0.219233  | 1.2756299 | 1.5646571 | 1.1357702 | -1.008602  | -0.73282  | -0.429602 | -0.955581 | -1.002624  | -1.000904 | -0.445857 | -0.178616 | -0.653379 | 0.2847316 | -1.177773 | -1.084006 |
| Sele      | 0.1139938 | 1.9845599 | 0.4655197 | 2.0510421 | 0.4341763 | 0.9241167 | -1.275978  | 0.321293  | -1.039116 | -1.046595 | -0.29996   | -1.191624 | -0.745772 | -0.64788  | -0.671941 | -0.414599 | 0.4024323 | 0.6362315 |
| Soat1     | 1.6587022 | 0.8635522 | 0.8625234 | 1.5839065 | 0.506798  | 1.9891719 | -0.967269  | -0.798267 | -0.863864 | -0.826941 | -0.910313  | -0.692986 | -0.919356 | -0.5503   | -0.355871 | 0.2090693 | -0.334008 | -0.49843  |
| Ptpn14    | 1.6645268 | 0.9368059 | 0.6578828 | 0.4445686 | 1.1637037 | 0.8696325 | -1.515463  | -0.890168 | 0.2731581 | -0.286139 | -0.337066  | -0.199496 | -0.390774 | 1.5697336 | -0.649911 | -1.627086 | -0.610473 | -1.075321 |
| Cenpf     | -0.816655 | -0.444189 | -1.073451 | -1.121407 | -0.956037 | -1.040831 | 1.7880981  | -0.050525 | 0.8005998 | 1.028338  | 0.0163155  | 0.3704208 | 0.4746061 | 1.7673337 | -1.16405  | -0.815691 | 0.766085  | 0.7058955 |
| Mark1     | 2.2696088 | 1.268647  | -0.043251 | 0.5598696 | 0.7470596 | 1.5583099 | -1.49189   | -0.857122 | -0.588369 | -0.847688 | -0.633594  | -0.407205 | -1.410694 | 0.4834768 | -0.173714 | -0.117584 | -0.040539 | -0.275322 |
| Nfk2      | -1.018998 | -0.986092 | -1.224475 | -1.243106 | -1.18373  | -1.1081   | 1.1179453  | 0.4583688 | 0.6655051 | 1.0270972 | -0.058213  | 0.8197977 | 0.2821797 | 0.8188249 | -0.305988 | -0.770607 | 0.8205244 | 1.8893374 |
| Atf3      | 1.6562163 | 0.0039499 | 1.1669653 | 2.5230466 | -0.031379 | 1.5070879 | -0.491422  | -0.396094 | -0.726298 | -0.734979 | -0.649559  | -0.531909 | -0.736759 | -0.69565  | -0.760924 | -0.113269 | -0.623954 | -0.45507  |
| Batf3     |           |           |           |           |           |           |            |           |           |           |            |           |           |           |           |           |           |           |



|            |           |           |           |           |           |           |            |           |           |           |            |           |           |           |           |           |            |            |
|------------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|------------|------------|
| Nup35      | -0.904898 | -0.989447 | -1.278683 | -0.847735 | -1.213036 | -1.219388 | 1.6541761  | 0.7045194 | 0.8360592 | 0.5374831 | -0.535301  | 0.932674  | 0.1279136 | -0.222713 | 0.7364454 | -0.114085 | -0.169464  | 1.9654778  |
| Dusp19     | -1.106455 | -1.109734 | -1.279282 | -0.937638 | -0.85902  | -1.092907 | 0.0616475  | 2.2001447 | 0.3776497 | -0.142351 | 0.9966789  | 0.1226179 | 0.7577554 | 0.2730615 | 0.8029642 | -0.597464 | -0.497085  | 1.0274168  |
| Ssfa2      | 0.6181377 | 2.6280456 | 0.8998556 | 0.3130438 | 1.1419166 | 1.2867243 | -0.054662  | -0.982999 | -0.531789 | 0.0076762 | -0.066349  | -0.687915 | -0.676715 | -0.272015 | -0.483513 | -1.168269 | -0.842733  | -1.128441  |
| ltga4      | 0.5734655 | 0.6273876 | 1.1239632 | 1.8487748 | 0.7931894 | 1.9804102 | -1.302932  | -0.913937 | -0.708649 | -0.993413 | -0.922015  | -0.562792 | -0.8088   | -0.662137 | -0.432733 | 0.6526632 | 0.0858374  | -0.378285  |
| Hat1       | -0.790739 | -0.924161 | -1.113114 | -0.951052 | -1.067329 | -1.084758 | 2.3598073  | 1.1745438 | 0.074906  | 1.1447638 | -0.30646   | 1.0776182 | 0.7535461 | -0.41366  | 0.7740318 | -0.266322 | -0.103195  | 1.6615475  |
| Stk39      | -0.704626 | -0.738691 | -0.712179 | -1.060998 | -0.606024 | -0.71675  | -0.635752  | 2.7536379 | 0.1060057 | -0.057995 | 0.9043392  | 0.9591656 | 0.3857977 | 0.3527603 | 0.8394421 | -0.476887 | -1.169912  | -0.3131282 |
| Ssrp1      | -1.251537 | -0.969965 | -1.05577  | -1.280127 | -1.110255 | -0.999009 | 2.1150784  | 1.5582493 | 0.6862438 | 0.1532671 | 0.2674837  | 0.1825416 | 0.3220206 | 0.3300389 | 0.9764145 | -0.490243 | -0.187054  | 0.7526217  |
| Slc43a3    | 1.5245215 | 0.401698  | 1.7630367 | 0.9996347 | 0.8935086 | 1.4767534 | -1.229574  | -0.876766 | -0.789051 | -1.09477  | -1.110944  | -0.889699 | -0.926372 | -0.448548 | -0.061652 | 0.4803619 | -0.062989  | -0.04915   |
| Smtnl1     | 2.3396427 | 1.7470086 | 0.7725005 | 1.2461963 | 0.4645541 | 0.3813759 | -0.875644  | -0.539733 | -0.920412 | -0.871877 | -0.948246  | -0.900472 | -0.948246 | 0.3995853 | -0.414069 | -0.488692 | -0.322119  | -0.121353  |
| Clp1       | -0.641313 | -1.285982 | -1.175542 | -0.780092 | -1.296947 | -0.610558 | 2.3672612  | 0.6503307 | 0.5294834 | 0.1454207 | -0.421775  | 0.1574106 | 0.5793802 | -0.422532 | 0.2506566 | -0.326255 | 0.4078751  | 1.8731781  |
| Med19      | -1.058411 | -0.769758 | -1.003118 | -1.023313 | -1.174481 | -1.112376 | 2.8824166  | 0.5088243 | 0.0892925 | 0.5215932 | -0.002966  | 0.2506264 | 0.880488  | 0.7007457 | -0.024539 | 0.1670104 | -0.36214   | 0.530105   |
| ltga6      | -1.4041   | -0.942371 | -0.724156 | -1.327029 | -1.017981 | -1.226863 | 0.902377   | 0.1476213 | 2.2305492 | 0.7547891 | 1.02065    | 0.0511049 | 0.5007085 | 0.4867511 | 0.8722203 | -0.430302 | 0.5007085  | -0.415018  |
| Kif18a     | -1.294312 | -0.884107 | -1.409167 | -1.306713 | -1.216114 | -1.197891 | 1.6697688  | 1.1082274 | 0.5263149 | 0.627149  | 0.3943977  | 0.1179484 | 0.4237994 | 0.0470442 | 0.6061044 | 0.1582735 | 0.0470442  | 1.5822311  |
| Slc12a6    | 1.1699036 | 1.0472287 | 1.0353851 | 1.6741188 | 0.9336436 | 1.222481  | -0.642956  | -0.846743 | -0.049733 | -1.041527 | -1.107414  | -1.079894 | -0.753701 | 0.4406553 | -0.656458 | 0.3447943 | -0.15791   | -1.531874  |
| Lpcat4     | -0.604042 | -0.972686 | -0.829633 | -0.240339 | -0.84583  | -0.757086 | 1.4553337  | 0.1195697 | -0.877528 | 0.0538851 | -0.043425  | 0.0060719 | 0.1870575 | -0.358636 | 0.0426289 | 0.311353  | 0.5483701  | 3.1658346  |
| Ccdc34     | -0.915176 | -0.931733 | -1.389073 | -1.308246 | -1.080039 | -1.202622 | 1.488028   | 1.4028777 | 0.1526894 | -0.191203 | 0.0702099  | 0.4794262 | 1.0848107 | -0.08682  | 0.9992885 | -0.161273 | 0.0553741  | 1.5334804  |
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| Cat        | 1.0796245 | 1.4860766 | 1.0431604 | 0.0931851 | 0.8941322 | 1.2064565 | -0.1766111 | -1.144341 | 0.164373  | -1.087813 | -0.720614  | -0.89457  | -0.521266 | 1.0504158 | -1.040633 | -0.765827 | -0.744617  | -1.272354  |
| Pamr1      | 0.8316598 | 0.0841857 | 0.8482972 | 0.919389  | 2.7903644 | 1.7205109 | -0.959907  | -0.77047  | -0.861338 | -0.477601 | -0.54175   | -0.326309 | -0.674177 | -0.736374 | -0.595331 | 0.0085434 | -0.841069  | -0.674975  |
| Sema6d     | -1.524765 | -0.948744 | -0.879052 | -1.133864 | -1.018396 | -0.927616 | -0.623396  | 0.1892443 | 1.2144298 | -0.83291  | -0.095298  | 0.6164681 | 0.2574525 | 0.9822848 | 1.5506875 | 1.222603  | 0.9340588  | 1.0164636  |
| Slc28a2    | 0.7108335 | 1.4853557 | 1.7770966 | 1.377029  | 1.3434807 | 0.94829   | -1.260997  | -0.654584 | -0.810665 | -0.815084 | -0.086869  | -0.887561 | -0.765475 | -0.782274 | -0.647245 | 0.2045689 | -0.255089  | -1.79665   |
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| Sord       | 1.3527063 | 0.8386348 | 0.9315491 | 1.033603  | 0.6944106 | 0.9236708 | 0.9068187  | 0.2105888 | -1.075604 | -0.741053 | 0.4456483  | -0.762381 | -0.782303 | 0.5080537 | -1.310189 | -0.585955 | -0.585955  | -1.577102  |
| Mdk        | -0.79979  | -0.844885 | -0.290813 | 0.2276662 | 0.0791389 | 0.0270102 | -0.902197  | -0.848667 | -0.710155 | -0.865853 | -0.739149  | 0.2761918 | -1.163348 | 1.7782876 | 1.6907476 | 1.3785566 | 0.9085492  | 1.1507082  |
| Lrp4       | 0.3780998 | 0.7677451 | 0.9124058 | -0.662438 | 1.0643844 | -0.015084 | 0.7745777  | -0.811005 | 1.6768977 | 0.4785016 | 0.9523819  | -0.846466 | 0.2863117 | -0.257781 | -1.345004 | -1.857851 | -1.319792  | -0.478727  |
| Jag1       | -0.91635  | -0.739931 | -0.694619 | -0.863561 | -0.721749 | -0.971541 | 0.6374513  | 2.6587173 | 0.668541  | 1.1789319 | -0.067174  | -0.409834 | 0.2818265 | 0.420728  | -0.283639 | 0.046288  | 2.151806   | -0.321629  |
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| Hba5       | -1.007297 | -0.664852 | -0.961181 | -1.078479 | -1.329452 | -1.163805 | 2.5782884  | 0.963511  | 0.1346903 | 0.8631916 | 0.4731818  | -0.239784 | 0.9496888 | 0.5326381 | 0.5723716 | -0.424696 | -0.106623  | -0.091673  |
| Uptox      | 1.3669617 | 0.9278376 | 0.8514567 | 1.9029262 | 1.2523535 | 1.5246133 | -0.779404  | -0.442205 | -0.851114 | -0.585142 | -0.407772  | -0.138889 | -1.110952 | -0.457097 | -0.746311 | -0.728621 | -0.47377   | -1.104872  |
| Nusap1     | -1.067467 | -0.816673 | -1.213076 | -1.255036 | -1.063735 | -1.083126 | 2.4619993  | 0.6418278 | 1.2954197 | 0.7055964 | 0.230119   | 0.5967716 | 0.6811786 | 0.0998111 | 0.2054431 | -0.317183 | -0.335347  | 0.234664   |
| Dl14       | -1.5593   | -1.498922 | -0.961037 | -1.387589 | -1.221081 | -1.066876 | 0.3826134  | 0.3084066 | 1.087632  | 0.401422  | 1.1422325  | 0.2718026 | 0.5037563 | 0.2110725 | 1.129156  | 1.3045455 | 0.7482688  | 0.2668181  |
| Adam33     | 1.0105552 | 0.7130298 | 1.712798  | 0.7630634 | 1.6253721 | 1.3293436 | -1.261643  | -0.508248 | -0.949391 | -1.069733 | -0.757374  | -0.557278 | -1.145502 | 0.7176316 | -0.069648 | -0.446033 | -0.306771  | -0.799638  |
| Signlec1   | 0.2170348 | 0.3186199 | 2.8084263 | 1.345549  | 1.4059918 | 0.7948368 | -0.785295  | -0.676056 | -0.643982 | -0.738475 | -0.7552    | -0.710486 | -0.703587 | -0.459162 | -0.437857 | 0.7007499 | -0.332987  | -0.654687  |
| Rad51      | -0.999441 | -1.040719 | -1.057286 | -1.156064 | -1.097967 | -1.378492 | 1.878632   | 1.3108516 | 0.0011353 | 0.9638181 | 0.9949773  | 0.1900988 | 0.5022563 | -0.514363 | 0.2687617 | 0.067276  | -0.171342  | 1.2378659  |
| Rpusd2     | -0.37975  | -1.219841 | -1.212272 | -0.961018 | -1.209978 | -1.253814 | 0.2998328  | 0.3814254 | 0.4726773 | 1.243577  | 1.2137436  | -0.316359 | 0.8163138 | -0.047906 | -0.105779 | -0.113688 | -0.473788  | 1.0736247  |
| Casc5      | -1.137626 | -0.9203   | -1.228494 | -1.317769 | -1.212097 | -1.187679 | 2.2683414  | 0.8489605 | 0.6729739 | 0.5997391 | -0.1829758 | 0.491833  | 0.5933601 | -0.083893 | 0.5031144 | 0.2825166 | -0.247099  | 1.0891423  |
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| D2Ertd750e | -1.159121 | -0.838089 | -1.149786 | -1.3672   | -1.012032 | -1.106651 | 2.6685614  | 0.7423049 | 0.3315378 | 0.5374476 | 0.3419534  | 0.0157139 | 0.5202324 | 0.2260454 | 0.817126  | 0.1890666 | -0.089038  | 0.9619277  |
| Rassf2     | 0.8358213 | 0.32787   | 0.9846917 | 1.6675206 | 1.5113754 | 1.6915788 | -1.165762  | -0.793313 | -0.838282 | -0.85515  | -0.928818  | -0.834813 | -0.892574 | -0.547158 | -0.505621 | 0.8654027 | -0.062993  | -0.459777  |
| Gcpdp1     | 0.2531271 | 2.4990501 | 0.4882055 | 0.4160572 | 0.9008692 | 1.5100131 | -0.453069  | -0.908239 | 0.2033323 | -0.236806 | -0.442353  | -0.154862 | 0.3775808 | 0.1981424 | -1.237439 | -1.155384 | -0.780871  | -1.477337  |
| Fam98b     | -0.659196 | -1.2619   | -1.296871 | -1.006575 | -1.385852 | -1.460487 | 2.2083629  | 1.481883  | 0.7326507 | 0.8127094 | 0.5127182  | -0.077683 | 0.088692  | 0.2681059 | 0.6224251 | 0.1037885 | -0.9220917 | 0.788322   |
| Mcm8       | -0.870021 | -0.97816  | -1.272087 | -0.846063 | -1.029322 | -1.205318 | 2.5207724  | 1.4817646 | 0.4726225 | 0.5421698 | 0.0284525  | -0.039816 | 0.5027126 | -0.24407  | -0.777929 | -0.225007 | -0.217392  | 0.597276   |
| Fermt1     | -0.954244 | -0.873646 | -0.206262 | -1.375893 | -1.105111 | -1.504689 | 1.110604   | 1.5102583 | 0.5230721 | 0.3521404 | 0.5599742  | -0.090022 | 0.6207608 | -0.726167 | 1.7961626 | 0.1226681 | 0.8357659  | 1.189733   |
| Bmp2       | -0.763116 | -0.865477 | -0.930675 | -1.467311 | -1.176724 | -1.155353 | 2.7285862  | -0.165105 | 0.1451381 | 1.3292922 | 0.2096929  | 0.2458375 | 0.6219402 | 0.7374711 | 0.1973872 | 0.9230032 | -0.91514   | 1.5509446  |
| Mrp5       | -1.247826 | -0.69791  | -0.70678  | -0.873894 | -0.926415 | -1.237428 | 1.6327714  | 0.9792494 | -0.518209 | -1.19187  | 0.2076626  | -0.13714  | 0.8538904 | -0.478375 | 0.4206385 | -0.35575  | -0.736425  | 1.9341437  |
| Bub1       | -1.093455 | -1.011252 | -1.094448 | -1.214801 | -1.102036 | -1.009998 | 2.1352263  | 1.6640119 | 0.4369596 | 0.397148  | -0.08914   | -0.183273 | 0.3817001 | -0.181743 | 0.8793538 | 0.0030924 | -0.01419   | 1.0968442  |
| Fcoln1     | 1.3184426 | 3.3681167 | 0.3867019 | -0.015607 | 0.3015447 | 0.6861687 | -0.580664  | -0.478386 | -0.488539 | -0.531949 | -0.569385  | -0.593871 | -0.599142 | -0.400459 | -0.184486 | -0.603395 | -0.441406  | -0.573686  |
| Axbl7      | 1.6181046 | 1.116106  | 1.4018042 | 2.4078609 | 0.2457306 | 1.3752592 | -0.825328  | -0.725734 | -0.595947 | -0.656736 | -0.766661  | -0.559947 | -0.79234  | -0.39456  | -0.363994 | -0.282864 | -0.21801   |            |



Pfn2 2.0786395 0.9175485 -0.11384 2.0543211 0.9158827 1.2694957 -0.804832 -0.401932 -1.066472 -1.031712 -0.549511 -0.541569 -0.703177 -0.086289 -0.438781 -0.452893 -0.296694 -0.748186

Mme 1.640897 1.1646429 0.417343 0.8946937 1.844346 1.9104981 -1.117576 -0.74131 -1.219072 -0.777272 -0.103295 -0.564886 -1.109251 -0.051073 -0.108622 -0.122076 0.264807 -0.614816

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Cd2 0.8015109 0.4798712 1.313898 2.2646015 1.3178662 1.1627854 -1.176431 -0.102764 -0.608458 -0.62779 -0.805103 -0.45727 -0.598865 -0.831057 -0.860609 0.3254177 -0.3446 -0.351808

Tbx15 1.2620119 1.2223023 0.3748126 1.3540843 0.8608302 1.6390747 -1.221971 -0.799083 -1.197754 -1.192006 -1.102605 -0.522235 -1.158268 0.3302346 -0.037826 0.6630505 -0.10033 -0.372514

Hsd3b6 2.4938835 -0.430127 -0.034028 0.8123904 2.0287389 1.5045752 -0.506249 -0.603382 -0.583137 -0.532566 -0.511455 -0.612214 -0.612214 -0.612214 -0.417627 -0.58293 -0.18923 -0.612214

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Syp12 1.577391 2.2282566 0.6122497 0.9561371 1.2503437 0.8620094 -0.952222 -0.704675 -1.003455 -0.941102 -1.118857 -0.835941 -0.503276 -0.375442 -0.366308 -0.114428 -0.29872 -0.27196

Dram2 0.7838579 0.9770565 1.2931422 1.6608157 1.8066023 1.4503848 -1.638155 -0.967367 -0.985683 -0.448334 -0.727658 0.4546797 -0.980496 -0.292535 -0.735307 0.593956 -0.585994 -0.658968

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Lce1m 2.4403212 1.6999981 0.5003138 -0.046778 1.3773639 1.2438212 -0.682818 -0.696155 -0.531447 -0.372289 -0.46419 -0.555718 -0.641042 -0.573067 -0.662583 -0.678988 -0.632114 -0.724092

Crc1 1.8434453 2.2054046 0.0104777 -0.069649 1.2620277 0.4939298 -0.763627 -0.897029 -1.442866 -0.097641 -0.561568 0.1370911 -0.078107 0.1887756 0.7525114 -0.587523 -1.377411 -0.888242

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Pmkv 1.986163 1.9112733 0.1704351 -0.214322 0.8471076 0.9681836 -0.996898 -1.429729 -1.094831 0.252546 -0.343307 0.660188 -0.676643 0.2527325 -1.145843 0.1203634 -0.946159 -0.294149

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Efn3a 3.0104037 1.0917588 -0.112187 1.0901476 0.6543703 0.1791876 -0.656922 -0.476247 -0.504753 -0.12971 -0.166798 -0.474864 -0.372211 0.2027025 -0.893995 -0.1609339 -0.602716 -0.968289

Cks1b -1.099722 1.216565 -0.946012 -1.311844 -1.178672 -1.0855 -0.11053 1.279443 0.4129536 0.8588644 0.3765321 0.4002451 0.248464 -0.732314 1.1146679 0.2992426 0.0250626 1.1956835

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Igkap3 -1.058991 -1.191558 -1.283124 -1.340012 -0.971231 -1.239273 1.0072419 1.4343816 1.3341206 1.130949 1.1505529 0.5872258 0.1195257 -0.064983 -0.39052 0.6891135 -0.139089 0.2166701

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Nudt17 3.0256203 1.4919035 -0.148141 0.7746517 0.8129966 0.682775 -0.565915 -0.464234 -0.587295 -0.374521 -0.377901 -0.481927 -0.618298 -0.418666 -0.660095 -0.708258 -0.582262 -0.800434

Ctsk 0.6444502 0.8872071 1.4641815 1.2137088 1.3559147 1.9760495 -1.04718 -0.836945 -0.954242 -0.959477 -0.82489 -0.659116 -0.998658 -0.157776 -0.352194 -0.200497 1.0467769 -0.697314

Mett14 -1.439822 -0.729502 -1.321457 -1.085289 -0.806837 -1.186182 1.2223704 1.2913008 1.4458853 0.7041618 0.0763432 -0.330099 1.489904 0.0965359 -0.374619 -0.237999 1.0508116 1.3629294

Bcar3 -1.06661 -1.1225 -0.718526 -1.041409 -1.049221 -1.210379 2.51518 0.7468616 0.694858 0.5098772 -0.075238 -0.059538 0.4637023 -0.572219 1.0265178 1.0016653 0.2938037 -0.3391

Abcd3 1.4201708 2.7022943 0.0368793 0.432572 0.8282552 0.8991228 -1.097375 -0.264468 0.1030206 -0.388312 -0.163119 -0.477362 -0.509595 0.3454357 -1.121368 -0.892468 -0.793811 -1.099055

Tem5m6 2.746945 2.0589726 0.0791203 0.0925054 0.824317 0.8695133 -0.640105 -0.531041 -0.550578 -0.461288 -0.571778 -0.606917 -0.607969 -0.470968 -0.459566 -0.639451 -0.496125 -0.635489

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Depdc1a -1.232884 -1.089692 -1.367002 -1.319688 -1.308143 -1.317829 0.8873638 1.2961498 0.6925419 0.6343702 0.0662512 0.5227256 0.0540655 0.1434977 0.6847142 0.1812831 1.3501923 1.1220818

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Lphn2 1.8133124 1.697624 0.5146104 0.8918518 1.2770619 1.128442 -1.523784 -0.750982 -0.374521 -0.236593 -0.488066 0.2519712 -0.4002 -0.231479 -0.842648 -1.139379 -0.797321 -0.789901

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Str16c5 1.4768756 2.5046784 0.7197527 0.2097937 1.0982626 0.8124765 -0.651626 -0.822029 -0.69617 -0.022679 -0.039806 -0.050116 -0.436299 -0.908708 -0.885377 -1.392895 -0.886815 -0.029318

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Cla2f 1.7595623 1.795647 0.6211644 1.7372399 1.2944541 0.4064424 -0.882325 -0.670075 -0.527903 -0.49307 -0.460999 -0.285609 -0.243077 -0.746493 -0.878425 -0.81368 -0.196982 -0.984172

Rragd 1.350825 1.8518481 0.9256448 1.4901899 0.9553408 1.2198622 -0.888305 -0.755622 -0.912053 -0.936701 -0.81663 -0.7946 -0.649225 -0.483123 -0.279387 -0.342186 -0.443212 -0.645668

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5830415F0 -0.406388 -0.845918 -0.651964 -0.715242 -1.280833 -1.011353 1.8465097 1.921853 0.2955648 0.0459179 -0.325323 -0.424564 0.7113811 -0.626541 0.6459461 -0.317642 -0.650446 -1.78871

Anp32b -1.122702 -0.863699 -0.951292 -0.940232 -1.138786 -1.112584 1.1727661 2.3178802 -0.005864 -0.267523 -0.0669312 -0.066931 0.480739 0.0780816 1.0211209 0.1360441 -0.243583 1.5758577

Col51a 0.482615 1.0466393 0.4694224 2.5479378 0.3559628 0.8856259 -1.400036 -0.317844 -0.836219 -0.99571 -0.864955 -0.109127 -0.873914 -0.028263 -0.110739 1.0354722 0.3984019 -0.683436

Tex10 -0.896155 -0.678672 -0.797332 -1.286703 -1.03795 -0.83441 0.5462837 1.9666819 0.1690617 -0.053669 -0.336478 0.2476275 1.3657571 -0.569524 0.4759735 -0.910341 0.7689762 1.8609414

Tmeff1 -0.736185 -0.753003 -0.988158 -0.731328 -0.743233 -0.804279 -0.



|          |           |           |           |           |           |           |            |           |           |           |            |           |           |           |           |           |           |           |
|----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Ifit74   | -0.751048 | -0.16153  | -1.364909 | -0.832575 | -1.154392 | -0.696862 | 0.4517743  | 2.0813684 | 1.5450865 | -0.309847 | -0.696254  | -0.05287  | 1.2447628 | 0.3090145 | 0.5397318 | -0.638836 | -0.772492 | 1.2598777 |
| Lapmt5   | 1.0444277 | 0.5137959 | 1.300722  | 2.2571999 | 0.3665299 | 1.4589184 | -1.059111  | -0.818975 | -0.769009 | -0.893756 | -0.888508  | -0.602255 | -0.920027 | -0.399513 | -0.652207 | 0.754304  | -0.246498 | -0.445004 |
| Orc1     | -0.94228  | -1.12675  | -1.046724 | -1.139552 | -1.168477 | -1.208686 | 1.2563874  | 0.8463482 | 0.0390762 | 1.1812995 | 0.2730936  | 0.2691695 | 1.1523014 | -0.760651 | 0.4942712 | 0.21968   | -0.326094 | 1.8993883 |
| Tnfrsf1b | 0.6760019 | 0.1934706 | 1.0727101 | 2.4454124 | 0.5780301 | 1.1602604 | -1.09349   | -0.674589 | -0.825748 | -0.905755 | -0.865735  | -0.713583 | -0.960759 | -0.681617 | -0.570273 | 1.2301531 | 0.1329058 | -0.197394 |
| Podn     | 1.3836501 | 0.4319575 | 0.885605  | 1.1674278 | 1.228195  | 1.4500461 | -1.293679  | -0.594823 | -1.218479 | -1.244608 | -1.044283  | -0.788372 | -1.221931 | 0.0840804 | -0.007519 | 0.7440996 | 0.414757  | -0.376134 |
| Scp2     | 1.8640053 | 2.4742352 | 0.1081224 | 0.559682  | 0.9865958 | 1.1272153 | -0.944428  | -0.365674 | -0.543504 | -0.51926  | -0.280374  | -0.620035 | -0.341481 | -0.435304 | -0.859953 | -0.782813 | -0.669589 | -0.89474  |
| Magoh    | -0.97247  | -0.774204 | -0.931304 | -1.09736  | -0.77684  | -0.998849 | 0.4481208  | 2.048176  | 1.6057838 | -0.12732  | -0.248611  | 0.3364197 | 0.9259356 | -0.759929 | 0.5093292 | -0.148521 | -0.623246 | 1.5848886 |
| Lrp8     | -1.314905 | -1.239207 | -0.175165 | -1.095088 | -0.998507 | -1.168964 | 0.5382227  | 1.8381137 | 0.9582014 | 1.5949768 | 0.2867508  | 0.3869516 | 0.77555   | -0.334432 | -0.265649 | 0.480208  | -0.124656 | 0.829598  |
| Tmem48   | -0.93439  | -1.046897 | -1.069892 | -1.128411 | -1.169628 | -0.774399 | 0.2979555  | 1.4802066 | 1.3064322 | 0.7562451 | 0.4049173  | 0.8042563 | 0.5724126 | -1.450618 | 0.5998409 | 0.4565576 | -0.52051  | 1.4159219 |
| Kcnq4    | -1.132148 | -0.752981 | -0.294779 | -0.975176 | -0.32209  | -0.903229 | -0.490614  | -0.937975 | 1.0227071 | 2.4077207 | 1.4312095  | -0.379628 | 1.3765906 | -0.592321 | 0.2323679 | 0.0798564 | -0.478482 | 0.7089724 |
| Ctps     | -0.966094 | -1.055092 | -1.108228 | -1.35329  | -1.227146 | -0.79471  | -0.12274   | -0.050676 | 1.3675672 | 0.1538522 | -0.266614  | 0.1956263 | 0.504056  | -0.018518 | 1.9447551 | 0.9130178 | 0.2037844 | 1.6804502 |
| Slc2a1   | -1.094729 | -0.963758 | -0.618003 | -1.036259 | -0.780814 | -1.114378 | 0.7718637  | -0.354228 | 2.7375683 | 0.9706386 | 0.4880598  | 0.0336036 | 0.7336516 | 1.1666496 | -0.10782  | -0.409489 | -0.194438 | -0.228119 |
| Fuca1    | 0.7568336 | 1.4097205 | 0.6587496 | 1.9041088 | 0.9556786 | 1.5615129 | -1.302049  | -1.3958   | -0.181279 | -0.862115 | -0.963052  | -0.768556 | -0.61227  | 0.0141278 | -0.721052 | 0.1266343 | -0.364437 | -0.216756 |
| Kif2c    | -1.21301  | -1.003898 | -1.203457 | -1.399957 | -1.048079 | -1.192299 | 1.1594161  | 0.0156451 | 1.9334635 | 0.8875969 | 0.4935624  | 0.6986231 | 0.5858302 | -0.009647 | 0.0750971 | 0.8819543 | -0.465242 | 0.8043998 |
| Eif2b3   | -0.722794 | -0.546328 | -1.317837 | -1.111217 | -1.149511 | -0.977295 | 0.4877574  | -0.42281  | 1.8548361 | 0.9081237 | 0.0790253  | 0.1219607 | 1.1417037 | -0.392977 | -0.430414 | 0.9571709 | -0.360575 | 1.8811826 |
| Mutyh    | -0.575326 | -0.039928 | -1.275177 | -1.516885 | -0.967691 | -1.211787 | 0.5508868  | 0.1839967 | -0.077267 | 1.1510812 | 1.0425954  | -0.021532 | 1.2465049 | -0.506706 | 0.1740664 | -0.354204 | -0.16608  | 2.363453  |
| Nasp     | -0.68386  | -0.704358 | -1.200015 | -1.21995  | -1.159222 | -1.143072 | 1.1497728  | -0.158219 | 0.8077313 | 0.7534353 | 0.1590362  | 0.1519071 | 1.1806129 | -0.668164 | 0.6251434 | -0.254582 | 0.008812  | 2.355018  |
| Rad54l   | -0.94379  | -0.759322 | -1.032304 | -1.161352 | -1.285002 | -1.143873 | 1.3815429  | -0.647335 | 0.82909   | 0.9689526 | 0.6612301  | 0.8454002 | 1.2099874 | -0.683332 | 0.5842094 | 0.185084  | -0.566503 | 1.5573194 |
| Mknl1    | 0.9259063 | 0.1976418 | 0.945006  | 1.6274026 | 1.1695743 | 1.982963  | -0.855005  | -1.511217 | -0.270245 | -0.870389 | -0.680416  | -0.949457 | -0.560781 | -0.837815 | -0.4594   | 0.5521137 | 0.2648197 | -0.670701 |
| Cyp4b1   | 2.1440386 | 0.9596987 | 0.3158751 | 0.7881635 | 1.5564992 | 1.7464063 | -1.015109  | -0.581986 | -0.220255 | -0.800854 | -0.7597    | -0.544729 | -0.707894 | -0.461942 | -0.604717 | -0.649768 | -0.285173 | -0.878553 |
| Pdzk1ip1 | 1.8448575 | 2.0829285 | -0.01394  | -0.110368 | 1.4526081 | 0.1304717 | -1.203039  | -1.260344 | -1.12022  | 0.690918  | 0.1247433  | 0.2771038 | 0.0202976 | -0.754882 | -1.135566 | -0.469073 | -0.387276 | -0.169521 |
| Stil     | -0.982812 | -0.908343 | -0.980759 | -1.23981  | -1.080342 | -1.175177 | 1.1013883  | 2.5607004 | 0.4963374 | 0.6250083 | 0.3630092  | 0.4223738 | 0.3587187 | -0.364393 | 0.1970343 | -0.246862 | -0.17244  | 1.026368  |
| Ebna1bp2 | -0.70956  | -0.695208 | -1.110846 | -0.992051 | -1.110316 | -0.669698 | 0.359652   | -0.115027 | 1.162427  | 0.5103557 | 0.0809667  | 0.3647533 | 0.6175104 | -0.927105 | 0.6295621 | -0.186128 | -0.12114  | 2.679827  |
| Mrt0a    | -0.832538 | -0.910465 | -1.130727 | -0.862331 | -1.326383 | -0.885074 | 0.6271229  | -0.315354 | 1.5045751 | 0.4325364 | 0.3294703  | 0.3434117 | 1.1389489 | -0.744761 | 0.6370124 | 0.2482701 | -0.589535 | 2.2362205 |
| Pla2gf   | 2.4698857 | 1.3777509 | 0.5119626 | 0.8701604 | 1.1198563 | 1.1432656 | -0.92376   | -0.895936 | -0.637595 | -0.223678 | -0.4220439 | -0.185954 | -0.470369 | -0.727573 | 0.3836684 | -0.754824 | -0.69638  | -0.772688 |
| Pla2ge   | 1.9836513 | 2.054696  | 0.4306103 | 1.113126  | 1.0570059 | 0.8160262 | -0.784085  | -0.822606 | -0.735751 | -0.541704 | -0.89185   | -0.848854 | -0.723438 | -0.6194   | -0.410671 | 0.1563121 | -0.351563 | -0.879691 |
| Pink1    | 1.5877357 | 1.2727287 | 0.7232863 | 1.406421  | 1.5433845 | 1.271651  | -0.871373  | -0.996348 | -0.029362 | -0.907292 | -0.753235  | -0.507097 | -0.721971 | -0.457919 | -0.753235 | -0.177017 | -0.562162 | -1.102419 |
| Kif17    | -0.85037  | -0.842997 | -0.699453 | -0.777113 | -0.751829 | -0.823374 | 1.0309229  | -0.257424 | 3.2024714 | 0.1513182 | 0.252251   | 0.1348699 | 1.0638857 | -0.310549 | -0.081402 | -0.602281 | 0.3351464 | -0.174075 |
| Ptpn12   | -0.762799 | -0.584255 | -0.800976 | -0.636419 | -1.209079 | -1.035904 | 0.8725461  | 2.1898805 | -0.166692 | 0.03796   | -0.12541   | -1.076522 | 1.0292903 | -0.761467 | 1.3442594 | 0.642883  | 0.3140382 | 1.0986457 |
| Fabp3    | 1.0016074 | 1.9584132 | 1.5033581 | 2.4370554 | 0.4734207 | 0.2012727 | -0.820938  | -0.591668 | -0.856699 | -0.82287  | -0.857269  | -0.81853  | -0.757041 | -0.236306 | -0.358567 | -0.266118 | -0.354904 | -0.464219 |
| Tinag1   | -1.188734 | -0.873718 | -0.473536 | -0.987495 | -1.189969 | -1.009094 | 2.3897787  | -0.309708 | 0.5625708 | 1.1840215 | 0.0354506  | 0.2622476 | 1.2380952 | -0.342266 | 0.6234577 | 0.9583141 | -0.678861 | -0.115052 |
| Adc      | -0.68965  | -1.04548  | -0.794334 | -0.513642 | -0.255221 | -0.365624 | -0.41237   | -0.445787 | -0.577999 | -0.394335 | -0.046304  | -0.025082 | -0.562371 | 1.610285  | 1.0816967 | 2.8934373 | 0.9273411 | -0.025082 |
| Ccdc28b  | 1.14335   | 1.3867905 | -0.169181 | 1.5785473 | 1.30722   | 1.3518079 | -1.567115  | -0.939896 | -0.440053 | -0.744174 | -0.497911  | -0.231175 | 0.3920829 | 0.2524829 | -0.881986 | 0.1387888 | -0.888196 | -1.183209 |
| Tmem50a  | 1.262262  | 1.1613974 | 0.7297289 | 1.4657391 | 0.9187311 | 1.5353113 | -1.105651  | -1.553061 | 0.7216854 | -0.785249 | -0.378279  | -0.659671 | -0.189058 | -0.533116 | -0.744431 | 0.2147145 | -0.684611 | -1.017793 |
| Trim63   | 1.0665474 | 1.8577001 | 1.236007  | 1.7464766 | 0.7612994 | 0.9790157 | -0.95639   | -0.839834 | -0.92415  | -0.934987 | -0.932312  | -0.938376 | -0.95639  | -0.142216 | -0.229981 | -0.250144 | -0.277335 | -0.264932 |
| Zfp593   | -0.819683 | -0.979912 | -1.064153 | -0.892259 | -1.114208 | -0.803626 | 1.2925669  | -0.127944 | 0.7968524 | 0.511388  | -0.127994  | 0.0545075 | 1.8028771 | -0.686088 | 0.0741007 | 0.3866873 | -0.499434 | 2.1962707 |
| Cnksr1   | -1.067333 | -0.796445 | -0.510409 | -1.195212 | -0.742396 | -1.266525 | 0.0368075  | -0.809699 | 0.2881938 | 0.2219764 | -0.117311  | 0.3118809 | -0.229817 | 0.5111866 | 0.5956569 | -0.421446 | -0.248473 |           |
| Cdc4a    | -1.251431 | -0.973088 | -1.186028 | -1.244941 | -1.043488 | -1.232523 | 0.801175   | -0.023898 | 1.6549246 | 1.0624077 | 0.7643178  | 0.3596867 | 0.6406699 | -0.235698 | 0.162298  | 0.086381  | -0.128243 | 1.7820771 |
| Rpa2     | -0.873208 | -0.638282 | -1.12869  | -1.187507 | -1.336566 | -0.945159 | 0.2635433  | -0.454481 | 0.1616298 | 0.6257832 | 0.7324849  | 0.5508158 | 1.1496201 | -0.592637 | 1.16147   | 0.2150683 | -0.648491 | 0.297146  |
| Yrdc     | -0.830868 | -0.808951 | -0.352889 | -0.938545 | -1.224314 | -0.939319 | 0.1683556  | 0.1070219 | 1.5208474 | 0.7526165 | 0.7081102  | 0.3004404 | 0.7270558 | -0.66896  | -0.16794  | 0.7759721 | -0.423447 | 2.2948127 |
| Inpp5b   | 0.8030271 | 2.1423838 | 0.6609435 | 0.5021717 | 1.497346  | 1.2015788 | -1.388385  | -1.420864 | -0.61546  | -0.504598 | -0.55197   | 0.2882474 | -0.733951 | -0.265996 | -0.103689 | -0.043391 | -0.839329 | 0.2819337 |
| Rcc1     | -0.963772 | -0.937832 | -1.06254  | -1.270431 | -0.949129 | -0.899656 | 0.9269353  | -0.354857 | 1.6510914 | 0.5090821 | 0.6914884  | -0.299342 | 0.7055356 | -0.199616 | 0.0887754 | 0.4143924 | -0.363346 | 2.3132204 |
| Plekhn2  | 0.8897931 | 0.2229919 | 1.7335641 | 2.5208504 | 0.183949  | 1.1392886 | -0.662764  | -1.131228 | -0.564556 | -0.428967 | -0.521945  | -0.805059 | 0.0241384 | -0.11672  | -0.700538 | 0.0724806 | -0.711546 | -1.142821 |
| Cdk14    | 1.1664011 | 0.9345519 | 0.7321943 | 1.6753844 | 1.0042397 | 1.7042578 | -1.292708  | -0.860497 | -1.031755 | -0.960696 | -1.0424    | -0.543015 | -1.18277  | 0.0734735 | 0.2333343 | -0.279403 | 0.0975161 | -0.428107 |
| Kcnab2   | 1.1359431 | -0.014151 | 0.8548227 | 2.2393589 | 0.3624423 | 1.5932001 | -1.38919   | -0.903665 | 0.296339  | -0.776392 | -0.492157  | -0.774503 | -0.854665 | -1.098656 | -0.149    | 0.7403051 | -0.058931 | -0.710561 |
| Xrcc2    | -0.945883 | -1.267036 | -1.079309 | -0.990591 | -1.353793 | -1.060783 | 0.249882   | 1.80021   | 0.60017   | 0.6614727 | 0.2873848  | -0.171244 | 0.6297938 | -0.303706 | 0.5925613 | 0.1820338 | -0.041556 | 0.4103927 |
| Nol9     | -0.617101 | -0.874827 | -0.420131 | -0.964165 | -0.828731 | -0.944674 | -0.006123  | -0.594602 | 2.3092402 | -0.236561 | 1.0184125  | 0.2565923 | 1.0407379 | -0.48695  | 0.4701969 | -0.3349   | -0.795616 | 2.0092008 |
| Smardc3  | 0.5982344 | 2.317771  | 1.0909221 | 0.8750888 | 1.0824804 | 1.0749129 | -1.493136  | 0.0692111 | -0.779116 | -1.00658  | -0.755141  | -0.699714 | -1.09288  | 0.2232461 | 0.0841278 | -0.440264 | -0.207028 | -0.854556 |
| Zbtb48   | -1.016417 | -0.461722 | -1.274725 | -0.73192  | -0.998026 | -0.992791 | -0.7267997 | -0.072262 | 1.7072535 | -0.394293 | 0.2450191  | 1.7300076 | 0.7693709 | 0.1102993 | 0.0624355 | -0.633004 | -0.757074 | 1.836558  |
| Abcb1b   | -0.816016 | -0.831165 | -0.818057 | -0.6853   |           |           |            |           |           |           |            |           |           |           |           |           |           |           |



|           |           |           |           |           |           |           |           |            |           |           |           |           |           |           |           |           |            |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|
| Pf4       | 1.6280828 | 0.4162039 | 0.1415801 | 1.6687764 | 1.1908059 | 1.6540586 | -0.872956 | -0.706105  | -0.823876 | -0.955478 | -0.961102 | -0.967377 | -0.761234 | -0.685846 | -0.387483 | 1.0466158 | -0.225914  | -0.398752 |
| Mthfd2l   | -0.666846 | -0.866506 | -0.046502 | -0.974139 | -0.136466 | -0.592819 | 1.288146  | 2.8903147  | -0.279781 | 0.0441967 | 0.0311974 | 0.4709667 | 0.7321387 | 0.1874329 | 0.4729962 | -0.062551 | -0.619817  | 0.3997768 |
| Areg      | -0.809189 | -0.953279 | -0.973024 | -1.115118 | -1.073823 | -1.053209 | 0.344368  | 0.2073767  | 0.0617378 | 0.1727283 | 0.1004582 | 0.3929866 | 0.2184254 | -0.367281 | 0.4974834 | -0.236883 | -0.51058   | 1.6680096 |
| Cxcl3     | -0.556342 | -0.64836  | -0.908519 | -0.700599 | -0.92757  | -0.574561 | 0.6274351 | 2.9007498  | -0.376633 | -0.518219 | 0.0766008 | 0.2603137 | -0.651234 | -0.894865 | -0.047263 | 1.0126573 | 0.53707    | 1.389338  |
| Ccng2     | -1.19715  | -0.70964  | -0.694625 | -1.231073 | -0.54326  | -0.750223 | 2.2380504 | 1.039618   | -0.071197 | 0.0619225 | 0.1133556 | -0.066869 | 0.2063728 | 0.0937491 | 1.0839608 | -0.214657 | -0.754254  | -0.424227 |
| Tcnn2     | -1.085744 | -1.118836 | -0.974717 | -0.759577 | -0.974259 | -0.737004 | 0.0684203 | 0.0876024  | 0.3238268 | 0.1875058 | 0.4368097 | 0.3081656 | 0.7050852 | -0.301032 | 0.1028575 | -0.459897 | -0.251547  | 2.4423402 |
| Eif2b1    | -0.853516 | -0.67132  | -1.594399 | -1.243036 | -1.393697 | -1.055479 | 0.5552416 | 1.1712308  | 0.1439718 | 1.1086063 | 0.5055113 | 1.0423663 | 1.3455005 | -0.042051 | -0.165383 | -0.06308  | -0.351876  | 1.5614095 |
| Rilp1     | 1.2892396 | 0.2319108 | 1.2280582 | 2.2641811 | -0.133397 | 1.9670528 | -0.592879 | -0.418218  | -0.934277 | -0.865266 | -0.772117 | -0.477382 | -0.724613 | -0.589637 | -0.581341 | 0.1607988 | -0.513941  | -0.538172 |
| Naaa      | 0.3108029 | 0.9421969 | 1.4311758 | 1.0505924 | 1.8839251 | 0.9972922 | 0.3666125 | -1.441997  | -0.324958 | -0.765981 | -1.074121 | -0.200933 | -0.978526 | 0.5158724 | -1.356033 | -0.526376 | -0.932503  | 0.1029582 |
| Kntc1     | -1.128288 | -0.804174 | -1.127066 | -1.300545 | -1.214382 | -1.193024 | 1.5238913 | 1.2089951  | 0.5352561 | 0.4938161 | 0.8386283 | 0.8487274 | 1.0605342 | 0.1510113 | 1.3219389 | -0.157642 | -0.540982  | -0.517592 |
| Sdad1     | -1.203469 | -1.123317 | -1.072549 | -1.246338 | -0.913741 | -1.121828 | 1.4164762 | 1.1766326  | 0.6954594 | 0.5509959 | 0.0863235 | 0.1571138 | 1.2308612 | -0.260946 | 0.1668037 | -0.067622 | -0.352961  | 1.8821058 |
| Ran       | -0.7013   | -0.902549 | -1.165417 | -1.284549 | -1.098631 | -1.147166 | 0.8294426 | 2.4524353  | 0.0824828 | 0.0354255 | 0.3351447 | 0.373164  | 0.9030693 | -0.2327   | 0.5236275 | -0.102934 | -0.298399  | 1.3988528 |
| Gbas      | 1.6688986 | 1.8696733 | 0.6877765 | 1.3636908 | 1.179812  | 0.9455605 | -0.566076 | -0.487425  | -0.808339 | -0.82431  | -0.84249  | -0.799968 | -0.08453  | -0.327686 | -1.051325 | -0.694915 | -0.165829  | -1.06262  |
| Psmd9     | -0.951089 | -1.220473 | -1.169622 | -1.218065 | -1.292523 | -0.749696 | 1.0554836 | 1.1147376  | -0.214019 | 0.2256885 | 0.2895133 | 1.3536965 | 1.0308388 | -0.475204 | 0.3121856 | 0.2765217 | -0.269728  | 1.9017516 |
| Cct6a     | -0.921768 | -0.945389 | -1.093775 | -0.995553 | -1.062174 | -0.967277 | 0.5819757 | 2.6385704  | -0.011321 | 0.0029443 | 0.0055725 | 0.3302251 | 0.4861054 | -0.14533  | 0.4680798 | -0.103439 | -0.159902  | 1.7616568 |
| Aldh2     | 1.4031165 | 0.8008873 | 1.5146874 | 1.1179152 | 1.6338712 | 1.2659474 | -1.393715 | -0.912674  | -0.80862  | -0.940469 | -0.412401 | -0.512546 | -0.727352 | 0.0536438 | -0.491243 | -0.157311 | -0.690931  | -0.742807 |
| P2rx7     | 0.4190972 | 0.3448613 | 1.1709387 | 1.9255814 | 1.586276  | 1.7844201 | -1.25682  | -0.6034872 | -0.540844 | -0.999283 | -0.621066 | -0.281834 | -0.525137 | -0.457599 | -0.524764 | 0.6541848 | -0.387794  | -0.926015 |
| P2rx4     | 0.8536163 | 0.5343623 | 0.9753318 | 1.2021911 | 0.8367824 | 1.8006961 | -0.876239 | -0.607517  | -0.909862 | -1.090494 | -0.101153 | -0.988269 | -0.732347 | -0.328759 | -0.342945 | 0.8464068 | -0.073079  | -0.727347 |
| Pde6b     | -0.877536 | -1.228219 | -1.092564 | -0.754615 | -0.59635  | -0.459704 | 1.5596385 | -0.710782  | 0.0606621 | 1.7619953 | 0.1966621 | -0.131837 | 0.5268258 | -0.182321 | 0.059206  | -1.129467 | 1.8269635  | 1.1625504 |
| Ddx51     | -1.657353 | -1.420829 | -1.274741 | -1.260944 | -1.157365 | -0.672758 | 0.7766054 | 1.1054675  | 0.086571  | 0.6750062 | 1.2137424 | 0.5175065 | 0.9304415 | 0.4467409 | 1.0790661 | -0.545555 | 0.5739984  | 0.5849506 |
| Pus1      | -1.147584 | -1.009791 | -0.981988 | -1.137655 | -1.33348  | -1.336026 | 1.2602778 | 1.1887837  | 0.5275173 | 0.1136677 | 0.1072549 | 1.3011123 | 0.2965991 | 0.8145398 | 0.6095191 | 0.0121347 | -0.201211  | 2.0873304 |
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| Chek2     | -1.287175 | -0.623028 | -1.331497 | -1.410327 | -1.246256 | -1.251113 | 0.9862337 | 1.7859762  | 1.1275216 | 0.5319533 | 0.3510428 | 0.5808303 | 0.6716532 | 0.6527428 | 0.3542216 | -0.052306 | -0.583558  | 0.7426848 |
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| Rbm19     | -1.364856 | -1.157078 | -0.296611 | -0.046889 | -1.37398  | -1.149202 | 1.5892167 | 0.6785931  | 0.3282057 | 0.6890332 | 1.3859619 | -0.152366 | 0.7340207 | -0.543752 | 0.7602317 | -0.949864 | 0.1736525  | 1.4626823 |
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|           | Aimp2     | -1.020798 | -0.858086 | -0.845035 | -1.537298 | -1.120046 | -0.325553 | 1.2801112  | 1.3139203 | 0.8417064 | 0.6619171 | 0.0925332 | 0.6734108 | 1.3285878 | -0.262706 | 0.447218  | -0.415365  | -0.685104 |
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| Flt1      | -1.075719 | -1.339697 | -0.631644 | -1.318962 | -1.139866 | -1.402777 | -0.27269  | 0.3139961  | 0.8932057 | -0.056604 | 0.4725018 | 1.0792255 | 0.4153349 | -0.105104 | 1.8044093 | 1.5930472 | 0.3325655  | 0.438777  |
| Sic46a3   | 1.1363429 | 1.5153862 | 0.664552  | 1.3017886 | 1.1750324 | 1.4234987 | -0.744111 | -0.690281  | -0.294955 | 0.0659928 | -0.505844 | -0.553783 | -0.966803 | -0.875192 | -0.83887  | -0.302993 | -0.907989  | -1.141772 |
| Tfp12     | -0.469068 | -0.983371 | -0.541977 | -0.617247 | -0.801762 | -0.298451 | -0.788617 | -0.477602  | -0.644724 | -0.711637 | -0.50472  | 0.0900106 | -0.256163 | 0.7678964 | 2.3393173 | 2.4963034 | 0.9032148  | -0.089804 |
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| Linn      | 1.5659608 | -0.018196 | 1.755254  | 1.9669177 | 1.7205211 | 0.9590793 | -1.026928 | -0.62353   | -1.00706  | -0.991137 | -0.561417 | -0.824239 | -0.101894 | 0.2939462 | 0.195842  | 0.111994  | 0.0719224  | -0.689977 |
| Hyal4     | 0.8659278 | 2.6327456 | 0.4392003 | -0.04844  | 1.1251934 | 0.6938113 | -0.810726 | -1.119343  | -0.488504 | 0.6600986 | 0.3203933 | -0.002142 | 0.3797865 | -0.556068 | -1.055341 | -1.180391 | -0.874937  | -0.981265 |
| Lmod2     | 2.2248914 | 0.7511577 | 1.303228  | 1.7347612 | 0.55685   | 0.3364339 | -0.906611 | -0.817461  | -0.976113 | -0.923655 | -0.965946 | -0.907732 | -0.935709 | 0.3264164 | -0.430965 | -0.188876 | -0.293281  | 0.114411  |
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| Mcm7      | -1.084431 | -1.181244 | -0.817241 | -1.368761 | -0.799194 | -1.145527 | 0.9019655 | 2.2676501  | 0.1677992 | 0.0542793 | 0.7382643 | -0.062034 | 1.111827  | -0.454512 | 1.1307269 | -0.010043 | -0.238167  | 0.7932819 |
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| Dlx5      | -0.836689 | -0.74736  | -0.706549 | -1.145271 | -0.985218 | -1.084169 | 1.9248013 | 0.0069821  | 1.5803106 | 1.4621179 | 0.1272914 | -0.056829 | 0.3131311 | 0.1350611 | -0.251284 | -0.106421 | -0.350918  | 1.0680072 |
| Pon3      | 1.4152336 | 1.5286597 | 0.7408874 | 1.4780013 | 0.5337499 | 1.5005246 | -0.887447 | -0.727248  | -1.418525 | -0.764727 | -1.175191 | -0.10975  | -1.060713 | 0.1603668 | -0.31921  | 0.0908553 | -0.08206   | -0.903409 |
| Akclb8    | -1.022653 | -0.911799 | -0.815051 | -0.815729 | -0.912314 | -0.733322 | 3.1691361 | 0.8039778  | -0.190039 | 0.1630229 | 0.4708002 | -0.335992 | -0.514444 | 0.9582213 | 0.325194  | 0.1839978 | 1.1373768  | 0.4626161 |
| Irf5      | 0.9802088 | 0.5209384 | 1.2172496 | 2.3595259 | 0.6062351 | 0.9950566 | 0.2411827 | -0.739484  | -1.182925 | -0.883387 | -1.156826 | -0.766943 | -0.832738 | -1.       |           |           |            |           |



|            |           |           |           |            |           |            |           |           |            |           |           |           |            |           |           |           |           |           |
|------------|-----------|-----------|-----------|------------|-----------|------------|-----------|-----------|------------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|
| Lrmp       | 0.9737587 | 0.4082357 | 1.2287609 | 1.7968236  | 1.2988578 | 1.6724394  | -1.19315  | -0.911749 | -0.780277  | -0.873992 | -0.867588 | -0.65951  | -0.840992  | -0.561498 | -0.468603 | 0.5261829 | -0.217579 | -0.530119 |
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| Camk1      | 0.9923495 | 0.5146337 | 0.561556  | 1.5466459  | 1.1417682 | 1.9209719  | -1.168851 | -0.656614 | -0.976408  | -1.099194 | -1.096342 | -0.451598 | -1.067629  | -0.174336 | 0.0299296 | 0.9412294 | -0.185714 | -0.778398 |
| Cidec      | -0.127696 | 1.4491366 | 2.1345548 | 1.2449248  | 1.4037602 | 1.4173232  | -0.684877 | -0.617919 | -0.684877  | -0.684877 | -0.661677 | -0.677158 | -0.682277  | -0.518847 | -0.525197 | -0.698874 | -0.429546 | -0.684877 |
| Med21      | -0.837357 | -0.927435 | -1.052686 | -1.348678  | -1.083425 | -1.05491   | 1.0513599 | 2.4643255 | 0.3393613  | 0.0885198 | -0.335547 | 0.3031082 | 0.4013578  | 0.4251504 | 0.690101  | -0.286273 | -0.171946 | 1.3379728 |
| Far2       | 2.213291  | 2.3997784 | 0.032429  | 0.2623253  | 0.6869708 | 1.3432787  | -0.54345  | -0.491755 | -0.601029  | -0.628679 | -0.61405  | -0.632958 | -0.608813  | -0.428513 | -0.488907 | -0.667871 | -0.535631 | -0.63136  |
| Tmtc1      | 1.4915242 | 1.0935901 | 1.4093294 | 1.0091833  | 1.4380815 | 0.5957952  | -1.312077 | -0.805242 | -0.403616  | -0.805958 | -0.771871 | -0.822389 | -0.1079221 | 1.0430323 | -0.22855  | -0.57209  | -0.288641 | -0.990431 |
| Caprinr2   | -0.720486 | -0.5015   | -1.044573 | -1.088233  | -1.08203  | -0.823757  | 2.40269   | 1.8965747 | 0.9294745  | 0.4557737 | 0.5021804 | 0.4144189 | 0.1424024  | 0.1745692 | 0.0971141 | -0.756157 | -0.266065 | -0.732396 |
| Dennd5b    | -1.63967  | -1.045425 | -0.961827 | -1.292003  | -1.300485 | -0.777972  | 0.8479596 | 1.2050658 | 0.5621791  | 1.1281016 | 0.3320729 | 0.9256825 | 0.130238   | 0.4476357 | 0.60484   | -0.277545 | 2.0475851 | 0.0635673 |
| Timp4      | 0.5234286 | 0.7211831 | 2.1518924 | 1.2316308  | 0.848603  | 2.0773917  | -0.750743 | -0.689584 | -0.750743  | -0.367692 | -0.750743 | -0.750743 | -0.750743  | -0.625069 | -0.358671 | -0.537621 | -0.471036 | -0.750743 |
| Rad51ap1   | -1.134272 | -0.944421 | -1.076652 | -1.397268  | -1.098472 | -0.902416  | 1.9713732 | 1.6490564 | -0.184387  | 0.6677948 | 0.4864244 | 0.8241124 | 0.2775768  | -0.169231 | 0.5957034 | -0.461341 | -0.105136 | 1.0015529 |
| Tspan9     | -1.066282 | -1.035562 | -0.413792 | -1.101125  | -0.622296 | -1.188179  | 1.2874179 | -0.481495 | 1.2912778  | 1.3762765 | 1.8768643 | -0.271837 | 0.0244458  | 0.9893598 | -0.554132 | -0.411706 | 0.8781784 | -0.577413 |
| Ckm        | 0.802951  | 2.8664484 | 0.4865145 | 0.6438432  | 1.1730662 | 1.2625183  | -0.693162 | -0.583478 | -0.695164  | -0.694875 | -0.695385 | -0.693338 | -0.695848  | -0.369643 | -0.518894 | -0.623736 | -0.399827 | -0.571991 |
| Rtn2       | 1.2695988 | 1.7932361 | 0.8193975 | 1.2358091  | 1.5898426 | 1.2242692  | -0.783013 | -0.792732 | -0.955774  | -0.900139 | -0.905723 | -0.673404 | -0.938805  | -0.215819 | -0.43933  | -0.504009 | -0.42018  | -0.401426 |
| Lilra6     | 1.6725033 | 0.5328332 | 0.7763061 | 2.1482293  | 0.3228688 | 1.6052158  | -0.957222 | -0.690284 | -0.800926  | -0.991397 | -0.91927  | -0.777741 | -0.828269  | -0.461693 | -0.573438 | 0.5118354 | -0.234805 | -0.426774 |
| Tmem238    | -0.892609 | -0.667954 | -0.913213 | -1.150223  | -1.048634 | -1.248737  | 1.2961529 | -0.02567  | 0.2427874  | 0.7080096 | 0.3603264 | 0.1622325 | 0.2346285  | 0.5498656 | -0.246703 | 0.5087343 | -0.607284 | 2.7382883 |
| Sbk2       | 2.7688359 | 0.1720034 | 0.9650618 | 1.5964988  | 0.4480294 | 0.8399457  | -0.777483 | -0.777483 | -0.647469  | -0.507325 | -0.777483 | -0.6669   | -0.777483  | -0.674045 | -0.527101 | 0.3563618 | -0.456615 | -0.557353 |
| Zdhhc13    | -1.121859 | -0.922334 | -1.071316 | -1.420423  | -1.140941 | -1.261594  | 0.9801814 | 1.1044261 | -0.54165   | 0.8937633 | -0.337191 | 0.8426776 | 1.1154254  | 0.7616254 | 0.8450702 | 0.4757934 | -0.727529 | 1.2375462 |
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| Sic7a10    | 0.1597412 | 2.7692765 | 1.9121513 | 0.5346767  | 0.902184  | 0.5779291  | -0.69177  | -0.675499 | -0.640611  | -0.615314 | -0.648921 | -0.69177  | -0.69177   | -0.359189 | -0.477814 | -0.648007 | -0.22575  | 0.525128  |
| Gas2       | -1.329672 | -0.656172 | -1.030279 | -1.063035  | -0.824399 | -0.753439  | 0.6455327 | 1.261691  | 2.7987924  | 0.0748426 | -0.208235 | -0.257515 | 0.1123325  | 1.1478815 | 0.4072294 | -0.213082 | 0.1129939 | 0.1075322 |
| SNRpa1     | -0.812468 | -0.758262 | -1.037929 | -1.26332   | -1.003386 | -0.821362  | -0.242181 | -0.032989 | -0.039762  | 0.2057313 | 0.7344531 | 0.3402296 | 0.1479155  | -0.238429 | 0.4066919 | -0.250885 | 0.6165594 | 2.9829664 |
| Pcsk6      | 2.0931391 | 1.4753571 | 0.9201294 | 0.7251564  | 1.4290683 | 0.8880301  | -0.086323 | -0.803494 | -0.54311   | 0.0730914 | -0.011909 | -0.32844  | -0.877043  | -0.768523 | -0.911097 | -0.871352 | -0.511866 | -0.890815 |
| Tarsl2     | -0.378195 | 1.9112411 | -0.409069 | 0.2334126  | -0.21116  | -0.2414123 | 0.596462  | 1.228931  | -0.25425   | -0.260691 | 0.6452156 | 1.1999811 | 0.0574057  | 0.1402975 | -1.100286 | -0.859493 | -1.629214 | -0.291618 |
| Phosphol1  | -0.748626 | -0.883735 | -1.123278 | -1.103266  | -1.175189 | -0.103642  | 0.3542432 | 2.4400102 | 0.4856001  | 0.1543805 | -0.19576  | 0.6456916 | 0.789654   | -0.104301 | 0.3960273 | -0.406542 | -0.233478 | 1.7222097 |
| Blm        | -1.13128  | -0.92379  | -1.099191 | -1.306387  | -1.159154 | -1.120752  | 1.0686233 | 1.7169272 | -0.418524  | 0.9508377 | 0.3728494 | 0.4095017 | 0.5282495  | -0.433865 | 0.456747  | 0.124657  | 1.9009079 | 1.7744954 |
| Sema4b     | -1.28427  | -0.855228 | -0.302541 | -1.611577  | -0.629484 | -1.582675  | 0.4695906 | -0.255648 | 1.8108484  | 1.5175824 | 0.9603269 | 0.0479782 | -0.271871  | 0.6455639 | 0.5406364 | -0.278338 | 1.1807616 | 0.028644  |
| Pex11a     | 2.7181578 | 1.7049078 | -0.005115 | 0.363936   | 0.6552135 | 0.9786165  | -0.082219 | -0.879388 | -0.308258  | -0.033233 | -0.551255 | -0.240032 | -0.013387  | -0.575296 | -0.623937 | -1.092657 | -1.032007 | -0.984047 |
| Plin1      | -0.195058 | 1.9375906 | 1.5421915 | 1.4520408  | 1.6780305 | 1.0492953  | -0.696894 | -0.58456  | -0.696984  | -0.687249 | -0.696984 | -0.696984 | -0.696984  | -0.456212 | -0.564797 | -0.666176 | -0.323193 | -0.696984 |
| Synn       | 0.9786753 | 1.9834769 | 1.1464826 | 1.2147679  | 1.4222057 | 1.1514718  | -0.106654 | -0.6699   | -0.791483  | -0.567572 | -0.676042 | -0.815489 | -0.907359  | -0.087461 | -0.632203 | -0.839912 | -0.244142 | -0.657863 |
| Lrrc28     | 0.6995161 | 2.647047  | 0.6167857 | -0.254663  | 1.6285703 | 0.8595935  | -1.022571 | -0.948049 | -0.598829  | 0.3263779 | 0.1963946 | -0.007283 | -0.517886  | -0.438762 | -0.888085 | -1.103271 | -0.736518 | -0.458268 |
| Tyrbp      | 0.947288  | 0.6695012 | 1.0160276 | 2.0501452  | 0.6113101 | 1.6596585  | -1.089896 | -0.82392  | -0.795668  | -0.954462 | -0.979853 | -0.688918 | -0.898552  | -0.551786 | -0.472379 | 0.9250639 | -1.138329 | -0.48523  |
| Rasgrp4    | 1.2675639 | 1.2078123 | 0.3018299 | 1.4367877  | 1.91395   | 1.2984727  | -1.333258 | -0.708757 | -0.563691  | -0.498388 | -0.618678 | -0.521105 | -1.060624  | -0.70795  | -0.96084  | 0.30475   | -0.375798 | -0.382077 |
| Ryrr1      | 0.9493789 | 1.47377   | 2.0453343 | 0.8611392  | 1.2728004 | 0.9323385  | -0.976488 | -0.832006 | -0.956257  | -0.93506  | -0.943848 | -0.940715 | -0.960231  | 0.1589293 | -0.589717 | -0.082217 | -0.145856 | -0.316848 |
| Mfge8      | 0.951136  | -0.025437 | 0.951136  | 2.9129326  | 0.1599436 | 1.4966935  | -0.893615 | -0.645891 | -0.707472  | -0.646916 | -0.67841  | -0.442101 | -0.816687  | -0.261491 | -0.456964 | 0.1954821 | -0.359404 | -0.732936 |
| Mrps11     | -1.409001 | -0.907389 | -0.869943 | -0.802791  | -0.78309  | -1.164367  | -0.151608 | 2.0981933 | 1.0453487  | 0.1863347 | -0.040886 | 0.2253418 | 0.1213993  | -0.438633 | 1.0663267 | -0.445171 | 0.3943217 | 1.8756131 |
| Sytl2      | 0.1319803 | 1.7918954 | 0.3820522 | 0.6845738  | 1.1793438 | 2.1846376  | -1.423723 | -0.887289 | -1.042324  | -0.881712 | -0.510517 | -0.264504 | -0.1079429 | 0.5156878 | -0.337962 | 0.3405129 | -0.299708 | -0.483515 |
| Me3        | 1.4990784 | 1.3237984 | 1.572059  | 0.4727668  | 1.2568209 | 1.1602525  | -1.401482 | -0.890747 | -0.077355  | -0.472052 | -0.49874  | -1.575175 | -0.21365   | -0.464955 | -0.542805 | -0.529999 | -0.253687 | -0.72165  |
| Zfand6     | 0.9215581 | 2.9021799 | 0.3686235 | 0.0830155  | 1.0790135 | 1.1263488  | -1.189133 | -0.374727 | -0.1002726 | -0.375568 | -0.542253 | -0.604036 | -0.255185  | 0.2569527 | -0.458044 | -0.916157 | -0.676927 | -0.255185 |
| 463243411i | -0.805107 | -0.841701 | -1.050997 | -1.112605  | -0.902205 | -1.110001  | 0.8243844 | 1.8883021 | 0.1748701  | 0.7173367 | 0.1123405 | 0.3717616 | 0.1870557  | -0.494813 | -0.257354 | -0.334301 | 0.2235246 | 2.4095078 |
| Xylt1      | 1.3058539 | -0.110383 | 0.932238  | 2.7210109  | 0.533305  | 0.909773   | -1.328972 | -0.263325 | -0.116879  | -0.467393 | -0.15026  | -0.99009  | -0.499277  | -0.685664 | -0.871669 | 0.3776505 | -0.220486 | -1.075433 |
| Mylpf      | 0.5612182 | 1.3884472 | 0.582505  | 0.7480228  | 0.8182693 | 0.6606093  | -0.761014 | -0.631787 | -0.75641   | -0.760032 | -0.766208 | -0.757531 | -0.761529  | 0.1371879 | -0.51512  | -0.192891 | -0.330999 | -0.462738 |
| Kif22      | -1.301954 | -1.065055 | -1.27399  | -1.368442  | -1.057593 | -1.190012  | 0.9720332 | 0.2483981 | 0.9599128  | 0.5062231 | 0.4883356 | 0.4582516 | 0.1083806  | 0.173002  | 0.1870018 | -0.085712 | 0.3632317 | 1.0428976 |
| Indo8e     | -1.392945 | -1.253141 | -0.80139  | -1.087106  | -1.062046 | -0.903233  | 0.2698214 | 1.8684112 | 1.2039567  | 0.3841276 | 0.4912674 | -0.00884  | 0.929634   | -0.081251 | 0.3160993 | 0.4555264 | -0.871695 | 1.5433105 |
| Aldoa      | 0.720736  | 2.9266541 | 0.720736  | 0.6935448  | 0.935683  | 0.720736   | -0.191398 | 0.5425473 | -0.585866  | -0.482356 | -0.828818 | -0.855233 | -0.797405  | -0.261846 | -0.423838 | -0.925058 | -0.688522 | -0.770299 |
| Gdpd3      | 0.8608527 | 2.2355125 | 1.1181599 | 0.86826017 | -0.208324 | 1.2746781  | -0.919954 | -0.166028 | -1.266135  | -0.596814 | -0.784549 | 0.3534599 | -0.420289  | -0.860414 | -0.104699 | -0.154499 | -0.960669 | 0.7981109 |
| Coro1a     | 0.5711318 | 0.5346612 | 0.8402991 | 2.0752973  | 1.0309272 | 1.330118   | -1.372719 | -1.020701 | -0.721094  | -0.92859  | -0.988975 | -0.482634 | -0.912955  | -0.507132 | -0.665085 | 1.2066621 | 0.1365587 | -0.12577  |
| Sult1a1    | 1.3307351 | 0.7502921 | 1.902777  | 1.0793265  | 1.5618389 | 1.4027961  | -0.727568 | -0.687942 | -0.62907   | -0.678178 | -0.73446  | -0.727063 | -0.814175  | -0.584675 | -0.564456 | -0.607919 | -0.533282 | -0.743478 |
| Kik7       | 1.8970934 | 1.9997733 | 1.2944196 | 0.9534703  | 0.8767757 | 0.5311023  | -0.066702 | -0.909902 | -0.975691  | -0.31764  | -0.265739 | 0.8014179 | -0.05193   | -0.127103 | -0.957249 | -0.557627 | -0.915364 | -1.243535 |
| Nupr1      | 1.9542093 | 1.        |           |            |           |            |           |           |            |           |           |           |            |           |           |           |           |           |



|           |           |           |           |           |           |           |           |           |           |           |            |            |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| Ophn1     | 1.1543751 | 0.993605  | 0.8454257 | 1.779786  | 1.0896434 | 1.6621039 | -1.184009 | -0.099827 | -0.614824 | -0.89483  | -0.895458  | -0.955669  | -0.826468 | 0.0472567 | -0.256111 | -0.023593 | -0.653839 | -1.167568 |
| Star8     | 1.1878309 | 0.3683338 | 1.0374126 | 1.5879356 | 1.497509  | 1.8876766 | -0.962445 | -0.727039 | -0.823345 | -0.921254 | -0.823605  | -0.72896   | -0.873454 | -0.42969  | -0.489511 | 0.2242832 | -0.269253 | -0.742431 |
| Efnb1     | -1.119519 | -0.971345 | -0.665166 | -1.411408 | -1.053808 | -1.255695 | -0.184855 | -2.153407 | 0.6162142 | 0.9309932 | -0.479343  | -0.0364445 | 0.5948937 | 0.6632685 | -0.334582 | 1.5023035 | -0.08211  |           |
| Awat2     | 3.0157978 | 1.8875454 | -0.197925 | 0.2207192 | 0.4187737 | 0.8872084 | -0.50546  | -0.373743 | -0.555161 | -0.407018 | -0.56045   | -0.548249  | -0.531849 | -0.567763 | -0.4781   | -0.622939 | -0.513659 | -0.567728 |
| SrpX2     | -0.804299 | -0.62862  | -0.510716 | -0.570368 | 0.0422485 | 0.3959711 | -1.251231 | -0.754325 | -0.927301 | -0.810524 | -0.432761  | 0.4602947  | -0.993509 | 1.4026342 | 1.4167714 | 1.9724275 | 1.5795491 | 0.2337488 |
| Cstf2     | -1.123224 | -0.558692 | -1.051188 | -1.155105 | -1.393321 | -1.307016 | 0.824163  | 1.1543137 | 0.8126374 | 0.4858846 | 0.3170261  | 0.1459086  | 0.5386495 | -0.272172 | 0.435988  | -0.709335 | 2.1935875 | 0.6618968 |
| Xkrx      | 1.0234423 | 1.3146454 | 0.1929173 | -0.051295 | 0.796657  | 0.371368  | -0.58021  | -0.679118 | -0.719967 | 0.6109361 | 0.0100628  | -0.366183  | -0.202271 | 0.2256356 | -0.906418 | -1.027104 | -0.864906 | -0.948193 |
| Cenpi     | -1.067554 | -0.967016 | -1.120639 | -1.280939 | -1.158338 | -1.169797 | 0.7898756 | 2.3744977 | 0.0262265 | 0.2820726 | -0.072262  | 0.8570303  | 0.2192632 | 0.2082378 | 0.4704102 | -0.158285 | 0.473132  | 1.294083  |
| Btk       | 1.1411584 | 0.6469167 | 1.4052849 | 1.8532277 | 0.8531365 | 1.4020852 | -1.295075 | -0.83634  | -0.901923 | -0.831465 | -1.00539   | -0.666999  | -0.936838 | -0.536666 | -0.347905 | 0.5390958 | 0.0285382 | -0.510842 |
| Gla       | 1.4117779 | 0.0416803 | 1.1199786 | 2.2912156 | -0.228265 | 1.7353595 | -0.760264 | -0.056343 | -0.876857 | -0.91701  | -0.751761  | -0.739065  | -0.824824 | -0.782643 | -0.536495 | 0.547153  | -0.217946 | -0.455691 |
| Chrd1     | 0.9185381 | 2.2150775 | 1.2334474 | 1.3501149 | 1.0336328 | 0.8317161 | -0.939125 | -0.648025 | -0.810282 | -0.881024 | -0.939125  | -0.882869  | -0.939125 | -0.222494 | -0.289163 | 0.1022485 | -0.365137 | -0.768408 |
| Pak3      | 2.2319811 | 2.0278864 | -0.076895 | 1.3751752 | 0.9292549 | 0.5229813 | -1.034059 | -0.49313  | -0.715231 | -0.488219 | -0.278899  | -0.474674  | -0.62144  | -0.910157 | -0.08808  | -0.419268 | -0.709069 | -0.778157 |
| Gpr64     | -0.863542 | -0.925132 | -0.572678 | -0.916104 | -1.000607 | -0.723929 | 0.69051   | -0.947742 | 0.6046788 | 0.5107754 | 0.7478807  | 1.4145537  | -0.862843 | -0.028267 | -0.390848 | 2.6113158 | -0.001522 | 0.6535009 |
| ltgblp2   | 1.5846586 | 2.1229644 | 0.970881  | 0.7629606 | 0.9980397 | 0.4563894 | -0.758984 | -0.560385 | -0.962783 | -0.810502 | -1.099685  | -1.273875  | -0.889288 | 0.648061  | -0.660335 | 0.1813747 | -0.442528 | -0.266948 |
| Gpm6b     | 0.7700585 | 0.6970555 | 0.217057  | 1.5477286 | 1.0264972 | 2.0270941 | -1.023363 | -0.383147 | -1.180722 | -1.109836 | -1.073757  | -0.857951  | -1.165524 | -0.120662 | 0.1495537 | 0.4221087 | 0.5733503 | -0.23673  |
| Hccs      | -0.622276 | -0.75126  | -1.608241 | -0.89623  | -1.506637 | -1.012986 | -0.219789 | 1.7534718 | 1.1678588 | -0.189051 | 0.0565388  | 0.1635834  | 0.8138356 | -0.580301 | 1.2790431 | 0.1735108 | 0.683823  | 1.2951078 |
| Arhgap1   | 1.6499811 | 0.3936705 | 0.4932208 | 2.6388317 | 0.4803345 | 1.2550228 | -0.897491 | -0.527599 | -0.838834 | -0.771119 | -0.883428  | -0.582436  | -0.812262 | -0.51037  | -0.280542 | 0.2354759 | -0.448667 | -0.593789 |
| Adbp6     | 0.7838955 | 1.82431   | 1.3135227 | 2.3576498 | 0.7445378 | 1.4326123 | -1.155277 | -0.60466  | -0.707    | -0.910788 | -0.983541  | -0.805987  | -0.887775 | -0.45693  | -0.580122 | 0.6190443 | -0.029485 | -0.31204  |
| Piga      | -1.097507 | -0.914927 | -0.782722 | -1.162228 | -1.118905 | -1.310136 | 2.016427  | 0.0266556 | 0.1256001 | 0.6015466 | -0.292962  | 1.1335572  | 0.3017114 | -0.086867 | 0.4584236 | 0.2271632 | -0.154335 | 1.964903  |
| Asb11     | 1.1123481 | 1.6510798 | 1.7946777 | 1.1080002 | 1.12907   | 0.982788  | -0.797729 | -0.843571 | -1.040353 | -0.929778 | -0.95463   | -0.234071  | -1.047461 | -0.31638  | -0.204747 | -0.787877 | -0.440125 | -0.181241 |
| Dusp9     | -0.861903 | -1.046708 | -0.904012 | -0.954203 | -1.044054 | -0.870432 | -0.210662 | 2.3853212 | -0.40665  | 0.7364642 | -0.070787  | -0.025479  | 0.1145394 | -0.606577 | 1.7008578 | 1.0646189 | 0.1596171 | 0.8400483 |
| Renbp     | 1.1212985 | 0.0532257 | 0.9350401 | 1.8536633 | 0.7550805 | 1.5236374 | -1.11557  | -0.922005 | -0.990556 | -1.058185 | -1.050373  | -0.700292  | -0.980555 | 0.763795  | -0.004015 | 0.6465631 | -0.190831 | -0.731611 |
| Dkc1      | -1.003085 | -0.707555 | -1.071195 | -1.334513 | -1.167346 | -1.313425 | 0.7464852 | 2.2465838 | 0.5599052 | 0.2101834 | 0.1596114  | 0.6572684  | 0.2948366 | -0.05345  | 0.3143107 | -0.351151 | 0.1636479 | 1.6488873 |
| Plp1      | 0.835583  | 1.4546947 | 1.0701422 | 1.7146288 | -0.239104 | 0.601948  | -0.037479 | 1.5053059 | -0.472372 | -1.020573 | -1.716113  | -1.171226  | -0.789326 | 0.1254875 | -0.862135 | -0.505135 | 0.8214196 | -1.303748 |
| Tsc22d3   | 2.2159091 | -0.108991 | 1.5407292 | 1.1303046 | 0.1938997 | 1.9670037 | -0.331918 | -0.855033 | -0.373388 | -0.856367 | -0.824055  | -0.606023  | -0.655502 | -0.609038 | -0.426405 | -0.194171 | -0.527997 | -0.677176 |
| Morc4     | -1.010474 | -0.735031 | -1.100764 | -0.725916 | -1.192045 | -1.121056 | 0.5601657 | 1.8164515 | 0.3430007 | 0.3246955 | 0.2965497  | 0.046468   | -0.459251 | -0.081935 | 0.658529  | 0.241575  | 2.5252311 | 0.096958  |
| Rnf128    | 1.8635188 | -0.032088 | 0.7759693 | 2.5948248 | 0.0005006 | 1.1820035 | -0.883459 | -0.659917 | -0.66425  | -0.577761 | -0.755059  | -0.53663   | -0.781123 | -0.546191 | -0.485919 | 0.2663881 | -0.234344 | -0.726464 |
| Mcf2l     | 2.3111525 | 1.3621418 | 0.0713296 | 0.3932768 | 0.5409899 | 0.701686  | -1.285458 | 0.0810697 | -0.584246 | -0.405957 | -0.034995  | 0.9612725  | -0.73156  | -1.18536  | -0.695912 | 0.7940724 | -0.943299 | -1.350205 |
| Gas6      | 0.597061  | 0.6170958 | 1.0176111 | 1.9922    | 1.9823271 | 1.1952528 | -0.958021 | -0.55771  | -0.822897 | -0.912315 | -0.652899  | -0.83972   | -0.977797 | 0.0229329 | -0.564751 | -0.139056 | -0.148025 | -0.84856  |
| Myom2     | 1.4569475 | 1.1143041 | 1.8581385 | 1.4591585 | 1.222263  | 0.6728347 | -0.890428 | -0.807899 | -0.894802 | -0.809486 | -0.981156  | -0.872036  | -0.881236 | -0.157598 | -0.559344 | -0.166755 | -0.195011 | -0.576579 |
| Angpt2    | -0.643426 | -0.679723 | -1.282957 | -0.7692   | -1.548073 | -1.439134 | 1.2045556 | 0.4093022 | 1.8537267 | -0.400925 | -0.681174  | 0.2411784  | 1.1577258 | 0.0644477 | 1.300206  | 0.4789718 | 0.0962995 | 0.638199  |
| Andr3     | -0.837656 | 1.8629403 | 1.1877865 | 0.4202754 | 1.6380534 | 1.2723238 | -0.232976 | -1.084581 | -0.23206  | 0.0920842 | 0.746154   | -0.975424  | 0.2783328 | 0.340143  | -1.143555 | -1.337735 | -0.29135  | -1.34089  |
| Eif4ebp1  | -1.006438 | -1.062157 | -0.701212 | -1.096176 | -0.741611 | -0.963531 | 2.9417613 | 0.8806191 | 0.4573256 | 0.2561996 | 0.3002473  | 0.051544   | 0.9719686 | -0.25868  | -0.518799 | -0.333188 | 0.1301127 | 0.6929351 |
| Cd209a    | 1.9821343 | 2.2046883 | -0.083172 | 0.3864157 | 1.5709932 | 0.9836612 | -0.76285  | -0.433556 | -0.731858 | -0.738999 | -0.72486   | -0.717972  | -0.717214 | -0.437584 | -0.513498 | -0.197146 | -0.510181 | -0.680332 |
| Cd209d    | 2.1281612 | 1.5686442 | 0.2232894 | 0.4979932 | 1.8141462 | 1.203348  | -0.741808 | -0.581305 | -0.73802  | -0.736087 | -0.73808   | -0.712172  | -0.729147 | -0.549448 | -0.606179 | -0.103106 | -0.514367 | -0.685864 |
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| Ankrk10   | -0.525119 | -1.228431 | -0.925187 | -0.62626  | -1.107779 | -0.976454 | 0.9852459 | 2.3807439 | 0.5615234 | -0.947948 | -0.561603  | -0.615254  | -0.104987 | 0.345198  | 0.5615234 | 1.0308331 | 0.749281  | 0.9783514 |
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| Eri1      | -0.826011 | -0.947176 | -1.151385 | -1.146015 | -1.095564 | -0.952738 | 2.1750299 | 1.7674013 | 0.0895163 | 0.0175438 | -0.10152   | 0.4620034  | 0.2637304 | -0.392037 | 0.6148921 | 0.0143014 | -0.188392 | 1.3964183 |
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Sca2a1 -1.044884 -1.052071 -0.700504 -1.094589 -0.60103 -0.876843 -1.300455 2.3364779 0.6457612 1.171608 0.3316203 0.0936984 -0.144958 -0.9373 0.7713379 -0.007382 1.2919746 0.669088
Sprbr -1.082255 -1.25651 -1.145864 -0.861921 -1.546861 -1.117178 0.1158606 1.3544648 0.8850539 1.1700016 0.3671954 1.3215225 0.4046077 -0.268032 0.9402626 0.5348622 -0.694957 0.881383
Trf 0.1308456 0.914698 1.4448418 1.7036762 1.3003387 1.8842703 -0.80031 -0.781041 -0.85045 -0.890699 -0.858185 -0.780638 -0.81935 -0.570209 -0.561171 0.7687003 -0.133708 -0.71169
Topbp1 -1.329324 -0.103138 -1.095239 -1.358816 -1.358463 -0.107692 0.5863765 1.2624568 0.1114349 0.2275064 0.1012762 1.139399 0.599357 -0.21695 1.169866 1.5425386 0.0737214 1.6532661
Acpp 1.0838646 2.008947 0.4023248 0.3080723 1.7927174 0.7425628 -1.19315 -1.062008 0.4789136 -0.083508 0.2355019 0.3462932 -0.262039 -0.844468 -1.153627 -0.080859 -0.870069 -0.869489
Nudt16 1.2518958 0.2259793 0.8979017 2.3335981 0.7133098 1.0757753 -0.939709 -0.736647 -0.937119 -0.980055 -0.918379 -0.771941 -0.877199 -0.650628 -0.294589 1.1517501 -0.21756 -0.326384
Mst1r -1.060126 -0.85966 -0.413747 -1.632027 -0.649037 -1.444665 0.9200339 1.1492045 0.7049688 1.2636615 1.2136557 0.2287356 0.8797433 -0.051478 0.4130082 0.5943687 -0.259266 -0.920214
Traip -1.094407 -1.125322 -1.149219 -1.27075 -1.217228 -1.231939 0.8187574 1.4232108 0.4618298 0.8906922 -0.387722 0.2530905 0.7633835 -0.42629 0.0948426 1.101447 -0.292872 1.617051
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Thsd4 1.0347522 0.648446 1.1944888 1.3920952 1.2406462 1.2811527 -0.995468 -0.536088 -0.80578 -0.1023662 -0.705007 -0.866995 -0.859925 -0.584337 -0.251162 -0.329742 -0.074194 -0.662018
Pygm 0.9930242 2.267214 1.2801549 0.7468428 1.49190654 1.1426156 -0.751626 -0.633556 -0.770152 -0.764411 -0.757762 -0.759178 -0.766443 -0.471051 -0.501949 -0.668503 -0.342546 -0.661749
Crebl2 1.280586 0.5349297 0.5126922 0.4074288 1.2678583 1.2652089 0.7634413 -0.251673 -0.826697 -0.969437 -0.577348 -0.289904 -0.423908 -0.462525 -1.080613 -0.431313 -1.28692



|            |           |           |           |            |           |           |           |           |           |           |           |           |           |           |           |           |            |           |
|------------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|
| Npat       | -0.770141 | -0.519361 | -1.338894 | -1.260192  | -1.489473 | -1.214065 | 1.0645341 | 1.7241359 | 0.1927233 | 0.0995729 | 0.2516669 | 1.1854615 | 1.6615075 | 0.1157858 | 0.3158489 | -0.541603 | -0.00498   | 0.5229217 |
| Pfkm       | 1.0612239 | 2.0019689 | 1.4617287 | 1.0612239  | 1.3741599 | 1.0050125 | -0.8626   | -0.592255 | -0.841437 | -0.828181 | -0.812253 | -0.792569 | -0.813448 | -0.280049 | -0.522508 | -0.564185 | -0.387988  | -0.667935 |
| Gas7       | 1.8300062 | 0.779364  | 0.6176924 | 1.937663   | 0.5493079 | 1.3404666 | 0.1672345 | -0.701936 | -1.226872 | -0.834172 | -0.988024 | -1.24009  | -0.486206 | 0.0231957 | -0.590272 | 0.1872552 | -0.589034  | -0.765529 |
| Tbcl1d4    | 0.5327865 | 1.624022  | 1.179209  | 1.8544376  | 1.0065537 | 1.3747502 | -1.095968 | -0.880672 | -0.631235 | -0.237059 | -0.727799 | -0.186534 | -1.002979 | 0.0511492 | -0.755791 | -0.264345 | -0.861911  | -0.978615 |
| Rnfl125    | 1.255239  | 1.623994  | 0.5305614 | 0.9128877  | 0.4401165 | 1.3949688 | -1.132867 | -0.423131 | -0.789883 | -1.268303 | -1.222368 | -1.052144 | -0.765144 | -0.951691 | 0.1077428 | 1.2276849 | 0.2683162  | -0.065913 |
| Phldb2     | -1.742464 | -0.801934 | -0.729425 | -1.238791  | -0.516491 | -1.04723  | 1.5261484 | -0.401478 | 0.5774475 | 0.6933287 | 1.1202152 | 0.3013623 | 0.2450658 | 0.4221106 | 1.8084082 | -0.263675 | 0.8014131  | -0.744828 |
| Atpla1     | -1.134495 | -0.813074 | -0.565035 | -0.894016  | -0.818414 | -1.136473 | -0.195298 | 0.603001  | 2.3185452 | 0.4128841 | 1.3560269 | -0.015651 | 0.6128578 | 1.7165332 | 0.0416577 | -0.261688 | -0.473158  | -0.754205 |
| Dis3       | -1.050425 | -0.850717 | -1.085345 | -1.1927657 | -1.233994 | -1.240448 | 0.4739361 | 0.4595046 | -0.226338 | 0.8488881 | 0.3434061 | 1.0376509 | 0.2638673 | 0.3117212 | 0.8323546 | 0.1052907 | -0.363106  | 2.5014116 |
| Card10     | -0.936529 | -1.046527 | -0.764733 | -1.38227   | -1.099199 | -1.238542 | 0.3971911 | 1.1081818 | 0.6126748 | 0.7049183 | 0.792593  | 1.0687311 | 0.3552905 | -0.884695 | 0.4170945 | 1.0310111 | -0.840716  | 1.7055245 |
| Mgil       | 2.3450752 | 1.7530358 | 0.303459  | 0.5709421  | 1.1210617 | 1.4092201 | -0.703964 | -0.665813 | -0.587788 | -0.653937 | -0.631152 | -0.6768   | -0.701124 | -0.48654  | -0.543653 | -0.663795 | -0.475978  | -0.71225  |
| Kbtbd12    | 1.0150775 | 2.3520184 | 0.9581747 | 1.0802243  | 0.9469493 | 1.1968653 | -0.844333 | -0.744739 | -0.902524 | -0.876978 | -0.935678 | -0.935678 | -0.348111 | -0.271724 | 0.04299   | -0.273057 | -0.523799  |           |
| BC016579   | 2.158472  | 1.9413239 | -0.023062 | 1.0559378  | 1.4608054 | 0.3504238 | -0.624694 | -0.775827 | -0.662651 | -0.172528 | 0.0175079 | -0.177028 | -0.505591 | -0.861697 | -0.91395  | -1.068047 | -0.490927  | -0.753969 |
| Myh2       | 0.7058163 | 1.2293617 | 1.8642984 | 2.1573894  | 0.687631  | 0.0449596 | -0.676279 | -0.75168  | -0.876981 | -0.876515 | -0.875715 | -0.876482 | -0.878506 | 0.7744727 | -0.608562 | -0.310779 | -0.272831  | -0.259601 |
| Tpsg1      | 0.8967423 | 2.1228505 | 1.6097197 | 0.9653088  | 0.6966833 | 1.3722184 | -0.737024 | -0.065844 | -1.048149 | -0.842166 | -0.784725 | -0.553504 | -0.905271 | -0.376773 | -0.474462 | -0.912928 | -0.345266  | -0.617412 |
| Mamdc2     | 1.6372247 | -0.190063 | 0.7819091 | 2.0531521  | -0.161418 | 1.8782005 | -1.065601 | -0.184146 | -0.860566 | -0.988089 | 0.1203572 | -0.996792 | 0.3612794 | -0.045001 | 0.0125551 | -0.209671 | -0.565275  |           |
| Rac2       | 1.0129455 | 0.5909095 | 1.327863  | 1.8859928  | 0.9239832 | 1.4205749 | -1.121682 | -0.91318  | -0.709077 | -0.992818 | -0.96929  | -0.789923 | -0.845526 | -0.628494 | -0.723134 | 0.7880728 | -0.098845  | -0.158373 |
| Tlf2       | -1.309124 | -1.061335 | -1.177542 | -1.282271  | -1.383483 | -1.061335 | 0.7895847 | 1.5934959 | 1.1804693 | 0.648416  | 0.5208851 | 0.7410875 | -0.000262 | 0.1217718 | 0.340975  | -0.003553 | -0.165687  | 1.4047853 |
| Hsf4       | -0.297902 | -0.963628 | -0.863845 | -0.827189  | -0.662802 | -1.054772 | 1.7417676 | 1.3525228 | -1.277573 | 1.0383025 | 0.4397929 | -0.719974 | -0.340323 | 0.1168292 | 1.8949077 | -0.439973 | 1.7571545  | -0.193296 |
| Duo01      | -0.865299 | -1.017509 | -0.812943 | -1.192766  | -1.042568 | -1.049708 | 2.5077678 | 0.1964401 | 0.4897254 | 0.416579  | 0.6177065 | -0.817878 | -0.211906 | 1.1498318 | 0.1036451 | -0.320462 | -0.7690734 | 0.1502689 |
| Noc41      | -1.206395 | -1.398045 | 0.0309009 | 1.162157   | -0.963299 | -1.581354 | 0.8118241 | 0.6065515 | 0.4699923 | 0.5044233 | 0.5812996 | 0.0743904 | 0.5725806 | -0.221147 | 0.0660168 | -0.295146 | 0.6505339  | 2.4644298 |
| Mif        | -1.078621 | -0.489659 | -1.083825 | -1.129963  | -0.928274 | -1.261041 | 0.3423131 | 2.2268001 | 1.465725  | 0.1227271 | 0.0717831 | 0.0530431 | 1.1847363 | 0.6223042 | 0.9977914 | -0.596471 | -0.550466  | 0.031096  |
| Fbx18      | -1.009068 | -0.98825  | -0.929643 | -0.489297  | -0.788296 | -1.038683 | 3.2106445 | 0.681031  | 0.3246218 | 0.3438689 | 0.4708627 | -0.769961 | 0.4690854 | 0.0204548 | 0.0558056 | 0.198306  | -0.103969  | 0.3424861 |
| Gstt2      | 1.2053236 | 0.3508409 | 1.424145  | 1.2801388  | 1.2397337 | 1.4901733 | -1.486567 | -1.045763 | -0.90256  | -0.951038 | -1.14634  | -0.34306  | -0.624642 | -0.679454 | -0.500095 | 0.4692909 | -0.425489  | -0.205524 |
| Tnxb       | 2.2279426 | 0.3701085 | 1.3740116 | 1.5278444  | 1.3263087 | 0.8628045 | -0.726183 | -0.633178 | -0.727436 | -0.741354 | -0.611191 | -0.749279 | -0.742145 | -0.375559 | -0.682605 | -0.318623 | -0.191923  | -0.733146 |
| Chst2      | -1.364    | -1.777496 | -0.979639 | -1.299298  | -1.215093 | -1.158648 | 0.4548517 | 0.9542058 | 1.5172175 | 0.7219822 | -0.731191 | -0.076029 | 1.2336365 | 0.7020651 | 0.6012542 | -0.733367 | -0.5192506 | 0.9952851 |
| Pus7l      | -0.744109 | -1.445892 | -1.174033 | -0.96123   | -1.011051 | -1.088431 | 1.1783311 | 1.6921292 | 2.244035  | 0.8611638 | 0.0307233 | 0.5409603 | 1.22634   | -0.005792 | -0.130158 | -1.12387  | -0.400936  | 1.718193  |
| Palmd      | 0.0386203 | 1.6370921 | 0.0366292 | 0.5338776  | -0.47804  | 1.4764341 | -0.451497 | 0.5068065 | 0.6009971 | 0.6882979 | 0.3905256 | 0.3199697 | 0.1415839 | 0.3292886 | -1.784525 | -0.34805  | -1.742419  | -1.899117 |
| Ag1        | 0.9145589 | 2.2380412 | 0.5822348 | 1.4772871  | 0.7247931 | 1.5947322 | -0.665176 | -0.612652 | -0.659651 | -0.284115 | -0.788815 | -0.913144 | -0.636285 | -0.083036 | -0.638091 | -0.66735  | -0.396107  | -1.097224 |
| Nudt15     | -0.648098 | -0.846327 | -1.338677 | -1.144689  | -0.846327 | -1.021523 | 1.731399  | 0.1382403 | -0.632503 | 1.1872367 | 0.8012971 | 0.6525679 | 0.6605939 | 0.7802546 | -0.156343 | -0.53897  | -0.61393   | 1.8357993 |
| Snap91     | 1.520239  | 2.579024  | -0.293074 | 0.5074266  | 0.9648733 | 1.593359  | -0.67262  | -0.69416  | -0.520747 | -0.214364 | -0.495932 | -0.580615 | -0.622819 | -0.366907 | -0.715106 | -0.71072  | -0.506461  | -0.767796 |
| Adamts15   | 1.2604247 | 0.7261796 | 0.4988952 | 1.5657204  | 1.2753855 | 1.4551659 | -1.031565 | -0.49456  | -0.914871 | -1.073759 | -1.109377 | -0.840434 | -1.129067 | -0.303319 | -0.232064 | 1.1794924 | -0.240622  | -0.587138 |
| Asprv1     | 0.228039  | 3.4557356 | 0.4508623 | -0.132653  | 0.7940685 | 0.6676841 | -0.712912 | -0.741649 | -0.57824  | -0.229729 | -1.004869 | -0.104869 | -0.15217  | 0.1183488 | -0.694481 | -0.718631 | -0.693204  | -0.851512 |
| Apof6      | -0.442632 | 0.9266911 | 2.5955334 | 1.6709179  | 0.8039665 | 0.7259333 | -0.714581 | -0.736457 | -0.849046 | -0.483399 | -0.802741 | -0.718359 | -0.667631 | -0.621697 | -0.420887 | -0.497071 | 0.0200381  | 0.5764228 |
| Myo6       | 1.0932416 | 2.951684  | 0.0439637 | 0.0953307  | 1.1203206 | 0.8105433 | -1.059764 | -0.461036 | -0.58341  | -0.29473  | -0.479214 | 0.7706089 | -0.443758 | 0.5832707 | -1.00691  | -0.521051 | -0.408328  | -1.755228 |
| Fa2h       | 2.5984722 | 1.7504877 | 0.3821491 | 0.181013   | 1.0419722 | 1.241227  | -0.648948 | -0.587924 | -0.606954 | -0.626564 | -0.57334  | -0.672884 | -0.666645 | -0.428141 | -0.534583 | -0.668759 | -0.513791  | -0.666787 |
| Ndn        | 1.7789311 | 0.7387425 | 0.0995848 | 0.9089249  | 1.409677  | 1.3031818 | -1.231016 | -1.022756 | -1.15586  | -1.182682 | -1.048709 | -0.38054  | -1.181906 | 0.7159953 | 0.2603078 | 0.3989613 | -0.148534  | -0.262306 |
| Rfwd3      | -1.005539 | -0.692718 | -1.007738 | -0.86813   | -1.029645 | -1.064343 | 1.4246074 | 1.7930605 | 0.497106  | 0.0213841 | -0.111017 | -1.352001 | 0.0006928 | 0.7182909 | 1.6613738 | -0.133114 | -0.111362  | 0.9358646 |
| Pank1      | 2.3500525 | 2.2943611 | -0.073388 | -0.045246  | 0.7936352 | 1.264279  | -0.400572 | -0.129411 | -0.787918 | -0.485103 | -0.444866 | -0.606225 | -0.574954 | -0.657699 | -0.575252 | -0.646899 | -0.473674  | -0.801141 |
| Zfp7       | -0.558408 | -0.843886 | -1.304087 | -1.326309  | -1.327885 | -0.872744 | 0.8554082 | 1.9486454 | 0.9128149 | -0.060507 | -0.402693 | 0.6851923 | 0.4012934 | -0.51136  | 0.4681987 | -0.378412 | -0.262621  | 1.7721476 |
| Gabbr3     | -0.879939 | -0.983626 | -0.881908 | -0.806359  | -0.684559 | -0.726312 | -0.312034 | -0.430687 | -0.586156 | 0.3585715 | 0.3536994 | 2.5729732 | -0.634325 | 1.5807801 | 1.5187079 | 0.1810064 | 0.0727248  | 0.2601418 |
| Arhgap39   | 1.7430625 | 0.5556059 | 1.740536  | 1.9484144  | 0.8169281 | 0.5311095 | -0.660218 | -1.364938 | -0.527885 | -0.91312  | -0.011156 | -0.698689 | -0.452957 | -0.41131  | -0.504706 | -0.554637 | -0.974937  | -0.244723 |
| Fuk        | -0.614512 | -1.127374 | -1.07101  | -0.755162  | -0.91813  | -1.111059 | 1.9978874 | 0.9335502 | 1.5499123 | -0.106448 | 0.2410788 | -0.764156 | 0.074407  | 0.5391735 | 0.5768675 | -0.462151 | -0.121819  | 0.1689441 |
| Star1      | 0.7559664 | -0.154721 | 0.9451568 | 1.7108235  | 1.4739208 | 2.0718013 | -0.967521 | -0.867495 | -0.877488 | -0.919379 | -0.863471 | -0.637834 | -0.888702 | -0.149326 | -0.248956 | 0.3806451 | 0.0383298  | -0.801751 |
| Akrc1c14   | 0.8001254 | 0.1768267 | 0.4154737 | 1.9454386  | 1.639135  | 2.2717043 | -0.682518 | -0.653828 | -0.629045 | -0.66489  | -0.675334 | -0.662707 | -0.616017 | -0.582352 | -0.653322 | -0.280455 | -0.490139  | -0.658097 |
| Adra2a     | -0.608227 | -0.488103 | -0.557119 | -0.607312  | -0.73421  | -0.632711 | -0.513752 | -0.368574 | -0.507937 | -0.177641 | -0.569093 | 1.753521  | -0.540382 | 0.1062117 | 1.1713065 | 0.3269681 | 0.1266639  | 0.5556431 |
| St18       | 1.49516   | 0.591467  | -0.367824 | 2.4516621  | 0.3605286 | 1.06779   | -1.04616  | -1.176135 | -0.782646 | -0.051281 | -0.801394 | 0.4460556 | -0.628136 | -0.873004 | 0.7391039 | -0.266782 | -0.058801  | -1.135515 |
| Gadd45gip1 | -0.926598 | -0.839463 | -0.743588 | -0.746342  | -0.943615 | -0.864557 | 2.1931248 | 0.994773  | 0.1956739 | 0.228335  | 0.2003861 | -0.503195 | 0.3598087 | -0.653792 | 0.4060705 | -0.398955 | -0.309454  | 2.3513867 |
| Mnd1       | -1.088561 | -0.38769  | -1.341762 | -1.54381   | -0.193844 | -1.137493 | 0.5451117 | 1.331142  | -1.29842  | 0.1310114 | 2.360209  | 0.0527812 | 0.9735126 | -0.544821 | 0.6443303 | -0.494924 | 0.5758864  | 0.5353407 |
| Recq4      | -1.022084 | -1.08846  | -0.96926  | -1.270037  | -1.12293  | -1.248662 | 1.3104635 | 0.9852496 | 0.4415481 | 0.7744207 | 0.790546  | 0.8354608 | 0.4390519 | -0.420169 | 0.1055378 | 0.0365588 | -0.553242  | 1.9759712 |
| Rpap2      | -1.510416 | -0.807078 | -1.220453 | -1         |           |           |           |           |           |           |           |           |           |           |           |           |            |           |



|           |            |           |           |           |           |           |            |           |           |           |           |           |           |           |           |           |           |           |
|-----------|------------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Ptpn13    | -1.219739  | -0.586691 | -0.965917 | -1.059631 | -0.777574 | -1.222441 | 2.0606477  | 0.328232  | -0.033512 | 0.0887674 | -0.15884  | -0.358193 | 0.5932697 | -0.540839 | 0.6124582 | 1.5950884 | -0.066345 | 1.7112582 |
| ExpH5     | 0.00779781 | 1.7620832 | 0.1091002 | -0.782199 | 0.9151757 | -0.106484 | 0.2904524  | -1.033742 | 0.2963763 | 1.1057352 | 1.5626778 | 1.0917009 | -0.060421 | -0.37585  | -0.799463 | -1.54791  | -1.223365 | -1.281126 |
| 8430429K0 | -1.360736  | -1.022674 | -1.037774 | -0.822883 | -1.169177 | -0.60618  | 1.564286   | 1.3611422 | 0.296668  | 0.2035025 | -0.471193 | 0.6444618 | 0.6019172 | 0.086136  | 0.1701536 | -0.977674 | -0.384972 | 0.200889  |
| Slc41a2   | 1.3378503  | 0.3243545 | 0.2019471 | 1.287718  | 0.9412273 | 1.5353434 | -0.556525  | -0.973015 | -0.955609 | -0.462914 | -0.849476 | -1.111902 | -1.081235 | -0.430996 | -0.418505 | 0.6509141 | 0.4142753 | -0.753453 |
| Myo5a     | 0.99914    | 0.3241997 | 0.1731502 | 0.2170036 | 0.4087514 | 1.7665434 | -0.764172  | 0.2059022 | -0.377315 | -0.709407 | -0.76298  | -0.987381 | -0.732558 | 0.470624  | -0.783352 | 0.1354254 | -0.435672 | -1.700923 |
| 2700049A0 | -0.175493  | 0.2956323 | -1.064983 | -1.252771 | -1.258954 | 1.9279748 | 0.7791969  | 1.3837769 | 0.3028053 | 0.1943138 | 0.0201842 | 0.8055714 | 1.5103388 | 0.1082974 | -0.403019 | -0.354014 | -0.847229 |           |
| Pof1b     | 1.1719883  | 2.4494391 | 0.2025821 | 1.083996  | 1.0688896 | 0.3031779 | -0.518869  | -1.144962 | -1.218149 | 0.352549  | -0.023929 | 0.5388907 | 0.7489553 | -0.10346  | -0.468477 | -1.193668 | -1.31005  | -0.963307 |
| Ppm1h     | 1.0358461  | 0.117381  | 1.1878072 | 1.7561141 | 0.8738508 | 1.6561924 | -1.303     | 0.1366035 | -0.752029 | -1.026815 | -1.162854 | -0.568631 | -1.161763 | -0.795487 | -0.562944 | 0.7602257 | -0.048281 | -1.42218  |
| Tipar     | -0.914274  | 0.969293  | -1.042984 | -1.054289 | -1.339829 | -0.727182 | 2.5978205  | 1.2738321 | 0.372295  | 0.5664449 | -0.236009 | 0.7149202 | 0.6659142 | 0.4590903 | 0.1417582 | -0.099997 | -0.721836 | 0.3136185 |
| Cd300a    | 0.9707878  | 0.5464017 | 1.9944676 | 2.0983339 | 2.049126  | 1.4785073 | -0.76954   | -0.651165 | -0.747741 | -0.902165 | -0.812976 | -0.672673 | -0.791295 | -0.583117 | -0.528892 | 0.0380616 | -0.335875 | -0.536034 |
| Cacna1a   | 3.0716972  | 0.5538656 | 0.2416851 | 0.7719118 | 0.1810467 | 1.4553046 | -1.074834  | -0.636679 | -0.853635 | -0.643089 | -0.815116 | -0.596632 | -0.342808 | -0.485725 | 0.1386522 | -0.480196 | -0.177136 | -0.308315 |
| Tmem109   | 2.2556807  | 1.5252787 | 0.4137766 | 0.7842418 | 1.0179146 | 1.0361363 | -0.791765  | -0.791765 | -1.334952 | -0.620187 | -0.287302 | -0.590021 | -0.931507 | 0.4211188 | -0.965792 | -0.726322 | -0.5587   | 0.1441664 |
| Xpot      | -1.366764  | -0.935189 | -1.146834 | -1.508117 | -1.187279 | -1.070739 | 0.2958934  | 1.3368193 | 0.3527698 | 0.3242287 | -0.062146 | 1.3010175 | 0.715945  | 0.4738612 | 0.275058  | 1.0050726 | -0.34316  | 1.5395395 |
| Tdg       | -1.064097  | -1.208489 | -1.513152 | -1.219566 | -1.122707 | -1.349046 | 1.0171525  | 1.2918727 | 0.5775544 | 1.0880327 | 0.559707  | 0.5775544 | 0.5683932 | -0.557814 | 0.4205959 | 0.9085373 | 0.002734  | 1.0223726 |
| Gns       | 0.8378222  | 0.043122  | 1.6814433 | 2.1101856 | 0.7911583 | 1.4096776 | -1.218579  | -0.780804 | -0.758058 | -0.8363   | -0.73998  | -0.514922 | -0.854305 | -0.396725 | -0.580574 | 0.532509  | 1.082158  | -0.743889 |
| Ttyh2     | 1.4711309  | 0.0910126 | 1.2915791 | 2.3589074 | 0.4499307 | 1.4015706 | -1.123323  | -0.707561 | -0.748567 | -0.824378 | -0.694517 | -0.674727 | -0.843575 | -0.442622 | -0.381675 | 0.1250962 | -0.110368 | -0.637915 |
| Sirt6     | -1.044634  | -1.366894 | -1.385292 | -0.862524 | -0.873999 | -1.776279 | 0.4843402  | 0.8601258 | 0.4027893 | 0.5359219 | 1.0396663 | 0.6903153 | 0.5677106 | 0.17029   | 0.1909864 | 1.0660151 | 0.0537268 | 1.1297348 |
| Mast4     | -0.735797  | -1.309123 | -0.670227 | -1.362544 | -0.954246 | -1.148822 | 0.0101427  | 1.7998705 | 0.4699686 | 0.922623  | 1.4556497 | -0.537507 | 0.1615893 | 0.0822631 | 0.9004668 | 0.029664  | 1.5042737 | -0.618003 |
| Tle6      | -0.314763  | 2.3483865 | 0.5794871 | -0.029814 | 1.2765009 | 1.2701715 | -0.970436  | -0.497955 | -0.458103 | 0.3693985 | 0.1013646 | -0.431439 | -1.130799 | 0.7131774 | -0.403179 | -0.918538 | -0.86287  | -1.089741 |
| BC030867  | -1.103105  | -1.163468 | -0.051985 | -1.166    | -1.071456 | -1.046162 | 2.3129056  | 1.2208061 | 0.186716  | 0.950696  | 0.6499095 | 0.208531  | 0.0354338 | -0.381096 | 0.4294897 | 0.2109551 | -0.242931 | 1.0207148 |
| Cd207     | 1.4037632  | 1.7444409 | 0.2755452 | 1.2970437 | 1.8021147 | 0.9154929 | -0.940066  | -0.845393 | -0.503284 | -0.252595 | -0.338892 | 0.3121157 | -0.665303 | -0.713156 | -0.856804 | -0.977789 | -0.837973 | -0.819224 |
| Gpsm3     | 1.4938583  | 0.0540621 | 0.8255194 | 2.2397902 | 0.1061521 | 1.3349907 | -1.124944  | -0.721581 | -0.869217 | -0.78599  | -1.069642 | -0.406914 | -0.91892  | -0.680896 | -0.617875 | 1.0531721 | 0.0432629 | 0.0550721 |
| Scn7a     | 1.6665435  | 0.9007054 | 0.9180522 | 1.863542  | 1.0771188 | 1.5735245 | -0.924521  | -0.714774 | -0.925881 | -0.907646 | -0.863068 | -0.832111 | -0.926163 | -0.377699 | -0.283642 | 0.21187   | -0.352312 | -0.825441 |
| Grip1     | -1.476278  | -0.837802 | -0.942563 | -1.036724 | -1.170543 | -1.427945 | -1.666269  | 0.2718648 | 0.9404255 | 0.3477836 | 0.3419435 | 1.051033  | 0.9558638 | 1.101954  | 0.8537999 | -0.192975 | -0.339573 | 1.634688  |
| Nup54     | -1.10058   | -1.199591 | -0.935682 | -1.426387 | -1.019408 | -1.045868 | 1.5297503  | 0.2028852 | -0.009568 | 0.1710841 | 0.3316812 | 1.1987415 | 1.3988416 | 0.5236902 | 0.8771925 | -0.192454 | 0.0617295 | 1.8024365 |
| Tespa1    | 0.6014106  | 1.3206119 | 1.3330152 | 1.4423131 | 1.8882816 | 0.8302338 | -0.968774  | -1.360639 | 0.0912328 | -0.680557 | -0.897008 | 0.0110864 | -0.409015 | -0.995177 | -0.935696 | -0.718102 | -0.345048 | -0.204575 |
| Ttc21b    | -0.99382   | -0.924327 | -0.889596 | -0.928999 | -1.072636 | -0.889596 | 2.1688943  | 0.4231334 | 0.4862889 | -0.293489 | 0.3192754 | 1.0728653 | 0.7241321 | 1.8876337 | -0.240439 | -0.956516 | 1.896179  |           |
| Mfsd12    | 1.726583   | 0.2094019 | 0.9772376 | 2.7690648 | 0.1163771 | 0.9464701 | -0.647106  | -0.666561 | -0.707612 | -0.624555 | -0.685272 | -0.643428 | -0.662179 | -0.533025 | -0.631529 | 0.178672  | -0.455979 | -0.666561 |
| BC031353  | 0.2602961  | 0.4846972 | 0.764582  | -0.336124 | 1.1568523 | 1.1820567 | -0.44963   | -0.459704 | -0.000451 | -0.024111 | 0.6960598 | -0.229058 | -0.10864  | 0.038704  | -1.233554 | -0.851182 | -1.55613  |           |
| Ano8      | 0.7159147  | 2.7852466 | 1.0026948 | 0.1022753 | 0.9726162 | 0.7348339 | -0.488394  | -0.539541 | -0.645148 | -0.053186 | 0.5610111 | -0.095935 | -0.27013  | -0.659833 | -1.121492 | -0.781465 | -1.09847  | -1.184116 |
| Lrr1      | -1.072842  | -0.864422 | -1.156753 | -1.166411 | -1.206619 | -1.174307 | 1.8475101  | 0.7275163 | 0.5722173 | 1.4819998 | 0.534896  | 0.6795649 | 0.8326684 | -0.576936 | 0.4477894 | -0.293022 | -0.490026 | 0.9226805 |
| Cactin    | -1.054327  | -1.465383 | -0.288885 | -1.527688 | -1.224178 | -1.571917 | 1.0365105  | 0.4192535 | 0.1974132 | 0.7615664 | 1.043297  | 1.1077247 | 0.5183641 | 0.2598362 | -0.026301 | 0.3613383 | -1.805005 | 1.6338807 |
| NcapH     | -1.159184  | -1.026549 | -1.195688 | -1.406277 | -1.186093 | -1.177826 | 1.2679595  | 1.8532288 | 0.9392083 | 0.6495118 | 0.2849791 | 0.5734001 | 0.6823478 | -0.249217 | 0.3528772 | -0.303815 | 0.1659823 | 0.9360378 |
| Tip3      | 1.6182456  | 2.3707249 | 0.4957687 | 0.2209517 | 1.249351  | 0.68578   | -0.866743  | -1.14483  | -0.688188 | -1.174475 | 0.4894646 | 0.424425  | -0.962797 | -0.800301 | -1.155849 | 0.621989  | -0.596018 | -0.084991 |
| Dhcr24    | 3.192256   | 1.1935878 | 0.167525  | 0.715792  | 0.7886391 | 0.585697  | -0.618527  | -0.764462 | -0.603977 | -0.371899 | -0.391812 | -0.438579 | -0.736864 | -0.554687 | -0.623675 | -0.557759 | -0.365432 | -0.615824 |
| Ar1ad     | -1.159011  | -0.409075 | -0.752851 | -1.084333 | -0.602332 | -0.985879 | 2.051379   | -0.845808 | 1.1458403 | 1.3628866 | 0.600409  | 0.9344977 | 0.4459095 | 1.209742  | -0.960254 | -0.462752 | -0.457628 | 0.0511594 |
| Tmem106a  | 0.7942092  | -0.008558 | 1.6639785 | 1.8941441 | 1.3232806 | 1.5033539 | -0.84818   | -0.813359 | -0.594541 | -0.893861 | -0.937728 | -0.615712 | -0.936133 | -0.628511 | -0.42519  | 0.4804801 | -0.294504 | -0.66317  |
| Cebpa     | 1.494649   | 1.613449  | 0.6079777 | 1.3381206 | 0.8957801 | 0.8820414 | -1.032058  | -1.604897 | -1.040683 | 0.0848944 | 0.2252039 | 0.2300986 | -0.405375 | -0.019711 | -1.425377 | -0.411728 | -1.025073 | -0.408529 |
| 5031414D1 | 0.1226825  | 0.9705748 | 0.7463642 | 0.9528166 | 1.2066795 | 1.7475    | -0.207906  | -1.469397 | -1.439493 | -0.357406 | -1.222376 | 0.1039445 | -1.23908  | -1.13749  | -0.086026 | 1.2103646 | -0.698343 | 0.5010411 |
| Vat1      | 1.7959143  | 0.2747733 | 1.0403355 | 2.1748777 | 0.6288895 | 1.4086632 | -0.218729  | -1.003878 | -0.995346 | -0.796304 | -0.466965 | -0.681322 | -0.647151 | -0.530168 | -0.746918 | -0.109493 | -0.215976 | -0.908472 |
| Igfbf     | 1.0764023  | 0.2767941 | 0.9429922 | 2.3453679 | 0.2257132 | 1.679273  | -0.918205  | -0.655246 | -0.816405 | -0.922404 | -0.954685 | -0.700158 | -0.776892 | -0.769982 | -0.529386 | 0.8392076 | 0.0328694 | -0.384194 |
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| Ncapd3    | -1.232079  | -0.485459 | -0.138908 | -1.48052  | -1.295037 | -1.395114 | 0.6524216  | 1.3644938 | 0.7480866 | 0.7852668 | 0.7719954 | 1.5461373 | 0.8491672 | 0.0830662 | 0.5219518 | -1.557575 | -0.435885 | 0.6141708 |
| Eef2k     | 0.4200428  | 0.7819335 | 0.9410365 | -0.187186 | 0.863049  | -0.116986 | 0.9237739  | -0.544995 | 0.9512941 | 0.7726203 | 1.3931283 | -0.441052 | 0.3932125 | -0.813507 | -1.730382 | -0.525278 | -1.139949 | -1.88072  |
| 1700020L2 | -1.125284  | -0.318525 | -0.582108 | -1.150235 | -1.071804 | -1.268317 | 1.0153303  | -1.02505  | 2.0068647 | 1.083685  | 0.6574024 | 0.4681588 | 0.3957768 | 1.37216   | 0.321461  | -0.639119 | -0.668952 | 0.5285561 |
| Secisbp2  | 1.8994381  | 1.8394602 | 0.4545495 | 0.7785315 | 1.0083907 | 1.656384  | -0.626531  | -0.745053 | -0.691112 | -0.753414 | -0.712992 | -0.891316 | -0.800109 | -0.35549  | -0.368975 | -0.395926 | -0.301092 | -0.994743 |
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| Mitr      | 1.4316049  | 1.0740648 | 0.8207172 | 2.1897827 | 0.7771585 | 1.427945  | -0.845992  | -0.050676 | -0.752664 | -0.824412 | -0.840106 | -0.810587 | -0.71129  | -0.668784 | -0.51954  | 0.0115848 | -0.407621 | -0.845255 |
| Zc3h12c   | -1.364294  | -1.224434 | -0.827679 | -0.696831 | -1.071179 | -0.917466 | -0.2199706 | 1.3891574 | 0.7535677 | 0.8035353 | 0.20718   | 1.3900718 | -0.205327 | -0.846714 | 0.1745717 | 0.5232932 | 0.1567092 | 1.9797659 |
|           |            |           |           |           |           |           |            |           |           |           |           |           |           |           |           |           |           |           |



|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Tdp2      | -0.742011 | -0.432939 | -0.902521 | -1.080826 | -0.888355 | -0.818113 | 1.0608871 | 3.110283  | 0.2908351 | 0.1212525 | -0.235818 | -0.63022  | 0.4556478 | 0.1698737 | 0.7844424 | -0.463671 | -0.336576 | 0.5378277 |
| ApeX1     | -1.202356 | 0.044705  | -0.978784 | -1.129883 | -1.293625 | -1.011134 | 0.6289971 | 1.2256605 | -1.012965 | 0.1246177 | 0.2139304 | 0.6156996 | 0.6198424 | 0.4509788 | 0.5689196 | -0.234511 | -0.109005 | 0.502874  |
| Ddx26b    | 1.1423723 | 1.4508429 | -0.142657 | 0.8945211 | 0.9472045 | 0.729425  | -0.945283 | -0.663362 | -0.181968 | 0.0280355 | -0.850512 | -0.017448 | -1.125585 | 1.9624576 | -1.273791 | -0.803256 | 0.1562927 |           |
| Zfp57     | -0.905323 | 0.3583752 | -1.190816 | -0.224064 | -1.495291 | -0.971987 | -0.807771 | -0.300231 | -0.203515 | -0.76702  | -0.261617 | 0.1782527 | 0.2731797 | 0.653973  | 2.4246412 | 1.0430649 | 0.9403497 | 1.2557996 |
| 5031439G0 | 1.7210198 | 0.2262681 | 0.8743775 | 2.7691833 | 0.9121342 | 0.6925408 | -1.158247 | -0.535524 | -0.778266 | -0.684136 | -0.1847   | -0.642483 | -0.957076 | -0.178527 | -0.929786 | -0.074466 | -0.243546 | -0.107958 |
| Fmnl2     | -1.005363 | -0.939529 | -0.52347  | -0.488296 | -1.06624  | -1.393761 | 0.9341746 | -0.091165 | 0.384492  | -0.329718 | -0.57098  | 0.0703504 | 0.3958498 | 0.160136  | -0.154105 | 0.320964  | 0.6991104 |           |
| Ptpn23    | -0.766567 | -1.439943 | -0.772726 | -0.669744 | -1.495905 | -1.512004 | 1.5692448 | 0.3915274 | 0.460253  | 1.3913893 | 1.2895971 | -0.530723 | 0.2503641 | 0.5949467 | 0.1909432 | 1.2300623 | 0.1078282 | -0.288544 |
| N28178    | 2.8219727 | 1.9737537 | -0.199885 | 0.0539749 | 0.0747433 | 1.090876  | -0.926157 | -0.194008 | -0.285097 | -0.409419 | -0.114487 | -0.820022 | -0.270195 | -0.376951 | -0.77981  | -0.141599 | -0.980857 |           |
| Colec12   | 1.0513214 | 0.2717363 | 0.5904016 | 2.0749507 | 0.3796146 | 1.9256278 | -1.129171 | -0.548521 | -0.973817 | -1.072413 | -0.129667 | -0.793269 | -0.977717 | 0.2231942 | -0.003411 | 0.6830553 | 0.0196393 | -0.691556 |
| Mbn13     | -0.310773 | -0.596103 | -1.532048 | -1.491936 | -1.255132 | -1.524616 | 1.7230884 | 1.106631  | -0.118838 | 0.6276576 | 0.1661277 | 0.0117742 | 0.0919996 | 0.5815036 | 1.5320732 | 0.2538045 | 0.8242954 | -0.08951  |
| Fam110c   | -1.444593 | -0.81609  | -1.125058 | -1.480198 | -1.35478  | -1.250903 | 1.5679267 | 0.5340591 | 1.6104706 | 0.5392162 | 0.186402  | 0.3543005 | 0.3594457 | 0.8182816 | 0.7489142 | 0.2884251 | 0.071806  | 0.3923745 |
| Acaa1a    | 2.1843291 | 1.3564977 | 1.0880824 | -0.015948 | 1.2427874 | 0.8385815 | -0.996345 | -1.183518 | -0.562132 | -1.015241 | 0.4171563 | 0.4144354 | -0.834186 | -0.747882 | -0.719572 | -0.7893   | -0.688988 | 0.0112411 |
| Prickle1  | -0.678834 | -1.161407 | -0.3721   | -0.625122 | -0.164011 | 0.7681524 | -1.391945 | -0.328395 | -0.896354 | -1.021789 | -0.338176 | 0.5024673 | -0.221731 | 2.0251042 | 1.8430777 | 1.026606  | 1.0865758 | -0.05212  |
| Ccdc38    | -0.983531 | -0.189674 | -1.375568 | -0.95179  | -1.196419 | -0.655629 | 1.4593322 | 2.6982197 | 0.3166559 | 0.4346389 | -0.166644 | 0.7043549 | 1.0924635 | 0.4016809 | -0.168656 | -0.640745 | -0.668633 | 0.889942  |
| Fam69b    | -1.310018 | -0.880116 | -1.094403 | -1.047016 | -0.893031 | -0.318965 | 1.2202491 | 2.677289  | 0.3071658 | 0.0381552 | 0.1040205 | 0.0774587 | -0.272585 | -0.326298 | 1.3716671 | -0.199508 | -0.111393 | 0.6573276 |
| Rif1      | -0.892696 | -0.655473 | -0.889644 | -1.132123 | -1.218021 | -1.186736 | 2.5190776 | 0.5952329 | 0.3617128 | -0.1393   | -0.154637 | 0.1486379 | 0.9967033 | -0.369346 | 1.0457856 | -0.181115 | -0.1284   | 1.2803405 |
| Sh3bp4    | -1.124339 | -1.407711 | -0.053097 | -1.161563 | -0.85132  | -1.204754 | 0.8617549 | -0.955646 | 2.296449  | 1.0685665 | 0.4153026 | 0.4127722 | -0.113926 | 0.0486781 | 1.1712101 | 0.2700225 | -0.325529 | 0.7096617 |
| Ska1      | -0.96221  | -1.023615 | -0.105126 | -1.07525  | -1.044249 | -1.03812  | 1.2412931 | 1.7008105 | 0.4786116 | 0.7501951 | 0.4994477 | 0.6820809 | 0.4411275 | -0.247608 | 0.7281122 | -0.789447 | -0.393192 | 0.2020008 |
| Gmp10     | 0.4380244 | 0.471076  | 2.0593576 | 1.866891  | 0.6437617 | 1.432952  | -0.405493 | -0.668924 | -0.167977 | -1.047292 | -0.367302 | -0.327139 | -0.681247 | -0.527114 | -1.042542 | 0.0668065 | -0.14406  | -1.599781 |
| Zbtb20    | -0.799698 | -0.867734 | 0.0664385 | -0.816543 | -0.695631 | -0.873643 | 0.7301492 | 2.1631133 | 1.4097695 | -0.665287 | 0.1865751 | -0.338462 | 1.5498702 | 0.8513849 | -0.249816 | -0.780517 | -0.858622 | -0.743428 |
| Noa1      | -0.970277 | -0.989624 | -0.596804 | -0.938545 | -1.363401 | -1.115297 | 0.4319519 | 1.5835462 | 1.1494137 | -0.062023 | 0.6864015 | 0.623121  | 0.8850199 | 0.3656721 | -0.818261 | 0.2964068 | -0.969238 | 1.8019379 |
| Gramd1c   | 1.1170919 | 2.3570634 | 0.1983288 | -0.542021 | 1.5654591 | 1.0257815 | 0.2100507 | -0.951037 | -0.601204 | 0.2593361 | -0.099186 | -0.234267 | 0.4407407 | -0.940382 | -0.642299 | -1.249522 | -0.104244 | -0.89952  |
| P2ry14    | 0.204462  | 0.7206756 | 2.3230875 | 1.4945207 | 0.6140787 | 1.5316719 | -0.965077 | -0.753772 | -0.035331 | -0.425507 | -1.2182   | -0.767028 | -0.624657 | -0.965976 | -0.580837 | 0.2948569 | -0.263457 | -0.361912 |
| Glib12    | 0.9957908 | 1.5440022 | 0.825376  | 2.2181424 | 1.6160402 | 0.5389543 | -0.729658 | -0.698507 | -0.640432 | -0.545571 | -0.654451 | -0.574351 | -0.570645 | -0.691574 | -0.646199 | -0.780078 | -0.407891 | -0.79895  |
| Npy1r     | 1.6293688 | 1.1288268 | 0.2737615 | 1.66676   | 1.01261   | 1.885042  | -0.428056 | -0.297907 | -0.844886 | -0.7652   | -0.953279 | -0.886758 | -0.661919 | -0.091053 | -0.603366 | -0.408343 | -0.716098 | -0.939504 |
| Arhgap26  | 0.8087064 | 1.4262903 | 0.594629  | 1.6253221 | 0.5193104 | 1.3706514 | -1.287519 | -0.292408 | -0.614935 | -1.498117 | -1.087814 | -0.668512 | -1.113521 | -0.312575 | -0.73005  | 1.0949688 | -0.158858 | 0.3940965 |
| Wtip      | -1.266033 | -1.155308 | -1.246428 | -1.435051 | -1.171454 | -1.271565 | 0.8629889 | -0.057371 | 1.2023669 | 0.3697675 | 0.5371155 | 0.9587472 | 1.6387034 | 0.7639084 | 0.4516018 | 0.324124  | -0.103852 | 0.5765908 |
| 1-Mar     | 0.1532101 | 0.7787599 | 1.5680134 | 1.1655343 | 1.1930971 | 1.2851325 | -1.304727 | -0.980142 | -0.753356 | -0.887337 | -0.172592 | -0.506506 | -0.992499 | -0.586545 | -0.512973 | 1.5606888 | 0.0440662 | -0.151826 |
| Rnf13     | 1.4778324 | 1.2529765 | 0.3707225 | 1.6634118 | 0.6717537 | 1.6723587 | -0.2664   | -0.648129 | -0.984153 | -1.05654  | -0.925939 | -0.8858   | -0.456625 | 0.1355603 | -0.335253 | 0.3942739 | -0.710075 | -1.369978 |
| Sh3t1c    | 1.1042114 | 0.5663313 | 1.0106825 | 2.2337942 | -0.038777 | 2.0161469 | -0.924908 | -0.341469 | -0.772358 | -0.218028 | -0.386848 | -0.382536 | -0.733064 | -1.015062 | -1.13229  | -0.052164 | -0.088655 | -0.953117 |
| Fxyd1     | 1.0058185 | 1.2553698 | 0.9939235 | 1.5221282 | 1.4060904 | 1.4483417 | -1.257488 | -0.744281 | -1.023707 | -0.994125 | -0.102091 | -0.738833 | -1.051359 | 0.2763396 | -0.487877 | -0.114483 | -0.176571 | -0.478804 |
| H2-Aa     | -0.338133 | 1.3504285 | 1.8753613 | 1.3912062 | 1.5393504 | 0.8213629 | -1.085348 | -0.966544 | -0.669499 | -0.811687 | -0.942646 | -0.44309  | -0.968928 | -0.422132 | -0.620966 | 0.5365246 | 0.1434864 | -0.216655 |
| Eepd1     | 0.8452782 | 1.562021  | 1.2973251 | 1.3224993 | 1.4848436 | 1.4355234 | -0.838554 | -0.756885 | -0.792776 | -0.902498 | -0.101177 | -0.370997 | -1.047428 | -0.39621  | -0.699934 | -0.384113 | -0.614331 | -0.142498 |
| Atp13a2   | 1.2233369 | 0.3627067 | 1.1364739 | 2.817053  | 0.8535829 | 1.1751735 | -0.887655 | -0.71128  | -0.687226 | -0.870443 | -0.719772 | -0.903112 | -0.821844 | -0.584146 | -0.6402   | 0.8802199 | -0.30691  | -0.727755 |
| Clnr7     | 1.13766   | 0.1008288 | 1.9797765 | 1.8838638 | 0.5492055 | 1.1651811 | -0.101585 | -0.19429  | -0.741858 | -0.543675 | -0.049424 | -0.95607  | -1.021535 | -0.736456 | -0.413651 | 0.0265329 | 0.2180083 | -1.392513 |
| Cenpt     | -1.152018 | -0.91435  | -0.999362 | -1.078015 | -1.140045 | -1.20783  | 1.4263202 | 0.7468307 | 1.1063629 | 0.8678718 | 0.560398  | -0.44966  | 0.3638761 | -0.433063 | 0.7426014 | -0.654282 | 0.3721567 | 1.8422974 |
| Nop14     | -0.130505 | -0.969769 | -1.122436 | -1.103969 | -0.847929 | -1.157583 | 0.9395401 | 2.0617608 | 0.2132077 | 0.3828832 | 0.4304496 | 0.1921383 | 0.9703309 | 0.1928405 | -0.183861 | -0.091911 | -0.702379 | 1.8606407 |
| Micall2   | -0.439068 | -0.733463 | -0.93977  | -0.707691 | -0.889107 | -0.643049 | 1.4006244 | 1.0399141 | -0.634777 | 0.1835868 | -0.443561 | -0.098516 | -0.198557 | -0.767343 | -0.049817 | -0.048521 | 1.1228881 | 2.8462275 |
| Zscan12   | -0.708416 | -0.491762 | -1.183759 | -0.9751   | -0.902689 | -1.221883 | 2.230519  | 1.3487128 | 0.0228613 | -0.035621 | 0.3114132 | -0.66408  | 1.3319582 | 1.1021045 | 0.2304247 | -0.409365 | -0.718202 | 0.7328829 |
| Dnajc12   | 1.5019074 | 1.5128208 | 1.0118919 | 1.084162  | 0.7402839 | 1.1781415 | -0.701961 | -0.769289 | -0.330278 | -1.177331 | -1.104448 | -0.975929 | -0.512549 | -0.106477 | -0.540635 | 1.0598129 | -0.918186 | -0.032938 |
| Kif15     | -1.204508 | -0.899671 | -1.332799 | -1.432383 | -1.253182 | -1.342519 | 0.8414767 | 1.7000017 | 0.7732519 | 0.9561064 | 0.5279567 | 0.6135154 | 0.7587444 | -0.051052 | 0.2440479 | 0.1236923 | -0.078278 | 1.0555974 |
| Anln      | -1.151163 | -0.795493 | -1.239998 | -1.215497 | -1.144981 | -0.969612 | 0.9703161 | 2.4355395 | 0.5550579 | 0.3779422 | 0.1765057 | 0.8904474 | -0.158046 | -0.03282  | 0.3721043 | 0.8015949 | -0.542071 | 0.7390283 |
| Jmjd4     | -0.298477 | -1.075985 | -1.449214 | -0.991681 | -1.258468 | -1.355744 | 0.948726  | 1.9577633 | 0.9141955 | 0.917541  | -0.273863 | 0.8694005 | 0.3736104 | 0.3510444 | -0.738602 | -0.187839 | 0.248286  | 1.0493058 |
| Tmem149   | 1.0030136 | 2.290516  | 1.452075  | 2.1278679 | 1.3143304 | -0.106027 | -1.112077 | -1.625978 | -0.284839 | 0.2658747 | 0.151563  | -0.006276 | -0.69513  | -0.191898 | -0.793238 | -0.527235 | -0.666089 | 0.5841469 |
| Lpar3     | 1.0795753 | 1.2967794 | 0.0195881 | 1.3599284 | 1.3804285 | 0.8112515 | -1.143628 | -0.931786 | 0.3706537 | 0.7092786 | 0.3540315 | 0.4541882 | -1.084017 | 0.0002132 | -1.161722 | -1.376823 | -0.863941 | -1.208999 |
| Pnpl7     | 0.7988547 | 0.5883972 | 1.5174512 | 1.8379427 | 0.6983019 | 1.6050531 | -1.195325 | -0.748689 | -0.954503 | -0.869477 | -0.933754 | -0.571246 | -0.755485 | -0.169033 | -0.488033 | 0.7160703 | -0.044989 | -1.031575 |
| Hspb6     | 1.1853401 | 1.2666395 | 2.3132894 | 1.3897552 | 1.0086303 | 0.2575975 | -0.626145 | -0.573288 | -1.041529 | -0.798105 | -0.618397 | -1.071161 | -0.819008 | -0.01951  | -0.5794   | -0.62549  | -0.177873 | -0.471345 |
| Vnt4      | -1.377488 | -0.484731 | -0.47055  | -1.396064 | -0.762216 | -1.17964  | 0.7229991 | -0.953159 | 1.0212873 | 1.7068374 | 1.7714749 | 0.3225715 | 0.8357157 | 0.4387356 | 0.4317446 | -0.874113 | -0.208939 | 0.4512335 |
| Phkb      | 1.4404867 | 2.0687295 | 0.1219418 | 0.8336971 | 0.8158635 | 0.9059946 | 0.6176983 | -0.303543 | -0.438755 | -0.68746  | -0.587833 | -1.713389 | -0.366193 | 0.2310062 | 0.408724  | -1.533748 | -0.234057 | -0.200373 |
| Acaa2     | 2.2559861 | 1.4649042 | 0.        |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |



|            |           |           |           |           |           |           |            |           |            |           |            |           |           |           |           |           |           |           |
|------------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|------------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BC022687   | -0.785725 | -1.419978 | -1.536675 | -0.999774 | -1.119349 | -1.118335 | 1.5829104  | 0.9523912 | 1.13006    | 0.7832777 | 0.3091306  | -0.710145 | -0.205048 | 0.8795898 | 0.6124461 | 0.2581148 | 0.2581148 | 1.1289932 |
| 181001911f | -0.789472 | -0.817429 | -0.828672 | -1.235882 | -1.100993 | -1.280543 | 0.785092   | 0.351857  | 2.3398215  | 0.9449957 | 0.5994989  | 0.8698898 | 1.209465  | -0.152104 | -0.155051 | -0.358531 | -0.442512 | 0.742468  |
| Nme1       | -0.368917 | -0.624476 | -1.121177 | -1.324106 | -1.018763 | -1.056524 | -0.600012  | 0.0684268 | -0.484644  | 0.5214954 | 0.1399153  | 0.8424731 | 0.0731846 | -0.48967  | 1.4493248 | 0.0635155 | 0.0588811 | 1.7210721 |
| Lphn3      | 2.2920115 | 1.011145  | -0.265945 | 1.5229254 | 0.8929611 | 1.3180966 | -1.092536  | -0.513336 | -0.778376  | -0.90961  | -0.70608   | -0.62976  | -0.998679 | 0.131505  | -0.134275 | -0.607729 | 0.218727  | -0.751046 |
| Tnfrsf23   | -1.156833 | -1.276991 | -1.004508 | -1.236036 | -1.273001 | -1.17003  | 1.6826185  | 0.4117088 | -0.198879  | 0.8459516 | 0.3886271  | 0.1089346 | 0.6621693 | 0.2696055 | 1.0452766 | 0.5116127 | 1.3033868 | -0.614514 |
| Cdkn3      | -1.087405 | -1.051195 | -1.333984 | -1.397312 | -1.069372 | -1.022584 | 1.5421288  | 0.2544014 | -0.039529  | 1.2687405 | 0.5523053  | 0.7660989 | 0.5523053 | 0.8613838 | -0.463373 | 0.6017738 | -0.376471 | 1.4420872 |
| H2-DMA     | 0.0038964 | 0.7405633 | 1.9216971 | 1.5339152 | 1.3732507 | 0.7397716 | -1.258361  | -1.041506 | -0.604807  | -0.86565  | -0.968005  | -0.3128   | -1.075786 | -0.635426 | -0.646519 | 1.0770814 | -0.077497 | 0.0961806 |
| Slc20a2    | -1.190562 | -0.971894 | -0.931904 | -1.266225 | -1.045886 | -1.200934 | 2.003689   | 1.056263  | 0.5816224  | 0.2752054 | 0.4181729  | -0.8731   | 0.1984456 | 0.2266379 | 0.1667287 | 0.148781  | 1.4485739 | 0.9549857 |
| Cdkn1c     | 1.8074997 | 0.0167951 | 0.9603143 | 1.890464  | 0.3542177 | 2.1818187 | -0.650166  | -0.58278  | -0.634225  | -0.639084 | -0.650094  | -0.59043  | -0.637726 | -0.569516 | -0.563358 | -0.555271 | -0.539493 | -0.589866 |
| Atp8a1     | 1.7525182 | 1.980517  | 0.8535272 | 0.506197  | 1.3616757 | 1.0581183 | -1.247108  | -0.929637 | -0.646802  | -0.650228 | -0.695835  | -0.731866 | -0.922311 | -0.089873 | -0.710569 | -0.266573 | -0.047005 | -0.574747 |
| Dhdn1      | 1.8675556 | 1.6238794 | 0.6908607 | 1.9182087 | 0.5619834 | 0.8573589 | -0.195334  | -0.460002 | -0.943346  | -0.817039 | -0.909179  | -0.781341 | -0.883705 | -0.737914 | -0.5246   | -0.144133 | -0.101544 | -0.397509 |
| Ckap2      | -1.134746 | -0.677075 | -1.212268 | -1.334572 | -1.044273 | -1.134561 | 1.6705207  | 1.4377119 | 0.783327   | 0.7700213 | 0.3109735  | 0.2452922 | 0.4130117 | 0.6854553 | -0.890523 | -0.627911 | 0.6915093 | 1.0481076 |
| Themis2    | -0.354524 | 0.5403618 | 2.5676056 | 1.1650781 | 1.2353179 | 0.6447247 | -1.378573  | -0.576516 | -0.468729  | -1.060857 | -0.765583  | -0.485104 | -1.024504 | -0.580336 | -0.567264 | 0.7088787 | 0.1837503 | 0.2162731 |
| Dzip1l     | -1.187547 | -0.36445  | -0.852982 | -0.889253 | -0.886464 | -1.402397 | -0.550983  | 1.1065339 | 1.503304   | 0.2763886 | 1.1580359  | 0.5335852 | 0.6648362 | 0.147898  | 1.9928303 | -0.865731 | 0.4597577 | -0.547569 |
| Iars       | -0.104914 | -1.457758 | -0.997939 | -1.416715 | -1.138439 | -1.166461 | 0.4703124  | 0.8652242 | 0.8929952  | 1.3664455 | 0.6056202  | -0.595163 | 1.0041951 | -0.500491 | 0.7096311 | 1.1349679 | 0.6976103 | 0.5408785 |
| Egr2       | 2.5322118 | 0.5551327 | 0.3303355 | 1.4644984 | 0.9914084 | 1.2560082 | -0.838951  | -0.527291 | -0.800871  | -0.719602 | -0.718039  | -0.115528 | -0.736644 | -0.802857 | -0.741704 | 0.2276664 | -0.469151 | -0.886624 |
| Darc       | 1.657957  | 0.8203833 | 1.54434   | 1.4787909 | 1.1202668 | 1.2126696 | -1.219038  | -0.825013 | -0.806789  | -0.397589 | -0.994342  | -0.841517 | -0.856938 | -0.694222 | -0.33985  | -0.356621 | -0.144246 | -0.358152 |
| Sirpa      | 0.7410485 | 0.0410151 | 1.2329139 | 2.0730229 | 0.7391818 | 1.5260902 | -1.020166  | -0.811748 | -0.773785  | -0.826745 | -0.653614  | -0.80692  | -0.720823 | -0.617845 | -0.58775  | 0.8370036 | -0.103363 | -0.654219 |
| Ankrd9     | -0.829677 | -0.570026 | -0.520254 | -1.045226 | -0.7886   | -1.154327 | -0.018211  | -0.410695 | 0.3043532  | 0.8035449 | 0.372926   | 2.559486  | -0.175748 | 1.5593862 | -0.191772 | 0.3572672 | -1.224619 | 0.9721962 |
| Ccdc5      | -1.056671 | -0.615739 | -0.819413 | -1.401127 | -1.338969 | -1.186227 | 1.4458462  | 1.6002203 | 0.2696078  | 0.4130639 | -0.649935  | 0.4316634 | 1.5431793 | 0.6536882 | 0.4816341 | -0.502662 | -0.148355 | 0.9891926 |
| Fam101a    | -0.8896   | -0.798902 | -1.204842 | -0.829844 | -0.506542 | -0.401192 | 0.0054441  | -0.836449 | -0.754433  | 0.244452  | 0.1528028  | 1.1919256 | 0.2536375 | 2.7916453 | 1.4743681 | -0.133324 | 0.0408102 | -0.163959 |
| Nin1j      | 0.7390737 | 0.5197672 | 0.8862879 | 1.8054874 | 0.6718117 | 1.8082933 | -0.0951009 | 0.3914956 | -1.228108  | -1.187867 | -0.393923  | -1.168197 | -0.597144 | -0.187703 | -0.503745 | 0.9376004 | -0.355266 | -0.497355 |
| Snn        | -1.219693 | -0.875225 | -1.163504 | -1.395723 | -0.705398 | -1.42207  | -0.001235  | 0.506185  | -0.011514  | 2.1592837 | 0.2851517  | -0.079222 | -0.225901 | 0.9657694 | 0.3959577 | 0.7104815 | 1.2256614 | 0.8929204 |
| Ccdc138    | -1.018572 | -0.781519 | -0.878703 | -0.981985 | -1.045449 | -0.931274 | 2.0582397  | 0.1884556 | 1.7615116  | 1.1841706 | 0.12217271 | 0.4039849 | 1.1133304 | 0.1946078 | -0.087275 | -0.762007 | -0.444869 | 0.4048249 |
| Rnmt1l     | -0.3223   | -0.939432 | -1.026945 | -0.903195 | -1.198133 | -1.387572 | 0.1523536  | 0.3154991 | -0.4648836 | 1.2738706 | 0.1005477  | 0.8396521 | 0.6899284 | 0.6344504 | -0.15754  | -0.569805 | -0.496187 | 2.5774259 |
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| 2010002N0  | -1.538212 | -1.240364 | -0.907365 | -1.247484 | -1.137998 | -0.94691  | -0.04311   | 0.7908059 | 1.5904149  | 0.8033286 | 1.1597959  | 0.8086278 | 1.2319341 | -0.583931 | 0.793911  | -0.086268 | 0.526315  | -0.018498 |
| 2410066E1  | 0.3753608 | 0.2717626 | 0.6086455 | 1.4582414 | 0.9911481 | 1.9009017 | -1.426346  | 0.8528131 | -0.095002  | -0.352664 | -0.71518   | -0.965125 | 0.5828504 | -0.870795 | -0.384874 | 0.4739904 | -0.101831 | -1.686897 |
| Camk4      | -0.695591 | -0.738801 | -1.279117 | -0.933745 | -1.034481 | -0.770625 | 1.4319597  | -0.191129 | 0.5531363  | 0.1113815 | 0.1901303  | 2.6216268 | 0.5971662 | 0.785806  | -0.285126 | -0.460679 | -0.792916 | 0.8273047 |
| Rbm24      | 1.2337557 | 1.7660802 | 0.720001  | 1.1739153 | 1.4509987 | 0.6272844 | -1.031206  | -1.009862 | -1.008485  | -0.851776 | -1.007616  | -1.006087 | -1.085017 | -0.100055 | -0.494972 | 0.8046635 | -0.174284 | -0.007344 |
| Cd84       | 1.1681676 | 0.4371554 | 1.0903702 | 2.3698056 | 0.303942  | 1.6422894 | -0.852725  | -0.738662 | -0.760738  | -0.812627 | -0.919292  | -0.693128 | -0.775141 | -0.644656 | -0.522594 | 0.5793287 | -0.286307 | -0.687262 |
| 5033430I15 | -0.98324  | -1.088485 | -0.981374 | -0.846597 | -0.798259 | -0.937941 | 0.8660437  | 2.1049089 | 0.5568721  | 1.8621247 | 0.9239245  | 0.276131  | 0.7954185 | -0.39981  | -0.741305 | -0.836689 | -0.343657 | 0.2870177 |
| Spon1      | -0.747278 | -0.896655 | -0.346002 | 0.3583087 | -0.025001 | 0.0797251 | -1.090143  | -0.873043 | -0.740252  | -0.78952  | -0.554889  | -0.080183 | -0.98672  | 1.2736328 | 1.7260091 | 1.9455818 | 1.6001599 | 0.1482689 |
| Plkthg6    | -0.802318 | -0.561304 | -0.704907 | -1.17224  | -0.729315 | -1.17224  | -0.228893  | -0.583424 | 0.2242072  | 0.9377269 | 0.9008905  | 0.1189933 | 0.3351274 | 1.9937488 | 0.953409  | -0.353073 | -0.02666  | 0.3250575 |
| Pde4dip    | 1.106342  | 1.2001015 | 1.6811339 | 1.430552  | 1.4076477 | 1.0523303 | -0.99131   | -0.693907 | -0.597269  | -0.916873 | -0.871626  | -1.07275  | -1.01989  | -0.261494 | -0.284163 | -0.208127 | -0.247972 | -0.712726 |
| Slc43a2    | 1.2258712 | 0.242187  | 0.9323429 | 1.0601233 | 0.9570695 | 0.9500284 | -1.329365  | -0.430605 | 0.6960298  | -1.061652 | -0.783659  | -1.137539 | -0.598464 | -0.501245 | -1.102475 | 0.3253925 | 0.6139518 | -0.990475 |
| Slamf7     | 0.5579266 | 0.335975  | 0.9332741 | 1.7342515 | 0.3306792 | 2.07946   | -0.849503  | -0.743452 | -0.572954  | -0.710857 | -0.707401  | -0.435267 | -0.631296 | -0.692336 | -0.483583 | -0.512172 | -0.311508 | -0.531806 |
| Rcnp       | 1.2764539 | 1.013751  | 0.2535071 | 2.4007218 | 0.9282469 | 1.2925736 | -0.8057    | -0.646925 | -0.987177  | -0.782808 | -1.044698  | -0.2518   | -0.597929 | -0.521489 | -0.994118 | 0.3107651 | -0.194819 | -0.648317 |
| Kan7       | 1.9803742 | 2.0918954 | 1.2066318 | 0.8529305 | 0.2389469 | 0.7083871 | 0.2421794  | -0.575693 | -0.812448  | -0.573194 | -0.866777  | -1.158456 | -0.711944 | -0.482533 | -0.711123 | -0.782035 | -0.782558 | 0.1354171 |
| BeD3       | -0.963254 | -1.445139 | -0.788615 | -1.405755 | -1.311889 | -1.355491 | 1.2962009  | 1.2029997 | 0.6882011  | 1.1652372 | 0.7708203  | 0.5209262 | 0.646748  | -0.113299 | 0.1257585 | -0.281915 | 0.0337948 | 1.2146696 |
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| Tlcd2      | 1.9859547 | 1.9761902 | 0.907232  | 1.1079104 | 1.0257747 | 1.5443685 | -1.007482  | -0.298547 | -0.966445  | -0.541741 | -0.519496  | -0.556226 | -0.722579 | -0.200142 | -0.445142 | -0.728084 | -0.477577 | -0.876759 |
| F11r       | -0.876542 | -0.585801 | -0.662351 | -0.968831 | -0.870569 | -1.134218 | 0.9784885  | -0.118069 | 0.3608296  | 0.8283693 | -0.49165   | 0.8109587 | 0.5765192 | 2.8216363 | -0.173608 | -0.258884 | 0.4831096 | 0.1806135 |
| Hrc        | 0.974332  | 2.123012  | 1.4062528 | 1.3857605 | 1.0708605 | 0.835862  | -0.826602  | -0.785611 | -0.448862  | -0.786243 | -0.807968  | -0.828322 | -0.882854 | -0.043718 | -0.532666 | -0.451838 | -0.479961 | -0.451444 |
| Aox4       | 1.023384  | 2.999292  | 0.2731038 | -0.101246 | 1.5348496 | 0.6127521 | -0.798485  | -0.719953 | -0.443097  | -0.22849  | 0.3788923  | -0.656668 | -0.533261 | -0.491962 | -0.60515  | -0.875179 | -0.604017 | -0.524693 |
| Ncapd2     | -1.459408 | -1.084202 | -0.888822 | -1.491324 | -1.014675 | -1.088226 | 1.5960408  | 0.762462  | 1.8883706  | 0.4200663 | 0.7663992  | 0.4663913 | -0.293276 | 0.2135284 | 0.4773333 | -0.017644 | 0.0869453 | 0.622462  |
| Sema7a     | -0.851604 | -0.724117 | -0.339034 | -0.751347 | -0.864772 | -0.438218 | -0.454949  | -0.116014 | -0.407417  | -0.356301 | -0.526803  | 0.4117428 | -0.413681 | -0.200847 | 1.6368324 | 0.3120467 | 1.0418741 | 0.3408071 |
| Iffo1      | 0.9710441 | 0.3016926 | 0.6488494 | 2.3832724 | 0.6319124 | 1.0801908 | -1.031491  | -1.316416 | -0.357481  | -0.518162 | -0.480608  | -0.988482 | -0.85099  | -0.387496 | -0.920808 | 1.0889226 | 0.3164396 | -0.470388 |
| Nop2       | -1.152777 | -1.194132 | -1.07826  | -1.284374 | -1.188062 | -1.325775 | 1.2344768  | 1.5503637 | 0.7196678  | 0.6147913 | 0.5129893  | 0.5258187 | 0.237858  | -0.156789 | 0.2972012 | 0.1326526 | -0.09046  |           |



|            |           |           |           |           |           |            |           |           |           |           |            |           |           |           |             |           |           |           |
|------------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-------------|-----------|-----------|-----------|
| Plcl2      | 0.7555613 | 0.8100699 | 1.294169  | 1.9390568 | 1.0830339 | 1.5966749  | -1.14505  | -0.862138 | -0.671705 | -0.838077 | -0.958169  | -0.713278 | -0.869547 | -0.614383 | -0.662888   | 0.4586081 | -0.210295 | -0.391642 |
| Prc1       | -1.386402 | -0.956517 | -1.253022 | -1.427068 | -1.246065 | -1.068378  | 0.8554886 | 2.1292804 | 0.9675622 | 0.6306772 | 0.410577   | 0.3468284 | 0.0916955 | 0.551609  | 0.5694769   | 0.2257981 | 0.0244057 | 0.5340627 |
| Cnst       | 0.6988432 | 1.9888456 | 0.7734979 | 0.2778551 | 1.6193144 | 1.0497553  | -0.614205 | -1.400988 | 0.9607682 | -0.218701 | -0.184942  | -0.211069 | -0.233309 | 0.2365893 | -0.123662   | -0.477649 | -0.640292 | -1.12904  |
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| Pdk2       | 0.8765631 | 1.3962905 | 2.0667325 | 1.4315189 | 1.3011706 | 1.0762322  | -0.991545 | -0.899988 | -0.567013 | -0.832769 | -0.604193  | -0.740557 | -1.137331 | 0.1302272 | -0.739559   | -0.413003 | 0.2733935 | -0.657561 |
| L9         | 0.7946853 | 0.510205  | 1.366316  | 1.2634915 | 0.6147994 | 1.4515902  | -0.653579 | -0.801754 | -1.233526 | -1.100357 | -0.245117  | -0.820151 | -0.969884 | 0.0611035 | -0.423017   | 1.7213868 | -0.299645 | -0.256904 |
| Pgcp       | 0.7615445 | 0.3529076 | 1.4723339 | 1.4149775 | 1.3569599 | 1.9696282  | -1.052002 | -0.868908 | -0.990569 | -0.970325 | -0.953526  | -0.258108 | -0.878391 | -0.608233 | -0.270034   | 0.2885942 | -0.221019 | -0.545831 |
| Arhgap18   | 1.4073628 | 1.0056444 | 0.4407039 | 1.1367621 | 0.8631548 | 2.4314305  | -0.649219 | -0.661538 | -0.70868  | -0.842115 | -1.155604  | -0.001818 | -0.995781 | -0.478646 | -0.806308   | -0.00294  | -0.257101 | -0.730308 |
| St6galnac5 | 1.1807055 | 0.8515063 | 1.5320482 | 0.9510849 | 0.7135251 | 1.239169   | -1.309776 | -0.76677  | -0.979341 | -0.895093 | -1.259316  | -0.748579 | -1.281607 | -0.306963 | 0.6258453   | 0.3324498 | 0.8116218 | -0.690511 |
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| Eme1       | -1.290807 | -0.740226 | -1.216673 | -1.378764 | -1.337683 | -1.061298  | 0.7982117 | 1.4226204 | 0.1936422 | 0.621298  | 0.369649   | 0.1391514 | 0.5973799 | -0.094475 | 1.5024897   | -0.176936 | 0.0424597 | 1.6099606 |
| Anpep      | 1.680969  | -0.009442 | 1.525412  | 2.7273484 | 0.1812346 | 0.3646862  | -0.850287 | -0.731912 | -0.567905 | -0.444546 | -0.483193  | -0.76838  | -0.606215 | -0.530825 | -0.548822   | 0.1325359 | -0.31262  | -0.758038 |
| Cpa4       | 2.4272127 | 1.1752467 | 0.3130506 | 0.1625811 | 1.2717782 | 0.7258254  | 0.0780168 | -1.073502 | -1.180182 | 0.0443337 | -0.221607  | -0.308851 | -0.001267 | -0.563386 | 0.1856242   | -1.248648 | -1.138248 | -1.097979 |
| Zfp503     | -0.60921  | -0.872301 | -0.578493 | -0.85863  | -0.847644 | -1.125824  | 1.505553  | -0.63679  | -0.512705 | -0.016394 | 0.7675452  | 1.0404766 | -0.726872 | 2.6825864 | 0.5043694   | 0.4077834 | -0.140624 | -0.018826 |
| Sptlc3     | 2.7438908 | 1.7346418 | -0.033159 | 0.549892  | 0.6679979 | 0.5174132  | -0.364847 | -0.633005 | -0.891724 | -0.356441 | -0.50154   | 0.4990197 | -0.132961 | -0.096009 | -1.049321   | -0.851521 | -0.827619 | -0.974709 |
| F13a1      | 1.4968745 | 0.882301  | 0.4558651 | 0.9060333 | 2.000701  | 1.796809   | -0.796979 | -0.662482 | -0.801659 | -0.84149  | -0.829566  | -0.829641 | -0.769677 | -0.434213 | -0.556512   | 0.2091024 | -0.481751 | -0.743717 |
| Gpr126     | 1.0297412 | 1.5749189 | 0.4510037 | 1.3017284 | 0.4888829 | 0.9063833  | -1.416138 | -0.964854 | 1.5379605 | 0.1396852 | -0.315649  | -0.05456  | -0.425194 | -0.946992 | -0.101057   | -0.697568 | -0.76566  | -1.196363 |
| Gipc2      | -0.74625  | -0.283194 | -0.807997 | -0.77326  | -0.863542 | -0.838794  | 2.077788  | -0.286366 | -0.568836 | 0.7445561 | -0.100317  | -0.446897 | -0.269853 | 2.466889  | -0.523365   | -0.483496 | 0.6784255 | 1.024507  |
| Whrm       | -1.324873 | -1.108287 | -0.230935 | -0.671977 | -1.084925 | -0.965399  | 0.2392962 | 0.2514139 | 2.1014053 | 1.225736  | -0.5575999 | -0.62567  | 1.4102021 | -0.846311 | -0.051519   | -0.350569 | 0.0873178 | 1.3511544 |
| Akna       | 0.6640872 | -0.38768  | 1.7284614 | 1.9354253 | 1.1237892 | 0.7232182  | -1.337151 | -1.098286 | -0.560679 | -0.817774 | 0.759457   | -0.467591 | -0.912162 | -0.641963 | -0.820126   | 1.0113766 | 0.076004  | -0.160353 |
| Fanci      | -1.262341 | -1.088485 | -0.924148 | -1.346313 | -1.116582 | -1.282179  | 1.3704729 | 1.6149078 | 0.9408156 | 1.0031488 | 0.5491374  | 0.5131238 | 0.7344317 | -0.213945 | 0.2241681   | -0.254138 | -0.397959 | 0.9331829 |
| Nlrc4      | 0.2669043 | 0.1829957 | 1.1713761 | 1.949626  | 0.7153734 | 1.6759896  | -1.481561 | -0.105839 | -0.476434 | -0.726174 | -1.136485  | -0.782752 | -0.869303 | -0.380459 | -0.056973   | 1.2493624 | -0.089713 | -0.166527 |
| 1110008P1  | 2.8845704 | 0.8940073 | -0.446079 | 1.9661711 | 0.6066132 | 0.4670789  | -0.864447 | -0.924176 | -0.415586 | 0.2981287 | -0.266798  | -0.556329 | 0.3571679 | 0.0293383 | -0.771431   | -1.138172 | -0.295899 | -0.618159 |
| Orm1       | 3.4058364 | 0.9255454 | -0.01738  | 0.4533392 | 0.6959603 | 0.693812   | -0.510096 | -1.172523 | -0.591382 | -0.53649  | -0.735284  | -0.636827 | -0.378019 | -0.580093 | -0.593106   | 0.692734  | -0.514975 | -0.632865 |
| Daglb      | 1.2093364 | 0.446943  | 1.190737  | 2.4400147 | 0.6023622 | 1.5068993  | -0.855685 | -0.826356 | -0.610838 | -0.833777 | -0.840633  | -0.638413 | -0.656641 | -0.555376 | -0.549004   | 0.0331391 | -0.410512 | -0.717788 |
| Metrn1     | 0.9648874 | 1.2406292 | 0.9320379 | 1.8921038 | 0.5352016 | 1.3001591  | -1.378399 | -0.955797 | -1.372803 | -0.138493 | -0.404461  | 0.2678787 | -0.827159 | -0.598537 | 0.3833111   | -0.109603 | -1.340922 | -0.390036 |
| Suv39h1    | -1.274236 | -1.277881 | -0.862952 | -1.103878 | -1.095959 | -1.043651  | 0.3444957 | 1.7694194 | 0.1724639 | 0.54314   | 0.2882886  | 0.4451963 | 0.2154479 | -0.335853 | 0.909086    | 0.1427695 | -0.21149  | 2.1055759 |
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| Tgfb2      | -0.960842 | -1.184635 | -1.052084 | -1.109457 | -0.704356 | -0.830003  | -1.203618 | -0.37329  | 1.3731696 | 1.3349093 | 1.4976698  | 0.3798824 | 1.0760712 | 1.1717332 | 0.444748    | -0.302289 | 1.1962947 | -0.507904 |
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| Rftn1      | 0.9102986 | 0.0599602 | 0.9002555 | 2.420322  | 0.5559875 | 1.0747491  | -1.221904 | -0.947929 | -0.906424 | -1.029279 | -0.925293  | -0.51646  | -0.990694 | 0.0131798 | -0.214399   | 1.2014157 | 0.0255756 | -0.410262 |
| Atp6v0e2   | 1.2181389 | 0.5017778 | 1.4735325 | 1.8765512 | 0.7571809 | 1.562418   | -0.808057 | -0.889968 | -0.790045 | -0.973001 | -0.951556  | -0.761429 | -0.82767  | -0.656794 | -0.440095   | 0.807645  | -0.319279 | -0.55277  |
| C130074G1  | 0.6235315 | 1.465575  | 0.2679727 | 1.1836731 | 1.5794564 | 2.0664126  | -1.420817 | -1.105771 | -0.357723 | -0.729067 | -0.005504  | -0.573328 | -0.165376 | -0.410257 | -0.991544   | -0.796703 | -0.230916 | -0.351886 |
| Exosc2     | -1.081007 | 0.0073135 | -1.121765 | -1.242008 | -1.162578 | -0.667704  | 0.9054819 | 2.7904676 | 0.2147832 | -0.181736 | -0.001126  | 0.0829004 | 0.2308098 | 0.482955  | -0.024303   | 0.930388  | -0.243837 | 1.2170287 |
| Wfs1       | 1.8715674 | -0.056623 | 0.9066612 | 2.8264169 | 0.0724627 | 0.9060594  | -0.684918 | -0.612606 | -0.677926 | -0.66009  | -0.614269  | -0.539958 | -0.598568 | -0.517977 | -0.492569   | -0.063001 | -0.466546 | -0.598117 |
| Ntrn       | 1.287947  | 2.5262    | 0.0467778 | 0.6609961 | 1.0660686 | 0.2890643  | -1.025266 | -0.849614 | -0.762    | 0.5889662 | -0.183076  | 0.7579701 | -0.301954 | -0.231635 | -1.09478    | -1.025674 | -1.055381 | -0.694638 |
| Znfx1      | -0.189098 | -0.078402 | 3.3227718 | 0.841987  | 0.9387422 | 0.7327308  | -0.905052 | -0.933441 | -0.116417 | -0.280281 | -0.48493   | -0.141118 | -0.85246  | -0.536705 | -0.572415   | 0.4230694 | -0.016955 | -0.793198 |
| Ncam1      | -0.687062 | -0.693879 | -0.689346 | -0.602139 | -0.189547 | -0.129705  | -1.037987 | -0.635301 | -0.583391 | -0.718336 | -0.311452  | 0.4585562 | -0.834979 | 2.1105705 | 1.6688959   | 1.8132403 | 1.0911607 | 0.0336066 |
| Prx1       | 0.4545357 | 0.1901687 | -0.872923 | 0.0582606 | 0.8391439 | 0.4914977  | -1.418334 | -0.90684  | -0.618775 | -0.723538 | -0.729584  | -0.534523 | -1.097184 | -0.090091 | -0.606991   | 1.1670976 | 0.1232312 | -0.260562 |
| D2Wsu81e   | -0.906435 | -0.78061  | -1.053272 | -1.209865 | -1.143392 | -0.1019474 | 2.0284546 | 0.6289676 | -0.428396 | 1.464484  | 0.3899541  | 0.9625603 | 0.3788197 | -0.111173 | 0.5485613   | -0.11581  | -0.375491 | 2.0601513 |
| 57305281i  | -1.300927 | -0.910123 | -1.355216 | -1.164133 | -1.121471 | -0.96974   | -0.067737 | 2.2181176 | -0.130238 | 0.4867409 | 0.2799145  | 0.909091  | 0.2863139 | 0.2425333 | 0.2335944   | 0.3037467 | 0.4863222 | 1.5758924 |
| Ncoar      | 0.3869076 | 1.032394  | 1.0131446 | 1.2594149 | 0.7972797 | 2.1585973  | -1.624878 | -0.453696 | -0.195615 | -1.143274 | -1.17686   | 0.0276546 | -0.957242 | -0.458741 | -0.35812    | 0.7307483 | -0.524067 | -0.504549 |
| Lmbrd2     | 2.6382218 | 1.5472709 | -0.007784 | 0.9408749 | 0.5263982 | 0.9433614  | -0.284703 | -0.023816 | -1.491606 | -0.603621 | -0.587434  | -0.069362 | -0.206647 | -0.973159 | -0.69216    | -0.642771 | -0.804639 | -0.208362 |
| Prkrip1    | -0.689823 | -0.548073 | -0.512537 | -1.155338 | -0.969979 | -0.980976  | 0.483073  | 0.130366  | -0.400058 | 0.0195813 | -0.531754  | 0.2227853 | 0.7756087 | 0.7058829 | 0.2563913   | -0.233707 | -0.660084 | 0.933536  |
| Orai2      | -1.454149 | -1.163809 | -1.093193 | -0.93258  | -1.026325 | -1.258395  | 0.9376616 | 1.6168666 | 0.3592967 | 0.3602398 | 0.7723662  | -0.564209 | -0.271654 | -0.174723 | 0.8458237   | 0.7110436 | 1.4121408 | 0.9162472 |
| Exo1       | -0.915749 | -0.984114 | -0.132772 | -1.142909 | -1.268111 | -1.166993  | 1.252635  | 0.4755701 | 0.279194  | 0.884894  | 0.0388266  | 0.6489021 | 0.9777892 | -0.139757 | 0.2501274   | -0.617873 | 0.1579709 | 2.308643  |
| Fbx15      | -1.366506 | -1.026932 | -1.035416 | -1.199154 | -1.121932 | -1.156617  | 2.0513294 | 1.3525355 | 0.5935941 | 0.3676047 | -0.12443   | -0.143298 | 0.9530262 | 0.4670467 | 0.10561875  | 0.0726447 | 0.3847457 | -0.12443  |
| Alkbh4     | -1.204277 | -1.040483 | -0.855321 | -0.927205 | -1.14736  | -1.326787  | 1.4193392 | 1.164818  | 1.1865737 | 1.2998839 | 0.6877481  | -0.028845 | 1.4538334 | -0.199549 | 0.0204828   | -0.808774 | 0.126113  | 1.1798092 |
| Dnt1p2     | -1.11412  | -1.135907 | -1.277542 | -1.166985 | -1.407459 | -1.215765  | 0.4350239 | 1.5109469 | 0.314397  | 0.1623022 | -0.277581  | 0.4950212 | 0.5880398 | 0.1650796 | 0.7011076</ |           |           |           |



|           |           |           |           |           |           |           |           |            |            |           |           |            |           |            |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|------------|-----------|-----------|------------|-----------|------------|-----------|-----------|-----------|-----------|
| Mybbp1a   | -1.166615 | -1.285436 | -0.87592  | -1.111824 | -0.991832 | -1.190315 | 0.2195074 | 1.8577508  | 0.5923301  | 0.5123515 | 0.6652278 | 0.0067684  | -0.113813 | -0.035462  | 0.5309312 | -0.071933 | 0.3059717 | 2.1523121 |
| Gtpbb10   | -0.993878 | -0.375581 | -1.228601 | -0.739694 | -1.182805 | -0.509483 | 1.1604188 | 1.9671945  | -0.419181  | -0.20614  | -0.573913 | -0.460186  | 1.2263265 | 0.5489702  | 0.4476765 | -0.462761 | -0.180247 | 1.9818836 |
| Blvrb     | 1.0337434 | 0.7640859 | 0.8231068 | 2.3333678 | 0.8807613 | 1.2326652 | -0.204826 | -1.106293  | -0.708412  | -0.104427 | -0.992941 | -0.332541  | -0.877728 | -0.139977  | -0.634811 | 0.6104222 | -0.629637 | -1.00656  |
| AS30021E2 | -0.709014 | -0.785562 | -0.803617 | -0.816127 | -0.782006 | -0.644757 | -0.016479 | 0.0132347  | -0.636875  | 0.3718328 | -0.733552 | 0.1333687  | -0.680051 | -0.085313  | 1.1286064 | 0.7293962 | 1.5074994 | 2.8094144 |
| 9-Mar     | -0.958074 | -0.622114 | -1.136921 | -1.157202 | -0.896783 | -1.471722 | 1.8994002 | 0.5476719  | -0.432349  | 0.5963727 | 1.1408996 | 1.3206693  | 0.1783787 | -0.161131  | 0.1603525 | 0.088274  | -0.580792 | 1.2160311 |
|           | -1.173717 | -1.386185 | -0.84631  | -0.796511 | -1.386185 | -0.895078 | 1.3927704 | 0.5051029  | 0.1929305  | 0.560487  | 0.4878825 | 1.1657852  | 0.5195367 | -0.123732  | 0.248838  | 2.3158486 | -0.090533 | -0.134799 |
| Pvr       | 0.7264512 | 0.4064609 | 1.5639641 | 1.6694285 | 0.6796385 | 1.8258684 | -1.053011 | -0.743127  | -0.786156  | -0.972678 | -0.963679 | -0.873555  | -0.813325 | -0.669243  | -0.318554 | 0.9448467 | -0.133595 | -0.489779 |
| Tlr8      | 0.1812503 | 0.1780928 | 1.5245782 | 1.6687551 | 0.8351971 | 1.4217332 | -1.273902 | -0.98255   | -0.630811  | -0.963135 | -1.106752 | -0.45076   | -0.988271 | -0.552361  | -0.700791 | 1.2231544 | 0.1080566 | -0.031486 |
| Gm885     | 0.2805434 | 0.0566754 | 0.2032938 | 1.0410199 | 1.4606414 | 2.7970701 | -1.145441 | -0.695069  | -0.788993  | -0.753016 | -0.619056 | 0.0262147  | -0.877643 | 0.6846028  | -0.205997 | -0.438587 | -0.029909 | -0.996351 |
| Pitpnm3   | -1.166183 | -0.920846 | -0.39425  | -1.189831 | -1.006638 | -1.266995 | 2.180958  | 0.261343   | 1.5464577  | 0.5195562 | 1.1772085 | -0.234181  | 0.4764628 | 1.0396249  | 0.0109997 | -0.303379 | -0.299382 | -0.430927 |
| C3ar1     | 0.6368419 | 0.2152624 | 1.3706197 | 2.2122679 | 0.6358251 | 1.6370219 | -1.02461  | -0.891759  | -0.752381  | -0.868586 | -0.934254 | -0.828292  | -0.770051 | -0.431947  | -0.384828 | 0.8493724 | -0.119722 | -0.55078  |
| Gstm2     | 1.6873344 | 0.5814854 | 0.3659634 | 1.5978309 | 1.4452212 | 1.4730724 | -1.147597 | -1.204154  | -0.913273  | -0.646431 | -0.760854 | -0.098626  | -1.153172 | 0.3502278  | -0.494427 | -0.051013 | -0.393254 | -0.638334 |
| Apobec1   | 0.457403  | 0.1841802 | 1.3998834 | 2.1592829 | 0.8618624 | 1.7392714 | -0.727416 | -0.67461   | -0.775846  | -1.05257  | -1.05013  | -0.621937  | -0.956977 | -0.587197  | -0.675911 | 0.5526879 | 0.1422067 | -0.374184 |
| Tmem51    | -1.138615 | -1.00776  | -0.897307 | -1.031808 | -1.158611 | -1.126882 | 0.786494  | -0.572731  | 1.3409815  | 1.3227083 | 0.4866941 | 0.4487584  | 1.3258218 | -0.782596  | 0.0765165 | 0.4386143 | -0.188562 | 1.586128  |
| Gemin8    | -0.759414 | -0.704139 | -1.627731 | -0.934441 | -1.495425 | -0.514574 | 1.2320131 | 1.0698969  | 1.152673   | 0.4539257 | 1.2488597 | -0.1052953 | 1.1540284 | 0.0797477  | 0.9265642 | 0.0320478 | -0.775164 | 0.5340841 |
| Dok4      | -1.322002 | -0.955119 | -0.795814 | -1.172996 | -0.998544 | -1.09264  | 1.7180434 | 0.8961127  | 1.053527   | 0.8313863 | 0.8225994 | -0.857672  | 1.2583824 | 0.3586469  | 0.5162221 | -0.9679   | 0.4079442 | 0.2998227 |
| Cyp2b23   | 0.9623036 | 3.4567684 | 1.895091  | -0.229696 | 0.9854799 | 0.4509386 | -0.529733 | -0.529733  | -0.520245  | -0.437858 | 0.529733  | -0.479188  | -0.455747 | -0.319836  | -0.449236 | -0.529733 | -0.522727 | -0.529733 |
| B048355   | -0.810152 | -0.620785 | -1.080576 | -1.068623 | -1.021031 | -0.892062 | 0.348705  | 0.670603   | 2.6807396  | 0.7685838 | 0.2054277 | 0.1162552  | 0.1663752 | -0.095016  | 0.2260271 | 0.1166001 | -1.134474 | 1.4179253 |
| Clcf1     | -1.099292 | -1.127359 | -0.79303  | -1.093108 | -1.201263 | -1.089261 | 1.3084827 | 1.8910616  | 0.0144357  | 1.8445404 | 0.4552819 | -0.667626  | 0.1704002 | -0.7640667 | 0.1735822 | 0.1618007 | 0.4259682 | -0.048682 |
| Sh3bgr    | 0.0306843 | 3.1460189 | 1.039216  | 1.0647262 | 0.2685906 | 0.4217552 | -0.661399 | -0.544166  | -0.759264  | -0.72862  | -0.794627 | -0.528262  | -0.819365 | 0.6325411  | -0.418323 | -0.538755 | -0.508304 | -0.302446 |
| Phc1      | -0.494341 | -0.670351 | -0.828834 | -0.952495 | -1.25003  | -0.561453 | 2.8724028 | 1.0810759  | 0.4425761  | 0.0146779 | -0.256367 | -0.386874  | -0.144882 | -0.724763  | 1.1835799 | -0.295966 | -0.012058 | 0.9841019 |
| Mthfd1d   | -0.977963 | -1.156385 | -1.179553 | -1.136468 | -1.083178 | -1.002466 | 2.1386292 | 1.7274024  | 0.4962491  | 0.3133695 | 0.2026553 | 0.3963448  | 0.2508053 | -0.201849  | 0.717457  | -0.242746 | -0.258706 | 0.9984023 |
| Apobec2   | 2.2344036 | 2.2511755 | 0.6177077 | 0.9247662 | 0.4601027 | 0.8733357 | -0.740991 | -0.587213  | -0.708811  | -0.731599 | -0.737085 | -0.737752  | -0.737398 | -0.367306  | -0.536036 | -0.592526 | -0.463273 | -0.421503 |
| Cyp2s1    | -0.853713 | -0.84904  | -0.565001 | -0.906843 | -0.781383 | -0.87237  | 3.1287173 | 0.0945133  | -0.164243  | 0.56481   | 0.8227705 | 0.0233039  | 0.6283761 | 1.0777055  | -0.662648 | -0.220878 | -0.140871 | -0.053206 |
| A93001602 | 0.3687852 | 3.6171856 | 0.1462809 | 0.1318475 | 0.667989  | 0.6779    | -0.548396 | -0.378874  | -0.561441  | -0.55595  | -0.557584 | -0.5607    | -0.089903 | -0.454261  | -0.520546 | -0.363895 | -0.458574 |           |
| S8sia4    | 0.9689913 | 0.6427583 | 0.7488669 | 2.284416  | 0.4635388 | 2.0846588 | -0.963501 | -0.724203  | -0.702934  | -0.922507 | -0.900792 | -0.60518   | -0.762389 | -0.530752  | -0.459984 | 0.1144137 | -0.439286 | -0.324266 |
| Cre1      | 1.6723644 | 0.0157682 | 0.8694867 | 2.1745412 | 0.3735728 | 1.4223819 | -0.832302 | -0.804448  | -0.753425  | -0.831853 | -0.818561 | -0.530404  | -0.770494 | -0.408848  | -0.603363 | 0.0835581 | -0.481389 | -0.793937 |
| Rcsd1     | 1.1864015 | 1.1925036 | 1.4614995 | 1.3570132 | 1.1806031 | 1.2475331 | -1.285559 | -0.919779  | -0.76411   | -0.974571 | -0.902585 | -0.821317  | -1.063915 | -0.43523   | -0.334563 | 0.339362  | -0.050711 | -0.412576 |
| Cd53      | 1.0430184 | 0.5008223 | 1.1034708 | 1.6388554 | 0.4368597 | 1.4891413 | -1.143928 | -0.738829  | -0.939659  | -0.998393 | -0.983621 | -0.497816  | -0.969684 | -0.804102  | -0.479262 | 1.5924847 | -0.034598 | -0.214758 |
| Siah1b    | -1.077521 | -1.183979 | -1.209952 | -1.123078 | -1.321267 | -1.112156 | 1.0108273 | 1.1331353  | 0.5050526  | 0.7987537 | -0.033161 | 0.6338183  | 0.6452855 | 0.0068643  | 0.1341287 | 0.4174625 | -0.324979 | 2.1007663 |
| Lat2      | 1.2668033 | 0.3271039 | 1.1441881 | 2.4738288 | 0.4163014 | 1.5182706 | -0.921292 | -0.804738  | -0.72945   | -0.75264  | -0.823198 | -0.441975  | -0.808255 | -0.671962  | -0.611514 | 0.2642398 | -0.36565  | -0.480115 |
| Tex264    | 1.8948998 | 1.9627253 | 0.5597525 | 0.5877432 | 1.2710039 | 1.3406307 | -0.932756 | -0.662398  | -0.690347  | -0.553621 | -0.420609 | -0.165665  | -0.689183 | -0.30717   | -0.679228 | -0.717244 | -0.78342  | -0.105115 |
| Snrpd2    | -1.000915 | -0.822244 | -1.114894 | -0.839692 | -1.029602 | -0.981014 | 0.7468014 | -0.770806  | 0.9681026  | 0.2239484 | 0.3249043 | 0.7408032  | 0.7094064 | -0.222528  | 0.1098532 | 0.4863523 | -0.407523 | 2.7863171 |
| AS90579G1 | -1.050618 | -0.101925 | -0.614103 | -0.829678 | -1.263868 | -0.997724 | 1.099766  | -1.266844  | -0.0210813 | 1.0644256 | 0.9158149 | 0.6609248  | 1.9043401 | 0.0652626  | 0.9641954 | 0.071886  | -0.69121  | 0.9655731 |
| SiK5      | -0.806314 | -1.321114 | -0.711772 | -0.810658 | -0.969146 | -1.29715  | 1.4721737 | -0.803316  | 1.9811785  | -0.125262 | 0.4214498 | 0.9633493  | -0.581258 | 1.056378   | 1.1067673 | 0.5131537 | 0.0390979 | -0.127558 |
| Reps2     | 1.1744104 | 1.1450982 | 0.6242284 | 0.6373462 | 1.7636422 | 2.0129185 | -1.188103 | -0.085431  | -0.509823  | -0.497119 | -0.904615 | -0.119022  | -0.285549 | -0.669502  | -0.564782 | -0.262271 | -0.916953 | -1.354473 |
| ErF       | -0.403361 | -1.739697 | -0.899558 | -0.602069 | -1.188784 | -1.21687  | 1.1828931 | -0.870881  | 0.9209126  | 0.4671149 | 0.9846952 | 0.2870728  | 0.4476965 | -0.743628  | 0.874864  | 0.1618924 | 0.2829549 | 1.6251518 |
| Osbp10    | -1.059632 | -0.681415 | -0.657697 | -1.090173 | -0.779254 | -1.161225 | 1.2281166 | -0.63012   | 0.760019   | 1.5908534 | 0.9088525 | 0.8881992  | 0.1005758 | -0.879224  | -0.02449  | -0.03735  | -0.514959 | 2.0388764 |
| Wdr25     | -0.979166 | -0.103792 | -0.50159  | -0.101983 | -0.908051 | -1.238851 | 2.2647313 | -0.173258  | 1.5219869  | 1.1294461 | 0.6182656 | 0.1256166  | 0.6218709 | 0.9804508  | 0.0408856 | -0.634648 | -0.200105 | -0.610494 |
| Ccr6      | 1.629982  | 0.6480033 | 0.5307542 | 1.0331564 | 2.765557  | 0.523751  | -1.379934 | -0.942884  | -0.497919  | -0.440703 | 0.3153844 | 0.4711775  | -1.023384 | -1.08128   | -0.723206 | -0.427598 | -0.122646 | -0.789211 |
| Atp1a3    | 2.1084713 | 0.1321551 | 0.8060396 | 2.7184149 | -0.191122 | 0.5778923 | -0.680466 | -0.560118  | -0.161654  | -0.690542 | -0.674398 | -0.632979  | -0.687541 | -0.587202  | -0.511296 | 0.3638146 | -0.290548 | -0.57969  |
| Rcc2      | -1.040087 | -0.665714 | -0.652089 | -1.206312 | -0.901153 | -1.081182 | 0.2306175 | -0.02946   | 0.1663523  | 0.3260786 | 0.0800793 | -0.195838  | 0.5435762 | -0.255223  | 0.3345285 | -0.28817  | -0.444968 | 2.2789669 |
| Mgl2      | 1.8289466 | 0.2015222 | 0.2947311 | 1.2647952 | 1.201209  | 0.8195935 | -0.789578 | -0.505278  | -0.791223  | -0.76562  | -0.824095 | -0.761336  | -0.805688 | -0.591709  | -0.671057 | 0.3875158 | -0.606607 | -0.697735 |
| Gm11992   | 0.3186672 | 2.7965328 | 0.485834  | 0.1062551 | 1.5703451 | 0.4087054 | -0.958333 | -0.975648  | -0.675223  | 0.5070656 | -0.179881 | 0.0454008  | -0.449651 | -0.023697  | -1.045011 | -1.202027 | -0.895622 | -0.192806 |
| Mill2     | 1.5319904 | 1.1571279 | 1.6969523 | 2.0100334 | 0.658143  | 0.2939354 | -0.37147  | -0.902669  | -0.777595  | -0.722945 | -1.015031 | -0.833948  | -0.78651  | -0.545173  | -0.47901  | 0.3636742 | -0.677061 | -0.802791 |
| Cmtm8     | 2.8907045 | 1.4613175 | 0.4074943 | 0.3106924 | 0.9507588 | 0.1332097 | -0.76002  | -0.742582  | -0.457467  | 0.1673803 | 0.0939777 | -0.316619  | 0.1060865 | -0.874617  | -0.166762 | 1.322615  | -0.997771 | -0.120559 |
| Ramp3     | -1.238205 | -1.293898 | -0.78155  | -1.177568 | -1.111142 | -1.079258 | 1.2396594 | 0.0847812  | 2.1129983  | 0.1186475 | 0.1367826 | 1.1401282  | 0.9701307 | -0.006928  | 0.9842414 | 0.1582916 | -0.336315 | 0.0792036 |
| Wvwp1     | 0.743165  | 1.4939524 | 0.5881126 | 0.818411  | 1.5521523 | 1.6897065 | -1.114556 | -0.5072309 | -0.399209  | -0.726781 | -1.148388 | -0.926994  | -0.674685 | -0.323546  | -0.594698 | 0.8814734 | -0.570484 | -1.344864 |
| Pif1      | -1.073889 | -1.109984 | -1.182151 | -1.191993 | -1.210651 | -0.989798 | 1.6905221 | 1.0722491  | 1.1621849  | 0.5416583 | 0.2538077 | 1.4269955  | 0.0844905 | -0.364135  | 0.6122021 | 0.4444981 | -0.734569 |           |



|           |           |           |           |           |            |           |           |            |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Pgm5      | 1.3985771 | 0.8185857 | 0.4469535 | 1.687146  | 2.2044509  | 0.7612907 | -1.340972 | -0.683108  | -0.720671 | -0.919956 | -0.263019 | -0.448299 | -0.784198 | -0.055556 | -0.689845 | -0.173644 | -0.397805 | -0.839931 |
| Gml13178  | 2.3329153 | 2.5017819 | -0.137761 | 0.1740576 | 0.8992853  | 0.8509125 | -0.625564 | -0.593012  | -0.537748 | -0.534432 | -0.567522 | -0.607965 | -0.590167 | -0.414462 | -0.454945 | -0.625564 | -0.444248 | -0.625564 |
| Utp1      | -0.686264 | -0.866023 | -1.025869 | -1.042018 | -1.206109  | -1.006896 | 0.7770007 | 0.27934812 | 0.1327587 | 0.3493087 | -0.078622 | 0.4877604 | 0.6453728 | -0.398214 | 0.3699304 | -0.176662 | -0.310587 | 1.2416505 |
| Ccr1      | -0.214297 | -0.641117 | -0.50982  | -1.075195 | 0.0207903  | -0.5717   | 0.8681169 | 0.4671386  | 1.6638635 | 1.2292063 | 1.9846594 | 1.298723  | 1.0727611 | -0.800361 | -0.713602 | -0.431218 | -1.110508 | -1.36859  |
| Gpr155    | 1.4337652 | 1.7169474 | 0.4990055 | 1.3523318 | 1.0122811  | 1.1187534 | 0.3645103 | -0.776267  | -0.485333 | 0.2200851 | -0.510117 | -0.691463 | -0.573134 | -0.042627 | -1.509631 | -0.990455 | -1.008974 | -1.129684 |
| YdjC      | -0.162286 | -1.034464 | -1.100872 | -0.953771 | -0.963051  | -0.625409 | 0.3457763 | 0.8652524  | -0.111705 | 0.0425679 | 0.1450073 | 0.3560178 | 0.1325115 | 0.2720153 | 0.010138  | 0.0622265 | -0.660155 | 3.2911489 |
| Lad1      | -0.48686  | -0.800175 | -0.670649 | -0.840779 | -1.092661  | -1.37673  | 1.3112484 | -0.036226  | 0.3456288 | 1.9082873 | 0.1717639 | 0.3504468 | 0.1029501 | 2.1470808 | -0.205595 | -1.147927 | -0.164611 | 0.484807  |
| Abca9     | 0.7005976 | 0.7984624 | 1.1516815 | 1.1809539 | 1.7812125  | 1.999139  | -0.926628 | -0.69308   | -0.876659 | -0.89014  | -0.883987 | -0.742693 | -0.338136 | -0.41885  | 0.1449156 | -0.382578 | -0.754495 |           |
| Phlda3    | -0.850695 | -1.287906 | -0.632163 | 0.003863  | -1.421478  | -1.190101 | 1.7166129 | 0.0858474  | 0.1635861 | 1.2641414 | 0.0603474 | 0.1635861 | 0.4869839 | 2.0233952 | -0.038384 | -1.202433 | 0.0284772 | 0.626319  |
| Abca8a    | 1.2871794 | 1.1833449 | 1.5659696 | 0.8090723 | 1.0080304  | 2.0170344 | -0.85695  | -0.574017  | -0.812497 | -0.860001 | -0.861853 | -0.745931 | -0.867252 | -0.441341 | -0.488122 | -0.170018 | -0.418344 | -0.774305 |
| Syt13     | -0.186619 | 1.0971423 | 1.6664478 | 0.3500981 | 1.7920744  | 1.0947222 | -1.18365  | -1.448135  | -0.914963 | 0.2778894 | -0.149651 | -0.704264 | 0.0510467 | -0.957898 | -1.230655 | -0.514738 | 0.904519  | 0.0566331 |
| Haus1     | -1.07989  | -0.769274 | -1.213304 | -1.149249 | -1.068276  | -0.957506 | 0.5202608 | 1.9018704  | 1.2565338 | 1.0519396 | 0.5716034 | 0.7833701 | 1.0370011 | 0.3054937 | 0.385982  | -1.160454 | -0.459649 | 0.0345476 |
| Mcm3      | -1.067746 | -1.075119 | -0.720429 | -1.235412 | -1.123478  | -0.121703 | 0.6670012 | 1.2896087  | -0.020038 | 0.5076577 | 0.2486086 | 0.3109605 | -0.072945 | -0.706418 | 2.2743162 | 0.1370884 | 0.1561272 | 1.4519184 |
| Wipi1     | -1.225521 | -1.116854 | -0.741847 | -0.94679  | -0.870741  | -1.09929  | 1.0742889 | 0.8357308  | 0.5772059 | 0.0144176 | -0.211104 | -1.001073 | 0.1645713 | 0.3768297 | 1.8961573 | 1.2501659 | 1.4481902 | -0.424336 |
| Tmco7     | -1.183666 | -0.855512 | -0.750345 | -1.198179 | -0.940942  | -1.19942  | 1.1715158 | 0.596791   | 2.4260314 | 0.7263256 | 0.502645  | -0.870932 | 0.1883082 | 0.4277009 | 0.6621125 | -0.566205 | 0.2853315 | 0.5612505 |
| Elmod1    | 1.0782686 | 2.1370551 | 0.4621783 | 0.4055411 | 0.9114483  | 1.1896887 | -0.971909 | -1.063354  | -0.71155  | 0.1417697 | -0.077638 | 0.7856095 | 0.6044199 | -0.763729 | -0.642101 | -1.244729 | -1.121214 | -1.119755 |
| Hmr       | 1.4261904 | -0.995696 | 0.8541095 | 0.5085367 | 1.577389   | 2.4486666 | -0.705515 | -0.911739  | -0.424383 | 0.245347  | -0.145674 | 0.0012194 | -0.088733 | -0.677345 | -0.649146 | -0.828746 | -0.793266 | -0.841215 |
| Rappel5   | -0.560756 | -0.228402 | -1.183897 | -0.724903 | -0.903807  | -1.308469 | 1.4388083 | 0.3975979  | 0.4173141 | -0.039859 | -0.021865 | -0.405703 | 0.3968528 | 2.1581025 | 0.1509178 | -0.402301 | -1.051362 | 1.8717326 |
| Acab      | 1.5901772 | 1.4782937 | 1.6462333 | 0.3921804 | 1.5601996  | 1.2310079 | -0.755076 | -0.675166  | -0.740778 | -0.635002 | -0.405457 | -0.784789 | -0.694748 | -0.305877 | -0.581277 | -0.758993 | -0.670733 | -0.886586 |
| Ncapg2    | -1.085411 | -0.865257 | -1.337122 | -1.416001 | -1.317069  | -1.311016 | 1.9417343 | 0.562352   | 0.2278087 | 1.0988067 | 0.6526407 | 0.4236165 | 0.3993852 | 0.9995028 | 0.7467883 | -0.051705 | -0.060305 | 0.3912499 |
| Lce3b     | -1.155525 | -0.937783 | -0.672752 | -1.138738 | -0.885051  | -1.065331 | 0.582803  | 0.6771097  | -0.935657 | 0.2040367 | -0.342364 | 1.2851161 | 0.9664765 | 0.3782298 | 1.6233202 | 0.5419719 | -0.836839 | 1.7110681 |
| Igfs3     | -1.386859 | -0.860353 | -0.373901 | -1.334056 | -0.392674  | -1.255546 | -0.161599 | -0.616959  | 1.2930725 | 1.6017225 | 1.6531137 | 0.7018792 | 0.4546848 | 0.8748278 | 0.2130821 | -0.453887 | 0.7456851 | -0.019555 |
| Abhd14b   | 1.0605272 | 0.6199121 | 1.231918  | 1.5684351 | 1.1225671  | 1.1596107 | -1.085182 | -1.156749  | -0.744675 | -0.187472 | -1.199039 | -0.984926 | -0.980732 | -0.084661 | 1.1158752 | -0.888818 | -0.912358 | 0.0457665 |
| Ar5b      | 1.6463037 | 0.4138955 | 0.5258027 | 2.0836217 | 0.9259778  | 1.1629817 | -1.431104 | -0.335652  | -0.850005 | -0.042659 | -0.865827 | -0.390158 | -1.396095 | -0.10086  | 0.3821712 | 0.1545343 | -0.374127 | -0.907876 |
| Lce1c     | 0.7365991 | 2.3769022 | 0.9542006 | -0.027932 | 1.7971888  | 1.2318796 | -0.893958 | -0.858218  | -0.62054  | -0.964649 | -1.114515 | -0.443723 | -0.328741 | -0.478362 | -0.672378 | -0.398375 | -0.732137 | -0.947844 |
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| Vwa1      | -1.196859 | -1.448245 | -1.020371 | -1.148596 | -1.157028  | -0.9811   | 1.0028626 | 0.0223812  | 0.0439097 | 0.0985885 | 0.3602469 | -0.004349 | 0.0730236 | 0.3853327 | 0.5430913 | 0.9373909 | 2.0942855 | 1.3954356 |
| Lce1f     | 0.8698916 | 1.7194459 | 1.2724129 | 0.3238374 | 1.6231053  | 0.8142464 | -0.991427 | -1.176416  | -0.800674 | 0.3849109 | 0.1942165 | 0.2339046 | 0.0761918 | -0.30315  | -0.57371  | -1.298886 | -0.960967 | -1.406933 |
| Rassf4    | 1.6075766 | 0.5084353 | 0.8909749 | 2.3468275 | 0.6971753  | 1.4315012 | -0.932831 | -0.708772  | -0.758997 | -0.745511 | -0.782005 | -0.63215  | -0.813997 | -0.555235 | -0.538388 | -0.030004 | -0.321115 | -0.663485 |
| Cox10     | -0.985919 | -1.218751 | -0.989159 | -0.640087 | -0.1012301 | -1.409811 | 1.4686177 | 0.3462905  | 0.4920281 | 0.625475  | 0.2489309 | 0.6427419 | 1.0848296 | -0.684427 | 0.131073  | -0.762065 | 0.3862761 | 1.9741049 |
| Spr2i     | -0.938328 | -0.94855  | -0.909039 | -0.891253 | -0.908804  | -0.922516 | 0.7504699 | -0.490195  | -0.773069 | 2.0552591 | -0.402566 | 0.2191548 | 1.1797384 | 0.9176719 | -0.090888 | 1.0336887 | -0.477108 | 1.5960635 |
| Spr2d     | -0.910199 | -0.906529 | -0.816152 | -0.859006 | -0.792738  | -0.880118 | 0.3055158 | 0.7738715  | -0.820842 | 1.2243407 | -0.56521  | 0.2832179 | 1.1507151 | -0.807945 | 1.9482312 | 0.6494183 | -0.54825  | 1.6366431 |
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| Bag2      | -1.036411 | -0.929472 | -1.133707 | -1.132331 | -1.088969  | -1.026097 | 0.8033336 | 0.6828267  | 0.075937  | 0.7894175 | -0.257318 | 1.3833885 | -0.140919 | 1.9683412 | -0.433977 | -0.572045 | 0.8546744 | 1.1563261 |
| Tmc7      | -1.063501 | -1.103633 | -0.910934 | -1.153824 | -1.179733  | -1.197228 | 1.7413524 | 1.0135372  | 0.6386953 | 1.2806442 | 0.7096052 | 0.3832876 | 1.0919363 | -0.938935 | 0.7446643 | 0.3302159 | 0.0245011 | -0.41065  |
| Adrbk2    | 0.3123202 | 0.4187946 | 0.8470073 | 1.7166387 | 1.6493327  | 1.6194688 | -1.704103 | -1.285966  | -0.165489 | -0.002151 | -0.725382 | -0.067572 | -1.065041 | -0.619127 | -0.975852 | 0.2770993 | 0.0093014 | -0.239271 |
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| Itga1     | -0.869137 | -0.32485  | -0.422327 | -0.124558 | -0.727442  | -0.308834 | -0.577604 | -0.234057  | -0.586117 | -0.616619 | -0.719623 | -0.386297 | -0.648321 | 0.6916548 | 1.2196305 | 2.6380888 | 1.0458725 | 0.1036755 |
| Hsd3b7    | 0.8618635 | 0.1194864 | 1.1894252 | 2.5173772 | 0.4147266  | 1.4760844 | -1.081306 | -0.96401   | -0.531933 | -0.912341 | -0.865761 | -0.464758 | -0.888835 | -0.563928 | -0.227859 | 0.4522464 | 0.2183086 | -0.741787 |
| S100a13   | 1.1205716 | 1.2750266 | 0.0760451 | 1.6469095 | 0.3579055  | 1.6600034 | -1.330675 | -0.489716  | -0.9265   | -0.663998 | -0.883203 | -0.342828 | -1.077317 | -0.23651  | -0.258748 | 1.4338399 | -0.531843 | -0.828964 |
| Prox2     | -0.483946 | -1.330314 | -0.628273 | -1.005992 | -0.957927  | -0.701028 | 1.7403322 | 0.0635828  | 1.6901188 | 0.5715676 | -0.010256 | 0.0458447 | 1.3131101 | 1.6125573 | -0.483946 | -0.594679 | 0.1696127 | -0.101365 |
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| Gnl3      | -0.800648 | -1.03523  | -1.169532 | -1.249118 | -1.216319  | -1.000352 | 0.3587791 | 1.1258296  | -0.875659 | 0.6491018 | 0.1464336 | 0.606112  | 0.6669611 | 0.8787104 | 0.3049614 | 0.2911834 | -0.073971 | 2.3427567 |
| G5        | 0.8735524 | 2.5641445 | 0.1626015 | 0.123464  | 1.3779851  | 1.0212949 | -0.523375 | -0.911585  | -1.080574 | 0.3607809 | 0.1984237 | 0.1616585 | -0.12652  | -0.663258 | -0.951594 | -1.260911 | -0.903951 | -1.228539 |
| Gjb3      | 1.5227584 | 2.1502446 | 0.5013704 | 0.7436098 | 1.3623762  | 1.0808436 | -0.736067 | -0.773609  | -0.517912 | 1.1176504 | -0.347138 | -0.060496 | -0.610901 | -0.647712 | -0.97374  | -1.188186 | -0.489424 | -1.134445 |
| Esm1      | -1.076513 | -0.997171 | -1.072612 | -1.082808 | -1.001852  | -0.921453 | 0.3209955 | 1.192578   | 2.303403  | 0.3705545 | 0.8400026 | 0.8736628 | 1.1208137 | -0.234586 | -0.272993 | 0.404791  | -0.53117  | 0.6102592 |
| Dennd4b   | 1.3894671 | 0.5763088 | 1.577425  | 1.8200671 | 0.9052066  | 1.0598574 | -1.335849 | -1.095383  | -0.391299 | -0.650826 | 0.306161  | -1.435305 | -0.713864 | -0.177572 | -0.332163 | 0.1952406 | -0.52753  | -0.557584 |
| Dctpp1    | -0.860256 | -0.864768 | -0.805254 | -1.096941 | -0.848827  | -1.123941 | 0.5785863 | 1.8622006  | 0.5749712 | -0.146482 | -0.031434 | 0.2708654 | 0.2161592 | -0.658069 | 0.90337   | 0.291785  | -0.638717 | 2.3794612 |
| Hoxd4     | 1.7866736 | 0.040571  | 0.73457   | 1.4668344 | 1.3629895  | 1.1119264 | -0.855236 | -1.032302  | -1.317885 | -1.372147 | -0.774525 | -0.338103 | -0.956404 | -0.694461 | 0.3662997 | -0.204913 | 0.0687228 | 0.        |



|            |           |           |           |           |           |            |           |           |            |            |            |           |           |           |           |           |           |           |
|------------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Mrp150     | -0.436382 | -0.540703 | -1.309283 | -1.196247 | -1.013686 | -1.156415  | 0.9038919 | 2.145387  | 0.314206   | 0.3540064  | 0.3828242  | -0.007717 | 1.2041792 | -0.684119 | 0.7545617 | -0.55962  | -0.592097 | 1.437212  |
| Pcdhb21    | -1.183008 | -0.702018 | -0.92766  | -1.225993 | -1.070126 | -1.16798   | 1.1261599 | 1.0374729 | 0.8447444  | 0.4948455  | 1.790946   | 0.3262643 | 0.753133  | 0.4741905 | 0.1079125 | -0.656274 | 0.1099057 | -1.103764 |
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| Als2c      | -1.25381  | -1.149197 | -0.131129 | -1.202216 | -0.422019 | -1.14141   | 1.7769865 | -0.401288 | 1.0944772  | 0.6436803  | 1.8678496  | -0.117809 | 1.2071059 | -0.017014 | -0.915242 | 0.4983409 | 0.0862178 | -0.423526 |
| Fmn1       | 1.228442  | 1.3187532 | 0.4914227 | 1.7826837 | 0.6728088 | 1.3718778  | -1.139398 | -1.177018 | -1.255894  | -0.021842  | -0.699822  | -0.334262 | -1.061317 | 0.343323  | 0.0594928 | -0.265497 | 0.0439399 | -1.352149 |
| S100a1     | 1.7784872 | 0.4403402 | 1.1864823 | 2.0782389 | 0.3408616 | 1.662208   | -0.774969 | -0.765717 | -0.690513  | -0.711464  | -0.697363  | -0.766708 | -0.797157 | -0.460422 | -0.426937 | -0.205422 | -0.51396  | -0.666087 |
| Lmod3      | 1.4101789 | 2.1639931 | 0.8868093 | 1.5459989 | 0.9086207 | 0.2238608  | -0.950023 | -0.785963 | -0.950023  | -0.950023  | -0.916262  | -0.950023 | -0.924058 | 0.0342163 | -0.315902 | 0.1919564 | -0.204788 | -0.418571 |
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| Proca1     | 0.1377596 | 0.8079798 | 0.1987613 | 0.4544966 | 2.0728587 | 1.5809742  | 1.0889904 | -0.305905 | -0.626697  | 0.110768   | 0.4197487  | -0.054186 | -1.342225 | -1.4529   | -1.475505 | -0.042056 | -0.569691 | -1.003172 |
| Nkrf       | -1.019889 | -0.943989 | -1.120203 | -1.402053 | -1.256522 | -1.380337  | 1.2453311 | 1.4018018 | 0.765516   | 1.5239931  | 0.9636965  | 0.299746  | 0.7077573 | -0.247039 | 0.3645764 | -0.307033 | 0.509707  | -0.016096 |
| Naa38      | -0.52779  | -0.895474 | -0.896335 | -1.360717 | -1.264943 | -1.039811  | 0.8366868 | 2.5549177 | 0.5261523  | -0.145855  | 0.1285709  | 0.3646294 | 0.7865143 | -0.889688 | 0.9835047 | -0.159833 | 0.4467251 | 0.5527437 |
| Gpr146     | 1.1414724 | 0.5185186 | 1.2110289 | 1.6527382 | 1.3415205 | 1.2789844  | -1.249223 | -1.032956 | -0.534553  | -0.809191  | -1.070805  | -0.821102 | -0.708511 | -0.785524 | -0.397369 | 0.8729315 | -0.002413 | -0.605548 |
| Cdc25c     | -1.104162 | -0.903691 | -1.372106 | -1.451592 | -1.187097 | -1.150969  | 1.4106329 | 1.4597475 | 1.1860146  | 0.8009571  | 0.6467083  | 0.7652731 | 0.6130542 | 0.7646121 | -0.161072 | -0.029439 | -0.283492 | -0.003378 |
| Vsig4      | 0.9215159 | 0.5611785 | 0.6204805 | 0.7426663 | 1.4086612 | 2.4182905  | -0.947179 | -0.68412  | -0.911148  | -0.536662  | -0.881509  | -0.887577 | -0.901681 | -0.066392 | -0.75147  | 0.9842403 | -0.351628 | -0.737667 |
| Nhlrc1     | -0.468521 | -0.822155 | -0.571149 | -1.062063 | -1.315916 | -1.053206  | 0.5332268 | 1.9276731 | 1.9914334  | 0.4571578  | 1.2603108  | -0.151441 | 0.9206713 | -0.280191 | -0.202624 | 0.1014048 | -0.983025 | -0.281588 |
| Il20rb     | 1.9313986 | 1.5761193 | 0.19927   | 0.1418748 | 0.9242925 | -0.05705   | -0.936192 | -0.713624 | -0.110523  | 0.0957018  | 1.265007   | 0.9362306 | -0.200314 | -0.230774 | -1.248512 | -1.388083 | -1.188881 | -0.995942 |
| Osbp1a     | 1.1535494 | 2.6009245 | 0.707270  | 0.4054434 | 1.08229   | 1.2546874  | -0.600616 | -0.754972 | -0.714847  | 0.0750119  | -0.261448  | -0.713064 | -0.480025 | -0.229508 | -0.804315 | -0.772583 | -0.821125 | -1.126585 |
| Mab2113    | -1.183604 | -0.747452 | -1.006833 | -1.390352 | -0.21577  | -1.323593  | 0.6313991 | 0.1811742 | 1.2753218  | 1.5219821  | 0.9348441  | -0.462636 | 1.7231136 | 0.3741575 | -0.404918 | -0.826569 | -0.386973 | 0.9337807 |
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| Cxcr7      | -1.42977  | -0.689877 | -0.914787 | -0.967402 | -0.442105 | -0.702325  | 0.4794442 | -0.988894 | 1.2735667  | 1.6466493  | -0.547101  | 0.4167285 | 0.5435558 | -0.671807 | -0.002298 | 1.7934328 | 1.4133035 | -0.210104 |
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| Alkbh2     | -1.022928 | -1.284838 | 0.041673  | -1.04479  | -0.191907 | -1.103665  | 2.3888991 | 1.2954948 | 0.8471593  | -0.211046  | 0.2679481  | 0.3760877 | 0.8216347 | -0.056822 | 0.5644373 | 0.4237118 | -0.562693 | 0.3265083 |
| P2ry4      | 1.7983759 | 2.176912  | 0.6272228 | -0.123876 | 1.4800808 | 1.1700799  | -0.779876 | -0.807145 | -0.513141  | -0.298985  | -0.124986  | -0.102107 | -0.791996 | -0.680823 | -0.781835 | -0.810127 | -0.598976 | -0.838676 |
| Adig       | 2.6982851 | 0.2499564 | -0.075892 | 1.490589  | 1.9514759 | 0.205402   | -0.559293 | -0.583273 | -0.513206  | -0.533788  | -0.539463  | -0.753438 | -0.593247 | -0.568827 | -0.549111 | -0.491621 | -0.398924 | -0.622562 |
| Sptssa     | 1.1491832 | 2.7469928 | 0.2375563 | 0.0979978 | 1.1369999 | 0.7164145  | -0.669183 | -0.526258 | -0.624467  | -0.134159  | -0.3509    | 0.1060973 | 0.385264  | 0.1316963 | -0.090934 | -1.137906 | -0.151347 | -1.096048 |
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| Cnrip1     | 1.0099971 | 0.1725563 | 0.5978757 | 1.3828963 | 0.8649061 | 2.4352077  | -1.18057  | -0.929361 | -1.148451  | -0.97795   | -0.885854  | -0.348469 | -0.958409 | -0.146162 | 0.0229974 | 0.4961211 | -0.035562 | -0.452769 |
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| Rassf9     | 2.9509807 | 1.4734857 | 0.0448259 | 0.9625692 | 0.7245742 | 0.5604103  | -0.960779 | -0.420544 | -0.188373  | -0.409074  | -0.321246  | -0.71137  | -0.672902 | -0.323339 | -0.612659 | -0.796641 | -0.530203 | -0.769716 |
| Khlh31     | 0.8917194 | 2.496008  | 0.8514398 | 0.8745213 | 1.2833317 | 1.2120643  | -0.805852 | -0.690521 | -0.820443  | -0.812943  | -0.805205  | -0.826831 | -0.826831 | -0.227259 | -0.500401 | -0.431719 | -0.300212 | -0.560867 |
| Mylik4     | 1.6491228 | 2.9762572 | 0.2551809 | -0.277698 | 0.5622236 | 1.2368651  | -0.530878 | -0.489569 | -0.557661  | -0.554661  | -0.591606  | -0.554738 | -0.55653  | -0.468118 | -0.536628 | -0.513084 | -0.467197 | -0.581283 |
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| Napepld    | 1.6243601 | 2.1660783 | -0.577301 | 0.9358434 | 0.450613  | 0.7921715  | 0.2313743 | -0.103734 | -0.481071  | -0.3646201 | -0.175634  | -1.223617 | 0.8250313 | -1.076528 | -0.833117 | -0.619921 | -0.724066 | -0.60615  |
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| Acer1      | 2.1066795 | 2.4787177 | 0.3004731 | 1.036896  | 0.7812898 | 0.8271276  | -0.787124 | -0.919063 | -0.557734  | 0.179145   | -0.331642  | -0.305603 | -0.287679 | -0.000986 | -0.826165 | -1.136873 | -0.545022 | -0.698385 |
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| Arhgef37   | 1.2939135 | 0.2041931 | 0.462804  | 0.0695379 | 1.1462972 | 1.050182   | -0.871717 | -0.395381 | -0.518314  | 1.0538984  | 0.0032651  | -0.282346 | -0.169015 | 0.040     |           |           |           |           |



|           |           |           |           |           |           |            |           |           |           |           |            |           |           |           |            |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|------------|-----------|-----------|-----------|
| Jrk       | -0.734714 | -1.32657  | -1.145127 | -1.082606 | -1.058221 | -1.04965   | 1.0357713 | 1.9454983 | 1.2562772 | 0.3853469 | 0.9952356  | -0.399402 | 1.0963112 | -0.279777 | 0.48652    | -0.218383 | -0.541473 | 0.6349615 |
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| Scn4b     | 1.410822  | 1.7807765 | 1.4678870 | 1.0645653 | 1.3194516 | 0.9492686  | -0.902396 | -0.514397 | -0.837398 | -0.840549 | -0.869746  | -0.796889 | -0.830233 | -0.493866 | -0.306079  | -0.798562 | -0.29836  | -0.466663 |
| Kctd4     | 0.9426389 | 2.4302139 | 0.8164041 | -0.448617 | 1.6815471 | 0.8170589  | -0.506019 | -0.90573  | -0.841123 | 0.1053363 | -0.065049  | 0.3803052 | -0.253216 | -0.512086 | -0.493432  | -1.16027  | -0.936382 | -1.051581 |
| Ar        | 1.6985877 | 2.0369965 | 0.3246183 | 0.601501  | 1.1078969 | 1.3568956  | -0.999374 | -0.833579 | 0.7452142 | -0.573    | -0.646074  | -0.749645 | -0.931252 | -0.613851 | -0.596835  | -0.556296 | -0.580155 | -0.79165  |
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| Gj1b4     | 2.3715895 | 1.4506803 | 0.3735552 | 1.0783238 | 1.2697174 | 0.7033879  | -0.840271 | -0.824559 | -0.57983  | -0.122269 | -0.247277  | 0.0546782 | -0.52895  | -0.560807 | -0.897707  | -1.07613  | -0.509201 | -1.114933 |
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| Tifa      | 1.1591544 | 0.6157396 | 0.6405127 | 1.6526956 | 0.9375985 | 1.2662629  | -1.318381 | -0.300918 | -1.377222 | -1.052787 | -1.35189   | -0.599402 | -1.31364  | 0.2044166 | -0.022464  | 0.915942  | -0.137233 | 0.081614  |
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| Ppp1r3b   | -1.142593 | -1.1497   | -1.073322 | -0.801552 | -0.918195 | -1.103193  | 1.2359357 | 0.5264948 | 0.1816071 | 1.0137965 | 0.6593248  | 1.3751857 | 1.5622986 | -0.288978 | -1.206412  | 0.4334456 | -0.128241 | -0.075902 |
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| Fbl       | -1.415733 | -0.887823 | -0.953646 | -1.292882 | -1.280266 | -1.24633   | 0.9275891 | 0.1563587 | 1.6703177 | 0.0384636 | 0.6719443  | 0.2998902 | 0.8812657 | -0.183197 | 0.791518   | 0.2838422 | -0.099603 | 1.6418899 |
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| Spsb4     | 1.6685885 | -0.172424 | 1.2627035 | 2.2765452 | 0.1070293 | 1.0987215  | -0.877798 | -0.776729 | -0.445342 | -0.832243 | -0.489175  | -0.659046 | -0.904505 | -0.848012 | -0.452651  | 0.9369809 | -0.370562 | -1.072082 |
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| Tmem164   | 1.7077284 | 1.808445  | 0.2996388 | 0.819559  | 0.8934436 | 1.631545   | -0.910808 | -0.420581 | -0.961041 | -1.043721 | -0.645625  | -1.037351 | -0.920243 | -0.435138 | -0.02809   | -1.38661  | 0.3351814 | -0.954282 |
| Tigd5     | -0.602453 | -1.250411 | -1.116121 | -1.121683 | -1.544087 | -1.238306  | 1.3559944 | 0.5775727 | 0.2880077 | 1.0014828 | 0.9233885  | 0.7640201 | 0.8572951 | 0.4644427 | -0.231721  | -0.342875 | -0.416295 | 1.631569  |
| Disp18    | 2.8571455 | 1.5132821 | 1.1769661 | 0.8955273 | 0.5026555 | 1.0547949  | -0.385049 | -0.770621 | -0.691627 | -0.67342  | -0.578396  | -0.824231 | -0.713159 | -0.54709  | -0.456215  | -0.430719 | -0.580003 | 0.349812  |
| Fam185a   | -0.957175 | -0.543973 | -1.262339 | -0.381802 | -1.244696 | -0.953891  | 0.5529867 | 0.6144339 | 0.2156481 | 0.2579123 | -0.265278  | -0.457266 | 1.6753048 | -0.129195 | 0.6735907  | -0.309373 | -0.266686 | 0.7821532 |
| Gms127    | -0.648739 | -0.91879  | -0.857386 | -0.829698 | -1.014001 | -0.715373  | 0.3038616 | 0.4698179 | 0.056948  | 1.865119  | -0.394928  | 0.9415322 | 1.272769  | -0.145809 | -0.46683   | -0.592937 | -0.281435 | 0.0892532 |
| Hist1h2be | -1.306694 | -0.476513 | -0.921582 | -1.277897 | -1.052878 | -1.576135  | 1.3503096 | 1.3178532 | 0.2785027 | -0.563399 | 0.4543644  | -0.415181 | 0.6616138 | 1.0860761 | 0.7850702  | -0.081498 | 0.195959  | 1.5402078 |
| Sfn       | -1.126633 | -0.42255  | -0.660783 | -0.786064 | -1.002696 | -1.33741   | 0.3989171 | 0.2165767 | 0.3821109 | 2.2173147 | 1.5136575  | -0.045612 | 0.9848586 | 1.2954923 | -0.097663  | -1.073491 | 0.0497386 | -0.523763 |
| B3gnt1    | -1.232544 | -1.175283 | -0.717717 | -1.267359 | -0.579906 | -1.143083  | -0.144564 | 0.8191695 | -1.027088 | 1.5548409 | 1.5845919  | 0.4113526 | 0.6686978 | 0.9395717 | -0.598327  | 0.1013069 | 1.0188229 | 0.8602629 |
| Gpr68     | 1.3282737 | 0.7983628 | 0.9542075 | 2.2451005 | 1.0389362 | -0.024303  | -1.147331 | -1.093897 | -1.131696 | 0.5211213 | -0.54093   | -0.840798 | -1.141179 | -0.802342 | 0.1891984  | 0.3891578 | -0.154109 | -0.587774 |
| Cmya5     | 1.0563884 | 1.8014978 | 1.199513  | 1.2753334 | 1.3306972 | 1.3889651  | -0.844474 | -0.707428 | -0.841882 | -0.401284 | -0.838663  | -0.836597 | -0.839892 | -0.351339 | -0.464153  | -0.572945 | -0.298473 | -0.615709 |
| Fam180a   | 3.1577628 | 0.0872961 | -0.016828 | 0.0129648 | 1.3272324 | 1.2719974  | -0.801572 | -0.609517 | -0.700371 | -0.710156 | -0.236393  | -0.518861 | -0.405215 | 0.0756588 | -0.387046  | -0.700744 | -0.160269 | -0.685941 |
| Fam132b   | -0.685279 | -1.589644 | -1.12784  | -0.801562 | -1.152611 | -1.210379  | 1.212736  | -0.648839 | 0.4470713 | 1.7428903 | 0.680735   | 0.5308366 | 0.9467724 | -0.166111 | -0.521173  | 0.5741635 | 0.4717664 | 1.290129  |
| AS30099J1 | 1.1175622 | 0.3313034 | 0.9009506 | 1.3885342 | 1.0844141 | 0.7736569  | -0.722688 | -0.618401 | -0.832605 | -0.654521 | -0.740213  | -0.760282 | -0.779498 | -0.597228 | -0.545251  | -0.541063 | -0.349971 | -0.757162 |
| Adams12   | -0.773304 | -0.417172 | -0.541232 | -0.479627 | -0.368654 | 0.2479863  | -1.08659  | -0.622478 | -1.029642 | -0.608468 | -0.561212  | 1.0949072 | -0.950967 | 1.5240081 | 0.20999212 | 1.7267849 | 0.5951295 | 1.0506092 |
| Mis18bp1  | -1.13972  | -0.756361 | -1.316716 | -1.418868 | -1.183281 | -1.393352  | 1.5234205 | 0.5891373 | 0.9169334 | 0.8419332 | 0.3525093  | 0.3407923 | 0.6633111 | -0.077831 | -0.977814  | -0.369095 | 0.0928117 | 1.4832138 |
| Mmp10     | -1.099718 | -0.941559 | -0.37085  | -1.091069 | -1.040793 | -0.778878  | 0.8235972 | 1.0685147 | 1.3132927 | 2.8622338 | 0.0355936  | -0.173371 | -0.081292 | -0.902949 | 1.3116382  | -0.940038 | -0.516256 | -0.283006 |
| Nxpe5     | 0.8636878 | 1.0336729 | 0.0550545 | 0.9986039 | 1.9774531 | 1.8479987  | -1.026149 | -0.693251 | -0.894545 | -0.755149 | -0.827795  | -0.803592 | -0.92058  | -0.379974 | -0.508556  | 0.9603558 | -0.358225 | -0.56901  |
| Fcgbp     | -0.228628 | 0.4911422 | 2.4248009 | 0.8262861 | 2.210473  | 0.2796733  | -0.904851 | -0.952038 | -0.208455 | 0.3420547 | -0.066594  | -0.405559 | -0.406461 | -0.906031 | -0.912239  | -0.055503 | -0.502951 | -1.025119 |
| Fbxo40    | 1.0698051 | 1.9259882 | 0.7314105 | 1.8393707 | 0.5375797 | 0.9914789  | -1.014093 | -0.441755 | -0.988671 | -0.940898 | -0.967213  | -1.028988 | -1.055729 | 0.4713004 | -0.536562  | -0.023089 | -0.474549 | -0.0993   |
| Rnf150    | 0.307996  | 0.3525809 | 0.4717104 | 2.009526  | 1.0784289 | 1.8252476  | -1.360813 | -0.804725 | -0.382114 | -1.058289 | -0.984665  | -0.654955 | -1.191173 | -0.068806 | -0.237144  | -0.101555 | 0.3194438 | -0.569806 |
| Fancb     |           |           |           |           |           |            |           |           |           |           |            |           |           |           |            |           |           |           |



|           |           |           |           |           |           |           |           |           |           |           |           |            |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| Prmt6     | -1.212944 | -1.403004 | -1.379318 | -0.959255 | -1.419958 | -1.222349 | 1.1433124 | 0.8164209 | 0.6875073 | 0.4837178 | 0.1838192 | 0.600501   | 0.6710626 | 0.116785  | 0.5218346 | 0.0422753 | 0.5727942 | 1.7567978 |
| Setd8     | -0.86853  | -0.557202 | -1.199822 | -1.268121 | -1.197185 | -1.354445 | 1.5731379 | 1.0638016 | 0.227307  | 0.2397346 | 0.5452626 | 0.175837   | 1.7278989 | 1.4541915 | -0.249965 | -0.216605 | -0.474158 | 0.3819329 |
| Rarres1   | 1.9479336 | 2.316256  | 0.3446221 | 0.3279543 | 1.4252328 | 0.9852043 | -0.666744 | -0.59116  | -0.686878 | -0.671389 | -0.545418 | -0.646697  | -0.718924 | -0.584692 | -0.359977 | -0.697458 | -0.512983 | 0.663081  |
| Chchd10   | 1.8568863 | 1.5742846 | 1.4720534 | 1.2642616 | 0.9451089 | 0.6211842 | -0.72778  | -0.774495 | -0.975916 | -0.686884 | -0.354177 | -0.240482  | -1.009772 | -0.019046 | -0.953083 | -0.056285 | -0.52833  | -0.813528 |
| Htrb1     | -1.027914 | -1.241336 | -0.938247 | -1.108023 | -0.434173 | -0.938006 | 1.2710662 | 1.0819286 | 0.204119  | 0.2560194 | 0.4785261 | 0.15694524 | -0.498724 | 0.4920096 | 0.5276297 | 0.4963549 | -0.212265 | -0.615207 |
| Cdc42ep1  | -1.048708 | -1.111535 | -0.616374 | -1.205722 | -0.984361 | -1.21185  | 0.5366317 | 0.7801485 | 0.5683777 | 0.120209  | 0.3701268 | 0.777611   | 0.3818728 | -0.637682 | 0.2369912 | 0.3082893 | -0.040884 | 2.7777121 |
| Hist1h1a  | -0.85003  | -0.918214 | -1.025911 | -1.034453 | -0.873343 | -1.225525 | 1.9674136 | 1.5642144 | 0.7078363 | 0.6425591 | 0.5580083 | 0.0872237  | 1.2050595 | -0.919286 | 0.4257768 | -0.903706 | 0.1778412 | 0.4217429 |
| Clip1     | 2.1293528 | 1.4352735 | 0.4472993 | 1.0963113 | 0.9119114 | 1.1038432 | -0.719936 | -0.420154 | -1.074524 | -0.503245 | -0.008735 | -0.739796  | -0.489308 | 0.316912  | -1.173099 | -1.236664 | -0.047391 | -0.127933 |
| Aknad1    | -1.158899 | -0.398556 | -0.891743 | -1.115058 | -1.010139 | -1.124225 | 0.737139  | 0.3755263 | 2.254057  | 0.7918996 | 0.4753311 | -0.121333  | 0.4515443 | 1.5574787 | 0.6703869 | -0.913595 | -0.769777 | 0.1899631 |
| Ccdc69    | 0.6511967 | 1.3738681 | 0.7674934 | 1.3587294 | 2.0420036 | 1.0425548 | -1.096613 | -1.063547 | -1.233288 | -0.472036 | -0.475568 | 0.1838708  | -0.509828 | -1.015709 | -0.835648 | -0.380215 | -0.652223 | 0.3149586 |
| Lce1h     | 0.6945096 | 2.165349  | 0.9778188 | 0.1843037 | 1.8349802 | 1.2243718 | -0.945924 | -0.97131  | -0.778938 | 0.1028998 | -0.11725  | -0.160076  | -0.297152 | -0.641219 | -0.378866 | -0.965446 | -0.815897 | -1.112155 |
| Omg       | -0.73108  | -1.154419 | -1.270375 | 0.0439997 | -1.40266  | -1.453712 | 1.4807009 | 1.4298631 | -0.167318 | -0.015344 | 0.0510943 | -0.150576  | 0.8428398 | -0.018718 | 1.4560252 | -0.23927  | 1.490365  | -0.191416 |
| Cyp2g1    | 1.3513721 | 1.9967986 | 0.7438051 | -0.305957 | -0.322917 | 2.6663912 | -0.639309 | -0.507702 | -0.327459 | -0.508452 | -0.528166 | -0.257847  | -0.549311 | -0.587789 | -0.336204 | -0.639309 | -0.608637 | -0.639309 |
| Ucn2      | -1.29498  | -1.142478 | -0.726964 | -1.210846 | -0.892848 | -0.929522 | -0.853565 | 0.3918891 | 0.8856216 | 1.8507759 | 0.834387  | 0.0951789  | 0.0887528 | 1.0480579 | 1.6177307 | -0.393425 | 0.8094891 | -0.177264 |
| Lig4      | -0.868014 | -0.999251 | -1.428066 | -1.041422 | -1.131351 | -0.956452 | 2.096074  | 1.3390895 | 0.3708006 | 0.7106961 | 0.1408307 | 0.2007285  | 0.9163686 | -0.457096 | 0.6183205 | -0.553173 | 0.3792066 | 0.8448743 |
| Prss46    | 2.5731039 | 0.347244  | 0.765622  | 1.9528071 | -0.053519 | 1.1826836 | -0.749429 | -0.749429 | -0.697037 | -0.665649 | -0.696741 | -0.405648  | -0.749429 | -0.604828 | -0.490785 | 0.060253  | -0.331116 | -0.688104 |
| Mmp12     | 1.2242847 | 0.4788271 | 1.1066445 | 1.3216281 | -0.13329  | 0.7958576 | -0.728397 | -0.740667 | -0.775588 | -0.802885 | -0.792949 | -0.686715  | -0.689359 | -0.635093 | -0.481736 | 1.00637   | -0.429994 | -0.643741 |
| Arhgap15  | 0.8725488 | 1.0290449 | 1.4275606 | 1.9402584 | 1.2467089 | 1.0789092 | -1.074677 | -1.074677 | -0.437505 | -0.180123 | -0.188733 | -0.549165  | -0.704408 | -0.900487 | -0.658621 | 0.7277876 | 0.0396583 | -0.266979 |
| Zfp280b   | -0.362087 | -1.226492 | -1.073359 | -1.087419 | -1.023662 | -0.880576 | 1.4280144 | 0.026517  | 0.5528591 | 0.584261  | 0.1735777 | 2.786631   | 0.5288347 | -0.588133 | 0.4058858 | 0.107523  | -0.290777 | 0.1233967 |
| Fzd4      | 0.7764927 | 1.4220546 | 1.0737536 | 1.1044128 | 1.4465352 | 1.9317709 | -0.902443 | -0.103192 | -0.915225 | -0.805869 | -0.813517 | -0.940149  | -0.496068 | -0.66243  | -0.023186 | -0.783793 | -0.37299  | -0.941598 |
| Armcx4    | -0.730015 | -0.613301 | -0.728081 | -0.453364 | -0.627188 | 0.2657102 | -1.169541 | -0.759265 | -1.111694 | -0.947017 | 0.0066193 | 0.44661    | -0.329719 | 1.9269181 | 1.6872164 | 1.719113  | 0.7678264 | 0.6418925 |
| Zbtb12    | -1.136078 | -1.425729 | -0.163107 | -0.517203 | -0.8729   | -0.924691 | 2.3422036 | 0.9987725 | 0.7312588 | -0.258387 | 0.28625   | -0.451033  | 0.4195914 | -0.570791 | 0.8759528 | 1.1899775 | -0.33267  | 0.7067815 |
| Ceacam19  | 1.5372787 | 1.8999443 | 0.2951257 | 1.0462821 | 1.4657353 | 0.6077042 | -1.027009 | -1.164504 | -0.987075 | 0.5686208 | 0.5248708 | 0.599903   | -0.354562 | -0.85276  | -1.164304 | -0.984368 | -0.917683 | -0.193199 |
| Fam26e    | 0.7374556 | 0.4660756 | -0.058858 | 1.1991416 | 0.7600824 | 0.4014607 | -0.59312  | -0.525532 | -0.570774 | -0.545477 | -0.525767 | -0.522371  | -0.570646 | -0.477877 | -0.479761 | -0.483986 | -0.338721 | -0.509525 |
| Mettl21d  | -1.044837 | -0.731535 | -0.774658 | -1.124196 | -0.754027 | -0.859696 | 1.4875595 | -0.210419 | 0.3360956 | 0.5644279 | -0.270002 | 1.6958911  | 0.196589  | 2.0104373 | 0.1177144 | -0.841898 | -0.831551 | 1.0340666 |
| H2afx     | -0.832355 | -0.990821 | -0.877294 | -0.950911 | -0.955969 | -0.101608 | 1.0687428 | -0.346283 | 0.2984621 | 0.6751501 | -0.062005 | 2.1269774  | 0.7143545 | -0.511957 | 0.0337811 | -0.224725 | -0.26476  | 2.1157174 |
| Rpp38     | -0.707251 | -1.108032 | -1.106084 | -1.060274 | -0.99012  | -0.988061 | 2.3942795 | 0.9581279 | 0.9107318 | 0.2425122 | 0.331995  | 0.8329761  | 1.1558785 | -0.296658 | 0.3367445 | -0.25943  | -0.960372 | 0.3129468 |
| Ccdc137   | -0.723799 | -1.228432 | -1.096972 | -0.886568 | -1.205551 | -0.544302 | -0.443918 | 1.1880092 | 0.7457816 | 0.1428696 | 0.5440294 | 0.570016   | 1.0060218 | 0.1202734 | 1.8551967 | -0.291754 | -1.260684 | 1.5097816 |
| Gltd1d    | -1.101411 | -0.902141 | -1.099683 | -1.220393 | -0.951342 | -1.29536  | 1.8138526 | 0.8342478 | 0.9067724 | -0.064865 | 0.6334117 | 0.1372585  | 1.835821  | 0.6158146 | -0.045723 | -0.472942 | -0.265893 | 0.6425785 |
| Skint9    | 2.7448162 | 1.2430967 | 0.2443344 | 0.8863758 | 0.9144968 | 1.2220537 | -0.765641 | -0.741925 | -0.590556 | -0.155198 | -0.384298 | -0.618662  | -0.685486 | -0.636597 | -0.626133 | -0.765641 | -0.527128 | -0.757908 |
| Pitpn     | -0.974791 | -1.046064 | -1.135557 | -1.318607 | -1.195132 | -1.412213 | 2.1781225 | 0.7182014 | 0.0017695 | 0.9334243 | 0.7050503 | 0.3105939  | 0.9504027 | 0.2801802 | 0.5765545 | -0.356869 | 0.2696777 | 0.5151919 |
| Atmab1    | 1.6992609 | -0.170337 | 0.7079681 | 2.5863846 | 0.2247403 | 1.3626889 | -0.828359 | -0.200562 | -0.351873 | -0.562342 | -0.728592 | 0.2587342  | -0.811082 | -0.467652 | -0.93247  | -0.181249 | -0.679183 | -0.187076 |
| Bex1      | 0.9612664 | -0.299333 | 1.5420651 | 2.055209  | -0.236343 | 2.2113293 | -0.777344 | -0.699404 | -0.72117  | -0.770766 | -0.76211  | -0.253486  | -0.780106 | -0.356165 | -0.375039 | 0.3166805 | -0.366926 | -0.688718 |
| Agmo      | 2.0224855 | 1.1098658 | 0.861087  | 1.6304927 | 0.5898615 | 1.4156371 | -1.105506 | -0.188206 | -0.8427   | -0.314948 | -0.322562 | -0.825518  | -0.101543 | -0.590657 | -0.718947 | -0.448505 | -0.323239 | -0.933205 |
| Gsg2      | -1.44104  | -1.232189 | -0.917041 | -1.002409 | -0.496521 | -1.427595 | 1.0823542 | 1.2289353 | 0.6850061 | 1.314301  | 0.9840126 | 0.4115017  | 0.37169   | -1.051313 | -0.372646 | 0.4301335 | 0.1397914 | 1.2930285 |
| Cxcr3     | -0.141517 | 0.7349328 | 1.3891385 | 1.4031918 | 1.7053979 | 1.3842546 | -1.472046 | -1.218154 | -0.587127 | -0.54007  | -0.767204 | -0.652522  | -0.855818 | -0.61815  | -0.886366 | 0.6113537 | 0.1821447 | 0.3285688 |
| Hear1     | -1.092504 | -0.985114 | -1.052432 | -1.235558 | -1.374511 | -1.301256 | 0.7843551 | 1.2841301 | 0.7279636 | 0.4376777 | 0.0607869 | 0.0374097  | 0.5123009 | -0.033252 | 0.9896624 | 0.2462414 | -0.121009 | 2.0885077 |
| D8Ertdd2e | -0.760308 | -0.984408 | -0.739907 | -0.748864 | -0.832061 | -0.921067 | 2.8077727 | 0.6314731 | -0.158177 | 0.154754  | -0.0909   | -0.279556  | 0.0705554 | -0.518718 | 0.2786713 | -0.241871 | 1.9584088 | 0.3745467 |
| Synpo2    | 1.2306211 | 1.5663449 | 1.429979  | 1.7203997 | 0.8523095 | 0.7875963 | -0.92349  | -0.789757 | -0.999206 | -1.02933  | -0.937728 | -0.820843  | -0.987507 | 0.1980835 | -0.591924 | -0.298525 | -0.022784 | -0.377409 |
| Lgals3    | 1.3552432 | 0.9519737 | 0.5665364 | 2.6264265 | 0.230997  | 1.304308  | -0.547208 | -0.773334 | -0.95507  | -0.651856 | -0.529449 | -0.642393  | -0.73199  | -0.373197 | -0.839809 | 0.2913427 | -0.456618 | -0.825903 |
| Sprr1a    | -0.224394 | -1.222697 | -0.493586 | -0.908574 | -0.789067 | -1.174967 | -0.130788 | 0.5258311 | -1.387629 | 1.445584  | 0.7308593 | 0.6621555  | 1.8747487 | 1.0880625 | 1.0880625 | 0.7157734 | -0.972541 | -0.283171 |
| Tcf19     | -1.257261 | -0.662709 | -0.973452 | -1.511103 | -0.877256 | -1.188453 | 0.3949862 | 1.3623835 | 0.8873014 | 1.6263965 | 1.0927851 | 0.9604469  | 0.9302315 | 0.334376  | 0.3348558 | -1.245008 | -0.588468 | -0.741194 |
| Hmgrp2b   | 1.4490312 | 1.269415  | 1.4958937 | 0.621495  | 1.2670396 | 1.8393597 | -0.945779 | -0.609846 | -0.907289 | -0.562615 | -0.601556 | -0.837529  | -0.681892 | -0.56439  | -0.242907 | -0.682388 | -0.508269 | -0.798645 |
| Hy1s1     | -0.684796 | -1.350904 | -1.446624 | -1.222063 | -1.271136 | -1.13616  | 1.368796  | 1.0051916 | 1.1040171 | 1.0907956 | 0.2133411 | 0.6352927  | 1.3552633 | -0.261232 | 0.1478356 | -0.181686 | -0.078408 | 0.7117566 |
| Prokr2    | -0.774768 | -0.715759 | -0.765864 | -0.706894 | -0.575659 | -0.688353 | -0.671254 | -0.266475 | -0.542388 | -0.537372 | -0.198996 | 0.4985462  | -0.752348 | 0.2125668 | 1.191933  | 2.4423189 | 0.8507479 | 1.2726361 |
| Mmp13     | -1.122136 | -1.051777 | -0.688013 | -1.089648 | -1.038093 | -0.971369 | 0.303401  | 0.958287  | 0.0912382 | 0.7085569 | 0.6846991 | 0.3978702  | 0.1869448 | -0.868382 | 1.2847022 | 0.212186  | 1.7520899 | -0.950553 |
| Fam78a    | 0.6882104 | 0.1632883 | 0.9306027 | 1.6042823 | 1.2097806 | 0.6608819 | -1.587659 | -1.434329 | -0.823619 | -1.150407 | 0.0116614 | 0.7186849  | -0.396812 | -0.730196 | -1.065444 | 1.4821614 | -0.164124 | -0.116964 |
| 1700019N1 | -0.787712 | -0.843827 | -0.661552 | -0.81761  | -0.87304  | -0.701917 | 2.3487155 | -0.336468 | 0.7088663 | 1.6466714 | 0.0866074 | -0.993629  | 0.3173721 | 0.7720708 | 1.382933  | -0.35496  | -0.855536 | -0.037565 |
| Sprr2f    | -0.724552 | -0.732802 | -0.639893 | -0.716284 | -0.683623 | -0.705697 | 0.2447123 | 1.1794631 | -0.636409 | 0.5178374 | -0.5664   | 0.4884284  | 0.1138895 | -0.625421 | 1.0275308 | 1.3895761 | -0.514684 | 0.9459    |



|            |           |           |           |           |           |            |           |            |           |           |            |           |           |           |           |            |            |            |
|------------|-----------|-----------|-----------|-----------|-----------|------------|-----------|------------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|------------|------------|
| 1100001G2  | 2.3677413 | 1.9697121 | 0.0045759 | 0.5714689 | 1.1437362 | 1.1932734  | -0.744235 | -0.709501  | -0.546932 | -0.501326 | -0.525441  | -0.63818  | -0.662815 | -0.615708 | -0.622289 | -0.570894  | -0.475582  | -0.637604  |
| Mest       | -1.244374 | -1.005717 | -1.301642 | -1.177313 | -1.193714 | -1.070632  | 1.2441379 | 0.5134263  | 1.1235574 | -0.471279 | -0.087073  | 0.3672677 | 1.3552188 | 0.88949   | 1.5226649 | 0.6288014  | -0.091491  | -0.001329  |
| Cd209f     | 1.587548  | 0.68132   | 0.571467  | 1.2670144 | 2.2073734 | 1.1858521  | -0.793697 | -0.658181  | -0.793697 | -0.793697 | -0.785143  | -0.784032 | -0.793697 | -0.595371 | -0.573567 | 0.3409072  | -0.551145  | -0.719227  |
| Spats2     | -1.219693 | -1.061013 | -1.27647  | -1.033215 | -1.070948 | -1.074048  | 0.1661067 | 1.2021824  | 0.0469714 | 0.2908175 | 0.0908388  | 0.1793633 | 0.5971916 | 0.5204751 | 1.0641801 | -0.642193  | 1.1437402  | 0.20757123 |
| Lax1       | -0.236257 | 0.478611  | 1.7285928 | 0.7760237 | 1.5419384 | 0.1319808  | -1.401921 | -1.246837  | -0.171988 | 0.2171969 | 0.158693   | -1.130801 | 1.187992  | -0.107643 | -0.512947 | -0.312011  | 0.2442819  | -0.680904  |
| Btla       | 0.8419343 | 1.1754999 | 1.2067416 | 1.1943412 | 1.9482889 | 1.4845577  | -1.301389 | -0.56949   | -0.464778 | -0.239061 | -0.553401  | -0.715001 | -0.751772 | -0.979729 | -0.78675  | -0.395744  | -0.49952   | -0.576731  |
| Slc6a7     | 1.1213802 | 0.589884  | 0.5279593 | 2.6386024 | 0.9579308 | 1.3851059  | -0.856496 | -0.608529  | -0.819966 | -0.856496 | -0.856496  | -0.753024 | -0.804053 | -0.557208 | -0.234629 | -0.007126  | -0.1893    | -0.67754   |
| Pfdn4      | -0.922688 | -0.533341 | -1.216222 | -1.012543 | -1.118566 | -0.849227  | 1.8711528 | 0.892431   | -0.370585 | 0.2382556 | -0.189981  | 0.8503063 | 0.0372853 | -0.579767 | 0.607332  | 0.1217677  | -0.147985  | 2.3223739  |
| Pard3b     | 1.6487956 | 0.9927989 | 0.6986577 | 1.9699245 | 1.1886267 | 1.2547492  | -0.922371 | -0.755156  | -0.883208 | -0.922256 | -0.85464   | -0.580857 | -0.912304 | -0.236939 | -0.360696 | -0.188821  | -0.322556  | -0.813748  |
| Dock8      | 1.0518262 | 1.1144378 | 1.1598379 | 1.6192706 | 1.2758669 | 1.7526799  | -1.002697 | -1.075223  | -0.756258 | -0.462463 | -0.437018  | -0.614377 | -0.821312 | -0.610678 | -0.941448 | -0.333217  | -0.473062  | -0.446454  |
| Rgs14      | 0.816695  | 0.5351413 | 0.9982867 | 1.9131608 | 1.7891384 | 0.460204   | -1.26259  | -1.252472  | -0.662594 | -0.567447 | -1.022259  | -0.345313 | -1.133384 | -0.303741 | -0.889896 | 0.800073   | -0.126308  | 0.2533051  |
| Rasal3     | 0.2753483 | 0.0142976 | 1.6573667 | 2.0570027 | 1.15342   | 0.5224406  | -1.183433 | -1.036484  | -0.547631 | -0.656393 | -0.735704  | -0.395306 | -0.912419 | -0.990875 | -0.712822 | 1.451503   | 0.088166   | -0.048478  |
| Gm9869     | -0.888598 | -0.855287 | -0.825293 | -1.556881 | -0.845191 | -1.313026  | 1.6437003 | 1.3788558  | -0.318052 | 0.8167217 | -0.310169  | 0.5424885 | 1.0713432 | 0.7456921 | 1.2561295 | -0.367582  | -0.696412  | 0.5215589  |
| Pld4       | -0.105607 | 0.5072763 | 1.4561988 | 1.2982822 | 1.8967318 | 1.4166029  | -1.256917 | -0.957394  | -0.679056 | -0.966187 | -0.976191  | -0.828204 | -0.944878 | -0.164115 | -0.50817  | 0.7761965  | 0.0887331  | -0.053301  |
| Gm13476    | 0.1689747 | 1.5283935 | 0.7885629 | 1.8963677 | 0.5352055 | 1.6287514  | -1.06118  | -0.982261  | -0.844915 | -1.121341 | -1.122074  | -0.630835 | -0.946756 | -0.315595 | -0.178812 | 0.8218195  | 0.0629447  | -0.227251  |
| 5330438D1  | -1.199738 | -0.489432 | -0.653907 | -1.342271 | -1.058942 | -1.271125  | 1.1290884 | 1.0605405  | 1.1437878 | 0.8310274 | 1.0889293  | 0.5893767 | 1.876016  | -0.018004 | -0.442496 | -0.727817  | -0.40784   | -0.107192  |
| Taf9       | -0.612301 | -0.406407 | -1.176639 | -0.790949 | -0.818238 | -0.739963  | 0.5043237 | 3.2807567  | 0.0322062 | -0.168557 | -0.455881  | -0.44334  | 0.3194972 | 0.4305011 | 0.6082703 | 0.0651216  | -0.380848  | 1.1296468  |
| Doca2a     | -0.795766 | -1.060907 | -0.647732 | -1.041673 | -0.996101 | -1.150059  | 1.3804755 | 0.9250645  | 1.5495383 | 0.7900142 | 0.2591754  | 0.3110984 | 0.2559006 | -0.274641 | -0.220014 | -0.421957  | -0.990495  | 1.1280784  |
| Ankrd44    | 0.5593957 | 1.4369335 | 0.7623385 | 1.4450608 | 1.4527438 | 1.6620076  | -1.216839 | -0.742167  | -0.950441 | -0.804271 | -0.857121  | -0.644101 | -1.027809 | -0.352133 | -0.711833 | 0.5199324  | 0.0878509  | -0.61955   |
| 9930013L2  | -1.729372 | -0.78735  | -0.798874 | -1.519517 | -0.797369 | -1.25594   | 0.1266224 | 0.0017786  | 1.1105586 | 1.306428  | 0.7294501  | 0.7690325 | 0.1346594 | 1.9537718 | 1.115731  | 0.3444158  | -0.114442  | 0.4163848  |
| Actn2      | 1.0233313 | 0.6382658 | 2.1243086 | 1.833754  | 0.5765323 | -0.900696  | -0.946602 | -0.812356  | -0.971501 | -0.958532 | -0.984647  | -0.9645   | -0.973128 | 0.451374  | -0.544999 | -0.176785  | 0.0481886  | 0.7276317  |
| Lrrc33     | 1.0280711 | 0.7619233 | 0.851056  | 1.6100755 | 1.3651055 | 1.3892259  | -1.254397 | -0.847766  | -0.780792 | -1.009877 | -0.992474  | -0.898225 | -0.93471  | -0.413472 | -0.500511 | 1.0306407  | 0.0203865  | 0.424570   |
| Prrmt1     | -0.889915 | -0.852677 | -1.089644 | -0.830567 | -0.927133 | -0.909181  | 0.3395501 | 2.2796229  | -0.149308 | 0.1299091 | 0.0475753  | 0.1547626 | 0.067149  | -0.627925 | 0.4938877 | 0.2179793  | 0.130772   | 2.4151489  |
| Bmpr1b     | -1.295766 | -1.128855 | -0.90931  | -1.159486 | -1.217545 | -1.076094  | 1.4468131 | -0.287091  | 0.1674043 | 0.7207254 | 1.4688037  | 0.653661  | 0.9707035 | -0.108377 | 1.266441  | -0.181626  | 1.0799296  | -0.409327  |
| Zfp961     | -1.008464 | -0.668395 | -0.980888 | -1.488736 | -1.171149 | -0.1012681 | 2.3993944 | 0.139488   | 1.1657165 | 0.5417972 | 0.6866509  | 0.256621  | 0.9512408 | -0.443285 | -0.071034 | 0.1596779  | -0.314424  | 0.865669   |
| 2810055G2  | -0.160503 | 1.4240047 | -0.968516 | 0.1800097 | 0.6027875 | 0.7360928  | 0.238679  | -0.673758  | -0.794015 | -0.641637 | -0.007208  | 0.7992665 | 2.1476746 | 0.0285524 | -0.350297 | -0.116344  | -0.472994  | -2.044768  |
| Atp6v1a    | 2.142533  | 0.6377528 | 0.3875924 | 1.955409  | 0.2439516 | 1.045893   | 0.893366  | -0.652482  | -1.136993 | -0.389802 | -0.569144  | -0.55301  | -0.511788 | -0.890512 | -1.118589 | -0.423284  | -0.016134  | -1.044519  |
| C130026I21 | -0.149653 | 0.6773427 | 0.2094034 | 1.7993918 | 0.9662649 | 0.7501055  | -1.126926 | -0.814039  | -0.875568 | -0.827189 | -0.680921  | -0.758853 | -0.847407 | -0.80225  | -0.590485 | 1.0660344  | -0.167117  | 0.2818672  |
| Cherp      | -0.891542 | -1.116373 | -0.661534 | -0.963693 | -1.281799 | -1.513418  | 1.740644  | 0.5483823  | 0.5512889 | 1.4201503 | 1.6935679  | -0.266157 | -0.056223 | 0.4380625 | -0.193275 | -0.515146  | 0.5111053  | 0.5561372  |
| Epha3      | -0.510742 | -0.298203 | -0.401894 | -0.107093 | -0.318413 | -0.171417  | -0.781649 | -0.352028  | -0.766687 | -0.810469 | -0.689362  | -0.523304 | -0.78086  | 1.5718901 | 2.8169378 | 0.6263818  | 0.1472295  | 0.2578618  |
| Robo2      | -0.917843 | -0.855257 | -0.950761 | -0.860323 | -0.383687 | -0.858377  | 1.3335619 | 2.64087    | 1.3024456 | -0.475354 | -0.722654  | 0.2572759 | 0.4356556 | 0.2100033 | -0.289908 | -0.381284  | -0.238797  | -0.106563  |
| Magi3      | -1.272166 | -1.00471  | -1.075348 | -1.086278 | -1.158347 | -0.933358  | 0.5439466 | -0.046744  | 0.3842714 | 1.2767394 | -0.208769  | -0.078869 | 0.7800905 | 1.0414437 | 0.647769  | -0.167564  | 0.0884649  | 0.8963964  |
| 31026297   | 0.9216449 | 0.0553305 | 0.5841979 | 0.5992366 | 1.1522697 | -0.181025  | -0.635043 | -0.299982  | -0.268117 | -0.21723  | -0.107754  | -0.587353 | -0.360495 | -0.653781 | -0.824634 | -0.308791  | -0.97113   |            |
| Hist1h1d   | -1.293545 | -0.944899 | -0.985484 | -1.375104 | -0.945775 | -1.609154  | 1.3958276 | -1.2674918 | 0.2943887 | 0.5927007 | 0.3682173  | -0.204077 | -0.016593 | 0.9376024 | 0.1455592 | 0.3746367  | -0.304418  | 1.856239   |
| Asap2      | -0.829594 | -1.002987 | -1.074892 | -0.903421 | -1.131473 | -1.080985  | 2.7786453 | 0.9855986  | 0.7074915 | 0.5926922 | 0.2559868  | -0.556835 | -0.070181 | 0.7055729 | 0.2811775 | 0.2290082  | 0.4602029  | -0.346008  |
| 5430435G2  | 1.5052896 | 0.283515  | 0.7282019 | 2.5440608 | 0.4223177 | 1.7133777  | -0.577685 | -0.841029  | -0.712831 | -0.477477 | -0.613211  | -0.47714  | -0.520283 | -0.654093 | -0.720418 | -0.381503  | -0.456159  | -0.764941  |
| Repin1     | 1.3828674 | 0.2519822 | 1.1731515 | 1.4634551 | 1.4082452 | 1.5639104  | -1.402581 | -0.340765  | -0.866237 | -1.041704 | -0.518223  | -0.574283 | -1.128719 | -0.742981 | -0.444338 | 0.4878869  | -0.144866  | 0.526801   |
| Nup107     | -0.953967 | -1.066235 | -1.284862 | -1.100277 | -1.102858 | -0.96421   | 0.2132121 | 0.0235592  | 0.2784913 | 0.6040875 | -0.140531  | 1.2585112 | 0.4019625 | -0.517401 | 0.7346159 | 0.9114601  | -0.19205   | 1.7152495  |
| Junb       | -1.312959 | -0.999999 | -0.831375 | -0.947429 | -1.253802 | -1.273023  | 1.9136839 | 1.6907195  | -0.320557 | 0.9630767 | 0.696102   | -0.149422 | 0.2784537 | -0.204332 | 0.8067619 | 0.6853525  | -0.11487   | 0.4096176  |
| Reep1      | -0.95394  | -0.714535 | -0.788056 | -0.969306 | -0.871594 | -0.8123    | -0.266012 | 2.7785243  | 0.8710701 | 0.3051403 | 0.091715   | 0.2494872 | 1.5861485 | -0.402663 | 0.3319467 | -0.49821   | -0.619665  | 0.6822497  |
| Prkcb      | 1.1635059 | 0.8713624 | 0.990307  | 2.0662945 | 0.8724195 | 1.6928358  | -1.065835 | -0.753127  | -0.641787 | -0.59923  | -0.724801  | -0.51341  | -0.82326  | -0.625973 | -0.814943 | 0.2429661  | -0.496067  | 0.838887   |
| Ubxn8      | -1.106949 | -1.438663 | -1.028038 | -1.127592 | -1.490082 | -0.836583  | 1.8507699 | 1.1557568  | 0.9176565 | 0.9227477 | 0.0421665  | 0.0740341 | 0.2681002 | -0.158739 | 0.0048902 | 0.2054749  | -0.4647804 | 1.2802699  |
| Lamb2      | 0.9691266 | 0.1472164 | 1.1395996 | 1.2340431 | 1.2758394 | 1.291478   | -0.827545 | 0.2595784  | -1.653566 | -1.380371 | -1.196738  | -0.731379 | -1.194073 | 0.7089071 | -0.081702 | 0.5715871  | -0.230023  | -1.236648  |
| Arhgef15   | -1.199541 | -1.113241 | -0.957267 | -0.965128 | -1.213359 | -0.97216   | 0.3926675 | 0.320186   | -0.168863 | 1.0004433 | -0.1362912 | -0.487584 | -0.188855 | 1.2000513 | 0.836585  | -0.313256  | 0.0442117  | 1.0083251  |
| Cyp2f2     | 1.2715058 | 0.928157  | 0.868679  | 1.4916199 | 2.714933  | 1.2510951  | -0.717785 | -0.670191  | -0.699902 | -0.711664 | -0.708721  | -0.707978 | -0.70653  | -0.631764 | -0.59627  | -0.67517   | -0.431064  | -0.685358  |
| Uba2       | -1.255366 | -0.45128  | -1.096274 | -1.042078 | -1.263388 | -1.100778  | 0.4725386 | -0.739719  | 0.6631753 | 0.8513461 | 0.3857533  | -0.158361 | 0.8659113 | 1.2614868 | 0.3541646 | -0.736081  | 1.6747483  | 1.3138001  |
| Aph1c      | 1.1567131 | 0.4693339 | 1.2761783 | 2.2751897 | 0.1328128 | 1.9213458  | -0.830248 | -0.545137  | -0.626742 | -0.630815 | -0.767272  | -0.600882 | -0.762808 | -0.434129 | -0.671846 | 0.0058347  | -0.534387  | -0.824143  |
| Jam2       | 1.1941804 | 0.9394874 | 0.8743958 | 1.5822545 | 0.9796013 | 2.0549631  | -0.761886 | -0.317196  | -1.04782  | -1.044832 | -0.759625  | -0.842419 | -0.883699 | -0.460895 | -0.270146 | -0.433446  | 0.1278678  | -0.921784  |
| Clec12a    | 0.4194694 | 1.8277916 | 1.5131013 | 1.6893135 | 1.3884202 | 1.4192451  | -1.092843 | -0.812209  | -0.701467 | -0.916282 | -1.022011  | -0.775859 | -0.675551 | -0.715862 | -0.367166 | -0.0887371 | -0.2       |            |



|           |           |           |           |           |           |           |           |           |           |           |            |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Set       | -0.95961  | -0.565682 | -0.952428 | -1.017911 | -1.040092 | -0.945387 | 1.0204315 | 2.7373966 | 0.0703788 | -0.203456 | -0.088376  | 0.0978755 | 0.314709  | -0.2289   | 0.8478305 | -0.211018 | -0.358545 | 1.4827836 |
| Cadm4     | -1.103251 | -0.214877 | -0.720528 | -0.616823 | -1.031582 | -1.130048 | -0.115727 | 0.6893575 | -0.139416 | 1.3620318 | -0.815357  | -0.316606 | 0.0165245 | 0.6446787 | 0.4067786 | 0.6156869 | 1.0407179 | 2.4277834 |
| Elp6      | -1.135662 | -0.866307 | -1.142072 | -1.268728 | -1.123932 | -1.086915 | 0.3788094 | 0.8732799 | 1.3814583 | 0.6574793 | -0.8733296 | 0.6904814 | 0.7645968 | 0.1241611 | 0.0661011 | -0.172581 | -0.959911 | 0.9688909 |
| Tmem158   | -1.213569 | -1.048431 | -0.694889 | -1.201999 | -1.056143 | -1.392539 | 0.2289095 | 1.9731367 | 0.8469701 | 0.7526195 | 0.2116139  | -0.478421 | 0.0029421 | -0.09002  | 0.336364  | 1.6921119 | 0.1668156 | 0.9645277 |
| Zfp667    | 2.1801577 | 1.5467211 | -0.190004 | 0.9683385 | 0.509948  | 1.4211084 | -0.086069 | -0.91834  | -0.522019 | -1.18886  | 0.2866513  | -0.504343 | 0.4854295 | -0.855448 | -0.676381 | -0.426636 | -0.841775 | -1.188478 |
| Kcnmb4    | -0.916872 | -0.648043 | -0.705977 | -0.752829 | -0.789614 | -0.771956 | 0.3721954 | 1.3109929 | 0.7746111 | 0.124907  | 0.0039113  | -0.344769 | 1.4890926 | -0.273796 | -0.128804 | -0.489028 | -0.413485 | 0.349463  |
| Gm9958    | -0.318986 | -0.693941 | -1.314983 | -0.899168 | -0.838034 | -0.077109 | 2.4026233 | 1.6626055 | -0.312928 | 0.2363154 | 0.2168507  | -0.349716 | 1.4653569 | 0.7354669 | -0.429354 | -0.102625 | -0.507116 | 0.1256505 |
| 9130008F2 | -1.038794 | -1.020238 | -1.125459 | -1.247044 | -1.225463 | -0.791294 | 1.8597739 | 0.5993951 | 1.5547458 | 0.2122094 | 0.3165939  | 1.5793558 | 0.6587038 | -0.430508 | -0.203527 | -0.071352 | -0.09402  | 0.5719217 |
| Cntrn1    | -0.868326 | -0.765359 | -0.566004 | -0.842327 | -0.658579 | -0.811746 | 0.2646619 | -0.304557 | 2.9950677 | 0.378971  | -0.277135  | 1.7780082 | 0.4632313 | 0.2356784 | -0.666282 | -0.114568 | -0.485451 | 0.244716  |
| Smyd1     | 1.0889054 | 2.560611  | 0.7926071 | 0.8277347 | 1.1177635 | 0.9541556 | -0.926047 | -0.577454 | -0.954153 | -0.9418   | -0.95143   | -0.918778 | -0.689631 | 0.0791837 | -0.502406 | -0.371635 | -0.265911 | -0.321716 |
| Pdlm1     | -0.837294 | -1.323791 | -1.057856 | -0.935313 | -1.378299 | -1.237318 | 0.9175623 | 1.9458253 | -0.948335 | 0.6595856 | 0.8354045  | 0.2098553 | 0.8450087 | -0.03765  | 0.7505893 | 0.1090755 | 0.8580609 | 0.6248884 |
| C1ra      | 0.3257244 | 0.5147091 | 1.439131  | 1.649171  | 1.5187738 | 1.5549874 | -0.887078 | -0.671223 | -0.88011  | -1.006171 | -1.166764  | -0.454723 | -1.184423 | -0.47898  | -0.67     | 0.6317707 | -0.198162 | -0.036634 |
| Ntrk2     | 0.6767889 | 1.1764652 | 1.3351086 | 1.5488004 | 1.5375493 | 1.5401046 | -1.210868 | -0.828158 | -0.30492  | -0.726191 | -0.873132  | -0.692402 | -1.068365 | -0.153867 | -0.475748 | -0.59051  | -0.233549 | -0.657107 |
| Zfp93     | -0.705615 | -0.859044 | -0.94379  | -1.198984 | -1.200321 | -1.087331 | 1.3870464 | 1.4087307 | 1.7628457 | 0.6710398 | 0.1365753  | -0.030635 | 0.2274664 | 0.8096308 | 0.9221835 | -0.08543  | -1.322929 | 0.1085901 |
| Pgbd1     | -0.874361 | -0.726972 | -0.647691 | -0.946769 | -0.771362 | -0.927067 | 0.3040766 | 0.4912008 | -0.328732 | 0.7948016 | 0.4055661  | -0.43179  | 0.8876902 | 1.0874107 | -0.017417 | -0.546812 | -0.159457 | -0.322317 |
| Tns1      | 1.6115317 | 0.2986037 | 1.9340186 | 1.7449291 | 0.8928381 | 0.9547015 | -1.126978 | -0.809529 | -0.690792 | -0.854001 | -0.582216  | -0.784603 | -0.93242  | -0.090008 | -0.449114 | -0.174405 | -0.171578 | -0.770977 |
| Fat2      | -1.340791 | -0.621881 | -0.298718 | -1.226702 | -0.511141 | -1.173777 | 0.3226692 | -0.169389 | 2.403893  | 1.014773  | 1.6812363  | 0.0508477 | 0.3492525 | 0.6997155 | -0.817513 | 0.2377461 | 0.0842192 | -0.684477 |
| Snupn     | -1.44044  | -0.807551 | -1.124256 | -1.082444 | -1.451116 | -1.009357 | 1.4223971 | 1.1416291 | 0.5353631 | 0.0879535 | 0.3392046  | 1.4125911 | 0.9274903 | -0.615948 | 0.0798364 | 0.9261861 | -0.245596 | 0.9040577 |
| Slc6a2    | 3.6115708 | 0.3552364 | 0.0150117 | 0.9612577 | 0.1748159 | 0.182905  | -0.660276 | -0.209312 | -0.34073  | -0.2071   | -0.321907  | -0.636978 | -0.444145 | -0.671244 | -0.126081 | -0.686468 | -0.32142  | -0.667137 |
| Gm9968    | 1.0176959 | 1.8075013 | 0.8299121 | 1.3678164 | 0.447624  | 0.8384062 | 0.6028038 | -0.280448 | -0.865995 | -1.692351 | -1.113531  | -0.93971  | 0.3706629 | -0.450834 | 0.2395421 | 0.2688996 | -0.953758 | -1.351598 |
| Atp10b    | 2.0743554 | 2.0804474 | 0.256426  | 0.6174065 | 1.1763572 | 0.9995428 | -0.812698 | -0.9009   | -0.581434 | -0.158776 | 0.1368216  | -0.44955  | -0.411916 | -0.835657 | -0.869763 | -0.905832 | -0.571655 | -0.843176 |
| Epm2a     | 1.1062095 | 1.5914493 | 0.5723097 | 1.5259376 | 1.2624299 | 1.1599242 | -0.362916 | -0.29527  | -0.826142 | -1.359727 | -0.885494  | -0.7186   | -0.958546 | 0.6990132 | -0.863782 | 0.0511424 | -0.847992 | -0.849946 |
| Cdc47     | -0.296244 | -0.558349 | -0.972784 | -1.20768  | -1.121005 | -1.20363  | 2.1849247 | 1.0267741 | 1.528051  | -0.185437 | 0.0302565  | 0.4856233 | 0.5294773 | -0.138968 | 0.3054372 | -0.664741 | -0.916783 | 1.1750381 |
| B4galnt4  | -1.228811 | -0.640625 | -0.695498 | -0.917784 | -0.755928 | -1.145267 | 0.2379494 | 0.2543394 | 1.2951385 | 0.7435853 | 0.9137009  | -0.573318 | 0.8679833 | 0.8174618 | 0.042132  | -0.61939  | -0.941623 | 2.3723856 |
| Hmcn2     | 1.1514253 | 0.2494265 | 2.3374604 | 1.7440238 | 0.8019224 | 1.2320349 | -0.294189 | -0.530778 | -0.77215  | -0.780723 | 0.737027   | -0.841754 | -0.644813 | -0.611222 | -0.64139  | -0.595288 | -0.57356  | -0.516387 |
| Rras2     | -1.192838 | -1.2388   | -0.868939 | -1.142305 | -1.001231 | -1.210463 | 1.1163596 | 1.7261948 | 1.0542062 | 0.3183395 | 0.1754526  | 0.5061446 | 0.1716369 | -0.680871 | 0.3149737 | 1.7767459 | 0.1151571 | 0.0197378 |
| Ghr       | 0.5184869 | 1.9299602 | 0.7116089 | 1.5577559 | 1.4958593 | 1.4966683 | -0.751148 | -0.958629 | -0.5689   | -0.620341 | -0.6443    | -0.090959 | -0.768218 | -0.379139 | -0.568036 | -0.547689 | -0.931965 | -0.940929 |
| Gemin6    | -1.139172 | -0.947365 | -1.080745 | -1.053076 | -1.224667 | -1.21379  | 0.6238958 | 1.6882211 | 1.5819824 | 0.9447639 | -0.272738  | -0.1951   | 0.2873791 | 0.0309832 | 1.1390353 | 0.4576516 | -0.571486 | 0.9438666 |
| Abcd2     | 0.4503874 | 2.0148498 | 1.2725849 | 1.3678595 | 1.154314  | 1.5734438 | -0.807106 | -0.643685 | -0.744631 | -0.788954 | -0.835347  | -0.76465  | -0.749986 | -0.58567  | -0.561479 | -0.295492 | -0.373963 | -0.682477 |
| Fmnl1     | 1.0261813 | 1.0558804 | 0.8004418 | 1.3922077 | 0.4133848 | -0.666409 | -1.455859 | -0.314611 | -0.696647 | -0.613506 | -0.73315   | -0.722645 | -0.853934 | -1.021929 | -0.531093 | 1.4457334 | -0.702425 | -0.553574 |
| 1700034H1 | 2.3561195 | 1.8270011 | 0.7459521 | 0.4162995 | 0.5771657 | 0.6238681 | -0.363239 | -1.530008 | -0.313503 | 1.8848414 | -0.147459  | -0.402071 | -0.181399 | -0.453622 | -0.919071 | -1.360998 | -0.960353 | -0.103166 |
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| Fancm     | -0.724052 | -0.581393 | -1.467961 | -1.338489 | -1.383866 | -1.231317 | 0.2123953 | 0.2852027 | 0.4077525 | 1.3306381 | 0.7962478  | 1.382962  | 0.855619  | 0.5804833 | 0.7145332 | -0.600331 | -0.405828 | 0.3864421 |
| Skint4    | 1.6355664 | 2.3527905 | 0.1004912 | 0.609289  | 0.4587143 | 1.1517799 | -0.491593 | -0.293191 | -0.378707 | -0.28544  | -0.664548  | -0.385494 | 0.1218747 | -0.805641 | -0.979666 | -0.172204 | -0.386028 | 1.163028  |
| Cldn23    | 2.9295861 | 1.3514819 | -0.183014 | -0.030321 | 0.599722  | 1.0515134 | 0.2017065 | -0.846835 | -0.932971 | -0.042335 | -0.52983   | 0.2060959 | -0.963412 | -1.056056 | -0.799785 | -0.575262 | -0.35095  | -0.029335 |
| Fut2      | 1.0642305 | 2.6119553 | 0.3177662 | -0.25765  | 0.8947651 | 0.4416786 | -1.125587 | -1.03011  | -0.716074 | 0.5171643 | 0.2009948  | -0.114769 | -0.271881 | 0.7259171 | -1.338716 | -1.23726  | -0.872011 | 1.1895864 |
| Nod2      | -1.141384 | -0.14137  | -0.051084 | -0.95843  | -0.690136 | -0.932406 | 0.5320066 | -0.063272 | 1.1600652 | 0.7308717 | 0.0023296  | -0.384026 | 1.5067307 | -0.881664 | 0.2285047 | -0.078996 | -0.599542 | 0.6626715 |
| Clca1     | 0.8865626 | 0.3709801 | 0.6039439 | 0.4995537 | 0.6622192 | 0.1258664 | -0.981032 | 0.0438102 | 0.0063335 | -0.556234 | -0.319179  | 0.3587794 | 0.0896493 | -0.722814 | -0.945532 | -0.93634  | -0.768355 | -1.126312 |
| Lipm      | 1.0574485 | 2.4781913 | 0.4756813 | -0.134918 | 1.0841532 | 0.8752347 | -0.931176 | -1.170999 | -0.930137 | -0.114322 | -0.175295  | 1.042247  | -0.261979 | 0.122855  | -0.151547 | -0.718269 | -1.088505 | -0.458664 |
| St3gal5   | 1.9802756 | 0.1201909 | -0.320595 | 1.7307677 | 1.2694301 | 1.3125617 | 0.2631608 | -0.548564 | 0.4967894 | -1.392581 | -1.069404  | -0.452023 | -0.306013 | -0.156157 | -0.505027 | -0.301705 | -1.145385 | -0.974707 |
| B4gal6    | 0.870343  | 0.3990542 | 0.8045085 | 2.0815263 | 0.9627378 | 1.5878404 | -1.042602 | -0.538445 | -1.044787 | -0.977049 | -0.878343  | -0.773769 | -1.130932 | -0.246981 | -0.228977 | 0.7464656 | -0.063744 | 1.166848  |
| Ticam2    | 0.7686419 | 0.5385144 | 1.2721685 | 1.598139  | 1.2867174 | 1.9244176 | -0.935924 | -0.791274 | -0.797439 | -0.922862 | -0.848994  | -0.718933 | -0.84958  | -0.571564 | -0.55929  | 0.7089453 | -0.36961  | -0.691724 |
| Rdh9      | 1.2318408 | 2.2563288 | 0.2755575 | 0.0721729 | 1.0072889 | 1.1609512 | -0.821582 | -0.684812 | -0.60666  | -0.452245 | -0.419058  | 0.2757857 | -0.652441 | -0.676181 | -0.673451 | -0.693214 | -0.704318 | -0.796963 |
| Snx32     | 0.7032131 | 0.5053695 | 1.7031931 | 1.906753  | 0.8212692 | 1.6592937 | -1.195758 | -0.799468 | -1.301604 | -0.937839 | -0.640419  | -0.555042 | -0.621097 | -0.447773 | -0.340783 | 0.6270387 | -0.543187 | -0.998654 |
| Npm3      | -0.772707 | -0.838115 | -1.015522 | -1.300333 | -1.035243 | -0.972651 | 0.5553932 | 1.1143929 | -0.731336 | 0.7224549 | 0.3751282  | 0.8859571 | 0.8055307 | -0.12458  | 0.0004797 | -0.366128 | -0.252373 | 2.6829523 |
| Dendn1b   | 0.2534791 | 0.2031368 | 1.2410346 | 0.9213994 | 1.1192489 | 1.1331431 | -1.218698 | -1.260329 | -0.853656 | -0.276105 | 0.946321   | 0.1307037 | -0.646074 | 0.9622377 | -0.665172 | -0.778329 | -0.500531 | -0.653169 |
| Usp39     | -0.96923  | -0.822565 | -0.912864 | -0.928227 | -1.152777 | -0.706351 | 2.0725046 | 1.5052476 | 0.081932  | 0.2120131 | -0.18809   | 0.0980142 | 0.2968554 | -0.250901 | 0.1871264 | -0.23348  | 0.0063528 | 2.0744378 |
| 18100110I | -1.652192 | -0.61027  | -0.824584 | -1.301197 | -1.016107 | -1.286538 | 0.3848433 | 0.3659119 | 1.4591029 | 1.2392644 | 0.4526854  | 0.0740367 | -0.145861 | 1.5298917 | 0.6100448 | 0.3436383 | 1.1255833 | -0.748641 |
| Myh1      | 0.2813732 | 0.2550439 | 2.4231807 | 2.6252346 | 0.4727998 | -0.050398 | -0.707605 | -0.611806 | -0.707017 | -0.706874 | -0.705894  | -0.708101 | 1.376652  | -0.385276 | -0.315988 | -0.134597 | -0.455107 |           |
| Lig1      | -1.025639 |           |           |           |           |           |           |           |           |           |            |           |           |           |           |           |           |           |



|           |            |           |           |            |           |            |           |           |           |           |            |            |           |           |           |            |           |           |
|-----------|------------|-----------|-----------|------------|-----------|------------|-----------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|-----------|-----------|
| Fcer1g    | 0.5661304  | 0.2354915 | 1.4650102 | 1.6703822  | 0.5365462 | 1.8661617  | -1.127553 | -0.927475 | -0.734041 | -0.995951 | -0.999508  | -0.799415  | -0.853052 | -0.604191 | -0.321968 | 1.1833393  | -0.019614 | -0.140295 |
| Lin9      | -1.025356  | -0.156006 | -0.192748 | -1.386247  | -1.179333 | -0.72124   | 1.1748673 | 0.1819487 | 0.6442709 | 1.2087125 | -0.4344    | 0.2668456  | 1.1933461 | 0.2832157 | -0.34617  | -1.14387   | 0.7148394 | 1.9172876 |
| Hist1h1b  | -0.869291  | -0.797771 | -0.984963 | -1.065333  | -0.870407 | -1.23934   | 1.2602183 | 0.2091074 | -0.138289 | 0.5837255 | 0.2703988  | -0.053836  | 0.3026373 | -0.395562 | -0.127593 | 0.1800031  | -0.253277 | 2.1695726 |
| Nap1l1    | -1.069225  | -1.024455 | -1.176849 | -1.066655  | -1.221213 | -0.962442  | 0.404478  | 2.0421113 | -0.025905 | -0.496071 | -0.153637  | 0.9226192  | -0.175848 | 0.6462744 | 0.808855  | 1.4460943  | -0.001504 | 1.103372  |
| Col13a1   | -1.419864  | -1.357234 | -0.738942 | -1.387121  | -0.981505 | -1.204827  | 0.6182111 | 0.3028147 | 0.8290662 | 1.0374835 | 1.0268734  | 1.0913783  | 0.2352763 | -0.443894 | 1.6935675 | -0.302792  | 0.328687  | 0.6782116 |
| Lilrb3    | 1.26457    | 0.2685165 | 0.9290716 | 2.262242   | 0.5549786 | 1.7473062  | -0.959985 | -0.750172 | -0.798188 | -0.843862 | -0.866618  | -0.779926  | -0.811701 | -0.563565 | -0.539928 | 0.5305818  | -0.184791 | -0.458441 |
| Fam57b    | 1.5959382  | 2.6894106 | 0.4127757 | 0.5344288  | 0.8885895 | 0.98182    | 0.1586205 | -0.745259 | -0.591926 | -0.648412 | -0.596446  | -0.33782   | -0.647858 | -0.574364 | -0.746958 | -0.848635  | -0.7481   | -0.775788 |
| Vwa8      | 1.8106075  | 0.8869931 | 0.8773024 | 1.798418   | 0.6880681 | 1.0785334  | -0.801148 | -1.477896 | -0.877679 | -0.840391 | -0.686714  | -0.429157  | -1.114037 | -0.637162 | -0.042315 | -0.38629   | 0.5893719 | -0.436504 |
| Hnmpa3    | -1.213282  | -0.966599 | -0.101259 | -0.813721  | -1.215551 | -1.313999  | 1.3144264 | 1.3005836 | 0.2534927 | 0.4669121 | 0.5678823  | -0.101536  | 0.5528455 | 1.5183959 | 1.3144264 | -0.101284  | 0.5405774 | -0.157586 |
| Gm5506    | -1.245015  | -0.623832 | -0.961726 | -1.214897  | -0.989519 | -1.246724  | 2.0027404 | 0.1959819 | 1.7374283 | -0.097817 | 0.9750338  | 0.2105758  | 0.4869571 | 0.2036004 | 0.5944836 | -0.147033  | -0.774684 | 0.8944446 |
| Rad51l1   | -0.867828  | -0.739965 | -0.825383 | -0.935744  | -0.883183 | -1.20453   | 2.7148509 | 1.4001769 | 0.4661297 | 0.8376835 | 0.4086908  | 0.3260803  | 0.5501757 | 0.0977616 | 0.1744224 | -0.23214   | -0.929333 | -0.357866 |
| Pde1a     | 0.6831231  | 1.1139518 | 0.8862284 | 1.1352155  | 0.6247459 | 1.6832848  | -1.294238 | -0.974786 | -1.251162 | -1.123301 | -1.123614  | -0.644782  | -1.204879 | -0.255368 | 0.0541174 | 0.947554   | 0.6630096 | 0.0808998 |
| Lep       | 0.2420051  | 1.7695362 | 0.3174876 | 1.50419    | 0.8482502 | 2.4951592  | -0.588849 | -0.471003 | -0.70627  | -0.658935 | -0.70627   | -0.70627   | -0.70627  | -0.400314 | -0.586686 | -0.688659  | -0.29598  | -0.661124 |
| Olfr494   | 3.3210978  | 0.1069129 | -0.460439 | 1.427445   | 0.8821431 | 0.2896648  | -0.562188 | -0.262059 | -0.562188 | -0.16188  | -0.411402  | -0.562188  | -0.562188 | -0.562188 | -0.562188 | -0.562188  | -0.23434  | -0.562188 |
| Gzmd      | -0.526747  | -0.526747 | -0.341969 | -0.526747  | -0.484326 | -0.526747  | -0.412846 | -0.456769 | -0.432726 | -0.526747 | -0.434345  | -0.204757  | -0.4668   | 0.0224225 | 0.4766224 | 1.2264706  | 0.5416104 | 0.6011485 |
| R74862    | -1.188544  | -1.176688 | -1.435111 | -1.139264  | -0.662943 | -0.472906  | 2.0929054 | 0.4866028 | 1.0347352 | 1.0653902 | 1.2763972  | 0.4832127  | 0.7065439 | -0.293819 | -0.514672 | -0.388595  | -0.430211 | 0.5569648 |
| Hist1h3f  | -1.03002   | -1.133657 | -0.948237 | -1.118843  | -0.887763 | -1.207623  | 1.5742786 | 0.7130414 | -0.203704 | 0.8906936 | 0.1911585  | -0.187477  | 0.4260907 | -0.416941 | 0.2812182 | 0.3623487  | 0.3073605 | 2.388074  |
| Sic27a7   | 2.6291111  | 1.5593233 | 0.7223215 | -0.225024  | 1.1438695 | 1.0041625  | -0.296267 | -0.936944 | -0.943505 | 0.0454123 | -0.1671251 | -0.57084   | -0.408462 | 0.2054791 | -0.631555 | -0.866347  | -0.940633 | -0.886262 |
| Tonsl     | -1.535076  | -0.810478 | -0.969006 | -0.575819  | -1.601039 | -1.371186  | 1.1945116 | 0.3068144 | 0.528222  | 0.646939  | 1.2991091  | 0.6893405  | 0.500743  | -0.864973 | 0.5221015 | 0.3334962  | 0.1315508 | 1.5801492 |
| Csf2ra    | 1.040323   | 0.1529438 | 0.8953604 | 2.644912   | 0.260368  | 0.7198789  | -1.007293 | -0.868479 | -0.84404  | -0.813691 | -0.834701  | -0.226142  | -0.683875 | -0.551527 | -0.687962 | 1.4604195  | -0.210519 | -0.445756 |
| Fxyd2     | 3.2050699  | 0.385091  | 0.2896481 | 0.8028916  | 0.7025816 | 1.2129209  | -0.40641  | -0.600399 | -0.63315  | -0.741628 | -0.668649  | -0.686771  | -0.65539  | -0.404294 | -0.545451 | -0.207358  | -0.464247 | -0.584456 |
| Actg2     | -0.548994  | -0.782463 | -1.18147  | -0.834485  | -1.02387  | -0.1076919 | -0.61879  | 0.2943559 | -0.667224 | -0.454188 | 0.0489892  | 0.8172435  | -0.068178 | 1.2511009 | 2.3393267 | 0.1073254  | -0.034975 | 1.3680813 |
| Trp53     | -1.069066  | -1.072053 | -0.635985 | -0.875343  | -0.987656 | -1.241019  | -0.068976 | 1.1885933 | 1.5498256 | 0.876043  | 1.5662333  | -0.1015673 | 0.3397015 | -0.937736 | 0.9932035 | 0.2582405  | 1.1258577 | 1.0058081 |
| Nrm       | -0.968461  | -0.950564 | -1.25462  | -0.1018257 | -0.699046 | -1.237806  | 0.8495579 | 1.3423495 | 1.8183417 | 0.3043941 | 1.2681761  | 0.1090807  | 0.3840288 | 0.9948941 | -0.422142 | -0.139471  | -0.850857 | -0.330347 |
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| Zfp930    | -0.915225  | -0.602206 | -1.288183 | -1.37097   | -1.473799 | -1.167053  | 1.9333794 | 0.813624  | 0.6428735 | 0.2280085 | 0.0656192  | -0.008643  | 0.632589  | -0.003909 | 0.6357212 | 0.2924854  | -0.133957 | 1.7174123 |
| Mug1      | 1.3002273  | 1.182779  | 0.5080315 | 0.6393076  | 0.5669795 | 1.3271589  | -0.634803 | -0.711038 | -0.526512 | -0.615657 | -0.711038  | -0.711038  | -0.711038 | -0.637131 | -0.601711 | -0.711038  | -0.270445 | -0.682533 |
| 9430015G1 | -0.699172  | -1.068659 | -1.002834 | -0.747711  | -0.96077  | -0.638391  | 0.6774976 | -0.492143 | 2.1229999 | 0.7592437 | 0.4381782  | 0.1515928  | 1.2162455 | -0.101393 | 1.3841372 | 0.7275027  | -1.188262 | 0.3336383 |
| Chpt1     | 0.6161985  | 1.6312318 | 1.4230371 | 1.6379753  | 1.3484728 | 1.2323056  | -0.900847 | -0.767521 | -0.259888 | -0.863197 | -1.00203   | -0.904049  | -0.844331 | -0.321562 | -0.643015 | -0.383077  | -0.457557 | -0.542146 |
| Kif13b    | 0.6966902  | 1.4269352 | 1.0908006 | 0.9456622  | 1.4269352 | 1.0678473  | -0.780187 | -1.584974 | -1.50167  | 0.6388597 | 0.4165126  | 0.2902851  | -0.742008 | -0.286111 | -0.844411 | -0.965267  | -0.486646 | -0.806554 |
| Alox5ap   | 0.4148869  | 0.4052411 | 2.1747989 | 0.8099227  | 1.9741037 | 0.6893821  | -1.065349 | -0.891984 | -0.804926 | -0.879391 | -0.895973  | -0.698035  | -0.392364 | -0.731833 | -0.52425  | 1.0269898  | -0.453651 | -0.193979 |
| Hist1h4a  | -0.407839  | -1.483116 | -0.834948 | -0.782775  | -0.616607 | -0.855138  | -0.328193 | -0.108546 | 0.1081794 | 0.3443401 | 0.4086965  | -0.305784  | 0.5893759 | -1.4625   | 1.264932  | 0.619284   | 0.4821674 | 2.3922544 |
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| Alyref2   | -0.552142  | -0.791994 | -1.067915 | -1.034749  | -0.540855 | -0.860854  | 2.2117834 | -0.606744 | 0.1164113 | 0.7843505 | -0.247286  | -0.669066  | 0.6216622 | 2.0274178 | -0.314508 | -0.701464  | 0.9017102 | 0.724242  |
| Ppih      | -0.836468  | -0.762603 | -0.864928 | -1.082988  | -1.029329 | -0.917159  | 0.1637353 | -0.447946 | 2.0678243 | 0.4568629 | -0.098568  | 1.2884605  | 0.7649006 | -0.993766 | 0.6426954 | -0.053955  | -0.172726 | 1.8678664 |
| Zfp941    | -1.068294  | -0.449204 | -0.844886 | -0.825933  | -0.926795 | -0.627471  | 0.1324504 | 0.7503375 | -0.517907 | 0.1611718 | 0.8696836  | 3.0964584  | 0.2288445 | -0.751272 | 0.3512766 | 0.3866696  | -0.460677 | -0.869898 |
| Calm5     | -1.4662525 | 2.6065299 | 1.711428  | 0.0558795  | 0.4911956 | 1.5226969  | -0.462797 | -0.397627 | -0.47937  | -0.315244 | 0.0602596  | -1.059312  | -0.620248 | -0.370187 | -0.645056 | -0.872337  | -0.962873 | -0.890178 |
| C030014I2 | -0.866106  | -0.789337 | -1.146867 | -1.153868  | -0.926672 | -1.232201  | 0.8190691 | -0.540004 | -0.78197  | 0.6751824 | 0.1707748  | 0.036841   | 0.253572  | 2.0036318 | 0.2719165 | 0.8831009  | -0.654294 | 0.2654221 |
| Sntb1     | 2.9835903  | 0.9656356 | 0.2841748 | 1.20955    | 0.8727235 | 0.7441382  | -0.755266 | -0.667657 | -0.504271 | -0.400988 | -0.524133  | -0.636303  | -0.719618 | -0.615908 | -0.627834 | -0.578232  | -0.370845 | -0.658268 |
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| Ces4a     | 2.1203321  | 0.3112866 | 0.1397469 | 0.6145501  | 1.2066736 | 1.0389429  | -0.689433 | -0.551503 | -0.634466 | -0.511337 | -0.594128  | -0.689433  | -0.664128 | -0.489636 | -0.550117 | -0.68792   | -0.480598 | -0.689433 |
| H2-Eb1    | -0.370741  | 0.1304056 | 2.0987929 | 1.4498716  | 1.4824849 | 0.8669065  | -1.26722  | -0.983944 | -0.560503 | -0.817804 | -0.902886  | -0.349276  | -0.991319 | -0.45695  | -0.694853 | 0.4087757  | 0.066089  | -0.013359 |
| Layn      | 1.5958203  | 0.0061978 | 0.8699981 | 2.0097094  | 0.0560114 | 1.8114534  | -0.92303  | -0.57392  | -0.917857 | -1.010173 | -0.941239  | -0.606847  | -0.951076 | -0.561322 | 0.4562543 | 0.4910803  | -0.20159  | -0.603438 |
| Eno3      | 0.9380626  | 2.3583689 | 1.2286139 | 1.0109153  | 1.1854314 | 1.0907916  | -0.775892 | -0.669155 | -0.791022 | -0.807599 | -0.807226  | -0.793376  | -0.785544 | -0.306059 | -0.538724 | -0.541923  | -0.370525 | -0.625156 |
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| Hist1h4c  | -0.879186  | -0.301879 | -0.98704  | -0.964481  | -1.319721 | -1.180373  | 0.5875405 | 2.3512824 | 0.3567236 | 0.3271153 | 0.1428308  | -0.873934  | 0.4233567 | -0.328002 | 0.7298779 | -0.095463  | 0.1830776 | 1.8281758 |
| Cd302     | 0.7710043  | 0.3019065 | 0.4700318 | 1.5586697  | 1.0543809 | 2.1159662  | -1.113819 | -0.91506  | -1.065002 | -1.071175 | -1.045059  | -0.566787  | -1.008693 | -0.302404 | -0.035121 | 1.0274756  | 0.1716275 | -0.348572 |
| Gmfg      | 0.4949716  | 0.5602219 | 0.891735  | 1.6394683  | 1.1325752 | 1.4938239  | -1.328736 | -0.728536 | -0.87675  | -1.094961 | -0.173216  | -0.802129  | -0.916535 | -0.607388 | -0.437703 | 1.3942887  | 0.3985021 | -0.       |



Zfp599 -1.006433 -0.922048 -1.095164 -1.355027 -1.24354 -1.349219 1.3554253 1.8204721 0.7170894 0.3894825 0.2533892 0.8967549 0.7194558 0.2103935 0.8580703 -0.009445 -0.7207 0.4810434

I7rn6 -1.211468 -0.655406 -0.868403 -1.445561 -1.11946 -1.126832 1.2503137 1.9379106 0.6829719 0.8796254 0.253681 0.4459234 0.660456 0.3052956 0.0579375 -0.704948 -0.58418 1.2421429

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Impf1 0.7935615 0.701083 1.017895 0.9128324 1.3252337 1.3212183 -1.569491 -0.67293 0.131028 -0.922622 -0.87059 -0.618578 -1.237428 -1.163626 1.0852542 -0.486201 0.9139266

Cnmn2 -1.084426 -0.930445 -0.603718 -1.105193 -0.7711562 -0.777461 0.5421206 -0.33876 0.1651273 1.3541437 0.7874356 0.6296455 0.5708533 -0.761488 -1.192098 0.5807175 0.3941823 0.4811947

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|            |           |           |           |            |           |           |            |            |           |           |           |            |           |            |           |            |           |           |
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| SNORA61    | -0.343554 | -0.343554 | -0.343554 | -0.343554  | -0.343554 | -0.343554 | -0.343554  | -0.343554  | 2.7919372 | -0.343554 | 2.7049428 | -0.343554  | -0.343554 | -0.343554  | -0.343554 | -0.343554  | -0.343554 | -0.343554 |
| U1         | -0.235702 | -0.235702 | -0.235702 | 0.40069384 | -0.235702 | 0.235702  | -0.235702  | -0.235702  | -0.235702 | -0.235702 | -0.235702 | -0.235702  | -0.235702 | -0.235702  | -0.235702 | -0.235702  | -0.235702 | -0.235702 |
| U1         | 1.7290274 | -0.592805 | -0.816646 | -0.816646  | -0.09802  | 0.490185  | 2.0897673  | -0.529414  | 0.2919007 | 1.7391303 | -0.816646 | 0.6979901  | 0.4450003 | -0.546236  | -0.816646 | -0.816646  | -0.816646 | -0.816646 |
| U2         | 1.070088  | -1.84141  | -0.431878 | -0.487108  | 1.0780932 | 0.8975309 | 0.6775356  | -1.84141   | 0.0719231 | 0.0472681 | -0.539606 | -0.301263  | 0.5918948 | -1.841341  | 1.3151306 | 0.4068368  | 1.0304672 | -0.107708 |
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| U1         | -0.772516 | -0.929718 | -0.528088 | -0.850306  | -0.772516 | -0.72723  | -0.168848  | -0.909987  | 1.2803582 | -0.476622 | -0.219222 | 0.2359356  | -0.151944 | -0.925147  | 1.8351572 | 1.5508698  | 0.6597227 | 1.8701032 |
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| SNORA42    | -0.235702 | -0.235702 | -0.235702 | -0.235702  | -0.235702 | -0.235702 | -0.235702  | -0.235702  | -0.235702 | -0.235702 | -0.235702 | -0.235702  | -0.235702 | -0.235702  | -0.235702 | 0.40069384 | -0.235702 | -0.235702 |
| SNORA3     | 1.7225845 | -1.240649 | 0.1016570 | 0.6971535  | -0.59153  | -1.387835 | 1.4150674  | -0.698722  | 0.4884783 | 1.3533103 | -0.634068 | 0.0824325  | -0.959324 | -1.214428  | 0.0970006 | 0.3725913  | 0.4652252 | -0.98403  |
| U2         | 0.6919282 | -1.872583 | 0.231186  | -0.706348  | 0.035141  | 0.4631315 | 0.569984   | -1.861079  | -0.208088 | 0.9708708 | 0.3511773 | -0.410533  | 0.4997082 | -1.872     | 1.4227656 | 0.6919282  | 0.9067380 | 0.0680081 |
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| SNORA2     | -0.539377 | -1.346207 | 1.6134713 | 0.1636571  | 1.2290201 | -0.954823 | 0.2877908  | -0.299045  | 0.2444653 | 0.4123157 | 0.1669414 | 1.3557167  | -0.924684 | -1.669948  | 0.6696077 | -1.479014  | 1.1369268 | -0.066814 |
| U1         | 0.5174912 | -0.88189  | 0.1764112 | -0.136946  | -0.542914 | -0.357643 | 3.1961461  | -0.88189   | 0.9350819 | -0.768498 | -0.794459 | 0.6923529  | 0.3822262 | -0.784802  | -0.531012 | 0.6801146  | -0.450217 | -0.450453 |
| U1         | -0.235702 | -0.235702 | -0.235702 | -0.235702  | -0.235702 | -0.235702 | -0.235702  | -0.235702  | -0.235702 | -0.235702 | -0.235702 | -0.235702  | -0.235702 | -0.235702  | -0.235702 | -0.235702  | -0.235702 | -0.235702 |
| U1         | -0.845589 | -0.934444 | -0.654849 | -0.89506   | -0.779912 | -0.813502 | -0.151741  | -0.923607  | 0.8113556 | -0.439544 | -0.124863 | 0.6782089  | -0.096871 | -0.934444  | 1.3312315 | 1.8491063  | 1.0389475 | 1.8854872 |
| U1         | 2.7510397 | -0.511703 | 1.4268513 | -0.10078   | -0.273194 | -0.356613 | -0.872659  | -0.659222  | 1.5455562 | -0.872659 | -0.422392 | -0.872659  | 0.1485677 | -0.181991  | -0.872659 | 0.872659   | 0.4811048 | 0.05144   |
| U2         | 1.6364152 | -1.80762  | 0.2713426 | -0.5879    | 0.1014443 | 0.6732129 | 0.5051571  | -1.80762   | 0.0241757 | 0.7416647 | -0.214789 | -0.419338  | 0.4047459 | -1.807651  | 1.1568818 | 0.448212   | 0.9191156 | -0.239339 |
| Tacc1      | 1.231727  | 0.3599266 | 0.625354  | 2.1450612  | 0.7644379 | 1.595551  | -1.296739  | -0.96214   | -0.832269 | -0.92606  | -0.914766 | -0.657098  | -0.909532 | -0.327689  | -0.179048 | 0.7553469  | 0.0433074 | -0.515372 |
| Cd209b     | 1.6319928 | 1.8118384 | 0.956144  | 0.408162   | 1.6190623 | 1.3619493 | -0.769062  | -0.638544  | -0.769062 | -0.769062 | -0.769062 | -0.769062  | -0.751381 | -0.551398  | -0.605438 | -0.070017  | -0.588935 | -0.738123 |
| Dhrs3      | 1.3252071 | 0.711928  | 1.4854515 | 2.220857   | 0.5819353 | 1.3157213 | -1.027848  | -0.898944  | -0.458493 | -0.79135  | -0.64743  | -0.52088   | -0.775291 | -0.410998  | -0.652666 | -0.156777  | -0.461927 | -0.838475 |
| Gm1976     | -1.142558 | -0.507707 | -1.266222 | -0.176831  | -0.600522 | -1.142419 | -0.053151  | 1.1991515  | 1.5124404 | -0.161368 | 0.1128805 | 1.8005338  | 1.3446806 | 0.6994137  | -0.821202 | -0.488146  | -0.256463 | 0.8484895 |
| Adams1s1   | 0.8975963 | 1.2843911 | 1.1068424 | 0.5167495  | 1.2197997 | 1.960534  | -1.086852  | -0.288624  | -0.873026 | -1.195561 | -0.810989 | -0.687584  | -1.147955 | -0.103855  | -0.350473 | 0.8737892  | -0.491402 | -0.823382 |
| Prrp4      | -0.8899   | -1.158212 | -0.910002 | -1.117881  | -1.089268 | -1.16536  | 0.6894462  | 1.8753148  | 0.4982611 | 0.0666774 | 0.4101282 | 0.301288   | 1.0696344 | -0.827588  | 0.2315689 | -0.383465  | 0.9351556 | 1.8283191 |
| Slc31a2    | 1.5039397 | 1.6215291 | 1.1778726 | 1.2918971  | 1.1208456 | 0.514002  | -1.210996  | -0.664882  | -0.69336  | 0.2773673 | 0.0261379 | -0.150735  | -0.022319 | -0.890493  | -1.027671 | -0.488089  | -0.95783  | -1.427234 |
| AVS12931   | 1.5180588 | 1.2721787 | 0.2070094 | 1.7185828  | 0.7564317 | 1.4240707 | -1.368108  | 0.5297269  | -0.770319 | -0.694559 | -0.967293 | -0.790303  | -0.402735 | 0.2311827  | -0.66725  | -0.761673  | -0.030218 | -1.208804 |
| Yp537b     | -0.909326 | -0.105597 | -0.81277  | -1.146321  | -0.978532 | -1.112739 | 1.984008   | 0.2000809  | -0.359955 | 0.112888  | 0.1868621 | 0.2882826  | 0.8383549 | -0.582187  | 1.1298297 | 0.3012447  | -0.302865 | 0.4138391 |
| Serpina3c  | 1.3234994 | 2.4003758 | 1.2439738 | 1.21451    |           |           |            |            |           |           |           |            |           |            |           |            |           |           |



|           |           |           |           |           |           |           |           |           |            |           |           |           |           |           |           |           |           |            |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|
| Hist1h2ae | -1.041947 | -0.905254 | -1.111141 | -1.1658   | -0.991528 | -1.371398 | 1.6689238 | 1.3328462 | 0.1314118  | 0.6709138 | 0.4726091 | -0.156697 | 0.3344659 | -0.230188 | 0.3827972 | 0.160568  | -0.178379 | 1.9977971  |
| Hist1h3e  | -1.040137 | -0.883591 | -0.980205 | -1.207862 | -0.861988 | -1.336968 | 1.085069  | 1.3420726 | -0.107682  | 0.8124071 | 0.1663891 | -0.23274  | -0.123256 | 0.0488364 | -0.075454 | 0.4796742 | 0.1783811 | 2.0251154  |
| Hist1h4e  | -1.006209 | -1.164577 | -0.914308 | -1.023645 | -0.836476 | -1.286036 | 1.081560  | 0.9615668 | 0.1024142  | 0.4573469 | 0.2692137 | -0.558117 | 0.493569  | -0.033115 | 0.6728691 | 0.3134113 | -0.155578 | 2.6193021  |
| Hist1h2bj | -0.868607 | 0.0870605 | -0.822244 | -1.005233 | -0.844281 | -1.062043 | 0.8588114 | 3.3339207 | -0.048836  | -0.117655 | 0.1127617 | -0.38892  | 0.1750219 | 0.2256849 | -0.012119 | -0.163186 | -0.190374 | 0.7302373  |
| Hist1h2br | -0.900195 | -1.137881 | -0.875616 | -1.12588  | -0.643081 | -1.332973 | 1.44469   | -0.222757 | 0.5256463  | 0.406265  | 0.7228959 | 0.0119331 | 1.4674108 | -1.393563 | 0.6640498 | 0.6515826 | 0.1271883 | 1.6099381  |
| Hist1h4m  | -0.676223 | -1.139424 | -0.974667 | -1.00195  | -0.978828 | -1.23035  | 0.5803451 | 1.5668565 | 0.2160846  | 0.8422784 | 0.1967966 | -0.321325 | -0.105161 | -0.904808 | 1.1459809 | 0.1638262 | 0.4323126 | 1.284663   |
| Hist1h2bp | -0.122163 | -0.332076 | -0.938296 | -1.303941 | -0.959144 | -1.408341 | 1.5814126 | 1.8180685 | 0.3459875  | 0.8594442 | 0.5976655 | 0.0345325 | 0.4683886 | -1.427957 | 0.5651723 | 0.2581251 | 0.0434746 | 0.8241466  |
| Hist1h3c  | -0.639706 | -0.436995 | -0.529045 | -0.760025 | -0.58075  | -0.839606 | 1.350446  | -1.240621 | 1.0613063  | 0.8208494 | 0.645588  | -0.014909 | 0.325256  | -1.479709 | 0.9523429 | 0.3850736 | 0.17239   | 1.8680132  |
| Hist1h3h  | -0.609285 | -1.47246  | -0.517556 | -0.680764 | -0.530109 | -0.881129 | 1.6299064 | -1.181493 | 0.3223582  | 0.8649452 | 0.478061  | 0.0298936 | 0.5882112 | -1.39635  | 0.2982502 | 0.6348041 | 0.2586156 | 2.1640999  |
| Ctxn3     | 1.9658339 | 1.0669566 | 0.8911571 | 0.2517373 | 2.2532016 | 0.8214803 | -0.834344 | -0.819049 | -0.834344  | -0.834344 | -0.834344 | -0.753681 | -0.834344 | -0.377096 | -0.39937  | -0.047019 | -0.084769 | -0.597665  |
| Lyz1      | 0.8662786 | 0.8622507 | 0.7994753 | 1.9815571 | 0.2034353 | 1.8031605 | -0.951529 | -0.69267  | -0.912977  | -0.940845 | -0.940278 | -0.710477 | -0.87695  | -0.400777 | -0.324427 | 1.2390768 | -0.301871 | -0.702433  |
| Lyz2      | 0.4697328 | 1.5011887 | 0.6575772 | 2.3135858 | 1.9797931 | 1.4200882 | -0.915346 | -0.668098 | -0.873067  | -0.90562  | -0.893    | -0.743871 | -0.840407 | -0.35246  | -0.335088 | 0.9648231 | -0.280233 | -0.717799  |
| Cd300lh   | 0.4368419 | 0.2585489 | 0.9754947 | 1.7034812 | 0.5315346 | 2.6850727 | -0.978993 | -0.731432 | -0.74819   | -0.864069 | -0.859324 | -0.755181 | -0.85243  | -0.343679 | -0.41935  | 0.3946738 | -0.121471 | -0.311529  |
| Gm11710   | 0.813806  | 0.2045764 | 0.5996253 | 2.3532904 | 1.965547  | 1.5956376 | -0.101739 | -0.774669 | -0.829728  | -0.820382 | -0.856024 | -0.865983 | -0.864124 | -0.445759 | -0.555773 | 0.6591896 | 0.1123776 | -0.520875  |
| Sifn9     | -1.364867 | -1.087547 | -0.524242 | -1.27606  | -1.030066 | -1.32936  | 0.2546461 | 1.0739765 | 0.2341891  | 0.9226726 | 0.2614103 | 1.4713168 | -0.035722 | -0.820881 | 1.0123355 | 0.5415378 | 0.0018962 | 1.6947646  |
| Fbp1      | 0.2497746 | 1.1273795 | 0.2168582 | 1.5621409 | 2.072489  | 1.3479622 | -0.183407 | 0.3033931 | -0.768497  | -0.919641 | -1.083407 | -1.007815 | -0.688396 | -0.588805 | -0.269648 | 0.7303051 | -0.481944 | -0.718742  |
| Ahnak     | 0.6561224 | 1.7106646 | 0.4503929 | 1.3056498 | 0.5490494 | 1.2592605 | -0.32701  | 0.0554548 | -1.480332  | -0.10795  | -0.214474 | -0.494752 | -0.758124 | 1.2278209 | -1.090344 | -0.252634 | -0.607014 | -1.881782  |
| 049348A0  | 1.6053621 | 2.3437779 | 0.3272626 | -0.295906 | 1.244031  | 1.0726703 | -0.924817 | -0.628194 | -0.629177  | 0.5008732 | 0.0584664 | -0.563409 | -0.582558 | -0.563409 | -0.602006 | -0.968539 | -0.939562 | 0.2685006  |
| 9930111J2 | -0.40616  | 1.0366386 | 2.5241827 | 1.1144856 | 1.9558281 | 0.8772341 | -1.329728 | -1.01371  | -0.575981  | -0.488541 | -0.775221 | 0.0368417 | -0.900709 | -0.54799  | -0.617967 | 0.6133994 | -1.74015  | -0.481826  |
| 9930111J2 | -0.289388 | 0.635996  | 2.4781182 | 1.2634774 | 1.2573589 | 1.037608  | -1.271829 | -1.091172 | -0.582305  | -0.57389  | -0.774184 | 0.0612161 | -0.917385 | -0.725488 | -0.471174 | 0.4904294 | -0.081809 | -0.446183  |
| Cdc99     | -1.23149  | -1.182319 | -1.145476 | -1.216384 | -1.228267 | -1.223152 | 1.1627062 | 1.2048842 | 0.5617229  | 0.7964156 | 0.0477261 | 0.5855381 | 0.5001614 | -0.283333 | 0.3201637 | 0.4795616 | -0.026464 | 1.8780065  |
| Fam196b   | 1.1179113 | 0.7600739 | 1.1740014 | 0.0881395 | 0.9083103 | 1.3531805 | -1.204418 | -0.931483 | -0.490096  | -0.628508 | -0.77301  | -0.764289 | -0.911448 | -0.767753 | -0.582403 | 0.5151967 | -0.081623 | -0.781783  |
| Fcho1     | 0.5571288 | 2.4163308 | 1.5140535 | 1.0658311 | 1.0531375 | 0.8050498 | -0.760761 | -1.123366 | -0.909711  | 0.0507037 | 0.0539036 | 0.058582  | -0.336606 | -0.284689 | -1.144877 | -0.669481 | -1.104093 | -0.881136  |
| Sp140     | -0.664384 | 1.0260566 | 2.531835  | 0.8989399 | 1.022046  | 0.9744714 | -1.326743 | -0.437479 | -0.491886  | -0.507388 | -0.843508 | -0.74986  | -0.016845 | -1.258641 | -0.351919 | -0.34146  | 0.3755209 | -0.424897  |
| Fat1      | -1.282773 | -1.096215 | -0.711382 | -0.696252 | -0.694057 | -1.063334 | 1.327806  | 1.3376769 | 1.0931252  | 0.1856353 | 1.2941798 | -0.722192 | -0.083884 | 0.7969212 | 0.8869792 | -0.021126 | 1.5482614 | -1.231374  |
| 4930581F2 | -1.095712 | -0.861889 | -1.193495 | -1.45978  | -0.830004 | -0.643882 | -0.772921 | 0.2459399 | 1.4446066  | 0.307845  | -0.503703 | 1.1208505 | 0.5346427 | 0.4475749 | -0.22259  | 2.1477059 | 0.588236  | 0.742919   |
| Mmp27     | 2.0388245 | 2.4360498 | 1.2143705 | -0.230557 | 0.6402629 | 0.3696151 | 0.2157805 | 1.734452  | -0.809207  | -0.839223 | -0.751037 | -0.60763  | -0.652533 | 0.026866  | -0.340223 | 0.522471  | -0.581909 | -0.908528  |
| Ccnd1     | -1.155299 | -1.207447 | -0.929653 | -1.026751 | -1.035039 | -0.94746  | 0.1101025 | 2.692338  | -0.095036  | 0.3175732 | 0.523567  | 0.2906089 | 0.0917574 | 0.1762091 | 1.536792  | 0.2216514 | 0.0684133 | 0.3674855  |
| Env2b     | -0.791874 | -0.450316 | 0.8930757 | 1.0390093 | 0.3600483 | -2.373342 | -0.248714 | 0.1475145 | 0.2201088  | 0.9664305 | 0.0682355 | 0.383554  | -2.316566 | 0.5595716 | 0.4917638 | 0.4865894 | 0.9878104 | -0.422899  |
| Ampd1     | 0.3513995 | 3.282893  | -0.14511  | 0.1058443 | 0.8281629 | 1.2545503 | -0.284315 | -0.364789 | -0.824419  | -0.560241 | -0.729162 | -0.649516 | -0.733604 | -0.445343 | -0.515447 | -0.485618 | -0.50564  | 0.735355   |
| Nlrp1b    | 0.6081618 | 1.163838  | 1.0764783 | 1.6111291 | 0.9309944 | 1.567564  | -1.446098 | -1.258038 | -0.676831  | -0.853181 | -1.081091 | -0.189347 | -0.682993 | -1.022466 | -0.317596 | 1.3000618 | -0.107872 | 0.7378264  |
| Cyp3a57   | 1.9921472 | 2.536771  | -0.205756 | 0.3284917 | 1.0058494 | 1.2083589 | -0.624009 | -0.599805 | -0.599747  | -0.423857 | -0.549691 | -0.816268 | -0.590456 | -0.565886 | -0.563889 | -0.646124 | -0.501672 | -0.646124  |
| Adamt1s3  | 0.237866  | 0.3505795 | 0.8815393 | 1.2313616 | 1.3703288 | 2.6072292 | -1.122196 | -0.036613 | -0.348122  | -0.537101 | -0.093735 | -0.004282 | -1.231736 | -1.020345 | -0.136677 | -0.686175 | -0.844087 | -0.628195  |
| Ndn1e     | -0.871716 | -0.101781 | -0.068526 | -0.990013 | -1.149012 | -1.154051 | 1.8053475 | 2.0641649 | 0.0976407  | 1.0259709 | 0.3309782 | 0.6855907 | 0.6692764 | -0.202022 | -0.548412 | -0.42237  | -0.029825 | 0.6785755  |
| Mrgprb1   | 0.9559445 | 1.4625235 | 1.5555243 | 0.7203428 | 1.3947571 | 1.8478644 | -0.90696  | -0.663194 | -0.8757    | -0.599115 | -0.676417 | -0.700413 | -0.606246 | -0.543524 | -0.485002 | -0.744226 | -0.240282 | -0.895878  |
| Kc13177   | 1.4934251 | 2.9146228 | 0.1501961 | 0.3035352 | 1.1098103 | 0.934836  | -0.657836 | -0.567254 | -0.575044  | -0.410257 | -0.563625 | -0.657836 | -0.64669  | -0.558552 | -0.474189 | -0.657836 | -0.479468 | -0.657836  |
| Bttd8     | -0.995131 | -0.813293 | -0.585141 | -1.276925 | -0.949753 | -0.700651 | 0.5176125 | 0.5386466 | 1.1065206  | 0.0490024 | -0.003092 | -0.248679 | 1.5050363 | 0.8190395 | -0.409485 | -0.187576 | -0.838579 | 0.4724477  |
| Utp3      | -1.058697 | -0.992464 | -1.063289 | -1.06671  | -0.897471 | -1.155057 | 1.2405418 | 2.3625775 | -0.1516373 | -0.117756 | 0.0423755 | 0.4835101 | 0.9745368 | -0.127903 | 0.5498635 | -0.351598 | -0.253426 | 1.279328   |
| Sars2     | -1.010602 | -0.504209 | -0.983839 | -1.261826 | -0.752535 | -1.575167 | 0.8423621 | 0.3554029 | 0.6736464  | 0.5791472 | 1.2286014 | 0.6980507 | 0.7290202 | 0.4528261 | -0.5634   | 0.510009  | -0.566166 | 2.1978309  |
| Pla2g4d   | -1.061272 | -0.82738  | -0.649871 | -1.00939  | -0.831911 | -0.969877 | 0.1369293 | -0.050859 | -0.171124  | 2.1879529 | 0.4508228 | -0.18112  | 1.1007516 | 0.9814646 | 1.4666648 | -0.898609 | -0.820904 | 1.1497306  |
| Skint3    | 2.3104552 | 2.1322352 | 0.3269132 | 0.5449826 | 0.9133637 | 0.6432665 | -0.497837 | -0.140716 | -0.723336  | -0.203126 | -0.206514 | -0.076316 | -0.454177 | -0.365574 | -1.029932 | -0.925618 | -0.728152 | -0.1069887 |
| Rabepk    | -0.542906 | -0.488237 | -1.208271 | -1.328869 | -0.996014 | -1.220144 | 2.3016771 | 0.0973919 | 0.3155248  | 0.4398372 | 0.1926415 | 0.154096  | 0.078134  | 0.6853255 | 0.2714109 | -0.189998 | -0.599731 | 2.0381317  |
| Ccl19     | 2.6954019 | 0.5899992 | 0.4882351 | 1.3399756 | 1.1066831 | 1.1837921 | -0.767402 | -0.562508 | -0.503542  | -0.706881 | -0.638822 | -0.752401 | -0.67738  | -0.622576 | -0.536195 | -0.483483 | -0.360077 | -0.741821  |
| Sdr16c6   | 2.1621649 | 2.4855327 | 0.1057488 | 0.4351461 | 0.9467106 | 0.910487  | -0.673711 | -0.633534 | -0.651188  | -0.460567 | -0.526485 | -0.497634 | -0.550659 | -0.59786  | -0.570325 | -0.774256 | -0.50916  | -0.600411  |
| Zfp827    | -0.922168 | -0.710091 | -1.074074 | -0.955742 | -1.10538  | -0.879432 | -0.582725 | 1.1961852 | 0.2802604  | 0.1260781 | 0.0914943 | 0.2677628 | -0.303659 | 0.6568647 | 2.9657609 | 0.205074  | 0.3696185 | 0.3471726  |
| Ptges3    | -0.810022 | -0.880029 | -1.147874 | -1.140405 | -1.248858 | -1.21382  | 0.09369   | 2.0643072 | 0.5066342  | -0.006314 | 0.2612624 | 0.4319428 | 0.2804483 | -0.121524 | 0.338488  | -0.226551 | 1.4008288 |            |
| Gm10311   | -1.231831 | -0.438986 | -0.408999 | -0.918036 | -1.30444  | -1.341992 | 2.2931107 | 0.0726838 | 1.5210903  | 0.1599475 | 0.4319074 | 0.6013695 | 0.8768187 | 0.4097124 | 0.6330047 | -1.123299 | -0.109484 | -0.122579  |
| Naip5     | 0.5040242 | 0.4949976 | 1.0603907 | 1.9234911 | 0.3979541 | 1.6861711 | -1.295155 | -0.91981  | -0.815081  | -0.62962  | -1.172847 | -0.285163 | -0.797051 | -0.73426  | -0.544717 | 1.4524985 | -0.159078 | -0.166745  |
| Ct1qtnf9  | 0.6661015 | 1.5594449 | 1.086708  | 1.533319  | 0.6869441 | 1.7029754 | -0.991629 | -0.87318  | -0.107129  | -0.132704 | -1.238159 | -1.066607 | 0.0889988 | -0.015023 | -0.110677 | -0.781219 |           |            |



Mup11 0.112355 2.8731609 0.8742702 1.8845901 0.9196146 -0.238768 -0.587157 -0.351005 -0.585204 -0.587157 -0.583659 -0.587157 -0.587157 -0.426428 -0.500849 -0.585378 -0.459373 -0.584699

Mup7 -0.001288 3.5506199 0.4805617 1.2319576 0.356533 -0.293639 -0.496689 -0.21198 -0.496689 -0.496689 -0.496989 -0.496989 -0.293322 -0.40482 -0.494095 -0.420796 -0.496989

Al427809 1.3883237 -0.317005 0.1010543 2.522228 0.7695004 0.5126242 -1.147605 -1.05479 -0.797712 -0.885973 -0.624662 -0.879976 -0.329091 -0.505463 0.1905646 1.5828937 -0.028722 -0.199119

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Ggh 1.8475822 2.2743752 0.6026937 0.3726554 0.7139603 0.9914823 -0.96735 -0.784558 -0.765791 -0.532186 -0.667675 0.4333633 -0.218515 -0.749992 -1.183118 -0.000349 -1.141792 -0.224788

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Mlycd 1.1672514 0.6947308 1.5390064 1.9187457 0.6935999 0.7376083 0.1933895 -0.774691 -1.03185 -1.053227 -0.615791 -1.537528 -1.451664 0.3773367 -0.337557 0.0044674 -0.152398 -0.37143

Snmp40 -0.9303 -0.810528 -1.053625 -0.913966 -0.93735 -0.732074 -0.012358 -0.568373 1.8799508 0.5003005 -0.000636 0.6250375 0.7371117 -0.753502 0.7350349 0.0937199 -0.283085 2.4246413

Ntf5 -0.533067 -1.009257 -1.310626 -1.00738 -0.926358 -1.123712 1.7717015 2.1162408 0.6380933 0.6302564 0.7869456 0.0048575 0.6859507 -0.356011 0.1439962 -0.815285 -0.334663 0.6386151

Zfp319 0.2578807 -1.739822 -0.374051 -0.31139 -0.669719 -0.658496 2.0336045 0.5014777 2.5410841 0.0719315 0.5892126 -0.792365 0.0287642 0.28568 -0.461875 -0.64885 -0.197785 -0.455282

Klk5 0.339714 1.7391223 1.0580461 -0.139923 1.111931 0.914309 -1.139518 -0.931332 -0.574587 0.2976233 1.0203634 -0.396108 1.4798174 0.903546 -0.754054 -1.13708 -0.87296 -1.111817

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Adn1 1.3292169 0.6541243 0.8263343 0.7861807 2.5148197 1.9059582 -0.893105 -0.83043 -0.739486 -0.35898 -0.747009 -0.511475 -0.800718 -0.411143 -0.530669 -0.636137 -0.471391 -0.72609

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Cox7a1 1.5865827 1.0355193 1.5155853 2.1066513 1.0767104 0.3598702 -0.813474 -0.806365 -0.814068 -0.834242 -0.845291 -0.674213 -0.803466 -0.455631 -0.483802 -0.331568 -0.324019 -0.494781

Zfp568 -0.343747 -0.1016587 -1.118866 -0.721923 -1.43885 -1.111273 2.4321151 -0.4812 1.1638239 0.789533 -0.615 -0.037366 0.2331207 -0.288591 0.6304984 1.1037223 0.7068479 0.1137412

Gramd2 -0.993591 -0.703166 -0.800908 -1.10783 -1.060054 -1.20203 1.8796375 -0.111287 1.5717727 1.2369313 1.0814129 0.5593333 1.0631009 0.2946055 -0.366829 -0.266783 -0.702369 -0.371444

Amy1 0.7463026 1.8423488 1.6090624 1.120034 1.2328048 1.4048356 -0.096872 -0.80117 -0.236522 -0.96194 -0.756797 -0.546018 -0.513178 0.702204 -0.721305 -0.540221 -0.530972 -0.738188

Ovbp1 -0.946564 -0.865717 -1.080442 -1.143745 -0.919008 -0.412685 1.2163605 0.4525979 1.1240612 -0.282602 0.5306964 1.1847509 1.2253837 1.9801658 -0.678421 -0.322239 -0.60197 -1.160622

Adora3 -0.175447 -0.070393 0.334776 -0.457118 0.4185988 -0.368114 -1.441018 -1.23016 -0.130799 -0.174086 -0.978796 1.067237 0.1260504 -0.699586 2.2765019 2.1185478 -0.650115 0.0305198

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Hist2h3b -0.662671 -1.466777 -0.619334 -0.657063 -0.50107 -0.91145 1.5895294 -1.184763 0.5413777 0.8317608 0.2796267 1.3051804 0.5996518 -1.502582 0.1905257 0.1776134 0.195536 1.7749082

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Gml14548 1.6545433 0.3394371 0.8975164 2.3298679 0.316366 1.4888568 -0.925473 -0.692287 -0.787249 -0.8269 -0.863594 -0.762596 -0.803199 -0.497711 -0.543743 0.4011918 -0.26832 -0.456708

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Mex3a -0.741077 -1.224464 -1.15259 -0.711299 -1.077891 -0.92997 -0.413532 2.6322329 0.8710853 0.4582529 0.0516207 0.1881579 0.3133294 -0.410506 0.9202165 0.1442684 -0.253912 0.1360773

Mocm3 -0.873029 -1.007961 -0.89224 -0.948335 -0.988221 -1.231994 2.297515 0.8051564 0.1337488 0.8126634 0.3123605 0.6684609 1.1941814 -0.314062 0.0042282 -0.606605 -0.629103 1.2254367

Gam65c 1.4433596 1.6723694 0.8956624 -0.005066 1.3890362 0.7898781 0.0595968 -1.600135 -1.001615 0.5028071 -0.081938 -0.021088 -0.115436 -0.265956 -0.096694 -1.396277 -1.204299 -0.202908

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Lekr1 -0.991953 -0.885753 -1.260521 -1.179781 -1.041857 1.3635898 1.1419256 0.6500351 1.1972985 -0.39368 0.1833586 1.2880626 1.3085763 -0.460577 0.5294647 -0.773355 -0.28273

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Zfp850 -0.44662 -0.742422 -0.737519 -0.780702 -0.847728 -1.145564 0.5678446 -0.894896 -0.597099 -0.03488 0.7859479 2.1004778 1.447033 -0.421077 0.0695827 -0.235179 -0.177897 2.0176993

Gm826 -1.078411 -0.844622 -0.88293 -0.957454 -0.762034 -0.990616 1.6557464 -0.0115372 0.7813156 1.0467696 1.9180099 0.3630193 1.8397363 0.017495 -0.494573 -0.597698 -0.449432 -0.376849

Arhgap40 1.2365508 2.2197587 0.8484156 -0.021559 1.1643257 1.0808261 -0.893328 -0.791407 -0.733961 -0.496452 -0.416925 1.1724149 -0.559327 -0.564204 -0.778687 -1.033796 -1.039731 -0.393005

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Zcchc3 -0.803604 -1.049115 -0.804643 -0.6986 -0.925965 -1.000065 2.7379915 -0.968384 0.0012747 0.331491 -0.131421 1.2027617 0.0680453 -0.254865 0.7123295 0.331491 7.73E-05 1.2511994

Thbd -1.022036 -0.894658 -0.516117 -0.869688 -0.673316 -0.786757 0.360666 0.8827905 -0.256355 0.4908072 0.3280805 0.2847854 0.1820568 0.2029509 -0.192045 0.4670785 -0.209188 -0.175609

Ism1 2.7701228 0.4538226 1.2883454 1.1024591 0.9950909 1.5053111 -0.673193 -0.684142 -0.751977 -0.708661 -0.750947 -0.729386 -0.657018 -0.483874 -0.17069 -0.420038 -0.503516 -0.591717

Plknc1 0.6600265 0.9122108 0.948444 2.0813124 1.0523974 1.2233567 -1.159055 -0.863405 -0.461773 -0.789254 -0.88422 -0.485542 -1.002717 -0.390693 -0.895512 0.4610783 -0.342983 -0.59971

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Lcmt2 -1.153719 0.1826856 -1.066598 -1.028867 -1.097989 -1.123554 0.3890427 2.8641605 0.2634314 0.184794 0.1959271 0.4828466 0.2505094 0.8218232 -0.379244 -0.362694 -0.329997 1.0737556

B3galt5 -1.050478 -0.864688 -0.610133 -0.778082 -0.369086 -0.688698 1.5711881 -0.979872 -0.182647 1.829677 -0.322345 1.3655261 -0.359876 -0.590987 -0.583585 1.3965694 -0.188501 1.4069252

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Pak6 -1.42153 -0.973015 -0.289629 -1.41637 -0.948406 -1.387062 1.204588 -0.688097 0.6481546 1.6738133 1.049414 0.1616417 1.2862484 1.0148288 -0.227479 0.0219382 0.327903 -0.036941

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Prdm11 -1.230743 -1.186861 -0.288006 -0.926727 -1.12506 -0.825518 1.2677683 -0.807638 0.6154452 0.0178138 -0.596719 0.9506806 0.9540725 0.8370518 1.5829625 -0.193108 -0.558312 1.7126795

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Aarsd1 -0.79572 -0.937692 -1.607653 -1.055495 -1.031887 -0.682063 2.1390367 0.984228 -0.07666 0.3623007 0.3407357 0.4662299 -0.288262 -0.465763 1.4226449 -0.371217 0.2952392 1.3019687

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Dio3 -0.563375 -0.470037 -0.57868 0.2633169 -0.432171 -0.33989 -0.567088 -0.250304 -0.786654 -0.786654 -0.699426 -0.324799 -0.786654 0.7319262 1.2668841 3.1742904 0.7151415 0.432371

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lglkv2-137 -0.672518 -0.195906 2.0625444 1.8713168 1.0010013 2.0019097 -0.699993 -0.65864 -0.623331 -0.648121 -0.625279 -0.699993 -0.610725 -0.682881 -0.390789 0.0607585 -0.157905 -0.331432

lglkv4-79 -0.605263 0.1998424 1.6334492 2.0978922 1.6295479 1.0845424 -0.799561 -0.431977 -0.72518 -0.799561 -0.799561 -0.799561 -0.629388 -0.114961 -0.435405 -0.809297 -0.57462

lglkv4-56 -0.501997 -0.001



|           |           |           |           |           |           |           |            |            |           |           |            |           |           |            |           |           |            |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|------------|-----------|-----------|------------|-----------|-----------|------------|-----------|-----------|------------|-----------|
| Gm13212   | 0.6058449 | 1.0138958 | 0.9681499 | 1.3540241 | 1.059415  | 1.4840035 | -1.376796  | -1.088136  | -0.979252 | -0.97603  | -1.197465  | -0.785489 | -0.922863 | -0.59758   | -0.108836 | 1.0498973 | 0.1460551  | 0.3511614 |
| Gm438     | 1.4987157 | 2.9066735 | 0.1670227 | 0.0628522 | 1.2196646 | 0.917048  | -0.688332  | -0.556162  | -0.617079 | -0.369324 | -0.446058  | -0.674826 | -0.532291 | -0.501614  | -0.48555  | -0.688332 | -0.533557  | -0.678852 |
| Gm436     | 1.5361233 | 1.8409883 | 0.918127  | 0.355485  | 0.8980513 | 1.1915927 | -0.64646   | -0.538447  | -0.547018 | -0.64646  | -0.578822  | -0.64646  | -0.64646  | -0.616859  | -0.391084 | -0.64646  | -0.463079  | -0.64646  |
| Gm13124   | 2.3084684 | 2.2912031 | 0.1629623 | 0.1419415 | 1.1753241 | 0.9191654 | -0.659266  | -0.552017  | -0.606529 | -0.45209  | -0.583647  | -0.663826 | -0.630741 | -0.560508  | -0.510862 | -0.660366 | -0.459369  | -0.659844 |
| Aadac3    | 2.3588986 | 1.9011838 | 0.3210565 | -0.012165 | 1.1431936 | 1.161338  | -0.691063  | -0.685103  | -0.621199 | -0.410511 | -0.497458  | -0.480792 | -0.684875 | -0.623651  | -0.523164 | -0.705326 | -0.514632  | -0.705732 |
| Aunip     | -1.123718 | -1.032872 | -1.257817 | -1.026563 | -1.115203 | -1.118707 | -0.848938  | -0.6873564 | 0.3658899 | 0.803538  | 0.7388938  | 0.3694483 | 0.7929085 | -0.515578  | 0.7800185 | 0.5895953 | -0.858814  | 2.0726843 |
| Ebf1      | -0.23571  | -0.496824 | -0.348497 | -0.257325 | -0.454198 | -0.51056  | -0.510565  | -0.45643   | -0.056905 | 0.5511075 | -0.056905  | 3.8349696 | 0.1421296 | -0.510565  | -0.252897 | -0.053316 | -0.442568  | 0.1150571 |
| Bnip3     | -1.123464 | -0.954771 | -0.77272  | -1.031822 | -0.931498 | -0.945771 | 2.4417885  | 1.7873675  | 0.7188024 | 0.4220226 | 0.1685831  | 0.0342672 | 0.785623  | 0.5003379  | 0.1799608 | -0.44354  | -0.628322  | -0.215845 |
| Aoc2      | -0.631618 | -0.826375 | -0.688395 | -1.071573 | -0.97165  | -0.968147 | 2.6309075  | 0.4765061  | 1.0136734 | 0.8976822 | 0.4968269  | -0.795458 | 0.6953112 | 0.4127908  | 0.8374571 | -0.626583 | -0.897141  | 0.015784  |
| Psme3     | -0.988555 | -0.93465  | -0.947527 | -1.209435 | -0.957045 | -1.447611 | 1.9424877  | 1.1774221  | 0.5144156 | 0.6881213 | 0.0489214  | -0.340702 | -0.035605 | -0.312658  | 1.4161924 | -0.318792 | 0.6276165  | 1.0774019 |
| Lce1d     | 0.6502278 | 2.5607116 | 0.8959613 | 0.0903958 | 1.6416468 | 0.9876974 | -0.8256    | -0.881078  | -0.731814 | 0.0642536 | -0.207673  | -0.341869 | -0.190599 | -0.357142  | -0.298683 | -1.082409 | -0.92455   | -1.049477 |
| Fam174b   | 1.1789847 | 0.3244101 | 1.4785714 | 0.3689136 | 1.5025223 | 1.5176265 | -1.895459  | -0.293621  | -1.216853 | -0.538942 | -0.368862  | 0.4470368 | -0.811199 | 0.0846601  | -0.264734 | -1.423144 | 0.1434215  | -0.233331 |
| Mup19     | -0.043573 | 3.6292964 | 0.5645037 | 0.9631922 | 0.3691996 | -0.233823 | -0.490864  | -0.228782  | -0.489698 | -0.490864 | -0.487587  | -0.490864 | -0.488349 | -0.273798  | -0.413368 | -0.48919  | -0.41623   | -0.4892   |
| Mup18     | 0.0958443 | 2.9636044 | 0.7867003 | 1.7827571 | 0.9592115 | -0.233119 | -0.579984  | -0.354332  | -0.578945 | -0.579984 | -0.578768  | -0.579984 | -0.577978 | -0.407319  | -0.499738 | -0.578247 | -0.461198  | -0.578522 |
| Mup10     | 0.0240182 | 3.0967819 | 0.9414072 | 1.527852  | 0.8925256 | -0.197811 | -0.571385  | -0.359413  | -0.570872 | -0.571385 | -0.570748  | -0.571385 | -0.571385 | -0.41856   | -0.48239  | -0.567229 | -0.45937   | -0.570652 |
| Mup2      | -0.016394 | 3.5927401 | 0.5363073 | 1.0768733 | 0.3617952 | -0.241554 | -0.49717   | -0.200401  | -0.496322 | -0.49717  | -0.496093  | -0.49717  | -0.49717  | -0.290631  | -0.418444 | -0.496171 | -0.427077  | -0.495949 |
| Gm2002    | 0.5988774 | 2.7393753 | 0.0450433 | 1.2835455 | 0.3447507 | 1.0877993 | -1.184519  | -0.5103843 | -0.686406 | -0.859787 | -0.748426  | -0.88111  | -0.670039 | 0.4852990  | -0.425969 | -0.249346 | -0.492692  | -0.896773 |
| Haus5     | -1.448865 | -0.743928 | -0.911721 | -1.161008 | -0.959881 | -1.534522 | -0.5732975 | -0.205382  | 0.7072786 | 1.6617442 | 1.3843645  | 0.7984457 | 0.4152253 | -0.535563  | 0.2089206 | -0.271162 | 0.8008464  | 1.2208302 |
| Zfp566    | -0.723568 | -1.156295 | -0.875426 | -0.703077 | -1.025328 | -1.210553 | 1.7590787  | -0.1058789 | 1.4737828 | 0.4247289 | 0.3984286  | -0.099352 | 1.7821168 | -0.465271  | 0.3459809 | -0.282567 | -0.900742  | 1.1308842 |
| Evi2a     | 0.7139592 | 0.9115535 | 0.8936874 | 1.5839303 | 1.2909315 | 1.798689  | -1.263492  | -0.965442  | -0.797909 | -0.84562  | -0.971689  | -0.698423 | -1.027407 | -0.401157  | -0.481318 | 0.6842715 | 0.0439639  | -0.68531  |
| Rad54b    | -1.155371 | -0.871041 | -1.154061 | -1.136736 | -1.162818 | -1.201068 | 0.9244004  | 2.2420155  | 0.3633416 | 0.3906805 | 0.7206518  | 0.6019162 | 0.8418173 | -0.50313   | 0.6548835 | -0.256733 | -0.256733  | 0.9579854 |
| Cpt1b     | 1.1292175 | 1.941592  | 1.5672135 | 1.7826148 | 0.9037419 | 0.3096232 | -0.322112  | -0.54212   | -0.886716 | -0.557092 | -0.1035985 | -0.921553 | -0.7154   | -0.340417  | -0.551852 | -0.711735 | -0.561902  | -0.487119 |
| Taf9      | -0.042951 | -0.59658  | -0.955627 | -0.858539 | -0.875592 | -0.592719 | 0.8006999  | 2.7447043  | -0.009785 | 0.246829  | -0.15895   | 0.6005242 | 0.6009445 | -1.138316  | 0.1831801 | -1.10512  | -0.334972  | 1.4926293 |
| Naip6     | 1.0049349 | 1.0496669 | -0.127429 | 2.4750438 | 0.4726485 | 1.0711914 | -1.122383  | -0.291798  | -1.040813 | -0.52445  | -0.863904  | -0.177344 | -0.842764 | -0.4343174 | -0.921712 | 1.15901   | -0.14623   | -0.14462  |
| Naip2     | 0.380911  | 0.3861518 | 1.4501433 | 1.3745474 | 0.599851  | 1.458071  | -0.430383  | -1.225978  | -0.806142 | -0.971746 | -0.110396  | -0.116571 | -0.923932 | -0.86146   | -0.491711 | 1.3308287 | 0.320386   | 0.5320454 |
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| Samd1     | -0.485184 | -0.828088 | -0.846416 | -0.456674 | -1.123934 | -1.285637 | 2.8909372  | 0.3388421  | 0.289492  | 1.0705836 | -0.129723  | -0.988189 | 1.0275082 | 0.131996   | 0.531428  | 0.3667368 | -0.540279  | 0.9365985 |
| Serpina3j | 0.4644896 | 2.9591613 | 0.4758626 | 0.1774437 | 1.2113059 | 1.5411326 | -0.61092   | -0.582104  | -0.605584 | -0.587203 | -0.597052  | -0.608978 | -0.605628 | -0.440614  | -0.500958 | -0.609816 | -0.473727  | 0.606811  |
| Flrt3     | -0.578549 | -0.756163 | 1.171055  | -0.588565 | -0.736828 | -0.76802  | 0.3380304  | -0.731115  | 2.1236313 | -0.049456 | -0.557733  | -0.06793  | 2.436238  | -0.773963  | -0.599476 | -0.448171 | 0.8838349  | -0.347481 |
| Cyp4b3    | 1.0242164 | 0.2574425 | 1.4296645 | 2.3031602 | 0.3880182 | 1.4785629 | -0.758895  | -0.794589  | -0.779456 | -0.880592 | -1.055005  | -0.515745 | -0.881547 | -0.784856  | -0.449633 | 0.6519698 | -0.24674   | -0.385957 |
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| Dab2      | -0.658626 | -0.658626 | -1.32266  | -0.658626 | -0.658626 | -0.658626 | -0.658626  | -0.658626  | 2.5871384 | 0.9136163 | 0.3195488  | 0.9424521 | -0.658626 | -0.658626  | -0.658626 | 1.9212666 | -0.4871064 |           |
| Pms2      | -0.94545  | -0.935858 | -1.503519 | -1.013274 | -0.769334 | -1.245658 | 0.962442   | -0.355698  | 0.5318002 | -0.371928 | 0.1466473  | 0.7217044 | 1.3889087 | -0.02064   | 0.0772432 | 0.1695364 | -0.157166  | 0.6093424 |
| Capn3     | 1.0613377 | 1.6244079 | 0.420474  | 1.274869  | 0.9801685 | 0.37942   | -0.830487  | -0.501407  | -0.466378 | -0.622154 | -1.118101  | 1.6508103 | -1.227757 | 0.451862   | -1.255475 | -0.083044 | -0.845775  | -0.892772 |
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| Tlr5      | 1.1693851 | 0.1594486 | 0.6585583 | 0.5476198 | 0.790845  | 1.8735941 | 0.6890313  | -0.734463  | -0.866193 | -0.75185  | -1.100202  | -0.979075 | -1.542991 | 1.0394949  | -0.593084 | 0.5063277 | -0.018651  | -0.534638 |
| Cd209g    | 1.7169097 | 0.9402314 | 0.6554325 | 1.4152971 | 1.2167412 | 1.2735926 | -0.759787  | -0.688425  | -0.759787 | -0.759787 | -0.759787  | -0.746468 | -0.743192 | -0.619527  | -0.596057 | 0.3057274 | -0.480284  | -0.698932 |
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| Tmem233   | 0.8878223 | 2.8521424 | 0.195982  | 0.4695162 | 1.6448377 | 0.9426197 | -0.741815  | -0.499507  | -0.692109 | -0.547535 | -0.670804  | -0.688522 | -0.580037 | -0.487178  | -0.583901 | -0.691489 | -0.387983  | -0.422041 |
| Ccr1l     | 1.7243035 | 0.2932623 | 0.3170472 | -0.030835 | 0.8702437 | 2.9150026 | -0.47547   | -0.3086    | -0.228047 | 0.0017084 | 0.947362   | -0.872119 | -0.407088 | -0.531433  | -0.746596 | -0.888463 | -0.58599   | -1.141736 |
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| Gm11110   | -0.965978 | 1.261811  | -0.8362   | -1.199419 | -0.820188 | -0.631189 | 2.6325994  | -0.084336  | 0.1763835 | 0.0556672 | 0.1432272  | 0.9382037 | 0.3630225 | -0.029244  | 0.9067598 | -0.503717 | -0.682176  | 1.2157198 |
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| Gm7609    | 0.0147619 | -0.598402 | 2.5136352 | 1.8311626 | 1.3098804 | 0.72624   | -1.007515  | -1.004141  | -0.330568 | -0.319272 | -0.551857  | 0.0143924 | -0.554141 | -1.055288  | -0.436685 | 0.1902085 | 0.0531263  | -0.780119 |
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| Ssca1     | -0.747225 | -0.948689 |           |           |           |           |            |            |           |           |            |           |           |            |           |           |            |           |



|            |           |           |           |           |           |           |            |            |           |           |           |           |           |           |           |           |           |           |
|------------|-----------|-----------|-----------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Gm2986     | -0.520291 | -1.10329  | -0.729551 | -0.987582 | -0.95611  | -1.164395 | 1.1590537  | 1.1296991  | 0.2331289 | -0.068937 | 0.2111388 | 1.770317  | 2.0729596 | 0.6538392 | -0.980049 | -0.193173 | -0.352765 | -0.173993 |
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| 261002401  | 1.1924783 | 1.5563677 | 0.2361636 | 2.0815665 | 0.8844066 | 0.7048916 | -1.246543  | -0.427964  | -0.350032 | 0.0991977 | 0.3803522 | 0.2118883 | -0.386659 | -0.966004 | -0.826674 | -1.506867 | -0.65521  | -0.98145  |
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| U4         | -0.288339 | 0.7211652 | 3.8922602 | -0.288339 | -0.288339 | -0.288339 | -0.288339  | -0.288339  | -0.288339 | -0.288339 | -0.288339 | -0.288339 | -0.288339 | -0.288339 | -0.288339 | -0.288339 | -0.288339 | -0.288339 |
| SNORA61    | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702  | -0.235702  | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 |
| SNORA42    | 1.2016329 | 0.3147076 | -1.014358 | -1.014358 | -1.014358 | -1.014358 | -0.164869  | 0.5445351  | 0.3708157 | -1.014358 | 0.4406244 | -1.014358 | 0.6591741 | 0.3112187 | -0.181856 | 2.3211462 | -1.014358 | -1.014358 |
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| U2         | -0.588234 | -0.290718 | -0.588234 | -0.588234 | 0.9237609 | -0.588234 | 1.4280517  | -0.215391  | 1.7008687 | -0.588234 | 2.6872283 | -0.588234 | -0.588234 | -0.588234 | -0.588234 | -0.588234 | -0.588234 | -0.588234 |
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| U4         | -0.325114 | -0.325114 | -0.325114 | -0.325114 | -0.325114 | -0.325114 | -0.325114  | -0.351733  | -0.325114 | -0.325114 | -0.325114 | -0.325114 | 3.8519989 | 0.6729793 | -0.325114 | -0.325114 | -0.325114 | -0.325114 |
| U4         | 0.0069384 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702  | -0.235702  | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 |
| U2         | -0.252684 | -0.252684 | 3.9970371 | -0.252684 | -0.252684 | -0.252684 | -0.252684  | 0.0459067  | -0.252684 | -0.252684 | -0.252684 | -0.252684 | -0.252684 | -0.252684 | -0.252684 | -0.252684 | -0.252684 | -0.252684 |
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| U2         | 0.9217243 | -0.440572 | 0.9719765 | -1.25489  | -0.002677 | -0.720766 | -1.25489   | -0.237412  | 2.23756   | 1.1362656 | -0.258952 | -1.25489  | 0.8596307 | -0.296854 | 0.3205191 | -0.327929 | 0.8576126 | -1.25489  |
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| SNORA42    | 1.1583797 | -0.706877 | 0.4055223 | -0.706877 | 2.492262  | -0.706877 | -0.706877  | -0.61495   | 2.0527752 | -0.706877 | 0.1923066 | -0.706877 | 0.2576051 | -0.706877 | -0.706877 | -0.706877 | 0.1614288 | 0.2296615 |
| U2         | 2.2160979 | -0.256857 | 1.4407669 | -0.956591 | -0.691094 | -0.892334 | 0.2867017  | -0.318572  | 0.2586755 | 0.0707809 | -0.287535 | 1.7330471 | 0.942084  | -0.648705 | -0.478521 | -0.929736 | -0.070556 | -1.417653 |
| Y_RNA      | -0.522739 | -0.483368 | -0.522739 | -0.522739 | -0.522739 | -0.522739 | -0.522739  | -0.405027  | -0.522739 | -0.522739 | -0.522739 | -0.522739 | 1.4385774 | -0.522739 | 1.7301936 | 2.2040995 | 1.8338962 | -0.522739 |
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| SNORA48    | 0.1235372 | -1.702547 | -0.17038  | -0.17038  | -0.17038  | -0.17038  | -0.173824  | -1.214276  | 1.7760023 | -1.112414 | 1.0321796 | 0.9255993 | 1.4330771 | -1.538699 | 0.1235372 | 0.3936297 | 0.1235372 | 1.0321796 |
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|            |           |            |            |           |           |           |           |           |           |           |           |           |           |           |           |            |           |           |
|------------|-----------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|
| Gypc       | 0.9111154 | 0.0732006  | 0.852614   | 1.0061052 | 0.9815869 | 1.2120467 | -1.673904 | 0.0443545 | -1.361695 | -1.140394 | -1.103191 | 0.7168606 | -1.218133 | 0.0284646 | -0.51934  | 1.5435321  | -0.404584 | 0.0513599 |
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| Tnfrsf22   | 0.732015  | 2.9291029  | -0.583507  | 1.6804196 | -0.601654 | 0.0332    | -0.305422 | -0.601341 | -0.526125 | -0.411878 | -0.525805 | -0.417777 | -0.483365 | 1.2575425 | -0.562181 | -0.520735  | -0.599827 | -0.492663 |
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| Gm20390    | -0.787255 | -0.473884  | -1.027991  | -1.146351 | -1.300264 | -1.248633 | -0.712758 | 2.4721697 | 0.1671749 | 0.4891902 | 0.5736276 | 0.2677992 | -0.108347 | 0.0531016 | 1.0065381 | 0.2817992  | 0.0314601 | 1.4626219 |
| Vgll3      | 2.6900199 | 1.1394215  | 0.1410679  | 0.8467804 | 1.0503733 | 0.9149303 | -0.824463 | -0.642289 | -1.252307 | -0.60107  | -0.620782 | -0.172906 | -1.105043 | -0.223648 | -0.351521 | -0.577344  | 0.3132877 | -0.724509 |
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| Ly6g6c     | 1.5123108 | 1.2899453  | 0.5961723  | 0.7419825 | 1.3738531 | 0.9471472 | -1.325329 | -0.145364 | -0.668416 | 0.6410787 | 0.2818728 | -0.566458 | -0.509519 | 0.8252366 | -0.804079 | -0.191419  | -0.932853 | -1.301767 |
| Gm20442    | -0.619257 | -0.89965   | -0.834937  | -0.814584 | -1.036702 | -0.734917 | 1.9162936 | 1.7729952 | -0.189598 | 0.5843879 | 0.0764614 | -1.036702 | 0.2454742 | 0.1745118 | -0.562216 | 0.2821467  | -0.067722 | 1.9440137 |
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| U1         | -0.235702 | 4.0069384  | -0.235702  | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702  | -0.235702 | -0.235702 |
| U1         | -0.472713 | -0.472713  | -0.472713  | 2.0527106 | -0.472713 | -0.472713 | -0.472713 | -0.472713 | -0.472713 | -0.472713 | -0.472713 | -0.472713 | -0.472713 | -0.472713 | -0.472713 | -0.472713  | -0.472713 | 2.5745006 |
| U4         | 4.0069384 | -0.235702  | -0.235702  | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702  | -0.235702 | -0.235702 |
| U1         | -0.235702 | -0.235702  | -0.235702  | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | -0.235702 | 4.0069384 | -0.235702 | -0.235702  | -0.235702 | -0.235702 |
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| Gm20554    | 0.5655439 | -0.195242  | 0.4544178  | -0.508624 | 0.5151265 | -0.198116 | -0.830915 | 0.1330469 | 1.6577485 | 1.0491625 | 2.260791  | 0.1066931 | 0.3488495 | -1.162671 | -0.877306 | -1.188485  | -0.52728  | -1.506743 |
| Gm19357    | -1.388532 | -0.434301  | -1.157807  | -0.979964 | -0.65646  | -0.482496 | 1.972301  | -0.082244 | 0.8059515 | -1.126214 | 0.2313992 | 0.7979334 | 1.3246299 | 1.7993804 | -1.027726 | -0.40299   | 0.3406622 | -0.587523 |
| U1         | 0.0573114 | -0.846138  | 0.0625144  | -0.77218  | -0.846138 | 0.4583197 | 2.0569647 | -0.846138 | 1.2486726 | -0.846138 | -0.846138 | -0.846138 | 1.4565925 | -0.587902 | 0.0635719 | 0.1820133  | 1.6970852 | -0.846138 |
| Hist2h3c1  | -0.722349 | -1.209089  | -0.703873  | -0.802516 | -0.607761 | -0.862302 | 1.4450137 | -1.391781 | 0.4204975 | 0.8128802 | 0.455699  | 1.255881  | 0.6596717 | -1.313089 | 0.3989542 | 0.0962665  | 0.2771097 | 1.8726859 |
| U1         | 0.5626129 | -0.264923  | -0.6001869 | 0.6505298 | 0.5626129 | 0.6001869 | -0.264923 | 0.3967766 | 0.517774  | 0.4758391 | -0.176596 | -0.176596 | -0.176596 | -0.264923 | 0.517774  | 0.5813999  | 0.8341042 | -0.314449 |
| U1         | -0.710915 | -0.755779  | -0.576579  | -0.725099 | -0.685174 | -0.665173 | -0.487365 | -0.755579 | -0.16038  | -0.351981 | -0.545292 | 1.797524  | -0.191644 | -0.755579 | 0.6519964 | 0.1703387  | 1.0542048 | 1.7555082 |
| U2         | 0.7935754 | -1.6691721 | -0.4105065 | -0.105535 | 0.133312  | 0.2942398 | -0.441719 | -1.571745 | 0.1925389 | 0.8790284 | 0.3212907 | -0.793291 | 0.7115829 | -1.661223 | 1.1833226 | 0.637181   | 1.7067465 | -0.089017 |
| EVl2B      | 0.9053012 | 1.0323679  | 0.1756365  | 1.9628679 | 1.066514  | 1.7689919 | -0.941417 | -0.88594  | -0.747068 | -1.11737  | -0.105522 | -0.869055 | -0.30465  | -0.995773 | -0.512468 | 0.4986928  | 0.2315401 | -0.273334 |
| SL25A37    | 0.1521885 | -1.141375  | 0.5699587  | 0.1752865 | -0.843679 | 0.6524635 | -1.255165 | -1.065148 | 0.6470308 | -0.64061  | -0.607947 | -1.255165 | -0.783642 | 0.7219954 | 0.2337688 | 0.763731   | 0.7556199 | 1.1284983 |
| AC073565.i | -0.690521 | 0.8956754  | 2.2142747  | 1.8266468 | 0.2044474 | 1.2441292 | -0.816905 | -0.816905 | -0.481709 | -0.816905 | -0.64385  | -0.564934 | -0.816905 | -0.816905 | 0.6897439 | -0.357005  | 0.5645332 | -0.816905 |
| U2         | 0.3867122 | -1.728376  | 0.4808224  | -0.886948 | -0.0388   | 0.2831764 | -0.489084 | -1.690326 | 0.2663266 | 0.6820132 | 0.2494768 | -0.504209 | 0.7390336 | -1.725066 | 1.2795584 | 1.1255269  | 1.5452965 | 0.0248679 |
| U2         | 0.4223226 | -1.70837   | 0.5126557  | -0.881557 | -0.052619 | 0.2796339 | -0.463743 | -1.673638 | 0.2153371 | 0.671493  | 0.191906  | -0.513624 | 0.73      |           |           |            |           |           |



|            |            |           |           |             |           |           |            |            |           |           |            |           |           |           |           |           |            |           |
|------------|------------|-----------|-----------|-------------|-----------|-----------|------------|------------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|------------|-----------|
| Gm10592    | -0.189029  | 2.2499424 | 0.0167966 | 0.296607    | 0.4333116 | 0.8234478 | -1.310766  | 0.5969087  | 1.7672679 | -0.547483 | -0.480057  | -0.55321  | 0.9954597 | -0.322568 | -0.962174 | -0.90126  | -0.602427  | -1.310766 |
| U1         | -0.7493307 | -1.704543 | 0.2871849 | -0.171901   | 0.7290775 | 0.0305085 | 0.8938055  | -1.749407  | 0.5332281 | 0.1193539 | 0.4490736  | -0.702166 | 0.4665516 | -1.747931 | 0.1785403 | -0.012284 | 2.1233085  | -0.471731 |
| Samd11     | -0.914295  | -0.74871  | -0.819383 | -1.148348   | -1.011873 | -1.10606  | 0.10137367 | -0.385635  | 1.9842854 | 0.656287  | 0.5930612  | -0.061648 | 0.9136447 | 0.0020493 | 0.167061  | -0.266463 | -0.828748  | 1.9610369 |
| U1         | 1.0076652  | -1.279591 | -0.701709 | -0.177962   | 0.0097928 | 0.2725706 | 0.055714   | -1.211761  | 0.5206481 | -0.85957  | 2.5123537  | -0.847831 | 0.6671618 | -1.344677 | 1.0097916 | 0.8675109 | -0.457528  | -0.042581 |
| MOAP1      | -1.15733   | -0.914623 | -0.983317 | -0.704609   | -0.935957 | -0.468646 | 2.5009     | 0.1800663  | 0.2041103 | -0.364554 | 0.66885399 | 0.8833014 | 0.1934374 | 1.6856871 | -0.036446 | -0.2488   | -1.119298  | 0.6175379 |
| AC160990.1 | -0.734267  | -0.222856 | 2.5829072 | 0.7381122   | 1.6684842 | 1.5552706 | -0.734267  | -0.471193  | -0.321924 | -0.734267 | -0.734267  | -0.734267 | -0.734267 | -0.734267 | -0.305536 | -0.417032 | 0.3994071  | -0.065037 |
| Cdkn2d     | -1.141635  | -0.840487 | -1.157321 | -1.088533   | -0.687193 | -1.09377  | 1.494537   | 0.5726219  | 0.6261141 | 1.1909829 | 0.2369429  | 1.8299525 | 0.2313877 | 0.7932239 | -0.677728 | 0.9761602 | -0.882767  | -0.382489 |
| Gm10591    | 0.4818347  | 2.9277902 | 0.6796407 | 1.0753489   | 0.5814476 | 0.4340574 | -1.113871  | 0.0290584  | -0.791839 | -0.947258 | -0.633805  | -0.854894 | -0.810168 | 0.4808601 | -0.535464 | -0.987369 | -0.048651  | 0.0332815 |
| GM5849     | 1.2947465  | 1.6239476 | -0.077862 | -0.231107   | 1.4686669 | 2.5851084 | -0.601247  | -0.601247  | -0.601247 | -0.38545  | -0.364723  | -0.601247 | -0.502103 | -0.601247 | -0.601247 | -0.601247 | -0.601247  | -0.601247 |
| U1         | 0.553548   | -2.110452 | 0.5232341 | 0.4672944   | 0.5232341 | 0.5232341 | 0.553548   | -2.110484  | 0.4233038 | 0.4672944 | 0.1880847  | 0.1880847 | 0.1880847 | -2.110499 | 0.5232341 | 0.553548  | 0.9136371  | -0.257929 |
| Mup15      | 0.1449606  | 3.0527152 | 0.3908334 | 2.1327631   | 0.2801513 | -0.316372 | -0.522976  | -0.251662  | -0.522976 | -0.522976 | -0.522976  | -0.522976 | -0.522976 | -0.342729 | -0.44468  | -0.520752 | -0.464399  | -0.522976 |
| SLC12A6    | -0.630782  | -0.699612 | -0.662071 | -0.638501   | 0.8093967 | 2.0819388 | -0.289199  | 2.0943698  | -0.590563 | 0.5167488 | 0.0065458  | 1.6983644 | -0.533734 | -0.708318 | -0.646666 | -0.581602 | -0.68995   | -0.536367 |
| GM5796     | -0.309765  | -1.22435  | -0.358203 | 0.2721023   | 0.3572294 | -0.952381 | -1.054433  | -1.155311  | -0.672961 | -0.841433 | 0.783583   | -0.228684 | 1.6857495 | 0.6252796 | 2.2655318 | -0.237902 | 1.2031585  | -0.15721  |
| Hist1h2bm  | -0.664727  | -1.574714 | -0.573163 | -0.843274   | -0.61131  | -0.826325 | 1.6281059  | -1.175149  | 0.7444029 | 0.8076432 | 0.7026041  | 0.3064815 | 0.8478885 | -1.562293 | 1.0315468 | 0.1968128 | 0.2044975  | 1.3609722 |
| Ccl27b     | 0.741609   | 1.6732072 | 0.7171163 | 2.082764    | 0.7048403 | 1.3930562 | -0.997173  | 0.2339958  | 0.1651447 | -0.685049 | -0.402646  | -0.795603 | -0.635657 | -0.783566 | -0.7801   | -0.991983 | -0.640122  | -0.999833 |
| U1         | -0.817791  | -0.750958 | -0.657669 | -0.869124   | -0.818672 | -0.787659 | -0.418897  | 0.30890462 | 0.5486744 | -0.62344  | -0.453942  | -0.144514 | -0.411834 | 0.3490262 | 0.9310619 | 0.7304274 | 0.1344096  | 0.9718548 |
| AC158361.1 | -0.184961  | 2.4947313 | 1.7001644 | 0.2211212   | 0.6929951 | 0.9594917 | -0.844946  | -0.1059908 | -0.524547 | 0.0197345 | 0.5343444  | -0.072688 | -0.311191 | 0.253519  | -0.999715 | -0.906319 | -0.796054  | -1.175773 |
| mmu-mir-2  | 1.274422   | 0.1936809 | 1.6424329 | 2.0280426   | 0.0014099 | 0.935559  | 0.9377569  | -0.220991  | -0.003466 | -1.414822 | -1.272044  | -0.684687 | -0.868343 | 0.59413   | -1.072874 | -0.11036  | 0.0539116  | -1.113765 |
| RP23-25116 | 0.6065662  | 2.1426704 | 0.7018418 | -0.625958   | 1.1137156 | 1.8564847 | -0.924849  | -0.086313  | -0.851732 | 0.153274  | -0.419331  | 0.9460731 | -0.347675 | -0.940975 | -0.216757 | -0.618339 | -0.932412  | -0.556286 |
| AC153516.1 | -1.233101  | -0.439454 | -0.615635 | -1.386419   | -1.286136 | -0.868721 | 1.7270369  | 0.0450987  | -0.23628  | 1.3117139 | -0.208425  | 0.8313679 | 1.5432321 | 1.208917  | -0.318997 | -0.875582 | 0.2456512  | 0.5557323 |
| AC163537.1 | -1.038624  | 0.966999  | -0.951672 | -1.030321   | -1.015691 | -1.116727 | 2.1796031  | 1.8497218  | 0.671289  | -0.042948 | -0.038362  | 0.7759585 | 0.4075337 | 0.2113951 | 0.9388461 | 0.0412967 | -0.571178  | -0.30312  |
| CT025649.1 | -1.079681  | -0.94086  | -0.881234 | -0.996118   | -0.81849  | -0.904721 | -0.942517  | -0.466221  | 0.9169108 | 1.9951    | 1.2477768  | 0.8175981 | -0.704606 | 0.4112265 | 0.5175845 | -0.184394 | 0.4834947  | 1.5291516 |
| AC124998.1 | -0.625227  | -0.611303 | -1.01923  | -1.932672   | -1.446936 | -1.202    | 1.3329961  | 0.0214784  | 0.3053325 | 1.2903907 | 0.397249   | 0.259881  | 1.5806721 | 0.8478507 | 0.616458  | -0.523112 | 0.4956963  | 0.2124747 |
| AC122371.1 | -0.873181  | -0.96616  | -0.884771 | -0.852075   | -0.854339 | -0.935936 | 2.7143669  | -0.063798  | 0.2180542 | 1.2705702 | 0.331435   | 0.5944119 | 1.3477461 | -0.505573 | -0.41289  | 0.578907  | -0.269714  | -0.13342  |
| AC140326.1 | -0.788117  | -0.950016 | -1.036462 | -1.200292   | -1.010927 | -0.928099 | 2.3884749  | 1.9434021  | 0.6647291 | -0.025875 | 0.3313879  | 0.8634159 | 0.3659041 | -0.264629 | -0.299474 | 0.0182556 | -0.003572  | -0.068106 |
| AL732311.1 | -1.54355   | -0.377106 | -1.070768 | -1.695467   | -1.123639 | -0.407463 | 0.8441463  | 1.4793987  | 0.6395587 | 0.1448714 | 0.5006566  | 0.675044  | 0.0962347 | -0.609974 | 1.0329569 | -0.676276 | 0.3766726  | 1.7147564 |
| AL589650.1 | -1.036163  | -1.661401 | -1.196263 | -1.133418   | -0.946573 | -0.933101 | 1.5895151  | 0.3862891  | 0.6246327 | -1.11714  | 0.8297445  | 0.8407526 | 1.1684494 | -0.690903 | 0.3826832 | -0.254442 | -0.045375  | 0.9584413 |
| AL663030.1 | -0.819285  | -0.959986 | -0.539844 | -1.037871   | -1.073476 | -0.378115 | 2.2494429  | 1.94072    | 0.1067839 | 0.3418986 | 0.1285786  | -0.873271 | 0.4143644 | 0.0555153 | 0.1824477 | -0.333622 | -0.823003  | 1.4187406 |
| AC133646.1 | -0.94915   | -1.34877  | -0.912386 | -1.05453    | -0.941863 | -0.603557 | 1.7551492  | 1.3788753  | 1.0168915 | 0.676568  | 1.1633973  | 0.2571773 | 1.3838187 | 0.0533242 | -0.514896 | -0.264493 | -0.136817  | -0.95874  |
| AL672121.1 | -0.76609   | -1.704989 | -1.264369 | -0.869722   | -1.270948 | -0.712212 | 1.8276106  | 0.3424902  | 0.6795108 | 0.7833348 | 0.2645735  | 1.2263351 | 1.0043438 | 0.931541  | 0.6331698 | 0.4727987 | -0.288379  | 0.5879823 |
| AC132304.1 | -1.069073  | -0.783443 | -0.620641 | -1.020978   | -0.964841 | -0.97391  | 0.412168   | -0.223602  | 1.6502557 | 0.1819974 | -0.107639  | 1.7943629 | 1.6889403 | 0.2518919 | -0.917451 | 0.5600911 | -0.719842  | -0.038289 |
| AC125483.1 | -0.951894  | -1.037024 | -0.807455 | -0.700216   | -0.888372 | -0.787402 | 1.139308   | 0.4615673  | 1.0427729 | 0.6133945 | -1.115676  | 1.1908764 | -0.88346  | 1.9650191 | -0.28529  | 0.1183375 | 0.0627221  | 1.8627919 |
| RP23-302C  | -0.36029   | -0.65115  | -0.706252 | -1.070368   | -0.879327 | -0.004724 | -0.280607  | 0.1243054  | -0.643516 | -0.726774 | -0.634863  | -0.1295   | -0.597663 | 1.3432288 | 0.2049512 | 0.5211955 | -0.1718197 | 2.3195333 |
| AC117663.1 | -0.648559  | -0.990447 | -1.090826 | -1.083881   | -1.1341   | -1.174288 | 1.5297628  | 0.8527355  | 0.8250356 | 0.3248365 | 0.3675576  | -0.465722 | 2.0221114 | -0.763155 | 0.1204196 | 0.133353  | -0.108438  | 1.2836036 |
| RP23-399J8 | -0.997013  | -1.088702 | -0.450602 | -0.299714   | -0.855096 | -0.968396 | 2.6072634  | -0.03861   | -0.431693 | 0.2465315 | -0.209614  | 0.0295102 | -0.517887 | -0.126744 | -0.160603 | 0.6283432 | 0.4231227  | 2.2099031 |
| AC025794.1 | -0.921378  | -0.70655  | -1.046658 | -0.905374   | -0.874983 | -0.920567 | 0.2490763  | 1.0875848  | -0.861707 | 1.1483963 | 0.2046162  | 0.7005107 | 1.285633  | 0.0731827 | 0.7651663 | -1.384196 | 0.9187671  | 1.5484793 |
| CT025673.1 | -0.825036  | -0.656374 | -1.696707 | -1.013089   | -0.980869 | -0.779611 | -0.570121  | 1.7351113  | -0.460602 | 0.2854351 | 0.3789731  | 1.8389588 | 0.4731596 | 0.1323817 | 0.8122608 | -0.306275 | 0.1337757  | 1.4986284 |
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| mmu-mir-1  | 1.7008691  | 0.6987452 | 0.5089472 | 1.7963018   | 1.0209714 | 1.0432161 | -0.771842  | -0.289268  | 1.0266457 | -1.157145 | -0.63539   | -0.754113 | -0.609969 | -0.781632 | -0.476859 | -0.501645 | -0.259582  | -1.55825  |
| AC124550.1 | -0.4813    | -0.951271 | -0.82376  | -1.368246   | -0.42104  | -0.903826 | 0.9079522  | -1.066594  | 0.2050038 | 2.0502151 | 0.6256908  | 0.5135963 | 0.9392307 | 0.8304815 | 0.2797175 | -1.670392 | 0.9173636  | 0.4171783 |
| Tnfrs12    | 2.157191   | 0.1038269 | 0.7339732 | 2.2853677   | 0.502925  | 1.1032546 | -0.884336  | -0.745187  | -0.604005 | -0.765739 | -0.835919  | -0.64351  | -0.840134 | -0.529898 | -0.438217 | 0.2726339 | -0.250032  | -0.622197 |
| AC020971.1 | -0.965559  | -0.627695 | -0.961638 | -1.080519   | -0.897652 | -0.662305 | 0.2810593  | 2.8313832  | 0.0678779 | 0.6209689 | 0.694775   | -0.289858 | 0.5748561 | 0.7701464 | 0.6833574 | -0.335789 | 0.5239739  | -1.227382 |
| AL591113.1 | -0.526937  | -0.638489 | -1.043935 | -1.809626   | -1.064297 | -0.976926 | 1.8496884  | 0.5000047  | 0.1410821 | -0.215162 | -0.288371  | 0.3094239 | 1.8289806 | 0.0647832 | 1.2799962 | -0.226527 | -0.12771   | 0.9440211 |
| AC154200.1 | -0.316872  | -0.888092 | -0.793003 | -1.264011   | -1.291733 | -1.08349  | 1.2134094  | 0.8796224  | 0.8208283 | 0.2024033 | -0.281994  | 0.352477  | 1.7894954 | -0.520388 | 0.7673372 | -0.628762 | -0.38452   | 0.5272583 |
| AC124550.1 | -0.892228  | -0.860705 | -0.839145 | -1.042655   | -1.239005 | -1.17332  | 1.9781004  | 0.3082148  | 1.2838927 | 0.9129618 | -0.143613  | 0.245982  | 0.7407962 | 0.7278785 | 1.2594825 | -1.173752 | 0.202314   | -0.313118 |
| AC163637.1 | -0.893462  | -1.133915 | -0.750809 | -0.883053   | -1.066678 | -1.083261 | 2.0593131  | 0.2083141  | 0.8152661 | 0.0712322 | 0.9020044  | 1.6238426 | 1.3643073 | -0.229024 | -0.369638 | -0.269994 | -0.759764  | 0.3953186 |
| AC158898.1 | -0.860701  | -1.812015 | -1.296454 | -0.409798   | -1.123404 | -0.366963 | 1.8832103  | 0.3236126  | 0.2923838 | 1.5484587 | 0.595333   | 1.0280576 | 0.9104817 | -0.777761 | -0.355599 | 0.4415509 | 0.4530056  | -0.473401 |
| AC119214.1 | -1.009414  | -0.756972 | -1.007684 | -1.179151</ |           |           |            |            |           |           |            |           |           |           |           |           |            |           |



gene signature CHR-PAP

| Gene     | p-value   | fold change<br>PAP/CHR |
|----------|-----------|------------------------|
| Cdc45    | 6.483E-05 | 2.35                   |
| H19      | 2.508E-06 | 0.09                   |
| Cav2     | 1.301E-03 | 1.86                   |
| Ngfr     | 3.706E-02 | 2.02                   |
| Wnt9a    | 4.147E-02 | 2.21                   |
| Fer      | 1.137E-02 | 1.57                   |
| Gna12    | 3.071E-04 | 0.50                   |
| Slc22a18 | 2.946E-03 | 1.93                   |
| Pih1d2   | 1.447E-05 | 2.85                   |
| Ccnd2    | 8.032E-03 | 0.50                   |
| Slfn4    | 1.284E-02 | 2.32                   |
| Scnn1g   | 2.814E-03 | 3.31                   |
| Tspan32  | 2.500E-07 | 0.21                   |
| Gmpr     | 9.895E-08 | 0.34                   |
| Itgb2    | 3.874E-04 | 0.07                   |
| Hddc2    | 1.205E-05 | 2.34                   |
| Tpd52l1  | 1.182E-02 | 2.28                   |
| Pemt     | 1.514E-03 | 2.78                   |
| Ckmt1    | 2.228E-03 | 1.65                   |
| Bcl6b    | 3.206E-03 | 1.99                   |
| Clec10a  | 7.759E-06 | 0.02                   |
| Alox12   | 3.044E-02 | 2.29                   |
| Dbt      | 9.160E-03 | 0.64                   |
| Rem1     | 3.229E-04 | 0.25                   |
| Tbrg4    | 1.548E-05 | 1.67                   |
| Fap      | 6.386E-05 | 0.23                   |
| Lck      | 8.175E-03 | 0.46                   |
| Cttnbp2  | 1.643E-04 | 0.34                   |
| Pparg    | 1.221E-06 | 0.07                   |
| 1-Sep    | 1.304E-04 | 0.42                   |
| Acvrl1   | 1.744E-04 | 0.47                   |
| Itga5    | 4.647E-03 | 1.66                   |
| Adora3   | 1.233E-03 | 0.42                   |
| Hnrnpd   | 2.934E-04 | 1.80                   |
| Gm2a     | 1.086E-06 | 0.34                   |
| Hk2      | 2.033E-02 | 2.46                   |
| Cd52     | 7.606E-06 | 0.21                   |
| Loxl3    | 3.472E-02 | 0.49                   |
| Kat2b    | 7.443E-05 | 0.43                   |
| Dnmt3l   | 1.207E-03 | 3.16                   |
| Icosl    | 3.831E-02 | 1.56                   |
| Serpinf1 | 3.531E-04 | 0.30                   |
| Tcf7     | 3.880E-02 | 1.56                   |
| Car4     | 4.168E-02 | 0.33                   |
| Dnajc5   | 1.129E-02 | 1.53                   |
| Bcl11a   | 8.234E-03 | 1.53                   |
| Pxmp4    | 4.652E-04 | 0.44                   |
| Dlg3     | 1.568E-02 | 0.64                   |
| Gnb1l    | 2.769E-04 | 3.33                   |
| Nsun5    | 1.041E-05 | 1.82                   |
| Top1mt   | 5.985E-05 | 2.34                   |
| Hoxa4    | 1.826E-02 | 3.75                   |
| Mmp14    | 7.781E-03 | 0.55                   |
| Slc7a7   | 3.860E-05 | 0.35                   |
| Ilf2     | 1.184E-02 | 1.56                   |
| S100a4   | 5.467E-04 | 0.19                   |
| Nhp2     | 2.787E-04 | 1.56                   |
| Mfsd10   | 4.316E-07 | 1.83                   |
| Ift20    | 4.727E-03 | 0.62                   |
| Col6a1   | 3.630E-03 | 0.36                   |
| Cfp      | 1.996E-06 | 0.16                   |
| Timp1    | 2.641E-03 | 0.30                   |
| Oas1c    | 1.411E-03 | 1.91                   |
| Uhrf1    | 1.721E-06 | 2.45                   |
| Ramp2    | 1.184E-04 | 0.47                   |
| Gramd1a  | 3.355E-05 | 0.59                   |
| Hpn      | 5.174E-04 | 0.43                   |
| Ckb      | 1.143E-04 | 0.06                   |
| Itgb7    | 1.518E-03 | 0.36                   |
| Pfdn5    | 6.976E-04 | 0.66                   |
| Efnb2    | 3.423E-02 | 0.66                   |
| Rrp15    | 7.797E-04 | 1.59                   |
| Rnd2     | 2.525E-02 | 0.65                   |
| Srr      | 4.881E-03 | 1.51                   |
| Ube2c    | 4.310E-05 | 4.63                   |
| Smg5     | 2.094E-04 | 1.59                   |
| Col18a1  | 2.400E-04 | 1.92                   |
| Slc19a1  | 2.157E-05 | 2.73                   |
| Kpnb1    | 8.834E-04 | 1.66                   |
| Tubb6    | 6.130E-05 | 2.23                   |
| Pax9     | 2.626E-03 | 25.22                  |
| Itga3    | 5.279E-04 | 3.96                   |
| Sgca     | 1.671E-06 | 0.04                   |
| Foxm1    | 1.024E-04 | 3.20                   |
| Itfg2    | 1.658E-03 | 1.79                   |
| Gtf2h4   | 4.026E-03 | 1.79                   |
| Tubb5    | 2.547E-02 | 1.58                   |
| Ell2     | 7.671E-03 | 1.60                   |
| Jup      | 3.952E-02 | 1.50                   |
| Nom1     | 5.262E-03 | 1.52                   |
| Tnk1     | 1.224E-02 | 2.02                   |
| Tcea3    | 6.024E-08 | 0.08                   |
| Stk38l   | 7.827E-03 | 2.09                   |
| Gstt1    | 2.710E-06 | 0.06                   |



|          |           |       |
|----------|-----------|-------|
| Ddx18    | 2.858E-04 | 1.70  |
| Ubl3     | 2.183E-05 | 0.50  |
| Eef1e1   | 2.665E-02 | 2.38  |
| Il16     | 5.771E-07 | 0.25  |
| Tcirg1   | 1.768E-03 | 0.47  |
| Naglu    | 1.528E-04 | 0.26  |
| Smo      | 6.044E-07 | 2.03  |
| Pwp1     | 3.574E-03 | 1.55  |
| Lrp3     | 3.177E-05 | 0.15  |
| Air1l    | 3.244E-03 | 0.30  |
| Cpa3     | 2.609E-06 | 0.08  |
| Ltbp1    | 2.241E-03 | 2.50  |
| Slc1a5   | 5.669E-06 | 0.39  |
| Vwf      | 8.098E-04 | 0.56  |
| Gria3    | 1.849E-02 | 0.48  |
| Sipa1l2  | 7.094E-03 | 2.46  |
| Blvra    | 1.003E-03 | 0.57  |
| Srp3     | 2.516E-02 | 0.54  |
| Fam98a   | 3.951E-03 | 1.63  |
| Ltbp2    | 1.520E-02 | 0.43  |
| Cd3g     | 9.262E-06 | 0.28  |
| Spag5    | 9.841E-07 | 3.42  |
| Foxn1    | 2.134E-02 | 2.96  |
| Unc119   | 1.205E-03 | 0.51  |
| Ccne1    | 9.641E-05 | 2.92  |
| Acp2     | 1.154E-04 | 0.50  |
| Celf2    | 1.429E-06 | 0.12  |
| Nr1h3    | 6.978E-05 | 0.21  |
| Ddb2     | 4.467E-04 | 1.90  |
| Sfp1     | 2.110E-05 | 0.22  |
| Napsa    | 5.159E-04 | 0.41  |
| Paxip1   | 4.462E-05 | 1.88  |
| Rhoc     | 4.613E-04 | 0.30  |
| Ppard    | 3.071E-04 | 2.99  |
| Def6     | 6.445E-05 | 1.59  |
| Angptl4  | 1.906E-03 | 0.31  |
| Dbf4     | 1.514E-04 | 3.24  |
| Nr2f6    | 2.720E-04 | 1.63  |
| Abhd3    | 8.563E-04 | 0.21  |
| Snrpd1   | 8.759E-04 | 1.87  |
| Rpl3l    | 6.089E-09 | 0.05  |
| Slc9a3r2 | 7.045E-03 | 0.41  |
| Axl      | 8.567E-04 | 0.53  |
| Clpp     | 6.699E-04 | 1.61  |
| Dennd1c  | 7.674E-04 | 0.43  |
| Prkd1    | 2.836E-02 | 1.89  |
| Lcp2     | 1.093E-05 | 0.26  |
| Cse1l    | 6.821E-04 | 1.73  |
| Fkbp7    | 3.158E-03 | 0.47  |
| Jag2     | 1.509E-04 | 2.04  |
| Nudt14   | 1.136E-05 | 2.16  |
| Epdr1    | 4.452E-04 | 0.36  |
| Top3a    | 1.140E-04 | 1.80  |
| Atg4d    | 1.779E-04 | 1.54  |
| Qttr1    | 3.680E-04 | 2.06  |
| Plin4    | 2.939E-07 | 0.03  |
| Chaf1a   | 1.837E-07 | 3.06  |
| Pla1a    | 2.545E-03 | 0.29  |
| Mcm2     | 4.824E-05 | 2.51  |
| Tpra1    | 1.528E-07 | 0.62  |
| Nab1     | 2.010E-04 | 1.73  |
| Cd97     | 1.563E-04 | 0.24  |
| Lamb1    | 3.066E-02 | 0.61  |
| Cd36     | 1.305E-04 | 0.01  |
| Apoe     | 3.479E-06 | 0.17  |
| Apoc2    | 1.297E-02 | 0.49  |
| Klf4     | 1.720E-02 | 1.65  |
| Elf3     | 2.163E-02 | 7.50  |
| Lipe     | 2.151E-03 | 0.39  |
| Mical3   | 2.358E-03 | 1.58  |
| Zfp959   | 5.484E-04 | 1.50  |
| Ebi3     | 5.019E-05 | 0.44  |
| Ccdc94   | 2.135E-04 | 1.58  |
| Dvl3     | 3.749E-03 | 1.63  |
| Eif2b5   | 3.272E-03 | 1.56  |
| Dlgap1   | 2.463E-03 | 2.42  |
| Hck      | 3.582E-04 | 0.37  |
| Ap1m2    | 1.720E-03 | 1.73  |
| Fkbp11   | 4.327E-02 | 1.53  |
| Pld3     | 5.816E-05 | 0.29  |
| Etv3     | 8.589E-04 | 0.58  |
| St8sia6  | 8.001E-04 | 0.23  |
| Fcgrt    | 3.653E-07 | 0.11  |
| Inmt     | 1.946E-02 | 0.01  |
| Impdh1   | 1.676E-05 | 2.01  |
| Psg18    | 3.769E-05 | 12.02 |
| Dusp3    | 1.074E-03 | 0.35  |
| Dgcr14   | 9.167E-07 | 1.68  |
| Ier3     | 1.877E-02 | 4.05  |
| Klc4     | 2.290E-02 | 0.62  |
| Ercc1    | 2.137E-04 | 1.90  |
| Cyp17a1  | 1.244E-03 | 0.20  |
| As3mt    | 3.056E-04 | 0.33  |
| Homer3   | 2.332E-03 | 3.17  |
| Crtc1    | 4.893E-02 | 1.53  |
| Sec14l2  | 2.231E-02 | 1.92  |
| Aven     | 1.909E-06 | 1.78  |



|               |           |       |
|---------------|-----------|-------|
| Cp            | 2.564E-06 | 0.07  |
| Crot          | 3.264E-03 | 0.62  |
| Insig2        | 6.856E-04 | 0.33  |
| Man1a         | 3.096E-03 | 0.52  |
| Kif20a        | 2.422E-05 | 4.08  |
| Dnase2a       | 1.208E-03 | 0.64  |
| Syce2         | 9.234E-03 | 4.05  |
| Nob1          | 8.426E-03 | 2.16  |
| Gys1          | 3.564E-02 | 1.60  |
| Ruvbl2        | 1.152E-04 | 2.29  |
| Il7r          | 7.226E-04 | 0.12  |
| Zfp81         | 1.400E-03 | 1.83  |
| Mmd           | 4.980E-04 | 0.59  |
| Hlf           | 4.005E-03 | 2.08  |
| Fam162a       | 3.580E-06 | 3.38  |
| Fanc1         | 2.194E-03 | 1.51  |
| Gstm5         | 9.610E-03 | 0.44  |
| Stat5a        | 7.079E-05 | 0.64  |
| Hmox2         | 2.230E-05 | 0.63  |
| Col5a3        | 2.320E-02 | 0.45  |
| Dnmt1         | 1.283E-03 | 1.53  |
| Ppan          | 1.349E-05 | 2.12  |
| Trmt10a       | 4.684E-04 | 2.07  |
| Etv1          | 3.987E-05 | 0.21  |
| Psap          | 3.594E-04 | 0.22  |
| Wars2         | 2.758E-03 | 1.62  |
| Atn1          | 6.819E-03 | 2.17  |
| Ptpn6         | 3.579E-06 | 0.32  |
| Emg1          | 1.785E-03 | 1.73  |
| Il11          | 1.271E-02 | 2.40  |
| Ralb          | 2.753E-02 | 1.76  |
| Tbccd1        | 5.557E-05 | 1.62  |
| Clec11a       | 1.926E-02 | 0.57  |
| Gab2          | 2.282E-05 | 0.31  |
| Ctse          | 4.840E-03 | 0.47  |
| Ndrg2         | 2.975E-06 | 0.17  |
| Arhgef40      | 3.903E-03 | 0.50  |
| Pnpla6        | 1.053E-04 | 1.58  |
| Cd33          | 4.361E-05 | 0.31  |
| Nkg7          | 7.948E-03 | 0.43  |
| Sgce          | 1.549E-04 | 0.24  |
| Aqp1          | 2.271E-05 | 0.28  |
| Ly9           | 1.168E-04 | 0.11  |
| Emr1          | 1.581E-07 | 0.13  |
| Mtfp1         | 2.229E-04 | 2.75  |
| Pgf           | 1.676E-03 | 27.62 |
| Ulk2          | 8.942E-04 | 0.58  |
| Ccl24         | 1.490E-03 | 0.25  |
| Grap          | 3.776E-04 | 0.42  |
| Srpk1         | 1.439E-03 | 0.57  |
| Nes           | 4.317E-02 | 1.68  |
| Matk          | 8.144E-04 | 0.19  |
| Pias4         | 8.860E-06 | 1.51  |
| Rasa4         | 9.168E-05 | 0.30  |
| Fxyd4         | 4.869E-02 | 2.89  |
| Prkacb        | 2.413E-03 | 0.59  |
| Cstb          | 3.880E-02 | 0.52  |
| Sh2b2         | 1.354E-02 | 1.71  |
| Cd44          | 2.217E-03 | 1.54  |
| Ndrg1         | 2.101E-04 | 7.04  |
| 4930550C14Rik | 4.255E-02 | 3.04  |
| Man2b1        | 5.580E-04 | 0.26  |
| Klf5          | 8.542E-04 | 3.13  |
| Plekha8       | 2.006E-02 | 1.54  |
| Spc25         | 9.335E-06 | 3.20  |
| Ripk4         | 8.302E-06 | 2.54  |
| Prlr          | 3.515E-02 | 0.51  |
| Letm1         | 4.931E-05 | 1.52  |
| Cadm3         | 3.071E-05 | 0.14  |
| Fcer1a        | 1.014E-02 | 0.28  |
| Slc1a3        | 1.717E-04 | 0.32  |
| Msh6          | 4.407E-04 | 1.92  |
| Mlxipl        | 5.009E-05 | 0.09  |
| Tbl2          | 2.639E-05 | 2.57  |
| Nid1          | 3.123E-03 | 0.42  |
| Mcm5          | 1.300E-04 | 2.86  |
| Pafah1b3      | 2.202E-04 | 2.10  |
| Il27ra        | 8.855E-07 | 0.30  |
| Asf1b         | 3.211E-03 | 3.03  |
| Ddx39         | 1.802E-03 | 1.98  |
| Igf1r         | 1.054E-02 | 1.81  |
| Mef2c         | 2.604E-07 | 0.14  |
| Pcyt1a        | 1.560E-04 | 0.60  |
| Tmod4         | 1.640E-06 | 0.20  |
| Mthfd2        | 2.805E-02 | 1.98  |
| Kit           | 7.848E-04 | 0.40  |
| Pan2          | 3.937E-06 | 1.55  |
| Pard6a        | 3.797E-02 | 1.63  |
| Pvalb         | 2.402E-03 | 0.01  |
| Tfap4         | 1.679E-05 | 2.47  |
| Ranbp1        | 1.198E-03 | 1.91  |
| Cd247         | 1.113E-04 | 0.47  |
| Gata6         | 4.586E-02 | 0.37  |
| Rsl1d1        | 2.600E-03 | 1.83  |
| Reep5         | 3.950E-03 | 0.57  |
| Nr2c1         | 1.779E-04 | 2.02  |
| Smpd4         | 6.731E-06 | 1.52  |



|               |           |       |
|---------------|-----------|-------|
| Itgae         | 4.848E-04 | 0.36  |
| Ctns          | 5.778E-03 | 0.60  |
| Dnase1        | 1.833E-04 | 1.81  |
| Eps8l1        | 6.046E-04 | 0.34  |
| Prss16        | 1.414E-03 | 4.33  |
| Hspb7         | 4.985E-04 | 0.04  |
| Susd2         | 2.615E-05 | 0.14  |
| Ggt5          | 5.726E-07 | 0.16  |
| Crip2         | 1.625E-02 | 0.56  |
| Crip1         | 4.068E-04 | 0.15  |
| Gcat          | 1.409E-02 | 1.95  |
| Tek           | 2.967E-07 | 0.31  |
| Cdc20         | 1.911E-04 | 3.82  |
| Adamts4       | 3.183E-03 | 2.68  |
| Srm           | 8.089E-04 | 2.14  |
| Epha2         | 3.334E-04 | 2.17  |
| Rbm14         | 6.904E-04 | 1.51  |
| Actn3         | 2.719E-03 | 0.02  |
| Nelf          | 9.003E-03 | 0.60  |
| Pdk1          | 1.736E-02 | 2.66  |
| Ptbp1         | 1.432E-03 | 1.55  |
| Atp7b         | 4.757E-02 | 19.02 |
| Rundc3a       | 2.085E-04 | 2.48  |
| Gtf2h1        | 7.824E-04 | 1.84  |
| Hfe           | 9.602E-06 | 0.36  |
| Tcf23         | 1.238E-02 | 2.99  |
| Nphs1         | 1.302E-02 | 1.79  |
| Aplp1         | 2.864E-03 | 2.31  |
| Pola1         | 7.464E-06 | 2.01  |
| Gmnn          | 1.302E-02 | 2.91  |
| B4galnt1      | 1.108E-02 | 1.51  |
| Mettl1        | 4.210E-06 | 1.80  |
| Saal1         | 3.319E-04 | 2.08  |
| Krt23         | 3.085E-04 | 0.24  |
| Cnp           | 8.053E-04 | 0.64  |
| Sulf2         | 1.550E-04 | 0.34  |
| Tmco6         | 9.982E-03 | 1.54  |
| Stambp        | 2.502E-04 | 1.74  |
| Leprel4       | 1.068E-03 | 2.60  |
| Vars          | 3.868E-03 | 1.52  |
| Hspa1l        | 1.058E-04 | 2.04  |
| Msh5          | 1.329E-02 | 1.99  |
| Ddah2         | 2.063E-04 | 0.46  |
| Lsm2          | 1.874E-06 | 2.57  |
| Pole          | 9.472E-06 | 3.38  |
| Atp1a2        | 4.492E-09 | 0.02  |
| Casq1         | 3.361E-05 | 0.02  |
| Stx1a         | 9.677E-06 | 3.13  |
| Scube2        | 2.556E-03 | 0.29  |
| Dennd2c       | 3.068E-04 | 2.00  |
| Mark3         | 3.212E-04 | 1.89  |
| Mc5r          | 4.593E-04 | 0.06  |
| Tinf2         | 1.349E-03 | 1.63  |
| Rad51c        | 6.396E-04 | 2.97  |
| Arpp19        | 1.205E-04 | 1.51  |
| Khrrp         | 8.238E-04 | 1.72  |
| Cct4          | 3.215E-02 | 1.57  |
| Ankrd26       | 6.239E-04 | 2.29  |
| Ift43         | 5.858E-04 | 1.64  |
| Tcap          | 1.286E-06 | 0.01  |
| Crif1         | 4.027E-02 | 2.09  |
| Ctsd          | 1.558E-04 | 0.31  |
| Hmgcll1       | 2.037E-02 | 12.19 |
| Fzd3          | 2.383E-02 | 0.53  |
| Mid1ip1       | 1.200E-03 | 0.54  |
| Fhl2          | 2.155E-03 | 2.67  |
| Clstn3        | 3.576E-03 | 0.04  |
| Fbxw9         | 4.539E-02 | 1.62  |
| Lass4         | 4.700E-04 | 0.10  |
| 1700109H08Rik | 3.128E-02 | 1.78  |
| Elk3          | 3.789E-03 | 1.83  |
| Nutf2         | 1.470E-02 | 1.50  |
| Mgst1         | 1.779E-04 | 0.34  |
| Nfib          | 1.745E-03 | 0.57  |
| Rbfox1        | 3.964E-05 | 0.10  |
| Gprc5b        | 1.571E-03 | 0.33  |
| Cd163         | 1.107E-06 | 0.12  |
| Hdac5         | 6.052E-06 | 0.57  |
| Bcl2l13       | 7.464E-04 | 1.60  |
| Dqx1          | 2.585E-02 | 2.07  |
| Ascl2         | 1.128E-05 | 5.08  |
| Rarres2       | 8.989E-09 | 0.03  |
| Met           | 4.878E-03 | 1.54  |
| Fpgs          | 4.122E-06 | 2.19  |
| Cbx5          | 5.404E-04 | 1.59  |
| Sardh         | 2.178E-04 | 0.20  |
| Bcr           | 9.607E-04 | 1.72  |
| Fxyd5         | 1.487E-05 | 0.31  |
| Wnt3a         | 1.765E-05 | 5.42  |
| Aldh3a2       | 4.127E-04 | 0.39  |
| Ifrd2         | 2.353E-06 | 2.30  |
| Tnfrsf13b     | 2.602E-04 | 0.26  |
| Raver1        | 1.992E-06 | 1.92  |
| Tmem86a       | 1.754E-04 | 0.42  |
| Tsacc         | 1.283E-02 | 1.54  |
| Mettl16       | 2.356E-04 | 1.68  |
| Psen2         | 2.469E-05 | 0.20  |



|               |           |      |
|---------------|-----------|------|
| Plcd1         | 1.557E-02 | 1.95 |
| Fads1         | 4.261E-04 | 0.38 |
| Tnfrsf22      | 2.215E-03 | 3.25 |
| Phlda2        | 9.131E-03 | 3.06 |
| Grid2ip       | 1.796E-02 | 3.48 |
| Mcoln2        | 9.838E-06 | 0.12 |
| Panx3         | 1.228E-03 | 0.02 |
| Adssl1        | 6.485E-08 | 0.06 |
| Odc1          | 2.321E-04 | 4.85 |
| Thg1l         | 3.199E-03 | 1.58 |
| Adam19        | 2.061E-03 | 0.47 |
| Pabpc4        | 1.497E-02 | 1.51 |
| Exoc3l2       | 1.058E-05 | 2.21 |
| Zfp296        | 3.441E-04 | 2.40 |
| Dhdh          | 2.644E-05 | 0.35 |
| Pgam1         | 2.227E-04 | 1.98 |
| Tjap1         | 1.199E-03 | 1.73 |
| Ehf           | 2.144E-02 | 1.72 |
| Nanog         | 2.179E-05 | 3.37 |
| Steap4        | 1.158E-03 | 0.12 |
| Kif11         | 3.673E-05 | 2.92 |
| Rpa3          | 3.928E-04 | 1.69 |
| Mikl          | 2.193E-02 | 1.75 |
| Retn          | 3.924E-05 | 0.01 |
| Enkd1         | 1.466E-02 | 2.62 |
| Atp6v0d1      | 5.321E-04 | 0.65 |
| Zfp651        | 2.842E-02 | 0.61 |
| Card14        | 2.015E-03 | 0.36 |
| D16H22S680E   | 3.599E-05 | 0.60 |
| Cad           | 1.499E-04 | 2.19 |
| Pea15a        | 3.886E-04 | 0.54 |
| Tnfaip8l2     | 7.078E-05 | 0.21 |
| 1500003O03Rik | 5.779E-06 | 0.44 |
| Trpv4         | 4.190E-03 | 0.58 |
| Pigl          | 7.609E-03 | 1.52 |
| Bicc1         | 2.942E-04 | 0.29 |
| Mertk         | 3.449E-04 | 0.10 |
| Ankrd52       | 1.321E-02 | 1.52 |
| Mrps25        | 2.052E-04 | 1.83 |
| Csf1          | 1.606E-04 | 0.48 |
| Kif1a         | 4.132E-04 | 0.27 |
| 2310061C15Rik | 2.333E-03 | 1.94 |
| Hoxa2         | 1.613E-03 | 5.02 |
| Dll1          | 7.701E-04 | 2.87 |
| Elmo3         | 1.360E-02 | 1.89 |
| Stc1          | 2.171E-03 | 3.32 |
| 4931428F04Rik | 9.646E-03 | 5.22 |
| Tppp3         | 2.300E-02 | 0.35 |
| Msh3          | 2.443E-03 | 1.76 |
| E2f4          | 1.080E-02 | 1.83 |
| Surf2         | 4.089E-04 | 1.53 |
| Naf1          | 7.313E-04 | 2.84 |
| Yes1          | 4.225E-04 | 1.71 |
| Gata2         | 6.538E-06 | 0.35 |
| Entpd2        | 2.468E-02 | 0.60 |
| Clic3         | 6.012E-03 | 0.54 |
| Slc25a13      | 7.510E-04 | 1.57 |
| 0610007P22Rik | 1.519E-05 | 1.72 |
| Sirt2         | 7.797E-05 | 0.58 |
| Nolc1         | 9.323E-04 | 2.02 |
| Hmgb3         | 2.129E-03 | 2.15 |
| Mtap2         | 7.932E-03 | 0.55 |
| Abca1         | 8.451E-06 | 0.25 |
| Ubl4          | 8.045E-04 | 1.57 |
| Sash1         | 6.023E-05 | 0.50 |
| Endog         | 1.995E-03 | 2.19 |
| Cybb          | 1.027E-03 | 0.09 |
| Pcolce2       | 7.746E-05 | 0.17 |
| Cd48          | 2.059E-07 | 0.16 |
| Fam116b       | 1.191E-02 | 2.52 |
| Cd83          | 4.019E-04 | 0.15 |
| C4a           | 4.406E-04 | 0.19 |
| Notch4        | 1.006E-03 | 2.34 |
| Ppt2          | 1.137E-03 | 0.56 |
| Hivep2        | 4.852E-04 | 1.62 |
| Itga2         | 4.963E-04 | 4.47 |
| Lpl           | 1.514E-05 | 0.02 |
| Srf           | 6.666E-04 | 1.57 |
| Lama5         | 3.416E-03 | 2.15 |
| Steap1        | 1.849E-02 | 7.35 |
| Steap2        | 3.546E-02 | 2.53 |
| Awat1         | 1.378E-03 | 0.03 |
| Anxa9         | 8.970E-04 | 0.28 |
| Lass2         | 6.333E-04 | 0.48 |
| Plekho1       | 1.136E-04 | 0.21 |
| Anp32e        | 5.080E-03 | 1.56 |
| Eps8          | 2.554E-04 | 0.21 |
| Gnrh1         | 8.975E-03 | 2.22 |
| Sqstm1        | 9.603E-04 | 0.55 |
| Fcrls         | 2.763E-04 | 0.20 |
| Ncapg         | 5.176E-06 | 3.57 |
| Dstn          | 1.213E-02 | 1.55 |
| Bola1         | 7.267E-04 | 1.59 |
| Gatsl2        | 1.459E-03 | 1.74 |
| Fcgr1         | 3.003E-02 | 0.42 |
| Ncf1          | 9.765E-04 | 0.14 |
| Il17rb        | 9.899E-03 | 1.92 |



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|---------------|-----------|-------|
| Chdh          | 2.019E-02 | 1.60  |
| Lrrc27        | 3.199E-02 | 0.49  |
| Lbp           | 3.099E-06 | 0.08  |
| Celsr1        | 2.369E-02 | 1.53  |
| Fli1          | 6.758E-06 | 0.28  |
| Camk1g        | 3.631E-03 | 5.84  |
| Diexf         | 1.749E-05 | 1.58  |
| Hsd11b1       | 8.247E-07 | 0.10  |
| H2-M3         | 1.994E-03 | 0.38  |
| Lonrf3        | 1.041E-03 | 0.33  |
| Ctsz          | 8.284E-05 | 0.11  |
| H2-M2         | 3.329E-03 | 0.35  |
| Pdpf          | 1.053E-02 | 1.58  |
| Eef1a2        | 1.455E-06 | 0.01  |
| Cd46          | 3.635E-02 | 2.09  |
| Cd34          | 5.456E-03 | 0.40  |
| 5033414D02Rik | 9.604E-05 | 0.59  |
| Cd274         | 2.743E-02 | 0.38  |
| Pdcd1g2       | 4.729E-02 | 0.61  |
| Gtf3a         | 3.062E-04 | 1.59  |
| Mtif3         | 4.665E-05 | 1.67  |
| Lrx2          | 4.591E-06 | 2.22  |
| Il19          | 6.139E-03 | 10.30 |
| Dyrk3         | 1.096E-03 | 2.92  |
| Il10          | 3.996E-02 | 3.12  |
| Foxred2       | 1.852E-03 | 0.50  |
| Pacs1n2       | 2.334E-03 | 0.66  |
| Cmah          | 5.952E-03 | 1.55  |
| Ttll12        | 2.396E-05 | 1.89  |
| Sulf1         | 8.849E-03 | 0.38  |
| Etaa1         | 3.595E-07 | 1.87  |
| Matn4         | 1.386E-03 | 0.20  |
| Brca1         | 1.228E-04 | 3.11  |
| Cntnap1       | 4.928E-02 | 2.04  |
| Gsdma         | 5.485E-04 | 0.33  |
| Dnrtip1       | 1.067E-03 | 1.51  |
| Tnnc2         | 3.582E-05 | 0.01  |
| Cd300lg       | 5.493E-04 | 0.56  |
| Mpp2          | 4.816E-02 | 2.05  |
| Vtn           | 8.350E-07 | 0.12  |
| Traf4         | 2.625E-03 | 1.70  |
| Aldoc         | 1.672E-04 | 2.73  |
| Stac2         | 3.516E-03 | 0.17  |
| Plxdc1        | 3.491E-05 | 0.34  |
| Psm11         | 2.635E-03 | 1.51  |
| C1qtnf1       | 8.750E-03 | 0.41  |
| Timp2         | 1.129E-05 | 0.14  |
| Igfbp4        | 2.630E-03 | 0.45  |
| Cdc6          | 6.406E-04 | 2.76  |
| Atad5         | 2.591E-05 | 2.52  |
| Tns4          | 1.325E-04 | 2.82  |
| Serinc3       | 3.595E-07 | 0.43  |
| Birc5         | 1.935E-06 | 3.77  |
| Wfdc2         | 1.990E-03 | 10.76 |
| Etv4          | 1.306E-02 | 3.16  |
| Mmp9          | 2.905E-03 | 6.16  |
| Pltp          | 2.047E-06 | 0.12  |
| Ctsa          | 1.529E-07 | 0.31  |
| Jph2          | 3.535E-05 | 0.19  |
| Hspb9         | 7.954E-03 | 1.61  |
| Mybl2         | 2.853E-04 | 2.91  |
| Eya2          | 3.165E-02 | 0.57  |
| B4galt5       | 1.324E-03 | 0.23  |
| Ddx27         | 1.410E-04 | 1.85  |
| Cyth4         | 3.132E-05 | 0.15  |
| Rac3          | 5.818E-03 | 3.67  |
| Ints2         | 1.720E-05 | 1.66  |
| Med13l        | 3.737E-02 | 1.52  |
| Erbp3         | 1.072E-02 | 1.58  |
| Ikzf3         | 3.035E-04 | 0.39  |
| Mfng          | 3.495E-04 | 0.54  |
| Pmp22         | 3.488E-06 | 0.10  |
| Zcchc10       | 5.088E-04 | 2.99  |
| Gpx3          | 7.811E-06 | 0.16  |
| Anxa6         | 8.309E-06 | 0.25  |
| Kpna2         | 5.266E-05 | 2.27  |
| Shroom1       | 6.154E-03 | 5.76  |
| 8-Sep         | 5.876E-04 | 0.57  |
|               | 1.183E-03 | 2.03  |
| Myo1b         | 1.183E-03 | 2.03  |
| Ypel2         | 7.539E-04 | 0.57  |
| Nol11         | 1.188E-06 | 1.60  |
| C1qbp         | 9.580E-05 | 1.81  |
| Kdm6b         | 1.559E-03 | 1.90  |
| Adora2b       | 2.153E-02 | 1.57  |
| Trpv2         | 2.165E-04 | 0.21  |
| Pcgf2         | 2.363E-05 | 2.08  |
| Trim37        | 3.024E-03 | 1.67  |
| Slc2a4        | 8.662E-06 | 0.31  |
| 2810408A11Rik | 4.470E-02 | 3.30  |
| Sparc         | 8.798E-03 | 0.46  |
| Tada2a        | 1.044E-05 | 2.00  |
| Ikzf1         | 1.298E-05 | 0.25  |
| Copz2         | 9.829E-04 | 0.47  |
| Slc25a39      | 2.443E-04 | 1.80  |
| Sp2           | 8.382E-03 | 1.91  |
| Pex12         | 5.283E-05 | 1.95  |
| Slc25a35      | 7.510E-03 | 1.87  |



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| BC096441      | 5.271E-04 | 0.10  |
| Cd68          | 1.171E-04 | 0.09  |
| Acs1          | 2.218E-04 | 0.44  |
| Smyd4         | 1.639E-03 | 1.52  |
| Lsp1          | 3.259E-05 | 0.17  |
| Avpi1         | 2.208E-02 | 1.58  |
| Myh11         | 7.876E-06 | 0.14  |
| Unc45b        | 5.962E-07 | 0.10  |
| Sult4a1       | 1.873E-02 | 22.68 |
| Pnpla5        | 1.191E-03 | 0.03  |
| Mrpl45        | 1.607E-03 | 1.84  |
| Mb            | 1.201E-03 | 0.03  |
| P4ha2         | 3.342E-04 | 1.90  |
| Alox12e       | 8.160E-04 | 0.04  |
| Arrb1         | 1.621E-02 | 0.65  |
| Pelp1         | 1.929E-06 | 1.94  |
| Alox15        | 1.870E-04 | 0.18  |
| Ccl6          | 1.672E-05 | 0.06  |
| Sart3         | 6.503E-05 | 1.68  |
| Slfn3         | 4.708E-02 | 2.24  |
| Nars2         | 1.727E-04 | 1.95  |
| Mfsd3         | 1.337E-05 | 2.26  |
| Dnase111      | 1.814E-06 | 0.36  |
| Aldh3a1       | 1.664E-02 | 0.14  |
| Ccl9          | 1.717E-05 | 0.06  |
| Scrn1         | 2.930E-04 | 0.21  |
| Rnf145        | 1.745E-02 | 1.60  |
| Scn1b         | 7.596E-08 | 0.20  |
| Chtf18        | 1.039E-08 | 3.51  |
| Ppp1r12c      | 1.580E-04 | 0.54  |
| Mtap1s        | 9.740E-03 | 0.53  |
| 2610027L16Rik | 1.628E-03 | 1.60  |
| Atp6v0a1      | 8.372E-05 | 0.51  |
| Psmc3ip       | 3.456E-03 | 3.40  |
| Aoc3          | 2.752E-05 | 0.21  |
| Sec14l4       | 1.105E-03 | 0.08  |
| Tlcd1         | 2.527E-03 | 0.60  |
| Ptger1        | 1.542E-03 | 0.35  |
| Arhgef25      | 4.790E-02 | 0.55  |
| Cops6         | 6.443E-06 | 1.58  |
| Gyg           | 5.771E-08 | 0.14  |
| Rcn3          | 5.496E-03 | 0.33  |
| Slc6a8        | 9.198E-04 | 0.66  |
| Pdk4          | 1.590E-02 | 0.11  |
| Sema6a        | 1.911E-04 | 0.22  |
| Akt3          | 1.933E-03 | 0.50  |
| Lyst          | 1.308E-05 | 0.40  |
| Pr18a1        | 1.488E-03 | 58.01 |
| Syne1         | 8.703E-05 | 0.36  |
| Fbxo5         | 8.594E-07 | 2.72  |
| Frk           | 3.442E-02 | 1.76  |
| Trdn          | 5.940E-08 | 0.02  |
| Trmt11        | 3.773E-04 | 1.81  |
| Lrp11         | 4.881E-02 | 2.85  |
| Adat2         | 1.565E-06 | 2.00  |
| Pex3          | 5.949E-03 | 0.58  |
| Cep57l1       | 1.553E-04 | 2.48  |
| Ltv1          | 1.504E-05 | 1.51  |
| Mical1        | 1.260E-04 | 0.41  |
| Rab32         | 3.220E-05 | 0.46  |
| Slc16a10      | 6.151E-04 | 0.43  |
| Fyn           | 4.189E-05 | 0.42  |
| Tube1         | 3.599E-06 | 3.77  |
| Lama4         | 1.739E-04 | 0.45  |
| Popdc3        | 3.342E-02 | 2.16  |
| Prep          | 5.407E-07 | 2.47  |
| D10Bwg1379e   | 2.714E-02 | 0.26  |
| Hebp2         | 3.087E-02 | 0.53  |
| Rtn4ip1       | 1.101E-04 | 1.59  |
| Smpd13a       | 1.115E-02 | 0.46  |
| Fabp7         | 7.358E-03 | 0.30  |
| Pkib          | 8.842E-05 | 0.27  |
| Echdc1        | 4.221E-03 | 0.38  |
| Ccdc59        | 2.778E-03 | 1.71  |
| Lama2         | 2.042E-05 | 0.11  |
| P4ha1         | 1.426E-02 | 1.67  |
| Dcn           | 1.656E-06 | 0.03  |
| 2310015B20Rik | 3.818E-03 | 0.34  |
| Cdk1          | 3.900E-05 | 3.27  |
| Actr6         | 1.006E-03 | 1.56  |
| Poc1b         | 9.832E-05 | 1.77  |
| Tmpo          | 2.734E-06 | 1.74  |
| Sgk1          | 2.151E-02 | 0.63  |
| Cep290        | 1.709E-02 | 1.63  |
| Ikbip         | 3.773E-02 | 0.64  |
| Hbs1l         | 2.728E-06 | 1.52  |
| Epb4.1l2      | 2.081E-04 | 0.41  |
| Arg1          | 3.203E-02 | 6.19  |
| Nedd1         | 3.751E-04 | 2.04  |
| Pde7b         | 2.282E-04 | 0.25  |
| Fam54a        | 5.295E-06 | 2.72  |
| Moxd1         | 4.896E-02 | 2.10  |
| Vnn3          | 3.321E-03 | 0.03  |
| Gm872         | 5.070E-03 | 4.24  |
| Hal           | 1.431E-04 | 0.24  |
| Snrpf         | 3.755E-04 | 1.97  |
| Tmcc3         | 4.110E-03 | 0.62  |



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| Ccdc41        | 3.189E-04 | 1.63 |
| Socs2         | 7.629E-03 | 0.56 |
| Tcp11l2       | 5.608E-05 | 0.66 |
| Btbd11        | 1.443E-04 | 2.60 |
| Timp3         | 2.196E-05 | 0.28 |
| Igf1          | 2.315E-06 | 0.18 |
| Dram1         | 3.152E-03 | 0.66 |
| Mybpc1        | 6.692E-06 | 0.01 |
| Slc5a8        | 4.107E-02 | 0.53 |
| Herc4         | 1.850E-03 | 1.52 |
| Mypn          | 3.912E-07 | 0.04 |
| Pbld1         | 1.100E-05 | 1.53 |
| Ddx21         | 3.706E-05 | 1.69 |
| Srgn          | 3.164E-04 | 0.43 |
| Supv3l1       | 4.067E-04 | 1.68 |
| 2010107G23Rik | 8.454E-03 | 1.82 |
| Sgpl1         | 1.841E-06 | 0.34 |
| Pcbd1         | 5.155E-03 | 0.40 |
| Slc29a3       | 7.590E-03 | 0.61 |
| 4632428N05Rik | 1.602E-05 | 0.12 |
| Slc16a7       | 4.221E-08 | 0.15 |
| Lrig3         | 1.399E-02 | 0.57 |
| Ddit4         | 9.471E-05 | 4.97 |
| Pno1          | 1.248E-04 | 1.72 |
| Plek          | 4.779E-04 | 0.20 |
| Avpr1a        | 1.191E-02 | 0.37 |
| Pcsk4         | 5.488E-05 | 2.52 |
| Peli1         | 1.021E-04 | 0.58 |
| Slc1a4        | 3.817E-03 | 2.24 |
| Dock2         | 1.700E-06 | 0.16 |
| Gamt          | 5.129E-04 | 0.46 |
| Ptpnb         | 2.355E-04 | 0.61 |
| Cnot2         | 9.804E-04 | 1.70 |
| Cobl          | 3.177E-03 | 0.20 |
| Grb10         | 6.523E-04 | 0.45 |
| Snrpd3        | 8.075E-04 | 1.83 |
| Nav3          | 2.962E-02 | 0.62 |
| E2f7          | 5.471E-06 | 8.50 |
| Phlda1        | 2.853E-04 | 8.01 |
| Sf3a2         | 3.130E-06 | 1.96 |
| Mdm1          | 4.001E-03 | 1.80 |
| Jsrp1         | 5.650E-06 | 0.02 |
| Tmbim4        | 2.375E-03 | 0.64 |
| Irak3         | 8.371E-05 | 0.37 |
| 4930404N11Rik | 9.508E-04 | 0.16 |
| Fzr1          | 2.848E-07 | 1.70 |
| Col6a2        | 2.643E-03 | 0.37 |
| Txnrd1        | 1.643E-05 | 0.43 |
| Ppm1m         | 1.388E-02 | 0.66 |
| D10Wsu102e    | 3.162E-04 | 1.51 |
| Aldh1l2       | 6.837E-03 | 4.32 |
| Glyctk        | 2.831E-04 | 3.14 |
| Adarb1        | 6.474E-04 | 2.50 |
| App12         | 3.588E-05 | 0.48 |
| Slc36a2       | 1.141E-04 | 0.29 |
| Stk10         | 1.255E-02 | 0.54 |
| Pfkl          | 1.090E-07 | 3.14 |
| Pex13         | 1.602E-02 | 0.58 |
| Xpo1          | 2.551E-05 | 1.53 |
| Cpeb4         | 3.047E-05 | 0.47 |
| Stc2          | 7.063E-03 | 2.05 |
| Chac2         | 8.184E-04 | 1.62 |
| Shc2          | 4.767E-05 | 0.15 |
| Spnb2         | 5.589E-05 | 0.52 |
| Fstl3         | 2.852E-02 | 1.53 |
| Ccng1         | 2.904E-04 | 0.55 |
| Fgf22         | 1.498E-03 | 0.31 |
| Nudcd2        | 1.544E-02 | 1.55 |
| Hmmr          | 2.495E-06 | 3.35 |
| Cyflp2        | 2.435E-06 | 0.32 |
| Sgcd          | 4.624E-07 | 0.09 |
| Hnnpab        | 4.452E-03 | 1.58 |
| Hspa4         | 1.790E-04 | 1.53 |
| Gfpt2         | 1.290E-04 | 0.24 |
| Rufy1         | 1.312E-04 | 0.61 |
| Rnf130        | 2.247E-05 | 0.48 |
| Ltc4s         | 1.666E-04 | 0.39 |
| Rad50         | 7.382E-04 | 1.54 |
| 3010026O09Rik | 1.319E-03 | 1.58 |
| Phf15         | 6.421E-04 | 0.50 |
| Pdlim4        | 2.421E-04 | 0.10 |
| Cdkl3         | 1.030E-03 | 1.86 |
| Cdkn2aipnl    | 7.182E-05 | 1.65 |
| Itk           | 1.965E-04 | 0.39 |
| Havcr2        | 5.375E-03 | 0.52 |
| Tnip1         | 6.315E-04 | 0.63 |
| Upp1          | 3.731E-03 | 6.29 |
| Hus1          | 5.070E-06 | 1.93 |
| Pttg1         | 6.711E-06 | 2.51 |
| Tns3          | 1.898E-04 | 0.34 |
| Gatsl3        | 4.052E-03 | 2.16 |
| Igfbp3        | 3.998E-02 | 2.16 |
| Tcn2          | 3.372E-06 | 0.35 |
| Osbp2         | 5.776E-05 | 4.72 |
| Myo1g         | 6.870E-05 | 0.18 |
| Smtn          | 1.990E-02 | 1.53 |
| Guk1          | 5.307E-04 | 0.47 |



|               |           |       |
|---------------|-----------|-------|
| Pnpt1         | 1.385E-03 | 1.56  |
| Efemp1        | 1.648E-05 | 0.11  |
| Myl7          | 1.369E-02 | 29.01 |
| Pold2         | 6.024E-04 | 2.01  |
| Aebp1         | 7.976E-05 | 0.17  |
| Pgam2         | 2.846E-08 | 0.06  |
| Xbp1          | 3.088E-06 | 0.49  |
| 4-Sep         | 2.943E-04 | 0.49  |
| Ska2          | 2.701E-04 | 2.07  |
| Prr11         | 1.124E-07 | 3.57  |
| Smg8          | 1.954E-05 | 1.68  |
| Tubd1         | 3.855E-06 | 2.02  |
| Mrpl22        | 3.001E-05 | 1.54  |
| Znhit3        | 3.063E-05 | 1.72  |
| Shmt1         | 1.443E-04 | 1.88  |
| Drg2          | 5.628E-06 | 1.51  |
| Tom1l1        | 6.667E-03 | 1.56  |
| Cox11         | 1.308E-04 | 1.68  |
| Elac2         | 6.794E-06 | 1.63  |
| Pctp          | 3.696E-04 | 0.06  |
| Twistnb       | 1.566E-04 | 1.51  |
| Atp6v1c2      | 1.209E-03 | 0.20  |
| Pik3cg        | 1.784E-06 | 0.30  |
| Tspan13       | 2.688E-05 | 0.34  |
| Fam49a        | 1.435E-04 | 0.44  |
| Lpin1         | 2.358E-07 | 0.33  |
| Nrcam         | 1.700E-06 | 0.10  |
| Arsg          | 7.873E-04 | 0.57  |
| Fam84a        | 7.602E-05 | 0.52  |
| Fam20a        | 8.747E-05 | 2.12  |
| Fkbp1b        | 4.166E-04 | 0.38  |
| Rnf144a       | 3.501E-06 | 0.22  |
| Id2           | 7.154E-05 | 0.43  |
| Dus4l         | 1.109E-04 | 2.56  |
| Rrm2          | 1.648E-04 | 2.75  |
| Bcap29        | 2.742E-05 | 1.59  |
| Efr3b         | 5.615E-03 | 0.35  |
| Cbl1l         | 7.056E-03 | 1.91  |
| Dnmt3a        | 8.040E-04 | 0.28  |
| Ddx52         | 1.441E-04 | 1.76  |
| Taf15         | 1.934E-03 | 1.78  |
| Ace           | 3.166E-06 | 0.07  |
| Mmp28         | 9.038E-03 | 2.39  |
| Cdc27         | 2.941E-03 | 1.63  |
| Nle1          | 2.115E-06 | 1.96  |
| Map3k3        | 2.427E-05 | 0.66  |
| Adap2         | 1.702E-05 | 0.22  |
| Pecam1        | 1.179E-04 | 0.51  |
| Cacng1        | 1.395E-05 | 0.07  |
| Nup85         | 3.787E-03 | 1.54  |
| Itgb4         | 3.265E-03 | 3.89  |
| Acox1         | 1.258E-06 | 0.49  |
| Tsen54        | 6.339E-06 | 1.68  |
| Lgl2          | 2.374E-03 | 1.67  |
| Camkk1        | 1.184E-02 | 0.58  |
| P2rx1         | 9.974E-05 | 0.30  |
| Atp2a3        | 5.443E-10 | 0.23  |
| Med31         | 3.922E-04 | 1.67  |
| Ube2o         | 3.830E-03 | 1.98  |
| Txndc17       | 4.082E-04 | 2.02  |
| 4933427D14Rik | 1.100E-02 | 1.51  |
| Fam64a        | 1.479E-02 | 3.55  |
| Cygb          | 3.972E-07 | 0.06  |
| Mxra7         | 9.211E-04 | 0.24  |
| Rabep1        | 9.580E-03 | 0.66  |
| Sec14l1       | 5.241E-04 | 0.64  |
| Dhrs13        | 4.268E-05 | 3.38  |
| Coro6         | 1.716E-04 | 0.22  |
| Tmigd1        | 9.537E-04 | 6.07  |
| Nxn           | 4.547E-04 | 1.77  |
| Rph3al        | 3.699E-03 | 2.68  |
| Tac4          | 5.763E-03 | 0.22  |
| Scrn2         | 1.642E-03 | 2.14  |
| Cacnb1        | 5.080E-07 | 0.21  |
| Dlg4          | 3.365E-02 | 0.55  |
| Tmem107       | 2.885E-02 | 1.55  |
| Aurkb         | 1.580E-07 | 3.33  |
| Ctc1          | 2.588E-03 | 1.75  |
| Pfas          | 4.320E-05 | 1.57  |
| Pik3r5        | 1.304E-04 | 0.15  |
| Ntn1          | 6.635E-06 | 0.20  |
| Top2a         | 6.093E-05 | 3.13  |
| Kat2a         | 6.075E-06 | 2.01  |
| Lsm12         | 7.918E-04 | 1.84  |
| Ccdc43        | 2.731E-03 | 1.54  |
| Eftud2        | 4.328E-05 | 1.63  |
| Dcald         | 7.866E-03 | 1.62  |
| Plcd3         | 2.123E-02 | 1.82  |
| Coch          | 7.627E-06 | 0.10  |
| Ston2         | 6.311E-03 | 1.80  |
| Sel1l         | 3.664E-05 | 0.62  |
| Dnaaf2        | 1.024E-05 | 2.00  |
| Pole2         | 1.913E-05 | 2.45  |
| L2hgdh        | 1.155E-04 | 1.76  |
| Galc          | 1.345E-04 | 0.16  |
| Polr2h        | 1.463E-02 | 1.58  |
| 1110008L16Rik | 2.318E-04 | 1.61  |



|               |           |       |
|---------------|-----------|-------|
| Mbip          | 5.080E-03 | 1.81  |
| Gstz1         | 3.146E-03 | 0.54  |
| 2700073G19Rik | 9.194E-03 | 1.97  |
| Nova1         | 1.768E-06 | 0.05  |
| Mthfd1        | 1.070E-05 | 1.75  |
| Sgpp1         | 6.469E-04 | 0.48  |
| Spnb1         | 3.444E-04 | 0.53  |
| Nin           | 6.075E-05 | 0.40  |
| Pygl          | 1.835E-03 | 0.55  |
| Bdkrb2        | 3.348E-04 | 4.34  |
| Serpina3n     | 5.963E-09 | 0.09  |
| Dhrs7         | 1.152E-03 | 0.48  |
| Mnat1         | 7.940E-03 | 1.52  |
| Hif1a         | 2.018E-03 | 2.77  |
| Snapc1        | 1.682E-04 | 2.32  |
| Eif2s1        | 8.574E-05 | 1.67  |
| Plek2         | 1.144E-03 | 2.45  |
| Galnt1        | 4.288E-05 | 0.18  |
| Erh           | 5.783E-06 | 1.74  |
| Slc10a1       | 3.426E-04 | 2.17  |
| Mta1          | 6.854E-04 | 1.64  |
| Gtpbp4        | 6.554E-03 | 1.54  |
| Cdca7l        | 3.076E-04 | 1.51  |
| Efcab11       | 5.884E-03 | 5.32  |
| Tdp1          | 3.371E-03 | 1.64  |
| Rps6ka5       | 1.711E-03 | 1.61  |
| Fbln5         | 1.896E-02 | 0.52  |
| Lgmn          | 3.886E-04 | 0.34  |
| Pitrm1        | 7.870E-05 | 1.87  |
| Chga          | 2.065E-03 | 0.23  |
| Pfkf          | 2.382E-04 | 1.90  |
| Asb2          | 2.232E-04 | 0.34  |
| Akr1c13       | 2.137E-03 | 0.45  |
| Akr1c18       | 1.669E-02 | 0.52  |
| Rgs6          | 1.318E-02 | 0.03  |
| Dcaf4         | 1.172E-03 | 1.57  |
| Papln         | 1.239E-03 | 3.63  |
| Acot2         | 1.707E-04 | 0.36  |
| Aldh6a1       | 1.439E-07 | 0.42  |
| Npc2          | 2.228E-03 | 0.58  |
| Mlh3          | 4.321E-03 | 1.88  |
| Vash1         | 7.252E-04 | 2.18  |
| Angel1        | 5.882E-04 | 1.86  |
| Ccnk          | 2.506E-03 | 1.97  |
| Evl           | 4.172E-03 | 0.46  |
| Slc25a29      | 3.524E-02 | 1.86  |
| Hsp90aa1      | 2.228E-03 | 2.04  |
| Cinp          | 6.566E-07 | 1.58  |
| Tnfai2        | 6.498E-04 | 0.40  |
| Xrcc3         | 2.833E-03 | 1.62  |
| Klc1          | 1.511E-04 | 1.51  |
| Kif26a        | 9.715E-04 | 5.30  |
| Gpr137b       | 3.742E-04 | 0.18  |
| Gli3          | 1.045E-03 | 1.76  |
| Sfrp4         | 1.374E-04 | 0.04  |
| Aoah          | 2.406E-04 | 0.28  |
| Trim27        | 1.185E-03 | 1.77  |
| Gpld1         | 1.239E-02 | 0.59  |
| Irf4          | 8.910E-04 | 0.35  |
| Tfap2a        | 3.656E-05 | 3.20  |
| Tbc1d7        | 2.880E-04 | 1.90  |
| Cap2          | 2.138E-07 | 0.08  |
| Tpmt          | 2.783E-02 | 1.63  |
| Id4           | 2.341E-04 | 0.29  |
| Susd3         | 4.005E-04 | 0.42  |
| Ogn           | 1.877E-05 | 0.09  |
| Cenpp         | 1.296E-07 | 2.90  |
| Nol8          | 2.805E-04 | 1.80  |
| Wrnip1        | 2.287E-02 | 1.84  |
| Pxdc1         | 3.167E-03 | 4.09  |
| Rpp40         | 1.092E-02 | 2.31  |
| Ly86          | 1.213E-04 | 0.18  |
| Riok1         | 9.321E-04 | 1.73  |
| Gadd45g       | 8.806E-04 | 0.57  |
| Fbp2          | 3.803E-04 | 0.13  |
| Syk           | 2.586E-04 | 0.20  |
| Ptch1         | 1.116E-04 | 1.73  |
| Msx2          | 1.448E-02 | 3.30  |
| Sfxn1         | 6.271E-05 | 1.55  |
| Ctsl          | 4.077E-04 | 0.27  |
| Mxd3          | 1.699E-06 | 2.76  |
| Prelid1       | 1.327E-05 | 1.56  |
| Pdlim7        | 5.025E-04 | 1.55  |
| Pitx1         | 3.649E-03 | 21.61 |
| Cxcl14        | 1.019E-02 | 0.43  |
| Slc25a48      | 1.579E-03 | 2.88  |
| Fastkd3       | 9.531E-05 | 2.02  |
| Naa35         | 3.628E-03 | 1.52  |
| Dapk1         | 5.130E-04 | 0.49  |
| Slc6a19       | 9.394E-03 | 0.09  |
| Trip13        | 2.799E-05 | 4.64  |
| Cep72         | 7.928E-04 | 3.15  |
| Ahrh          | 3.010E-02 | 0.48  |
| Srd5a1        | 7.137E-03 | 1.56  |
| Nsun2         | 7.192E-04 | 1.66  |
| Mctp1         | 1.314E-05 | 0.16  |
| Med10         | 2.340E-05 | 1.72  |



|               |           |       |
|---------------|-----------|-------|
| Lpcat1        | 3.970E-03 | 1.78  |
| Tert          | 1.632E-02 | 3.91  |
| Vcan          | 2.915E-03 | 0.34  |
| Ckmt2         | 3.734E-04 | 0.02  |
| Cd180         | 9.398E-04 | 0.26  |
| Snn1          | 1.350E-03 | 2.02  |
| Btf3          | 4.601E-02 | 1.65  |
| Hexb          | 2.409E-04 | 0.43  |
| Iqgap2        | 1.064E-06 | 0.26  |
| Pde8b         | 5.425E-04 | 0.45  |
| Dimt1         | 9.809E-03 | 1.98  |
| Ercc8         | 6.895E-03 | 1.73  |
| Elovl7        | 1.936E-03 | 0.36  |
| Depdc1b       | 6.995E-05 | 2.93  |
| Thbs4         | 9.660E-03 | 0.04  |
| Dhfr          | 9.149E-04 | 3.05  |
| Rasgrf2       | 6.849E-06 | 0.28  |
| Ppwd1         | 3.229E-02 | 1.59  |
| Cenpk         | 6.411E-03 | 4.03  |
| Rgs7bp        | 1.245E-02 | 3.50  |
| Rnf180        | 5.377E-03 | 0.44  |
| Emb           | 9.176E-04 | 0.31  |
| Mrps30        | 1.183E-02 | 1.56  |
| Slc4a7        | 1.232E-03 | 1.73  |
| Acox2         | 1.617E-03 | 0.09  |
| Il6st         | 3.701E-05 | 0.44  |
| Ppap2a        | 2.264E-03 | 0.49  |
| Dusp13        | 1.109E-04 | 0.27  |
| Dlg5          | 8.912E-03 | 1.75  |
| Ldb3          | 1.386E-07 | 0.02  |
| Cdhr1         | 9.627E-04 | 3.64  |
| Nid2          | 5.225E-04 | 1.88  |
| Dnajc9        | 8.681E-04 | 1.55  |
| Txndc16       | 1.296E-05 | 0.38  |
| Ero1l         | 1.642E-02 | 2.21  |
| Samd4         | 4.823E-03 | 0.50  |
| Rnase4        | 1.146E-03 | 0.44  |
| Rnase6        | 1.203E-03 | 0.24  |
| Hacl1         | 4.851E-02 | 0.31  |
| Gpr65         | 1.514E-04 | 0.29  |
| Sh3bp5        | 2.632E-04 | 0.57  |
| Asb14         | 3.460E-05 | 0.44  |
| Phf7          | 1.926E-03 | 2.19  |
| Galnt12       | 2.152E-06 | 0.06  |
| Sema3g        | 1.412E-02 | 0.56  |
| Oxnad1        | 8.473E-03 | 1.75  |
| Nek4          | 5.090E-04 | 1.58  |
| Ctsb          | 5.629E-05 | 0.21  |
| Prkcd         | 2.062E-05 | 0.47  |
| Lats2         | 9.015E-06 | 0.54  |
| Ska3          | 1.925E-06 | 3.67  |
| Spata13       | 6.205E-04 | 0.58  |
| Cacna2d3      | 3.204E-02 | 4.13  |
| Wnt5a         | 1.201E-02 | 3.68  |
| Lcp1          | 1.160E-04 | 0.17  |
| Nufip1        | 2.899E-03 | 1.68  |
| Tsc22d1       | 2.892E-03 | 0.64  |
| Epsti1        | 4.080E-04 | 0.24  |
| 1190002H23Rik | 3.230E-04 | 0.36  |
| Diap3         | 4.595E-04 | 2.15  |
| Mtrf1         | 1.528E-02 | 1.55  |
| Scara5        | 1.396E-05 | 0.00  |
| Pbk           | 2.622E-05 | 2.64  |
| Esco2         | 1.252E-04 | 2.63  |
| Clu           | 1.946E-03 | 0.46  |
| Ephx2         | 9.198E-06 | 0.20  |
| Trim35        | 3.324E-05 | 0.36  |
| Dpysl2        | 8.217E-05 | 0.26  |
| Bora          | 3.389E-08 | 2.87  |
| Pdlim2        | 5.395E-03 | 0.55  |
| Sorbs3        | 1.978E-05 | 0.22  |
| Ppp3cc        | 7.286E-04 | 0.61  |
| Dok2          | 2.891E-05 | 0.17  |
| Rcctb2        | 1.366E-03 | 0.59  |
| Spry2         | 4.429E-04 | 1.62  |
| Ednrb         | 2.071E-03 | 0.30  |
| Scel          | 8.937E-04 | 0.38  |
| Fbxl3         | 9.798E-04 | 0.66  |
| Nup155        | 4.601E-04 | 1.96  |
| Gdnf          | 1.357E-02 | 3.86  |
| Fyb           | 3.155E-05 | 0.24  |
| Dab2          | 2.909E-06 | 0.17  |
| Rem2          | 3.590E-03 | 8.49  |
| Haus4         | 2.386E-04 | 1.80  |
| Jub           | 2.222E-02 | 1.87  |
| 4931414P19Rik | 8.759E-03 | 1.69  |
| C6            | 1.436E-03 | 0.02  |
| Drosha        | 1.259E-03 | 1.78  |
| Fitm1         | 2.292E-06 | 0.03  |
| Emc9          | 4.733E-02 | 0.64  |
| Ripk3         | 5.359E-03 | 1.56  |
| Cma1          | 1.391E-05 | 0.08  |
| Mcpt2         | 3.215E-02 | 15.33 |
| Mcpt1         | 2.422E-02 | 26.18 |
| Atp12a        | 2.917E-02 | 0.04  |
| Cmbl          | 4.060E-09 | 0.10  |
| Tars          | 2.499E-06 | 1.56  |



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|---------------|-----------|------|
| Amacr         | 2.605E-02 | 1.72 |
| Brix1         | 1.339E-04 | 2.10 |
| Rad1          | 1.836E-03 | 1.68 |
| Nadkd1        | 1.633E-02 | 1.51 |
| Ank           | 3.061E-05 | 0.51 |
| Fam134b       | 1.484E-04 | 0.38 |
| Grhl2         | 1.996E-05 | 2.23 |
| Atp6v1c1      | 3.570E-02 | 0.66 |
| Fzd6          | 7.313E-04 | 1.99 |
| Dcstamp       | 1.104E-02 | 0.25 |
| Lrp12         | 2.321E-03 | 0.48 |
| Angpt1        | 9.890E-07 | 0.19 |
| Utp23         | 2.138E-02 | 1.67 |
| Rad21         | 1.887E-03 | 1.88 |
| Shcbp1        | 5.597E-03 | 3.97 |
| Pop1          | 2.705E-02 | 2.55 |
| Khdrbs3       | 5.382E-05 | 0.18 |
| Sybu          | 4.098E-02 | 0.56 |
| Kcnv1         | 1.013E-02 | 4.46 |
| Myc           | 1.875E-05 | 2.23 |
| Klh38         | 5.128E-07 | 0.08 |
| Fbxo32        | 6.227E-05 | 0.19 |
| Atad2         | 2.555E-02 | 1.86 |
| Wdr67         | 1.445E-03 | 1.91 |
| Has2          | 2.500E-02 | 3.50 |
| Mtbp          | 4.857E-03 | 1.91 |
| Mrpl13        | 2.618E-02 | 1.51 |
| Col14a1       | 3.276E-04 | 0.15 |
| Sla           | 6.859E-06 | 0.27 |
| Fam49b        | 2.904E-02 | 1.84 |
| Wnt7b         | 3.433E-02 | 1.50 |
| Ppara         | 1.240E-04 | 0.23 |
| Gtse1         | 1.760E-08 | 3.94 |
| Rangap1       | 1.177E-05 | 1.53 |
| L3mbtl2       | 8.678E-05 | 1.55 |
| Fam83f        | 2.616E-03 | 1.63 |
| Syng1         | 8.168E-05 | 0.06 |
| Dsc1          | 2.807E-04 | 3.74 |
| Enpp2         | 2.942E-06 | 0.10 |
| Csnk1e        | 8.771E-05 | 0.46 |
| Sh3bp1        | 3.049E-03 | 1.59 |
| Parvb         | 1.074E-02 | 0.49 |
| Parvg         | 6.970E-03 | 0.51 |
| Twf1          | 3.008E-03 | 1.64 |
| Naga          | 5.539E-05 | 0.48 |
| 3-Sep         | 1.793E-04 | 0.27 |
| Slc38a2       | 1.104E-03 | 2.11 |
| Rpap3         | 2.259E-05 | 1.61 |
| Endou         | 1.693E-02 | 1.63 |
| Rapgef3       | 3.241E-03 | 1.85 |
| Desi1         | 1.999E-02 | 0.64 |
| Poir3h        | 3.576E-04 | 1.79 |
| Nckap1l       | 2.651E-05 | 0.14 |
| Pde1b         | 1.967E-02 | 0.55 |
| Ppp1r1a       | 9.754E-06 | 0.07 |
| Ciita         | 1.497E-02 | 0.36 |
| Trp63         | 3.430E-04 | 2.33 |
| Cldn1         | 2.246E-03 | 0.45 |
| Mgrn1         | 5.074E-06 | 0.52 |
| Srl           | 4.476E-06 | 0.24 |
| Hes1          | 2.094E-03 | 1.77 |
| Mefv          | 3.056E-02 | 0.55 |
| Apod          | 3.354E-05 | 0.03 |
| Fam203a       | 6.201E-06 | 2.26 |
| Bop1          | 2.669E-05 | 1.55 |
| Heat7a        | 1.302E-03 | 0.50 |
| Gpaa1         | 9.458E-04 | 1.51 |
| Scrib         | 4.258E-05 | 1.59 |
| Tsta3         | 1.731E-03 | 1.55 |
| Pycrl         | 2.629E-04 | 1.76 |
| Gsdmd         | 1.295E-03 | 0.39 |
| Ly6f          | 1.193E-02 | 7.90 |
| Ly6c2         | 1.252E-02 | 0.51 |
| Slurp1        | 1.334E-03 | 0.07 |
| Arc           | 1.811E-04 | 4.64 |
| Mapk12        | 4.787E-04 | 0.39 |
| Lmf2          | 3.794E-06 | 1.80 |
| Arsa          | 3.534E-03 | 0.62 |
| Rabl2         | 1.019E-06 | 2.25 |
| Yaf2          | 1.546E-02 | 1.62 |
| Alcam         | 6.006E-04 | 0.12 |
| Pvrl3         | 2.852E-02 | 0.55 |
| Cd96          | 4.095E-04 | 0.43 |
| Cd200         | 2.675E-03 | 0.34 |
| Ccdc80        | 2.533E-04 | 0.28 |
| Cd200r1       | 1.972E-05 | 0.08 |
| Prkdc         | 2.051E-03 | 1.72 |
| Mcm4          | 2.785E-05 | 2.40 |
| Snai2         | 3.466E-05 | 3.43 |
| Parn          | 1.852E-03 | 1.67 |
| 2610015P09Rik | 1.931E-02 | 1.73 |
| Qtrtd1        | 3.193E-03 | 1.68 |
| Zbtb20        | 6.018E-08 | 0.23 |
| Cpox          | 3.037E-04 | 1.73 |
| Cldn25        | 9.118E-04 | 1.65 |
| St3gal6       | 3.762E-02 | 2.05 |
| Cmss1         | 1.032E-03 | 2.52 |



|               |           |      |
|---------------|-----------|------|
| Khl122        | 1.525E-02 | 0.53 |
| Tmem45a       | 1.849E-04 | 0.38 |
| Slc7a4        | 2.863E-02 | 1.63 |
| Sdf2l1        | 1.419E-02 | 0.65 |
| Fgd4          | 2.289E-04 | 0.28 |
| Tnk2          | 7.279E-04 | 1.66 |
| Yars2         | 1.192E-03 | 1.93 |
| B4galt4       | 3.027E-03 | 0.57 |
| Arhgap31      | 1.592E-05 | 0.34 |
| Umps          | 9.051E-05 | 1.69 |
| Fstl1         | 4.744E-04 | 0.24 |
| Abcc5         | 1.532E-03 | 0.49 |
| Hcls1         | 1.246E-05 | 0.29 |
| Ccdc14        | 3.757E-06 | 2.29 |
| Mylk          | 1.088E-04 | 0.43 |
| Cln2          | 5.124E-03 | 1.71 |
| Hspbp1        | 2.561E-04 | 2.45 |
| D16Ert472e    | 5.428E-05 | 1.73 |
| Adipoq        | 3.328E-05 | 0.01 |
| Rfc4          | 1.003E-04 | 2.53 |
| Robo1         | 3.330E-04 | 2.33 |
| St6gal1       | 2.333E-05 | 0.31 |
| Masp1         | 8.831E-03 | 0.44 |
| Adamts5       | 6.387E-06 | 0.35 |
| Ildr1         | 1.306E-02 | 0.21 |
| Cd86          | 2.802E-02 | 0.61 |
| Pros1         | 1.828E-05 | 0.45 |
| Psmg1         | 2.548E-06 | 1.91 |
| Fam3b         | 1.676E-02 | 2.21 |
| Ripply3       | 8.324E-03 | 1.83 |
| Chaf1b        | 5.022E-06 | 2.29 |
| Setd4         | 2.114E-04 | 2.05 |
| Itsn1         | 6.341E-08 | 0.35 |
| Donson        | 3.006E-06 | 1.55 |
| Gart          | 8.179E-05 | 1.67 |
| Ifngr2        | 1.920E-04 | 0.48 |
| Ifnar1        | 5.007E-04 | 0.58 |
| Il10rb        | 4.633E-05 | 0.37 |
| Ifnar2        | 7.052E-04 | 0.55 |
| 1110004E09Rik | 6.044E-05 | 1.66 |
| Mis18a        | 1.766E-06 | 1.93 |
| Scaf4         | 9.468E-04 | 1.56 |
| Enah          | 7.215E-05 | 2.90 |
| Wnt10b        | 1.034E-02 | 3.84 |
| Racgap1       | 3.758E-09 | 2.82 |
| Gpd1          | 4.730E-06 | 0.03 |
| Lass5         | 7.574E-03 | 0.54 |
| Dip2b         | 4.822E-04 | 1.63 |
| Slc11a2       | 1.052E-03 | 0.54 |
| Cela1         | 3.095E-04 | 0.17 |
| Slc4a8        | 3.840E-02 | 3.77 |
| Pcdhga3       | 2.216E-02 | 1.60 |
| Krt6b         | 3.387E-03 | 3.28 |
| Krt18         | 4.873E-02 | 7.25 |
| Igfbp6        | 6.971E-03 | 0.36 |
| Amhr2         | 1.231E-04 | 5.97 |
| Npff          | 2.217E-03 | 2.24 |
| Calcoco1      | 1.884E-05 | 0.48 |
| Sncg          | 3.865E-03 | 0.25 |
| Rttn          | 1.001E-04 | 2.02 |
| Rgn           | 2.608E-03 | 0.25 |
| Ccdc123       | 5.063E-03 | 1.68 |
| Mospd1        | 4.791E-04 | 0.41 |
| Cxcl13        | 1.479E-03 | 0.06 |
| Fhl1          | 8.138E-06 | 0.05 |
| Rfc2          | 8.003E-06 | 1.62 |
| Denr          | 4.908E-05 | 1.57 |
| Prmt5         | 4.091E-04 | 1.61 |
| Tmem52        | 1.757E-08 | 0.01 |
| Slc38a1       | 2.559E-04 | 0.41 |
| Bsg           | 3.947E-05 | 1.56 |
| Vwa5a         | 5.268E-05 | 0.39 |
| Serping1      | 4.190E-06 | 0.08 |
| Serinc2       | 7.810E-04 | 1.86 |
| Ccl25         | 2.815E-03 | 1.79 |
| Kcnk5         | 1.941E-03 | 1.93 |
| Parp3         | 3.860E-04 | 0.51 |
| Acy1          | 3.092E-05 | 2.09 |
| Frs3          | 2.973E-02 | 1.74 |
| Cd4           | 6.149E-04 | 0.20 |
| Twf2          | 3.341E-04 | 0.65 |
| Dtwd1         | 7.136E-03 | 2.05 |
| Wfdc1         | 1.946E-07 | 0.01 |
| Poc1a         | 8.020E-05 | 3.65 |
| Trip6         | 1.215E-05 | 2.50 |
| Clec4n        | 1.570E-05 | 0.22 |
| Tmem176a      | 5.448E-04 | 0.37 |
| Pisd          | 1.042E-04 | 0.56 |
| Tpi1          | 9.518E-04 | 2.08 |
| Cdca3         | 2.760E-05 | 3.39 |
| Rheb1l        | 5.266E-03 | 2.16 |
| Rps6ka2       | 1.156E-03 | 0.48 |
| Park2         | 2.604E-04 | 0.31 |
| Agpat4        | 2.178E-05 | 0.22 |
| Riok2         | 4.466E-03 | 1.52 |
| Mpc1          | 3.068E-04 | 0.47 |
| Zfp54         | 1.374E-03 | 1.57 |



|               |           |       |
|---------------|-----------|-------|
| Smoc2         | 6.388E-03 | 0.50  |
| Zfp51         | 2.416E-03 | 1.59  |
| Tnfrsf12a     | 3.885E-02 | 1.77  |
| Pkmyt1        | 1.951E-05 | 2.80  |
| Flywch2       | 7.343E-04 | 2.45  |
| Pla2g7        | 8.068E-04 | 0.23  |
| Cenpq         | 5.146E-05 | 3.02  |
| Aars2         | 2.561E-04 | 2.00  |
| Sgol1         | 9.509E-07 | 4.00  |
| Slc29a1       | 5.658E-05 | 0.34  |
| Nfkbie        | 6.299E-04 | 0.57  |
| Vegfa         | 9.231E-05 | 6.57  |
| Polh          | 3.305E-04 | 1.94  |
| Clic5         | 1.195E-08 | 0.10  |
| Enpp5         | 3.715E-05 | 0.18  |
| Enpp4         | 6.868E-04 | 0.32  |
| Cyp39a1       | 9.800E-04 | 3.00  |
| Ptk7          | 1.631E-02 | 1.89  |
| Bysl          | 3.309E-06 | 1.86  |
| Tfeb          | 6.054E-04 | 0.51  |
| Foxp4         | 3.275E-05 | 2.38  |
| Trem2         | 4.988E-04 | 0.04  |
| Ppil1         | 3.367E-08 | 2.13  |
| Pi16          | 5.965E-08 | 0.03  |
| Mtch1         | 7.684E-04 | 0.62  |
| Fgd2          | 6.338E-05 | 0.21  |
| Glo1          | 4.002E-05 | 1.96  |
| Abcg1         | 3.538E-04 | 0.25  |
| Slc37a1       | 2.175E-02 | 0.55  |
| Wdr4          | 3.026E-03 | 1.80  |
| Arhgap28      | 3.490E-02 | 0.55  |
| Myom1         | 2.058E-10 | 0.03  |
| Wiz           | 2.381E-03 | 1.63  |
| Emilin2       | 1.095E-05 | 0.25  |
| Ndc80         | 3.794E-05 | 4.22  |
| Clip4         | 1.245E-02 | 0.56  |
| Lbh           | 1.663E-05 | 0.24  |
| Dpy30         | 9.432E-03 | 1.66  |
| Slc30a6       | 2.048E-04 | 1.57  |
| Crim1         | 1.211E-02 | 1.93  |
| Ttc27         | 3.511E-04 | 1.85  |
| Cebpz         | 2.021E-03 | 1.60  |
| Man2a1        | 4.011E-03 | 0.66  |
| Cyp11b1       | 1.292E-08 | 0.10  |
| Srsf7         | 5.409E-04 | 1.53  |
| Prss41        | 2.208E-02 | 3.05  |
| 1600002H07Rik | 4.310E-06 | 1.73  |
| Abca3         | 4.930E-05 | 0.46  |
| Eci1          | 4.870E-03 | 0.50  |
| Srbd1         | 1.736E-03 | 1.62  |
| Dnase1l2      | 3.783E-04 | 0.29  |
| Mlist8        | 6.275E-05 | 1.56  |
| Rhoq          | 4.115E-04 | 0.63  |
| Pigf          | 2.135E-04 | 1.80  |
| Meiob         | 3.625E-03 | 1.78  |
| Hagh          | 7.840E-05 | 1.53  |
| C3            | 2.389E-08 | 0.04  |
| Hn1l          | 6.180E-05 | 2.09  |
| Rgs11         | 7.888E-05 | 3.09  |
| Itfg3         | 1.290E-05 | 0.40  |
| Milt1         | 7.244E-05 | 1.80  |
| Snrpc         | 6.277E-05 | 1.59  |
| Zeb1          | 7.481E-07 | 0.30  |
| Tmem178       | 4.688E-04 | 0.05  |
| Thumpd2       | 2.162E-04 | 1.90  |
| Pkdcc         | 2.037E-03 | 0.25  |
| Polr2d        | 2.800E-06 | 1.85  |
| Celf4         | 1.399E-03 | 4.34  |
| Tpgs2         | 2.960E-04 | 1.62  |
| Slc39a6       | 2.769E-06 | 2.30  |
| 2700062C07Rik | 1.641E-03 | 1.62  |
| Thoc1         | 7.547E-04 | 1.62  |
| Adamts10      | 8.213E-05 | 0.33  |
| Myo1f         | 1.417E-04 | 0.11  |
| Kifc5b        | 1.432E-04 | 3.78  |
| Dtna          | 1.596E-08 | 0.11  |
| Wdr46         | 1.647E-06 | 1.70  |
| Rnf138        | 1.271E-02 | 1.53  |
| Dsc2          | 1.160E-03 | 10.25 |
| Tmem173       | 7.024E-03 | 0.53  |
| Spata24       | 4.916E-03 | 2.09  |
| 2010001M09Rik | 1.696E-03 | 0.08  |
| Slc23a1       | 9.402E-05 | 1.70  |
| Hspa9         | 1.531E-02 | 1.61  |
| C2            | 5.799E-03 | 0.31  |
| Epb4.1l4a     | 7.866E-07 | 2.45  |
| Tslp          | 7.297E-04 | 10.62 |
| Bin1          | 7.520E-07 | 0.22  |
| Lims2         | 2.599E-03 | 0.57  |
| Aif1          | 1.820E-03 | 0.30  |
| Ltb           | 3.036E-03 | 0.50  |
| Zfp521        | 9.867E-07 | 0.29  |
| Lama3         | 8.625E-04 | 5.06  |
| Mrps18b       | 2.231E-04 | 1.73  |
| H2-M5         | 4.475E-04 | 0.22  |
| Gabbr1        | 1.143E-04 | 0.46  |
| Myot          | 9.675E-09 | 0.01  |



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|---------------|-----------|-------|
| Ap3s1         | 1.195E-04 | 0.54  |
| 4833403l15Rik | 1.151E-03 | 0.17  |
| Hbegf         | 3.202E-04 | 4.36  |
| Tcerg1        | 6.135E-06 | 1.73  |
| Dpysl3        | 1.193E-02 | 0.43  |
| Dtwd2         | 1.810E-03 | 1.83  |
| Hsd17b4       | 6.327E-05 | 0.55  |
| Mbd2          | 3.566E-02 | 1.61  |
| Pmaip1        | 3.925E-04 | 2.29  |
| Impa2         | 6.404E-05 | 2.23  |
| Cidea         | 3.730E-03 | 0.16  |
| Afg3l2        | 5.465E-06 | 1.54  |
| Srfbp1        | 7.563E-05 | 1.68  |
| Lox           | 1.795E-05 | 0.19  |
| Ptpn2         | 1.406E-03 | 1.66  |
| Cep192        | 8.010E-04 | 1.95  |
| Me2           | 1.130E-02 | 1.75  |
| Csnk1a1       | 1.892E-02 | 1.58  |
| Pcyox1l       | 3.135E-02 | 2.00  |
| Nars          | 2.077E-03 | 1.60  |
| Lmnbl         | 1.101E-05 | 2.32  |
| Slc27a6       | 1.450E-02 | 0.66  |
| Dctn4         | 1.337E-06 | 1.55  |
| Cd74          | 3.141E-04 | 0.21  |
| Tcof1         | 3.356E-04 | 1.78  |
| Camk2a        | 3.609E-06 | 0.04  |
| Pdgfrb        | 1.605E-03 | 0.38  |
| Csf1r         | 2.907E-06 | 0.14  |
| Psat1         | 1.482E-02 | 1.92  |
| Cndp2         | 2.083E-04 | 0.46  |
| Cyb5          | 1.181E-03 | 0.56  |
| Incenp        | 1.325E-04 | 2.55  |
| Fth1          | 1.048E-03 | 0.27  |
| Rab3il1       | 5.598E-06 | 0.15  |
| Tmem138       | 3.254E-04 | 1.93  |
| Cd6           | 2.370E-02 | 0.53  |
| Ms4a7         | 6.770E-06 | 0.21  |
| Ms4a6b        | 2.353E-04 | 0.25  |
| Ms4a4d        | 6.715E-06 | 0.14  |
| Ms4a6d        | 5.333E-06 | 0.24  |
| Ms4a2         | 1.715E-03 | 0.28  |
| Lpxn          | 1.290E-06 | 0.14  |
| Ms4a8a        | 5.686E-07 | 0.09  |
| Ccdc86        | 7.858E-04 | 1.90  |
| Slc15a3       | 6.388E-04 | 0.17  |
| Fen1          | 5.459E-03 | 2.01  |
| Lipa          | 1.956E-04 | 0.09  |
| Ak3           | 2.623E-05 | 0.50  |
| Snx15         | 5.498E-03 | 1.50  |
| Sac3d1        | 1.322E-04 | 2.01  |
| Cdca5         | 3.362E-04 | 4.40  |
| Tnfrsf25      | 2.286E-03 | 0.52  |
| Kif20b        | 1.675E-04 | 3.80  |
| Rpp30         | 4.863E-03 | 1.76  |
| Ankrd1        | 2.757E-02 | 0.08  |
| Il33          | 8.554E-03 | 2.50  |
| Slc25a45      | 1.909E-04 | 0.50  |
| Ighmbp2       | 8.847E-06 | 1.76  |
| Pola2         | 2.621E-04 | 1.59  |
| Banf1         | 4.928E-02 | 1.57  |
| Cst6          | 8.032E-03 | 0.07  |
| Pitpnm1       | 1.634E-03 | 0.60  |
| Pacs1         | 3.898E-04 | 2.05  |
| Doc2g         | 5.039E-03 | 1.92  |
| Cbwd1         | 1.500E-02 | 1.52  |
| Rin1          | 1.587E-03 | 2.64  |
| Aldh3b1       | 9.525E-05 | 0.18  |
| Asah2         | 8.014E-03 | 0.52  |
| Slc29a2       | 2.033E-04 | 4.69  |
| Pcx           | 3.912E-04 | 0.42  |
| Efemp2        | 2.085E-02 | 0.60  |
| Ctsw          | 5.901E-04 | 0.37  |
| Fosl1         | 9.519E-04 | 11.81 |
| Rnaseh2c      | 1.106E-03 | 1.84  |
| Kcnk7         | 2.751E-02 | 1.61  |
| Ehbp1l1       | 9.055E-04 | 0.63  |
| Ltbp3         | 2.235E-02 | 0.61  |
| Rps6ka4       | 1.017E-03 | 2.15  |
| Kcnk4         | 5.090E-03 | 9.27  |
| Fermt3        | 2.767E-05 | 0.23  |
| Stip1         | 1.245E-02 | 1.56  |
| Rcor2         | 1.201E-03 | 8.33  |
| Al846148      | 1.237E-02 | 1.59  |
| Lgals12       | 1.054E-04 | 0.33  |
| Pdcd4         | 2.244E-03 | 0.59  |
| Gpam          | 3.488E-05 | 0.31  |
| Acsf5         | 4.895E-04 | 0.56  |
| Hhex          | 1.797E-04 | 0.34  |
| Cep55         | 1.561E-03 | 3.85  |
| Rbp4          | 4.163E-06 | 0.02  |
| Noc3l         | 5.088E-05 | 1.76  |
| Hells         | 2.079E-03 | 2.68  |
| Ccnj          | 1.085E-03 | 1.62  |
| Pik3ap1       | 1.564E-04 | 0.30  |
| Slit1         | 1.085E-02 | 15.61 |
| Mxi1          | 1.267E-03 | 1.65  |
| Add3          | 3.786E-05 | 0.46  |



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|---------------|-----------|-------|
| Xpnpep1       | 7.035E-03 | 1.52  |
| Trim8         | 4.004E-03 | 1.61  |
| Sfxn2         | 3.121E-03 | 1.70  |
| Nt5c2         | 1.068E-02 | 0.65  |
| Msr1          | 3.444E-04 | 0.16  |
| Taf5          | 5.640E-04 | 2.02  |
| Pcgf6         | 2.936E-03 | 2.05  |
| Col17a1       | 2.911E-03 | 2.42  |
| Sfr1          | 1.995E-03 | 2.83  |
| Gsto1         | 2.893E-03 | 2.87  |
| Dclre1a       | 1.994E-03 | 1.77  |
| Vwa2          | 1.352E-04 | 2.80  |
| Gfra1         | 9.066E-04 | 0.19  |
| Slc18a2       | 1.424E-04 | 0.56  |
| 3110040N11Rik | 1.323E-04 | 1.54  |
| Bnc1          | 5.248E-06 | 4.98  |
| Ppp1r27       | 1.796E-03 | 0.15  |
| Alyref        | 8.358E-03 | 1.86  |
| Myadml2       | 2.707E-07 | 0.01  |
| Fasn          | 3.387E-03 | 0.59  |
| Arhgap19      | 2.131E-04 | 2.18  |
| Zdhhc16       | 1.415E-03 | 1.74  |
| Rfng          | 1.640E-04 | 3.34  |
| Slc16a3       | 1.261E-06 | 4.52  |
| Cd7           | 4.728E-02 | 0.48  |
| Sectm1a       | 1.184E-02 | 0.40  |
| 1110031I02Rik | 3.245E-03 | 1.58  |
| Ankrd2        | 4.712E-03 | 0.08  |
| Loxl4         | 2.385E-03 | 0.53  |
| Got1          | 2.254E-06 | 0.46  |
| Entpd7        | 3.046E-03 | 1.81  |
| Cutc          | 1.824E-02 | 1.57  |
| Cpn1          | 2.032E-02 | 11.36 |
| Cwf19l1       | 1.071E-04 | 1.94  |
| Scd3          | 1.653E-02 | 0.10  |
| Peo1          | 1.528E-03 | 1.65  |
| Poll          | 7.783E-04 | 1.60  |
| Sufu          | 1.436E-03 | 1.75  |
| Hexa          | 7.725E-06 | 0.13  |
| Bbs4          | 1.050E-04 | 1.63  |
| Adpgk         | 2.625E-04 | 1.55  |
| Fyco1         | 3.876E-05 | 0.56  |
| Zfhx4         | 3.864E-02 | 0.56  |
| Ribc1         | 1.069E-03 | 4.08  |
| Tsr2          | 3.526E-04 | 1.57  |
| Fgd1          | 3.858E-03 | 2.37  |
| Ptpnj         | 1.075E-02 | 0.65  |
| Itgb8         | 2.698E-03 | 0.41  |
| Padi1         | 4.861E-02 | 2.19  |
| Padi4         | 1.454E-02 | 0.26  |
| Itga7         | 1.441E-02 | 3.45  |
| Cd63          | 2.081E-03 | 0.45  |
| Dgka          | 3.566E-03 | 1.74  |
| Cdk2          | 6.660E-05 | 1.80  |
| Pa2g4         | 4.209E-04 | 1.88  |
| Esyt1         | 7.662E-05 | 0.33  |
| Baiap2        | 2.746E-03 | 0.62  |
| Nabp2         | 1.591E-02 | 1.73  |
| Aatk          | 4.124E-03 | 0.29  |
| Enthd2        | 9.690E-03 | 1.54  |
| Fscn2         | 4.332E-03 | 3.39  |
| 2310003H01Rik | 1.624E-03 | 1.83  |
| Prim1         | 8.564E-05 | 2.22  |
| Shmt2         | 4.372E-06 | 3.25  |
| Mbd6          | 1.111E-02 | 1.55  |
| Pstpip2       | 2.076E-02 | 0.52  |
| Xrcc6bp1      | 1.784E-03 | 2.53  |
| Gm9752        | 7.373E-03 | 1.54  |
| Nnt           | 7.929E-05 | 0.54  |
| Zfp511        | 6.758E-05 | 1.84  |
| Tubgcp2       | 5.619E-05 | 1.59  |
| Cyp2e1        | 3.074E-03 | 0.20  |
| 1190003J15Rik | 1.265E-02 | 2.13  |
| Cox8b         | 2.315E-07 | 0.01  |
| Ifitm1        | 2.435E-02 | 0.61  |
| Hras1         | 1.419E-03 | 1.51  |
| 1600016N20Rik | 7.634E-05 | 4.58  |
| Taldo1        | 5.253E-04 | 0.65  |
| Lrdd          | 1.147E-05 | 2.83  |
| Pnpla2        | 8.654E-06 | 0.19  |
| Tspan4        | 5.381E-04 | 0.36  |
| Zfp711        | 7.590E-04 | 1.72  |
| Gusb          | 4.473E-04 | 0.25  |
| Farp1         | 9.257E-03 | 0.65  |
| Slc15a1       | 3.819E-03 | 0.24  |
| Tmc6          | 2.543E-03 | 1.62  |
| Tk1           | 4.764E-06 | 2.08  |
| Cbx8          | 3.918E-03 | 1.64  |
| Gaa           | 4.420E-04 | 0.53  |
| Nptx1         | 5.779E-04 | 39.72 |
| Cpeb1         | 1.461E-05 | 0.13  |
| Tma16         | 3.252E-04 | 1.76  |
| Cct8          | 5.682E-03 | 1.65  |
| Phf6          | 1.185E-03 | 1.68  |
| Ccdc51        | 1.924E-07 | 2.51  |
| Col7a1        | 6.293E-03 | 2.84  |
| Rps6ka6       | 4.552E-03 | 0.38  |



|               |           |      |
|---------------|-----------|------|
| Tmem47        | 1.655E-02 | 0.52 |
| Alox5         | 3.354E-04 | 0.42 |
| 8-Mar         | 9.270E-06 | 0.49 |
| Wdr73         | 5.045E-06 | 1.71 |
| Sdc3          | 1.928E-02 | 0.45 |
| Agbl1         | 5.661E-04 | 0.02 |
| Plk4          | 1.847E-04 | 2.85 |
| Larp1b        | 4.857E-03 | 1.71 |
| Crispld1      | 1.659E-02 | 3.65 |
| Itih5         | 7.024E-05 | 0.08 |
| Taf3          | 7.567E-03 | 1.72 |
| Clec3b        | 1.020E-05 | 0.02 |
| Tgm4          | 2.915E-04 | 1.73 |
| Slco3a1       | 3.083E-02 | 0.56 |
| Pgm2          | 1.252E-03 | 1.67 |
| Hgs           | 1.569E-04 | 1.59 |
| Rassf3        | 4.482E-06 | 0.24 |
| Ccr1          | 4.926E-02 | 0.62 |
| Nrp1          | 2.085E-05 | 0.21 |
| Nudt5         | 1.451E-04 | 1.74 |
| Heatr2        | 6.740E-07 | 2.45 |
| Get4          | 1.491E-04 | 1.72 |
| Nop16         | 7.501E-04 | 1.95 |
| Arl10         | 1.300E-02 | 0.66 |
| Thoc3         | 5.360E-05 | 1.80 |
| Hk3           | 2.504E-04 | 0.06 |
| Smad7         | 1.749E-05 | 2.98 |
| Aasdhppt      | 3.273E-03 | 1.80 |
| Alkbh8        | 4.091E-03 | 1.56 |
| Mybl1         | 2.749E-03 | 2.47 |
| Terf1         | 1.188E-03 | 1.83 |
| Paqr8         | 1.245E-03 | 0.54 |
| Gsta3         | 2.813E-09 | 0.07 |
| Idh1          | 1.357E-03 | 0.66 |
| Klf7          | 1.430E-05 | 2.89 |
| Adam23        | 1.046E-04 | 0.29 |
| Nrp2          | 5.763E-03 | 0.40 |
| 9430016H08Rik | 1.151E-04 | 1.81 |
| Hspd1         | 1.607E-02 | 1.62 |
| Slc40a1       | 5.151E-06 | 0.22 |
| Lanc1         | 1.547E-03 | 1.96 |
| Icos          | 3.256E-02 | 0.56 |
| Cd28          | 1.467E-03 | 0.40 |
| Raph1         | 1.371E-03 | 1.53 |
| Wdr12         | 2.257E-03 | 1.63 |
| Nop58         | 1.963E-04 | 2.10 |
| Cflar         | 9.583E-06 | 0.66 |
| Orc2          | 5.921E-03 | 1.76 |
| Sgol2         | 4.239E-05 | 4.26 |
| Col5a2        | 2.917E-02 | 0.47 |
| Col3a1        | 6.339E-04 | 0.19 |
| Kdelc1        | 2.375E-02 | 1.65 |
| Tex30         | 1.362E-03 | 2.01 |
| Il18rap       | 3.591E-03 | 0.46 |
| Il1rl1        | 9.141E-03 | 0.28 |
| Il1r1         | 4.029E-05 | 0.38 |
| Npas2         | 3.292E-02 | 0.31 |
| 2010300C02Rik | 2.260E-03 | 4.22 |
| Stk17b        | 2.597E-04 | 0.64 |
| Pms1          | 1.346E-03 | 1.86 |
| Mstn          | 1.046E-02 | 0.00 |
| Inpp4a        | 9.305E-05 | 0.56 |
| Zap70         | 7.419E-03 | 0.59 |
| Sema4c        | 5.530E-04 | 2.79 |
| Ptpn18        | 2.012E-06 | 0.28 |
| Prim2         | 4.613E-06 | 2.05 |
| Wnt10a        | 4.488E-07 | 2.89 |
| Cyp27a1       | 1.846E-07 | 0.18 |
| Bcs1l         | 7.933E-04 | 1.51 |
| Rqcd1         | 3.612E-05 | 1.66 |
| Slc11a1       | 3.625E-04 | 0.10 |
| Igfbp5        | 2.054E-06 | 0.08 |
| Xrcc5         | 1.477E-05 | 2.04 |
| Pecr          | 1.371E-06 | 1.82 |
| Atic          | 1.960E-04 | 1.58 |
| Fn1           | 9.000E-04 | 0.26 |
| Bard1         | 1.653E-05 | 3.70 |
| Abcb6         | 6.099E-04 | 1.53 |
| Gilb1l        | 8.779E-05 | 0.56 |
| Speg          | 8.244E-04 | 0.34 |
| Des           | 7.811E-09 | 0.03 |
| Slc16a14      | 4.551E-02 | 2.69 |
| Sp100         | 7.839E-03 | 0.38 |
| Itm2c         | 4.230E-03 | 0.59 |
| Ncl           | 1.385E-04 | 1.73 |
| Farsb         | 1.245E-05 | 1.61 |
| Ngef          | 1.300E-02 | 8.30 |
| Gpr35         | 2.473E-04 | 2.85 |
| Pask          | 6.119E-04 | 1.86 |
| Inpp5d        | 9.126E-05 | 0.30 |
| Scly          | 7.879E-03 | 0.60 |
| Serpinb8      | 1.893E-02 | 0.62 |
| Cln8          | 1.787E-04 | 0.56 |
| Tnfrsf11a     | 4.597E-05 | 0.28 |
| Gin1          | 2.761E-04 | 1.63 |
| Pam           | 1.113E-03 | 0.60 |
| Tmem163       | 5.399E-03 | 6.87 |



|               |           |      |
|---------------|-----------|------|
| Mcm6          | 2.745E-04 | 1.53 |
| Rgs18         | 8.371E-05 | 0.24 |
| Rgs1          | 6.957E-04 | 0.10 |
| Rgs2          | 9.529E-04 | 0.40 |
| Cfh           | 2.010E-06 | 0.04 |
| Mki67ip       | 1.558E-06 | 1.62 |
| Dbi           | 7.859E-03 | 0.57 |
| Steap3        | 2.192E-05 | 0.19 |
| Nek7          | 2.820E-03 | 0.66 |
| Ptprc         | 4.763E-06 | 0.20 |
| Cd55          | 1.118E-06 | 0.27 |
| Ddx59         | 2.000E-03 | 1.73 |
| Cacna1s       | 7.274E-07 | 0.03 |
| Tnnt2         | 2.736E-02 | 6.66 |
| Fcamr         | 1.407E-03 | 2.21 |
| Il24          | 1.561E-04 | 9.46 |
| Srgap2        | 4.130E-05 | 0.65 |
| Arl8a         | 3.056E-02 | 0.67 |
| Ube2t         | 2.670E-04 | 3.26 |
| Slc45a3       | 3.851E-04 | 0.18 |
| Cdk18         | 3.783E-03 | 0.22 |
| Atp2b4        | 3.202E-03 | 0.56 |
| Tor1aip1      | 7.569E-03 | 0.65 |
| Mr1           | 1.156E-02 | 0.66 |
| Gilul         | 7.837E-06 | 0.12 |
| Lamc1         | 4.870E-03 | 0.65 |
| Lamc2         | 1.012E-02 | 4.07 |
| Ncf2          | 1.934E-04 | 0.17 |
| Rgl1          | 2.447E-05 | 0.19 |
| Adck3         | 2.836E-06 | 0.18 |
| Mnda          | 3.369E-04 | 0.36 |
| Slamf9        | 3.774E-02 | 0.60 |
| Uck2          | 7.126E-03 | 1.79 |
| Mpz1          | 5.299E-03 | 2.21 |
| Mpc2          | 3.302E-05 | 0.54 |
| Xcl1          | 3.102E-02 | 0.35 |
| Dpt           | 5.867E-06 | 0.06 |
| Nme7          | 1.082E-03 | 1.74 |
| Atp1b1        | 1.662E-03 | 0.20 |
| F5            | 3.230E-05 | 0.19 |
| Selp          | 1.268E-02 | 0.46 |
| Sell          | 3.180E-02 | 0.59 |
| Sele          | 2.136E-03 | 0.25 |
| Prrx1         | 1.369E-04 | 0.29 |
| Sec16b        | 7.469E-03 | 0.45 |
| Soat1         | 4.535E-06 | 0.13 |
| Ptpn14        | 8.379E-04 | 0.57 |
| Cenpf         | 3.584E-04 | 2.78 |
| Kctd3         | 5.327E-05 | 1.53 |
| Mark1         | 4.736E-04 | 0.32 |
| Nek2          | 1.684E-06 | 3.61 |
| Tmem206       | 5.820E-03 | 0.62 |
| Atf3          | 1.834E-03 | 0.23 |
| Batf3         | 1.858E-04 | 0.27 |
| Traf5         | 1.064E-03 | 0.55 |
| Lamb3         | 1.085E-03 | 4.52 |
| Olah          | 6.560E-03 | 0.11 |
| Suv39h2       | 1.849E-03 | 2.39 |
| Dclre1c       | 4.498E-05 | 0.57 |
| Fam107b       | 5.505E-04 | 0.53 |
| Fcgr2b        | 9.588E-07 | 0.19 |
| Frmf4a        | 1.035E-02 | 0.59 |
| Sepbs1        | 1.387E-03 | 1.62 |
| Mcm10         | 1.580E-05 | 3.58 |
| Optn          | 1.138E-03 | 0.54 |
| Ddr2          | 4.347E-03 | 0.43 |
| Rgs5          | 9.185E-05 | 0.38 |
| Nuf2          | 2.309E-06 | 3.67 |
| Mgst3         | 3.760E-03 | 0.59 |
| Mettl13       | 2.370E-03 | 1.57 |
| Myoc          | 2.494E-04 | 0.03 |
| Cenpl         | 1.297E-04 | 2.31 |
| Mrc1          | 3.205E-07 | 0.06 |
| Vim           | 5.366E-04 | 0.12 |
| Pip4k2a       | 8.140E-06 | 0.47 |
| Plxdc2        | 2.916E-03 | 0.54 |
| Lypd6b        | 3.366E-02 | 1.54 |
| Prkcq         | 2.284E-03 | 0.38 |
| Mastl         | 2.585E-05 | 3.66 |
| Pdss1         | 8.849E-03 | 0.53 |
| Pkn3          | 5.577E-03 | 1.52 |
| Apbb1ip       | 1.868E-04 | 0.21 |
| Stxbp1        | 2.453E-03 | 0.61 |
| Med27         | 8.094E-04 | 1.51 |
| St6galnac6    | 2.324E-04 | 0.28 |
| Gtf3c5        | 2.256E-03 | 1.57 |
| Lcn2          | 8.870E-03 | 0.15 |
| Dnm1          | 2.647E-03 | 0.33 |
| Gbg1          | 4.041E-07 | 0.20 |
| 1700007K13Rik | 2.724E-03 | 3.45 |
| Cytip         | 2.193E-04 | 0.48 |
| Olfr1         | 4.481E-04 | 0.43 |
| Acvr1c        | 2.018E-04 | 0.08 |
| Fubp3         | 5.366E-04 | 1.52 |
| Crat          | 8.437E-07 | 0.23 |
| Zeb2          | 2.966E-06 | 0.11 |
| Phf19         | 5.596E-03 | 2.68 |



|               |           |      |
|---------------|-----------|------|
| Hc            | 1.417E-02 | 0.29 |
| Traf1         | 1.785E-03 | 0.46 |
| Gsn           | 5.791E-08 | 0.14 |
| Stom          | 1.103E-04 | 2.79 |
| Dab2ip        | 4.990E-04 | 2.41 |
| Mrrf          | 1.029E-02 | 1.62 |
| Grb14         | 1.030E-03 | 0.26 |
| Gca           | 2.235E-04 | 0.19 |
| Strbp         | 9.940E-03 | 1.81 |
| Wdr5          | 1.255E-02 | 1.62 |
| Brd3          | 1.399E-03 | 1.57 |
| Pmpca         | 3.367E-03 | 1.51 |
| Card9         | 3.382E-04 | 0.42 |
| Gpsm1         | 2.323E-02 | 0.66 |
| Fcna          | 6.592E-04 | 0.19 |
| Mamdc4        | 3.464E-02 | 1.81 |
| Neb           | 1.547E-09 | 0.02 |
| 2010317E24Rik | 3.522E-05 | 4.18 |
| Uap1l1        | 8.777E-04 | 0.45 |
| Itgb6         | 3.089E-03 | 2.08 |
| Zmynd19       | 1.315E-03 | 2.16 |
| Ly75          | 4.250E-03 | 0.50 |
| Il1f5         | 3.859E-02 | 0.41 |
| Hnmt          | 1.328E-02 | 0.64 |
| Dapl1         | 4.911E-03 | 0.24 |
| Pkp4          | 7.730E-05 | 2.06 |
| Galnt3        | 1.025E-03 | 3.94 |
| Nup35         | 1.562E-04 | 1.94 |
| Dusp19        | 3.876E-04 | 1.85 |
| Ssfa2         | 1.958E-03 | 0.57 |
| Itga4         | 1.959E-05 | 0.24 |
| Cybrd1        | 3.332E-02 | 1.51 |
| Hat1          | 2.935E-03 | 1.85 |
| Xirp2         | 7.436E-05 | 0.03 |
| Stk39         | 7.822E-03 | 2.58 |
| Ssrp1         | 2.008E-04 | 1.70 |
| P2rx3         | 2.271E-02 | 3.53 |
| Prg2          | 2.019E-05 | 0.23 |
| Slc43a3       | 1.557E-06 | 0.18 |
| Slc43a1       | 2.403E-02 | 0.52 |
| Smtnl1        | 9.783E-05 | 0.05 |
| Clp1          | 3.921E-03 | 1.61 |
| Med19         | 3.091E-03 | 1.77 |
| Hoxd8         | 1.233E-04 | 0.47 |
| Ola1          | 1.690E-02 | 1.50 |
| Itga6         | 1.683E-04 | 3.25 |
| Kif18a        | 9.857E-06 | 3.19 |
| Slc12a6       | 1.563E-06 | 0.55 |
| Lpcat4        | 4.547E-02 | 2.01 |
| Ccdc34        | 2.150E-04 | 1.87 |
| B230118H07Rik | 5.835E-03 | 0.65 |
| Depdc7        | 4.189E-05 | 2.95 |
| Tcp1l1l       | 6.370E-03 | 1.60 |
| Cat           | 5.885E-05 | 0.48 |
| Pamr1         | 1.462E-03 | 0.18 |
| Gatm          | 4.066E-04 | 0.36 |
| Sema6d        | 5.679E-03 | 1.81 |
| Myef2         | 2.120E-03 | 0.48 |
| Fbn1          | 7.346E-05 | 0.18 |
| Fgf7          | 2.595E-03 | 0.07 |
| Meis2         | 1.137E-02 | 1.65 |
| Cd82          | 2.556E-04 | 0.54 |
| Slc28a2       | 2.731E-07 | 0.21 |
| Duoxa1        | 1.718E-02 | 2.09 |
| Sord          | 9.824E-03 | 0.63 |
| Wdr76         | 4.337E-04 | 1.91 |
| Harbi1        | 1.663E-02 | 1.80 |
| Jag1          | 1.513E-02 | 2.58 |
| 2210009G21Rik | 6.438E-04 | 2.06 |
| Snap23        | 9.497E-04 | 0.63 |
| Ehd4          | 4.554E-03 | 0.66 |
| Ubox5         | 1.235E-03 | 1.91 |
| Ptpa          | 2.346E-06 | 0.64 |
| Nusap1        | 9.691E-05 | 3.31 |
| Atrn          | 2.178E-02 | 1.54 |
| Dll4          | 1.906E-06 | 3.56 |
| Adam33        | 2.341E-06 | 0.20 |
| Siglec1       | 7.341E-04 | 0.05 |
| Rad51         | 4.157E-05 | 3.16 |
| Rpusd2        | 4.742E-04 | 2.27 |
| Casc5         | 5.925E-05 | 3.73 |
| 1700037H04Rik | 3.040E-04 | 1.63 |
| Cdc25b        | 9.923E-04 | 3.08 |
| D2Erttd750e   | 8.201E-04 | 3.91 |
| Smox          | 2.519E-03 | 1.95 |
| Rassf2        | 4.061E-06 | 0.15 |
| Gpcpd1        | 5.518E-03 | 0.61 |
| Fam98b        | 2.873E-04 | 1.82 |
| Mcm8          | 1.050E-03 | 3.08 |
| Fermt1        | 3.768E-05 | 2.46 |
| Crls1         | 1.034E-02 | 1.69 |
| Bmp2          | 8.125E-04 | 2.72 |
| Mrps5         | 7.703E-04 | 1.73 |
| Bub1          | 9.144E-04 | 5.16 |
| Acox1         | 1.220E-02 | 0.05 |
| Fbln7         | 3.444E-04 | 0.10 |
| Zc3h8         | 4.696E-03 | 2.85 |



|               |           |       |
|---------------|-----------|-------|
| Polr1b        | 4.583E-05 | 1.88  |
| Slc20a1       | 1.093E-02 | 2.01  |
| Tgm3          | 2.421E-03 | 4.35  |
| Snrpb         | 3.591E-03 | 1.57  |
| Nop56         | 7.457E-05 | 2.21  |
| Cpxm1         | 3.453E-03 | 0.18  |
| Bfsp1         | 1.766E-02 | 7.58  |
| 8430406i07Rik | 4.756E-04 | 3.06  |
| 1700010M22Rik | 1.099E-02 | 4.01  |
| Cd93          | 6.084E-03 | 0.39  |
| Cst3          | 7.504E-05 | 0.47  |
| Acss1         | 1.623E-04 | 0.14  |
| Gins1         | 4.606E-05 | 2.77  |
| Snph          | 1.483E-02 | 0.35  |
| Fam110a       | 7.629E-03 | 1.65  |
| Angpt4        | 5.163E-03 | 0.18  |
| Tbc1d20       | 5.766E-05 | 0.59  |
| Tpx2          | 3.863E-06 | 3.50  |
| Mylik2        | 7.370E-07 | 0.01  |
| Dnmt3b        | 3.225E-02 | 1.91  |
| Mapre1        | 1.856E-04 | 1.56  |
| Cdk5rap1      | 8.375E-04 | 1.67  |
| Snta1         | 4.602E-05 | 0.37  |
| E2f1          | 2.553E-02 | 1.51  |
| Aurka         | 6.130E-07 | 4.18  |
| Cstf1         | 2.839E-04 | 1.77  |
| Pkia          | 3.875E-07 | 0.10  |
| Rae1          | 6.862E-03 | 1.56  |
| Pck1          | 3.206E-03 | 0.01  |
| Fabp12        | 2.226E-02 | 16.64 |
| Impa1         | 4.298E-03 | 1.55  |
| Nfatc2        | 2.381E-05 | 0.28  |
| Zfp64         | 9.500E-04 | 2.38  |
| Car3          | 1.661E-05 | 0.01  |
| Car2          | 8.229E-04 | 5.12  |
| Zbtb46        | 2.097E-04 | 0.52  |
| Ahcy          | 1.507E-04 | 2.13  |
| Map1lc3a      | 1.315E-04 | 0.39  |
| Acss2         | 2.596E-02 | 0.62  |
| Gss           | 2.631E-03 | 1.79  |
| Procr         | 1.963E-04 | 6.16  |
| Eif6          | 2.702E-02 | 1.53  |
| Hps3          | 1.544E-04 | 0.57  |
| Dsn1          | 3.999E-04 | 2.29  |
| Rbl1          | 1.019E-03 | 2.01  |
| Src           | 2.324E-02 | 1.85  |
| Fam83d        | 3.398E-07 | 4.20  |
| Dhx35         | 1.306E-02 | 1.54  |
| Wisp2         | 2.263E-04 | 0.07  |
| Gnb4          | 7.967E-05 | 0.34  |
| Nceh1         | 9.344E-04 | 0.40  |
| Ect2          | 6.171E-05 | 3.35  |
| Acad9         | 2.367E-02 | 0.56  |
| Anxa5         | 1.135E-05 | 0.33  |
| Ccna2         | 3.401E-06 | 3.07  |
| Spata5        | 6.850E-04 | 1.53  |
| Aadac         | 3.668E-03 | 0.22  |
| P2ry1         | 9.455E-05 | 2.22  |
| Schip1        | 2.714E-03 | 1.83  |
| Ppm1l         | 1.788E-03 | 1.81  |
| Nmd3          | 6.259E-04 | 1.51  |
| Bche          | 1.042E-04 | 0.03  |
| Dclk1         | 2.177E-03 | 0.37  |
| Ppid          | 8.249E-03 | 1.56  |
| Pfn2          | 2.973E-04 | 0.32  |
| 4930579G24Rik | 1.501E-03 | 1.68  |
| Mme           | 5.062E-06 | 0.17  |
| Gmps          | 2.377E-03 | 1.68  |
| Wnt2b         | 4.439E-03 | 1.82  |
| Ptpn22        | 1.211E-03 | 0.47  |
| Dclre1b       | 1.575E-05 | 1.78  |
| Olfml3        | 2.305E-02 | 0.44  |
| Ngf           | 5.393E-03 | 2.63  |
| Cd2           | 2.279E-05 | 0.24  |
| Tbx15         | 1.740E-06 | 0.12  |
| Hsd3b6        | 6.393E-03 | 0.03  |
| Gpsm2         | 1.478E-03 | 1.73  |
| Sypl2         | 4.800E-06 | 0.08  |
| Slc16a4       | 4.510E-03 | 1.90  |
| Dram2         | 1.576E-04 | 0.54  |
| Ddx20         | 2.297E-06 | 1.92  |
| S100a11       | 3.248E-04 | 1.61  |
| Lce1m         | 6.873E-04 | 0.09  |
| Crcr1         | 6.031E-03 | 0.48  |
| Lce1g         | 8.262E-03 | 0.46  |
| Lce1b         | 2.900E-03 | 0.22  |
| Sprr2j-ps     | 4.567E-03 | 16.98 |
| Npr1          | 6.038E-06 | 0.21  |
| Creb3l4       | 5.672E-03 | 2.41  |
| Pmvk          | 1.543E-02 | 0.59  |
| Efna1         | 6.688E-03 | 1.64  |
| Fam198b       | 8.052E-03 | 0.62  |
| Tmem144       | 3.791E-05 | 2.12  |
| Sass6         | 5.130E-07 | 2.19  |
| Vcam1         | 4.793E-02 | 0.38  |
| Larp7         | 2.288E-05 | 1.81  |
| Prss12        | 1.232E-03 | 2.01  |



|               |           |      |
|---------------|-----------|------|
| Trim2         | 9.525E-04 | 0.35 |
| Tlr2          | 1.376E-03 | 0.47 |
| Casp6         | 3.563E-05 | 1.91 |
| Gar1          | 3.719E-06 | 2.20 |
| Ctso          | 1.192E-04 | 0.43 |
| Gstcd         | 1.272E-05 | 1.75 |
| Pdgfc         | 4.810E-03 | 0.47 |
| Enpep         | 6.336E-05 | 0.05 |
| Dkk2          | 9.456E-04 | 0.33 |
| Kcnq5         | 1.987E-02 | 2.67 |
| Ptgfr         | 4.731E-04 | 0.21 |
| Efna3         | 1.163E-02 | 0.34 |
| Cks1b         | 2.679E-04 | 3.06 |
| Thbs3         | 1.806E-04 | 0.22 |
| Rit1          | 4.143E-05 | 0.66 |
| Arhgef2       | 5.110E-04 | 0.42 |
| Sema4a        | 4.274E-03 | 0.66 |
| Pmf1          | 6.095E-07 | 2.57 |
| Iqgap3        | 1.056E-08 | 3.17 |
| Gpatch4       | 6.556E-06 | 2.13 |
| Pear1         | 9.378E-07 | 0.55 |
| Cd1d1         | 7.358E-03 | 0.50 |
| Nudt17        | 4.921E-03 | 0.20 |
| Tars2         | 3.015E-04 | 1.52 |
| Ctsk          | 7.885E-07 | 0.08 |
| Mettl14       | 1.801E-04 | 1.69 |
| Myoz2         | 8.177E-04 | 0.03 |
| Bcar3         | 1.206E-03 | 3.40 |
| Abcd3         | 5.809E-03 | 0.54 |
| F3            | 7.250E-03 | 2.32 |
| Tmem56        | 3.538E-03 | 0.05 |
| Them4         | 1.156E-04 | 1.62 |
| Rorc          | 1.176E-03 | 0.42 |
| Mttp          | 8.755E-04 | 4.72 |
| Dapp1         | 7.243E-04 | 0.58 |
| Manba         | 1.389E-02 | 0.61 |
| Depdc1a       | 4.546E-07 | 4.38 |
| Cth           | 6.236E-04 | 4.47 |
| Lphn2         | 2.457E-04 | 0.42 |
| Rpf1          | 2.199E-04 | 1.69 |
| Cryz          | 1.472E-02 | 1.85 |
| Trp53inp1     | 1.228E-02 | 0.61 |
| Ccne2         | 4.476E-04 | 2.72 |
| Fam92a        | 1.771E-02 | 1.96 |
| Sdr16c5       | 1.725E-03 | 0.43 |
| Atp6v0d2      | 3.170E-04 | 0.02 |
| Ubxn2b        | 6.867E-04 | 1.62 |
| Nsmaf         | 2.141E-03 | 0.51 |
| Sdcbp         | 6.166E-03 | 0.55 |
| Odf2l         | 1.271E-04 | 1.87 |
| Ndufaf4       | 4.159E-03 | 1.61 |
| Clca2         | 4.456E-05 | 0.19 |
| Gbp1          | 3.215E-02 | 0.11 |
| Ube2j1        | 8.627E-03 | 1.67 |
| Rragd         | 4.667E-08 | 0.07 |
| Smc2          | 4.979E-05 | 2.64 |
| Polr1e        | 1.995E-07 | 1.99 |
| Exosc3        | 1.905E-04 | 1.50 |
| 1300002K09Rik | 2.175E-03 | 0.11 |
| 5830415F09Rik | 1.188E-02 | 2.16 |
| Anp32b        | 4.486E-03 | 2.14 |
| Col15a1       | 4.774E-04 | 0.32 |
| Tex10         | 2.853E-03 | 1.53 |
| Tmeff1        | 2.209E-02 | 2.27 |
| Murc          | 2.264E-06 | 0.10 |
| Txn1          | 8.847E-04 | 2.38 |
| Svep1         | 3.301E-05 | 0.20 |
| Rod1          | 4.867E-03 | 1.58 |
| Snx30         | 2.550E-05 | 0.48 |
| Slc46a2       | 1.055E-03 | 0.09 |
| Alad          | 2.787E-03 | 0.46 |
| 2310002L09Rik | 3.678E-05 | 0.02 |
| Zdhhc21       | 5.503E-04 | 1.63 |
| Aptx          | 5.699E-03 | 1.54 |
| Tmem38b       | 4.338E-05 | 0.57 |
| Nol6          | 1.416E-05 | 1.80 |
| Ubap2         | 5.988E-04 | 1.60 |
| Aqp3          | 1.451E-03 | 2.67 |
| Kif24         | 8.991E-04 | 1.74 |
| Nudt2         | 2.564E-04 | 1.53 |
| Cntfr         | 1.193E-02 | 1.65 |
| Pigo          | 6.110E-03 | 1.52 |
| Stoml2        | 1.264E-05 | 1.56 |
| Sit1          | 4.789E-03 | 0.42 |
| Car9          | 3.190E-05 | 9.48 |
| Tpm2          | 4.153E-03 | 0.51 |
| Tln1          | 1.221E-03 | 0.59 |
| Npr2          | 2.771E-06 | 0.25 |
| Reck          | 3.851E-06 | 0.15 |
| Gilpr2        | 7.566E-06 | 0.24 |
| Plin2         | 2.763E-05 | 0.26 |
| Ptplad2       | 3.412E-06 | 0.41 |
| Ppap2b        | 1.533E-05 | 0.25 |
| Slc35d1       | 2.435E-03 | 1.75 |
| Ak4           | 2.293E-06 | 4.24 |
| Cachd1        | 1.693E-02 | 0.64 |
| 2610528J11Rik | 6.418E-04 | 2.53 |



|               |           |       |
|---------------|-----------|-------|
| St3gal3       | 1.153E-04 | 0.44  |
| Artn          | 4.818E-02 | 7.84  |
| Dph2          | 8.169E-04 | 1.89  |
| Slc6a9        | 3.070E-02 | 1.53  |
| Bend5         | 2.098E-04 | 6.90  |
| Itgb3bp       | 9.150E-03 | 4.16  |
| Ttc39a        | 5.160E-03 | 1.77  |
| Usp1          | 1.621E-04 | 1.70  |
| Ift74         | 1.933E-02 | 1.65  |
| 5830433M19Rik | 1.717E-05 | 1.70  |
| Laptn5        | 4.049E-05 | 0.16  |
| Pdpn          | 1.958E-02 | 0.37  |
| Orc1          | 1.043E-05 | 3.36  |
| Gpx7          | 2.939E-02 | 0.53  |
| Tnfrsf1b      | 1.850E-04 | 0.21  |
| Podn          | 6.553E-07 | 0.12  |
| Echdc2        | 2.237E-02 | 1.77  |
| Scp2          | 8.698E-04 | 0.52  |
| Magoh         | 2.017E-03 | 1.85  |
| Lrp8          | 1.651E-05 | 5.35  |
| Tmem48        | 3.328E-06 | 2.73  |
| Lrrc42        | 1.912E-03 | 1.62  |
| Cyb5rl        | 1.936E-03 | 1.74  |
| Mrpl37        | 1.564E-03 | 1.55  |
| Kcnq4         | 4.933E-02 | 3.02  |
| Ctps          | 4.650E-04 | 1.84  |
| Edn2          | 1.850E-02 | 6.16  |
| Ppcs          | 1.178E-02 | 1.81  |
| Tfap2c        | 4.667E-03 | 1.85  |
| 4930538K18Rik | 1.214E-04 | 3.70  |
| Slc2a1        | 3.345E-03 | 5.28  |
| Ppt1          | 1.178E-03 | 0.66  |
| Fuca1         | 1.327E-05 | 0.51  |
| Kif2c         | 2.029E-05 | 3.92  |
| Eif2b3        | 1.644E-03 | 1.54  |
| Mutyh         | 1.101E-03 | 2.03  |
| Toe1          | 1.009E-03 | 1.60  |
| Mmachc        | 1.182E-02 | 1.63  |
| Akr1a1        | 5.632E-04 | 0.64  |
| Nasp          | 6.540E-05 | 1.62  |
| Ipp           | 3.175E-04 | 1.56  |
| Rad54l        | 1.482E-04 | 2.62  |
| Mknk1         | 5.942E-05 | 0.53  |
| Mob3c         | 8.907E-04 | 0.66  |
| Cyp4b1        | 8.060E-05 | 0.17  |
| Pdzk1ip1      | 3.642E-02 | 0.52  |
| Stil          | 1.932E-04 | 4.25  |
| Ebna1bp2      | 5.249E-04 | 1.69  |
| Mrt4          | 1.479E-04 | 1.77  |
| Pla2g2f       | 1.614E-04 | 0.22  |
| Pla2g2e       | 2.137E-05 | 0.09  |
| Pink1         | 1.366E-06 | 0.41  |
| Kif17         | 1.409E-02 | 13.49 |
| Hspg2         | 3.456E-02 | 0.65  |
| Ptpn12        | 2.847E-02 | 1.55  |
| Fabp3         | 1.437E-04 | 0.05  |
| Tinagl1       | 2.507E-03 | 3.03  |
| Sema3c        | 2.211E-03 | 1.68  |
| Ccdc28b       | 2.087E-04 | 0.55  |
| Zfp362        | 4.084E-03 | 1.80  |
| Hdac1         | 9.818E-03 | 1.53  |
| Tmem50a       | 2.494E-04 | 0.61  |
| Stmn1         | 3.539E-02 | 1.53  |
| Trim63        | 2.443E-07 | 0.02  |
| Zfp593        | 2.246E-04 | 2.21  |
| Cnksr1        | 6.053E-03 | 2.46  |
| Hgf           | 3.042E-03 | 0.18  |
| Cdca8         | 1.181E-05 | 3.56  |
| Fgr           | 1.808E-03 | 0.48  |
| Rpa2          | 8.288E-05 | 1.61  |
| Smpdl3b       | 9.215E-03 | 0.62  |
| Yrdc          | 4.380E-05 | 1.66  |
| Inpp5b        | 4.850E-04 | 0.57  |
| Rcc1          | 6.724E-04 | 2.14  |
| Ptpru         | 4.518E-03 | 2.56  |
| Plekhn2       | 8.344E-04 | 0.54  |
| Cdk14         | 5.609E-07 | 0.19  |
| Padi2         | 5.261E-05 | 0.48  |
| Kcnab2        | 1.819E-03 | 0.39  |
| Xrcc2         | 2.639E-04 | 2.49  |
| Espn          | 2.106E-02 | 5.02  |
| Nol9          | 1.880E-02 | 1.59  |
| Smarcd3       | 1.283E-04 | 0.38  |
| Zbtb48        | 1.751E-03 | 2.01  |
| Abcb1b        | 7.920E-03 | 3.95  |
| Cort          | 1.484E-02 | 2.96  |
| Car6          | 1.667E-02 | 0.28  |
| Slc2a5        | 5.760E-03 | 2.62  |
| Casz1         | 2.749E-02 | 0.65  |
| H6pd          | 2.655E-05 | 0.38  |
| Ctnnbip1      | 4.598E-03 | 0.45  |
| Angptl7       | 7.737E-03 | 0.51  |
| Fam126a       | 2.725E-02 | 1.65  |
| Rbp7          | 2.593E-02 | 0.53  |
| Agtrap        | 8.297E-04 | 0.49  |
| Orc5          | 6.960E-03 | 1.59  |
| Dnajc2        | 5.575E-03 | 1.57  |



|               |           |      |
|---------------|-----------|------|
| Trp73         | 5.354E-03 | 2.30 |
| Dffb          | 1.347E-02 | 2.51 |
| Lrrc47        | 1.267E-02 | 1.62 |
| Arhgef16      | 1.112E-03 | 2.91 |
| Prkc2         | 9.744E-03 | 1.98 |
| Plch2         | 1.557E-02 | 1.96 |
| 2810405K02Rik | 3.551E-02 | 0.55 |
| Mmp23         | 2.287E-02 | 0.49 |
| Mxra8         | 1.348E-03 | 0.20 |
| Tas1r3        | 9.699E-03 | 1.61 |
| Ttll10        | 3.258E-02 | 2.18 |
| Kcnp4         | 6.020E-03 | 1.61 |
| Pacrgl        | 3.315E-04 | 1.67 |
| Gpr125        | 5.244E-04 | 0.31 |
| Sorcs2        | 3.782E-05 | 3.55 |
| Htra3         | 1.777E-05 | 0.13 |
| Acox3         | 3.923E-07 | 0.31 |
| Rgs12         | 7.761E-05 | 2.45 |
| Lrpap1        | 6.412E-04 | 0.57 |
| Pcdh7         | 5.608E-03 | 2.97 |
| Whsc2         | 3.828E-05 | 1.68 |
| Man2b2        | 6.174E-04 | 0.54 |
| Ngsl          | 1.729E-02 | 0.58 |
| Rbks          | 9.813E-05 | 1.65 |
| Ppm1g         | 1.834E-04 | 1.69 |
| Krtcap3       | 5.290E-06 | 2.33 |
| Cwh43         | 1.000E-03 | 1.89 |
| Cgref1        | 1.351E-02 | 1.92 |
| Emilin1       | 2.895E-03 | 0.38 |
| Agbl5         | 2.757E-03 | 1.61 |
| Mapre3        | 9.062E-04 | 1.78 |
| Pgm1          | 5.138E-03 | 1.53 |
| Sepsecs       | 1.464E-03 | 1.62 |
| Cenpa         | 5.210E-07 | 2.85 |
| Zcchc4        | 5.636E-05 | 1.52 |
| Pi4k2b        | 9.001E-04 | 1.85 |
| Sel1l3        | 1.973E-03 | 0.23 |
| Rfc1          | 3.185E-04 | 1.70 |
| Tada2b        | 1.535E-05 | 1.68 |
| Grpel1        | 3.234E-06 | 1.70 |
| Tec           | 4.333E-05 | 0.46 |
| Lnx1          | 1.776E-02 | 0.55 |
| Pdgfra        | 1.215E-04 | 0.13 |
| Ppat          | 3.111E-03 | 2.25 |
| Cenpc1        | 1.936E-03 | 1.65 |
| Stap1         | 4.209E-04 | 0.10 |
| Gilmn         | 1.224E-04 | 2.31 |
| Cdc7          | 9.139E-04 | 1.93 |
| Tgfbr3        | 2.401E-05 | 0.27 |
| Gbp9          | 2.508E-02 | 0.29 |
| Abcg3         | 3.793E-03 | 0.43 |
| Spp1          | 1.517E-02 | 0.33 |
| Sparcl1       | 3.823E-05 | 0.35 |
| Hsd17b11      | 2.148E-04 | 0.17 |
| Enoph1        | 1.702E-03 | 1.62 |
| Rasgef1b      | 1.267E-04 | 0.46 |
| Prkg2         | 4.975E-02 | 5.45 |
| Bmp3          | 2.326E-02 | 5.27 |
| Tesc          | 1.726E-02 | 0.24 |
| Nos1          | 2.453E-05 | 0.02 |
| Rfc5          | 7.051E-04 | 1.77 |
| Dck           | 3.002E-05 | 1.69 |
| Rassf6        | 2.548E-02 | 1.95 |
| Pf4           | 3.181E-05 | 0.08 |
| Mthfd2l       | 7.563E-03 | 2.37 |
| Areg          | 5.447E-04 | 4.69 |
| Cxcl3         | 4.006E-02 | 5.65 |
| Ccng2         | 5.185E-03 | 1.91 |
| Tctn2         | 6.638E-04 | 2.15 |
| Gtf2h3        | 2.716E-04 | 1.66 |
| Eif2b1        | 6.179E-06 | 1.65 |
| Ddx55         | 2.704E-05 | 1.65 |
| Rilpl2        | 9.534E-04 | 0.32 |
| Cdkl2         | 4.595E-03 | 1.61 |
| Pitpnm2       | 9.195E-03 | 1.79 |
| Abcb9         | 2.092E-03 | 1.91 |
| Naaa          | 6.235E-04 | 0.51 |
| Kntc1         | 4.248E-07 | 3.30 |
| Sdad1         | 1.146E-05 | 1.79 |
| Stx2          | 1.992E-04 | 0.46 |
| Ran           | 1.069E-03 | 1.91 |
| Gbas          | 1.014E-06 | 0.56 |
| Bcl7a         | 7.656E-05 | 1.67 |
| Psmid9        | 6.924E-05 | 1.58 |
| Cct6a         | 3.673E-03 | 1.95 |
| Aldh2         | 5.314E-07 | 0.31 |
| Gpn3          | 1.419E-03 | 1.64 |
| Anapc7        | 1.419E-03 | 1.56 |
| P2rx7         | 2.351E-04 | 0.41 |
| P2rx4         | 1.772E-05 | 0.25 |
| Camkk2        | 7.205E-03 | 0.57 |
| Dhx37         | 1.246E-04 | 1.57 |
| Mfsd7a        | 9.731E-03 | 0.56 |
| Pde6b         | 1.165E-02 | 2.42 |
| Ddx51         | 3.408E-06 | 1.78 |
| Pus1          | 2.225E-05 | 2.02 |
| Gpc2          | 5.493E-03 | 2.50 |



|               |           |       |
|---------------|-----------|-------|
| Ulk1          | 2.496E-02 | 1.53  |
| Cit           | 6.867E-05 | 2.49  |
| Chek2         | 6.614E-06 | 2.50  |
| St7           | 1.024E-02 | 1.66  |
| Srsf9         | 4.142E-08 | 1.85  |
| Psmg3         | 1.980E-05 | 1.53  |
| Tes           | 3.313E-02 | 1.84  |
| Tfec          | 9.171E-05 | 0.23  |
| Mad1l1        | 1.772E-03 | 1.85  |
| Ftsj2         | 7.279E-06 | 1.91  |
| Lfng          | 2.650E-06 | 0.46  |
| Mmab          | 2.202E-03 | 1.58  |
| Fscn1         | 3.197E-04 | 2.78  |
| Ung           | 3.799E-04 | 2.43  |
| Usp30         | 5.281E-04 | 1.61  |
| Rbm19         | 1.670E-04 | 1.75  |
| Ddx54         | 1.319E-04 | 1.51  |
| 1110008J03Rik | 8.759E-06 | 1.91  |
| Aimp2         | 4.785E-06 | 1.80  |
| Polr1d        | 3.572E-04 | 1.89  |
| Flt1          | 7.954E-05 | 1.96  |
| Slc46a3       | 3.860E-06 | 0.50  |
| 6330406I15Rik | 3.064E-04 | 0.31  |
| Col1a2        | 7.278E-03 | 0.40  |
| Wnt16         | 1.150E-02 | 3.91  |
| Fam3c         | 5.008E-04 | 0.52  |
| Auts2         | 1.112E-02 | 1.62  |
| Limk1         | 5.642E-03 | 2.51  |
| Eln           | 2.021E-04 | 0.06  |
| Hyal4         | 2.872E-02 | 0.49  |
| Lmod2         | 4.326E-05 | 0.04  |
| Ezh2          | 7.958E-03 | 1.55  |
| Srcrb4d       | 6.576E-03 | 2.83  |
| Rbm28         | 4.307E-03 | 1.51  |
| Lrwd1         | 3.509E-05 | 2.09  |
| Ephb4         | 7.435E-04 | 2.58  |
| Pop7          | 4.331E-04 | 1.55  |
| Pcolce        | 7.800E-05 | 0.22  |
| Gm20605       | 2.350E-03 | 0.65  |
| Cyp3a13       | 2.336E-02 | 2.04  |
| Mcm7          | 7.672E-04 | 1.98  |
| Asns          | 2.543E-03 | 2.47  |
| Dlx5          | 4.024E-04 | 4.78  |
| Pon3          | 1.214E-05 | 0.38  |
| Akr1b8        | 2.060E-02 | 3.21  |
| Ccdc136       | 3.035E-02 | 0.30  |
| Irf5          | 2.992E-04 | 0.44  |
| Ahcyl2        | 1.772E-03 | 1.95  |
| Adcyap1r1     | 8.323E-05 | 0.01  |
| Nt5c3         | 5.693E-04 | 0.38  |
| Tmem209       | 7.291E-04 | 2.02  |
| Tsga14        | 5.081E-05 | 2.16  |
| Herc3         | 1.217E-03 | 1.50  |
| Tmem176b      | 3.512E-04 | 0.33  |
| Igf2bp3       | 3.091E-02 | 1.53  |
| Gpnmnb        | 6.258E-04 | 0.02  |
| Nfe2l3        | 1.534E-02 | 0.61  |
| Cbx3          | 8.747E-03 | 1.69  |
| Hoxa1         | 1.636E-05 | 9.37  |
| 2010107G12Rik | 2.494E-02 | 2.24  |
| Epha1         | 4.034E-02 | 1.51  |
| Clcn1         | 1.893E-03 | 0.32  |
| Mad2l1        | 3.713E-04 | 3.13  |
| Prdm5         | 5.309E-04 | 0.28  |
| Clec5a        | 4.712E-04 | 0.38  |
| Tbxas1        | 4.204E-05 | 0.11  |
| Anxa4         | 8.935E-04 | 0.54  |
| Tgfa          | 9.416E-05 | 3.02  |
| Cct7          | 1.475E-02 | 1.71  |
| Reg3g         | 2.509E-02 | 0.10  |
| Lrig1         | 3.732E-03 | 0.42  |
| Kbtbd8        | 2.207E-03 | 2.22  |
| Wdr54         | 4.955E-05 | 3.28  |
| Mrpl19        | 1.119E-02 | 1.79  |
| Arhgap25      | 7.864E-04 | 0.16  |
| Ap1f          | 4.857E-05 | 1.56  |
| Rab43         | 2.014E-04 | 0.48  |
| 8430410A17Rik | 1.899E-04 | 1.75  |
| Uba3          | 2.144E-02 | 1.52  |
| Frmd4b        | 1.353E-03 | 0.61  |
| Gxylt2        | 1.388E-03 | 0.34  |
| Ruvbl1        | 4.110E-04 | 2.08  |
| Plxna1        | 1.155E-02 | 0.62  |
| Klf15         | 1.631E-04 | 0.35  |
| Slc41a3       | 7.261E-07 | 0.29  |
| Wnt7a         | 1.285E-02 | 14.11 |
| Tmem43        | 2.817E-04 | 0.65  |
| Grip2         | 1.819E-02 | 4.80  |
| Sumf1         | 7.698E-05 | 0.65  |
| Itpr1         | 2.890E-04 | 0.46  |
| Bhlhe40       | 7.506E-04 | 2.10  |
| Slc6a12       | 9.231E-03 | 0.09  |
| Mfap5         | 3.157E-04 | 0.06  |
| Gdf3          | 6.358E-04 | 0.45  |
| Plxnd1        | 1.933E-02 | 0.65  |
| Tmcc1         | 1.074E-04 | 0.61  |
| Bms1          | 1.205E-04 | 1.58  |



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|---------------|-----------|------|
| Clec4d        | 2.421E-03 | 0.21 |
| Zfp248        | 6.530E-04 | 2.52 |
| Clec4b1       | 5.426E-06 | 0.12 |
| Clec4a2       | 3.165E-06 | 0.12 |
| Klrk1         | 3.924E-03 | 0.34 |
| Cd69          | 4.704E-03 | 0.53 |
| Clec2d        | 2.305E-04 | 0.59 |
| Gabaraapl1    | 2.820E-06 | 0.35 |
| Ccdc77        | 9.065E-07 | 1.90 |
| Wbp11         | 8.536E-04 | 1.61 |
| Art4          | 5.622E-03 | 2.89 |
| Mgp           | 1.953E-03 | 0.04 |
| Ptpro         | 9.458E-06 | 0.13 |
| Strap         | 5.084E-03 | 1.68 |
| Dera          | 6.474E-04 | 1.70 |
| Ldhb          | 3.006E-03 | 0.27 |
| Kcnj8         | 2.278E-02 | 0.53 |
| Abcc9         | 3.417E-06 | 0.32 |
| Rad18         | 2.791E-04 | 2.58 |
| Sspn          | 3.958E-06 | 0.21 |
| Bhlhe41       | 6.184E-03 | 0.23 |
| Rassf8        | 5.673E-03 | 0.37 |
| Lrmp          | 2.099E-06 | 0.16 |
| Ogg1          | 5.476E-03 | 1.96 |
| Camk1         | 1.231E-05 | 0.27 |
| Ttll3         | 4.429E-03 | 1.64 |
| Cidec         | 8.681E-05 | 0.01 |
| 5730419I09Rik | 5.695E-03 | 1.83 |
| Il17rc        | 1.566E-02 | 1.57 |
| Cmas          | 2.296E-03 | 1.54 |
| Med21         | 2.064E-03 | 1.79 |
| Far2          | 1.891E-03 | 0.10 |
| Tmtc1         | 7.480E-07 | 0.27 |
| Caprin2       | 2.644E-04 | 2.67 |
| Dennd5b       | 4.425E-06 | 2.12 |
| Tamm41        | 5.412E-06 | 1.58 |
| Timp4         | 6.112E-05 | 0.04 |
| Pianp         | 2.351E-02 | 0.19 |
| Rad51ap1      | 1.248E-04 | 3.92 |
| Tspan11       | 5.141E-04 | 0.27 |
| Tspan9        | 1.849E-03 | 1.94 |
| Tead4         | 3.540E-02 | 2.00 |
| Klrb1a        | 3.588E-03 | 0.05 |
| Ckm           | 3.426E-04 | 0.01 |
| Rtn2          | 3.514E-08 | 0.11 |
| Dmpk          | 9.032E-05 | 0.34 |
| Lilra6        | 5.442E-05 | 0.09 |
| Tmem238       | 4.802E-05 | 2.95 |
| Sbk2          | 8.007E-04 | 0.04 |
| Psd3          | 2.476E-04 | 0.52 |
| Zfp719        | 7.589E-05 | 1.59 |
| Csrp3         | 2.414E-03 | 0.03 |
| Zdhhc13       | 1.250E-04 | 2.04 |
| Zfp108        | 2.508E-03 | 1.86 |
| C230052I12Rik | 7.359E-04 | 1.91 |
| Slc7a10       | 1.252E-03 | 0.02 |
| Gas2          | 6.741E-03 | 2.78 |
| Snrpa1        | 1.090E-04 | 1.87 |
| Pcsk6         | 1.124E-04 | 0.35 |
| Mphosph10     | 1.522E-03 | 1.67 |
| Blm           | 1.378E-04 | 3.36 |
| Sema4b        | 1.066E-03 | 1.90 |
| Pex11a        | 7.691E-03 | 0.55 |
| Plin1         | 1.075E-04 | 0.01 |
| Nr2f2         | 4.941E-05 | 0.44 |
| Synm          | 1.362E-07 | 0.19 |
| Lrrc28        | 1.544E-02 | 0.47 |
| Cd22          | 3.322E-04 | 0.14 |
| Tyrobp        | 7.153E-06 | 0.12 |
| Dpf1          | 4.529E-02 | 4.43 |
| Rasgrp4       | 1.508E-05 | 0.37 |
| Ryr1          | 4.112E-07 | 0.03 |
| Mfge8         | 2.576E-03 | 0.16 |
| Det1          | 4.081E-03 | 1.56 |
| Mrps11        | 1.741E-03 | 1.56 |
| Syt12         | 4.491E-04 | 0.28 |
| Me3           | 1.455E-05 | 0.34 |
| Zfand6        | 2.005E-03 | 0.56 |
| 4632434I11Rik | 1.265E-04 | 3.44 |
| Coq7          | 2.915E-03 | 1.50 |
| Pde2a         | 1.009E-03 | 0.60 |
| Xylt1         | 4.384E-03 | 0.51 |
| Nucb2         | 1.648E-02 | 0.63 |
| Pde3b         | 1.457E-05 | 0.30 |
| Mylpf         | 1.451E-03 | 0.02 |
| Kif22         | 8.052E-06 | 3.81 |
| Kctd13        | 7.180E-04 | 1.51 |
| Stard10       | 1.495E-02 | 1.90 |
| Ino80e        | 1.386E-04 | 1.76 |
| Fchsd2        | 5.441E-06 | 0.53 |
| Aldoa         | 3.550E-03 | 0.61 |
| Gdprd3        | 1.300E-03 | 0.42 |
| Coro1a        | 2.156E-05 | 0.25 |
| Sult1a1       | 2.025E-07 | 0.12 |
| Klk7          | 3.486E-03 | 0.40 |
| Nupr1         | 5.067E-05 | 0.34 |
| Ppme1         | 6.880E-05 | 1.60 |



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|---------------|-----------|------|
| Nfatc2ip      | 4.176E-05 | 2.19 |
| Lipt2         | 2.016E-03 | 2.34 |
| Atp2a1        | 1.634E-10 | 0.01 |
| Slco2b1       | 1.086E-07 | 0.08 |
| Myh14         | 6.701E-03 | 0.51 |
| Lat           | 7.271E-07 | 0.24 |
| Dgat2         | 9.131E-04 | 0.45 |
| Il4ra         | 1.895E-02 | 1.74 |
| Nsmce1        | 4.800E-05 | 2.47 |
| Jmjd5         | 2.861E-06 | 2.50 |
| Far1          | 3.576E-03 | 0.57 |
| Myo7a         | 7.850E-04 | 0.30 |
| Slc5a11       | 7.044E-03 | 0.07 |
| Parva         | 7.044E-03 | 1.66 |
| Trat1         | 2.585E-03 | 0.22 |
| Slc5a2        | 2.265E-04 | 1.83 |
| Cox6a2        | 8.151E-08 | 0.02 |
| Itgam         | 1.095E-04 | 0.24 |
| Lyve1         | 4.785E-02 | 0.55 |
| Itgax         | 2.012E-03 | 0.09 |
| Dkk1          | 3.701E-03 | 0.35 |
| Cd37          | 4.940E-06 | 0.14 |
| Prss8         | 1.018E-02 | 0.51 |
| Fbxl19        | 6.259E-05 | 1.52 |
| 9130019O22Rik | 8.669E-04 | 1.93 |
| Bcat2         | 3.528E-06 | 0.35 |
| Itgal         | 1.124E-03 | 0.47 |
| Sergef        | 2.581E-03 | 1.52 |
| Rgs10         | 1.380E-06 | 0.23 |
| Fgfr2         | 1.997E-02 | 2.10 |
| 2010110P09Rik | 1.341E-05 | 0.03 |
| Plk1          | 9.137E-09 | 4.24 |
| Ears2         | 2.118E-04 | 1.71 |
| Cdr2          | 2.271E-02 | 0.63 |
| Mrpl17        | 1.138E-06 | 1.64 |
| Dnhd1         | 1.676E-03 | 1.73 |
| Rrp8          | 1.856E-03 | 1.80 |
| Tmem159       | 1.793E-04 | 0.33 |
| Trim30a       | 3.887E-02 | 0.47 |
| 2610020H08Rik | 1.358E-03 | 1.57 |
| Eri2          | 1.820E-05 | 2.14 |
| Acsn3         | 5.090E-03 | 0.41 |
| Lhpp          | 7.880E-05 | 0.22 |
| Ctbp2         | 7.101E-04 | 1.57 |
| Rrm1          | 2.235E-04 | 2.34 |
| Art1          | 2.281E-06 | 0.03 |
| Mki67         | 4.813E-05 | 2.68 |
| Atp6ap2       | 1.369E-04 | 0.61 |
| Wee1          | 7.200E-03 | 2.00 |
| Mrgprf        | 1.048E-03 | 0.37 |
| Ano1          | 3.540E-03 | 1.88 |
| Fadd          | 1.338E-06 | 1.76 |
| Cttn          | 1.020E-04 | 1.59 |
| Dock11        | 8.319E-05 | 0.53 |
| Cul4b         | 1.241E-03 | 1.60 |
| Tnni2         | 5.288E-06 | 0.02 |
| Syt8          | 7.713E-04 | 5.92 |
| Sash3         | 1.228E-05 | 0.24 |
| Rbm2          | 2.660E-05 | 2.33 |
| 2610018G03Rik | 5.931E-03 | 2.69 |
| Slc9a9        | 7.979E-07 | 0.23 |
| Arhgef6       | 1.414E-06 | 0.17 |
| Prickle3      | 4.748E-04 | 1.55 |
| Praf2         | 2.607E-02 | 1.63 |
| Pim2          | 7.083E-03 | 1.53 |
| Hdac6         | 2.920E-05 | 1.69 |
| Was           | 9.362E-06 | 0.26 |
| Ftsj1         | 1.081E-03 | 1.61 |
| Rpgr          | 7.430E-04 | 2.06 |
| Vbp1          | 1.471E-02 | 1.51 |
| Ophn1         | 3.060E-06 | 0.33 |
| Stard8        | 2.533E-06 | 0.10 |
| Efnb1         | 7.214E-04 | 2.60 |
| Awat2         | 1.108E-02 | 0.10 |
| Itm2a         | 5.610E-03 | 0.34 |
| Hmgn5         | 9.182E-03 | 2.09 |
| Sh3bgrl       | 1.132E-05 | 0.34 |
| Tnmd          | 3.870E-02 | 0.34 |
| Cstf2         | 4.654E-06 | 1.71 |
| Xkrx          | 4.254E-02 | 0.46 |
| Cenpi         | 5.710E-04 | 4.11 |
| Btk           | 7.426E-07 | 0.20 |
| Gla           | 1.965E-03 | 0.33 |
| Acs14         | 2.614E-02 | 0.62 |
| Chrdl1        | 1.547E-06 | 0.04 |
| Pak3          | 9.346E-04 | 0.22 |
| Gpr64         | 2.089E-03 | 2.44 |
| Itgb1bp2      | 1.642E-05 | 0.28 |
| Gpm6b         | 4.460E-05 | 0.17 |
| Hccs          | 2.130E-03 | 1.53 |
| Arhgap6       | 4.170E-04 | 0.13 |
| Ctps2         | 4.260E-05 | 0.57 |
| Xlr4c         | 3.058E-02 | 0.54 |
| Grpr          | 3.373E-03 | 7.98 |
| Ap1s2         | 1.700E-04 | 0.53 |
| Bgn           | 1.710E-03 | 0.25 |
| Abcd1         | 8.678E-05 | 0.28 |



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|---------------|-----------|------|
| Piga          | 7.570E-04 | 2.32 |
| Asb11         | 4.225E-07 | 0.16 |
| Dusp9         | 1.043E-02 | 4.52 |
| Renbp         | 1.710E-05 | 0.17 |
| Naa10         | 7.671E-04 | 1.53 |
| Arhgap4       | 5.199E-04 | 0.57 |
| Plxna3        | 2.096E-02 | 1.50 |
| Dkc1          | 1.955E-04 | 2.37 |
| Plp1          | 4.189E-02 | 0.58 |
| Tsc22d3       | 1.112E-03 | 0.21 |
| Morc4         | 2.032E-04 | 3.09 |
| Rnf128        | 2.230E-03 | 0.16 |
| Mcf2l         | 3.427E-02 | 0.63 |
| F7            | 1.398E-02 | 0.05 |
| F10           | 1.461E-03 | 0.13 |
| Lamp1         | 1.717E-04 | 0.62 |
| Adprhl1       | 3.226E-05 | 0.08 |
| Gas6          | 1.702E-05 | 0.19 |
| Rasa3         | 2.789E-05 | 0.44 |
| Myom2         | 1.111E-07 | 0.01 |
| Angpt2        | 5.501E-03 | 2.00 |
| Nek3          | 1.330E-02 | 2.09 |
| Slc25a15      | 1.258E-02 | 1.80 |
| Gpr124        | 2.948E-02 | 0.57 |
| Brf2          | 1.543E-02 | 1.62 |
| Adrb3         | 1.806E-02 | 0.44 |
| Eif4ebp1      | 2.900E-03 | 2.51 |
| Cd209a        | 3.920E-04 | 0.04 |
| Cd209d        | 8.486E-05 | 0.02 |
| Tnfsf13b      | 3.188E-03 | 0.46 |
| Ptpn7         | 4.092E-05 | 0.40 |
| Ankrd10       | 4.547E-02 | 1.51 |
| Asb5          | 9.056E-06 | 0.02 |
| Dlc1          | 3.561E-05 | 0.37 |
| Erl1          | 1.494E-03 | 1.93 |
| Mrps31        | 1.877E-02 | 1.52 |
| Ap3m2         | 1.013E-03 | 0.58 |
| Gins4         | 2.013E-04 | 1.69 |
| Slit2         | 7.241E-06 | 0.13 |
| Tenm3         | 3.989E-04 | 5.21 |
| Dctd          | 5.621E-04 | 3.48 |
| Fgfr1         | 8.836E-04 | 0.43 |
| Rwdd4a        | 1.132E-04 | 1.92 |
| Star          | 4.255E-04 | 1.97 |
| Ash2l         | 1.237E-03 | 1.70 |
| Tti2          | 1.425E-03 | 1.61 |
| Mak16         | 1.449E-03 | 1.66 |
| Gsr           | 3.882E-03 | 1.69 |
| Gtf2e2        | 2.390E-03 | 2.12 |
| Frg1          | 6.528E-04 | 1.60 |
| Asah1         | 7.960E-04 | 0.63 |
| Pdgfri        | 8.863E-04 | 0.27 |
| Slc7a2        | 2.981E-04 | 0.25 |
| Cnot7         | 4.497E-03 | 1.64 |
| Sap30         | 2.356E-03 | 2.55 |
| Ednra         | 5.882E-03 | 2.08 |
| Nr3c2         | 1.539E-05 | 0.30 |
| Sorbs2        | 2.339E-04 | 0.42 |
| Casp3         | 5.388E-03 | 1.57 |
| Mlf1ip        | 1.633E-04 | 3.63 |
| 4933411K20Rik | 1.553E-03 | 1.59 |
| Slc25a4       | 6.834E-04 | 0.52 |
| Pdlim3        | 1.316E-06 | 0.02 |
| Sh3rf1        | 5.789E-04 | 2.56 |
| Nek1          | 1.851E-02 | 1.53 |
| Adcy7         | 2.839E-05 | 0.16 |
| Snx20         | 1.102E-02 | 0.45 |
| Rbl2          | 5.009E-04 | 0.64 |
| Gins3         | 1.732E-03 | 2.48 |
| Got2          | 2.420E-02 | 1.67 |
| Lsm6          | 1.227E-03 | 1.69 |
| Slc10a7       | 1.044E-04 | 1.51 |
| Orc6          | 3.120E-03 | 2.17 |
| Rfx1          | 2.226E-03 | 1.70 |
| Tecr          | 6.711E-03 | 0.60 |
| Tbc1d9        | 1.228E-05 | 0.42 |
| Il15          | 3.925E-04 | 0.43 |
| Smarca5       | 5.474E-03 | 1.63 |
| Hp            | 1.285E-04 | 0.05 |
| Txnl4b        | 2.545E-02 | 1.51 |
| Zfp821        | 2.210E-02 | 1.56 |
| Dhodh         | 1.873E-02 | 1.65 |
| Irx3          | 2.061E-03 | 1.99 |
| 4933436C20Rik | 9.687E-04 | 2.09 |
| Irx5          | 5.895E-04 | 2.02 |
| Mmp2          | 2.377E-04 | 0.17 |
| Gnao1         | 1.479E-02 | 2.21 |
| Il34          | 2.085E-03 | 0.44 |
| Nudt21        | 1.575E-02 | 1.74 |
| Cenpn         | 3.721E-04 | 3.76 |
| Cdyl2         | 6.875E-04 | 1.63 |
| Mt2           | 1.224E-02 | 2.48 |
| Mt1           | 1.761E-02 | 2.39 |
| Herpud1       | 6.141E-05 | 0.60 |
| Ccl22         | 2.066E-02 | 0.38 |
| Ccl17         | 2.501E-02 | 0.19 |
| Katnb1        | 1.768E-02 | 1.56 |



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|---------------|-----------|------|
| Kifc3         | 8.456E-04 | 0.65 |
| Mmp15         | 2.079E-04 | 3.34 |
| Tmem38a       | 4.323E-08 | 0.10 |
| Tpm4          | 3.037E-02 | 1.56 |
| Slc27a1       | 6.327E-06 | 0.33 |
| Taf1c         | 1.482E-02 | 1.54 |
| Ifi30         | 2.527E-05 | 0.45 |
| Mphosph6      | 1.505E-02 | 1.97 |
| Hsd17b2       | 4.249E-02 | 0.58 |
| Lpar2         | 8.195E-03 | 2.06 |
| Atp13a1       | 1.230E-04 | 1.61 |
| Cmtm3         | 4.704E-05 | 0.33 |
| Ces2g         | 1.947E-03 | 4.27 |
| Fam96b        | 8.133E-03 | 1.64 |
| Rrad          | 4.575E-02 | 2.78 |
| Ces2e         | 5.108E-03 | 6.23 |
| Tradd         | 1.029E-02 | 1.69 |
| Pla2g15       | 1.354E-05 | 0.25 |
| Has3          | 4.583E-03 | 8.22 |
| Cep57         | 5.834E-03 | 1.51 |
| Mre11a        | 2.235E-03 | 1.71 |
| Ankrd49       | 8.715E-06 | 1.62 |
| Panx1         | 2.050E-03 | 1.85 |
| Med17         | 7.254E-05 | 1.51 |
| Heph11        | 2.794E-02 | 0.57 |
| Vstm5         | 1.385E-02 | 1.66 |
| Taf1d         | 8.985E-04 | 1.75 |
| Adat1         | 1.426E-03 | 2.06 |
| Gabarapl2     | 6.067E-03 | 0.59 |
| Tmem170       | 1.628E-02 | 1.71 |
| Cfdp1         | 2.736E-02 | 1.50 |
| Bcar1         | 4.525E-04 | 2.16 |
| Ldhd          | 3.266E-02 | 2.06 |
| Wdr59         | 8.177E-03 | 1.81 |
| Bmper         | 5.219E-04 | 0.09 |
| Arv1          | 6.030E-03 | 2.17 |
| 2310022B05Rik | 3.843E-02 | 1.64 |
| 2810004N23Rik | 1.350E-02 | 1.82 |
| Egln1         | 7.561E-03 | 2.54 |
| Jam3          | 1.959E-02 | 0.66 |
| Trpc6         | 1.778E-02 | 2.50 |
| Dcun1d5       | 3.279E-03 | 1.64 |
| Pdgfd         | 2.741E-02 | 0.60 |
| Usp2          | 7.167E-05 | 0.40 |
| Thy1          | 2.892E-02 | 0.51 |
| Pvrl1         | 2.208E-03 | 2.30 |
| Pou2f3        | 1.722E-02 | 0.47 |
| Sc5d          | 4.954E-02 | 1.59 |
| Ubash3b       | 1.011E-03 | 1.55 |
| Clmp          | 3.815E-06 | 0.16 |
| Dcps          | 1.374E-04 | 1.88 |
| Tirap         | 4.446E-03 | 1.79 |
| Rpusd4        | 3.894E-04 | 1.57 |
| Fdx1          | 2.265E-04 | 1.62 |
| Pou2af1       | 2.150E-02 | 0.24 |
| Cryab         | 6.278E-04 | 0.12 |
| 2310030G06Rik | 6.736E-05 | 2.69 |
| Dixdc1        | 1.724E-05 | 3.71 |
| Bco2          | 6.383E-04 | 6.14 |
| Cadm1         | 1.088E-02 | 1.94 |
| Bud13         | 1.015E-04 | 1.76 |
| Tagln         | 4.657E-02 | 0.59 |
| Il10ra        | 1.676E-04 | 0.30 |
| Mpzl2         | 6.813E-04 | 2.13 |
| Cd3e          | 2.560E-02 | 0.56 |
| Cd3d          | 2.185E-02 | 0.55 |
| Pus3          | 3.560E-04 | 1.76 |
| Chek1         | 3.860E-04 | 3.72 |
| Fez1          | 4.884E-02 | 0.36 |
| Slc37a2       | 2.908E-06 | 0.28 |
| Robo4         | 7.891E-03 | 1.67 |
| Hmbs          | 1.217E-05 | 1.53 |
| Pin1          | 4.025E-06 | 1.88 |
| Olfm2         | 1.424E-02 | 2.36 |
| Scg3          | 1.221E-03 | 0.12 |
| Lysmd2        | 2.514E-03 | 1.70 |
| Tmod2         | 1.288E-03 | 0.31 |
| Bcl2l10       | 1.623E-02 | 2.91 |
| Gnb5          | 3.512E-03 | 2.10 |
| Ldlr          | 1.044E-02 | 1.59 |
| Kank2         | 6.825E-05 | 0.37 |
| Rsl24d1       | 8.109E-06 | 1.74 |
| Ccnb2         | 3.567E-06 | 3.07 |
| Cgnl1         | 1.420E-05 | 0.47 |
| Narg2         | 5.526E-05 | 1.77 |
| Rora          | 6.260E-03 | 0.53 |
| Calml4        | 7.824E-05 | 0.49 |
| Anp32a        | 1.382E-02 | 0.60 |
| Kif23         | 4.507E-06 | 2.68 |
| Ankk1         | 4.453E-03 | 8.60 |
| Elovl4        | 2.100E-03 | 0.29 |
| Zw10          | 1.108E-04 | 1.58 |
| Nnmt          | 7.520E-04 | 0.18 |
| Pkm           | 3.500E-03 | 1.73 |
| Neil1         | 1.413E-03 | 1.65 |
| Ulk3          | 1.820E-04 | 1.88 |
| Nrg4          | 2.134E-03 | 0.53 |



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|---------------|-----------|-------|
| Al118078      | 4.485E-06 | 6.10  |
| Cyp1a1        | 1.025E-04 | 0.04  |
| Pstpip1       | 5.359E-05 | 0.38  |
| Cyp11a1       | 1.210E-05 | 0.12  |
| Tspan3        | 3.740E-06 | 3.29  |
| Stra6         | 1.647E-02 | 9.83  |
| Loxl1         | 3.052E-04 | 0.28  |
| Mb21d1        | 5.814E-04 | 1.89  |
| Gsta4         | 2.793E-02 | 19.49 |
| Elovl5        | 8.508E-05 | 0.38  |
| Mlip          | 1.360E-06 | 0.03  |
| Fam83b        | 2.477E-04 | 1.63  |
| Ctsh          | 1.190E-06 | 0.48  |
| Tpm1          | 1.924E-04 | 0.25  |
| Plscr2        | 2.712E-06 | 0.17  |
| Car12         | 8.394E-05 | 3.03  |
| Plscr4        | 4.671E-03 | 0.50  |
| Parp16        | 2.316E-03 | 2.44  |
| Tipin         | 3.026E-05 | 1.86  |
| Snape5        | 2.993E-03 | 0.65  |
| Zwilch        | 5.124E-06 | 3.92  |
| Atr           | 5.911E-04 | 1.64  |
| Tfdp2         | 5.630E-04 | 1.69  |
| Ube2cbp       | 1.762E-05 | 2.49  |
| Me1           | 5.203E-03 | 0.46  |
| Syncrrip      | 3.208E-03 | 1.51  |
| Cmtm7         | 2.735E-03 | 0.61  |
| Tgfbr2        | 4.562E-06 | 0.40  |
| Nmnat3        | 2.441E-04 | 1.73  |
| Mrps22        | 6.199E-04 | 1.66  |
| Dbr1          | 5.198E-05 | 1.69  |
| Mras          | 3.898E-03 | 0.51  |
| Cdc25a        | 1.173E-06 | 2.38  |
| Nme6          | 7.290E-04 | 1.72  |
| Ptgs2         | 4.071E-02 | 13.18 |
| Nradd         | 3.019E-02 | 2.07  |
| Pth1r         | 4.822E-05 | 0.23  |
| Csrnp1        | 7.258E-03 | 1.83  |
| Hhatl         | 1.083E-06 | 0.03  |
| Slco2a1       | 3.029E-02 | 2.05  |
| Srprb         | 5.044E-06 | 1.77  |
| Trf           | 1.329E-05 | 0.04  |
| Topbp1        | 1.135E-05 | 1.99  |
| Nphp3         | 1.926E-04 | 1.81  |
| Acpp          | 1.215E-02 | 0.53  |
| Gnai2         | 7.581E-04 | 0.63  |
| Nudt16        | 5.121E-05 | 0.17  |
| Aste1         | 6.280E-04 | 1.51  |
| Col6a4        | 4.340E-03 | 5.38  |
| Mst1r         | 3.158E-04 | 2.13  |
| Traip         | 9.430E-07 | 4.57  |
| Mst1          | 1.237E-02 | 3.07  |
| Amigo3        | 7.876E-03 | 1.66  |
| Uba7          | 4.278E-02 | 0.46  |
| Slc25a20      | 2.705E-04 | 0.61  |
| Nicn1         | 4.677E-03 | 1.62  |
| Amt           | 2.370E-02 | 1.67  |
| Thsd7a        | 1.945E-06 | 0.11  |
| Gpr19         | 4.546E-02 | 1.71  |
| Pygm          | 2.494E-06 | 0.02  |
| Crebl2        | 1.393E-03 | 0.65  |
| 3-Mar         | 8.441E-04 | 0.44  |
| Fam189b       | 3.953E-02 | 0.55  |
| Pon2          | 6.224E-03 | 0.66  |
| Malt1         | 7.379E-03 | 0.65  |
| Lmo2          | 2.953E-06 | 0.18  |
| Trib3         | 4.999E-04 | 2.61  |
| Mdfr          | 2.683E-05 | 2.49  |
| Mansc1        | 3.567E-04 | 0.21  |
| Abtb2         | 2.272E-02 | 1.55  |
| Folr2         | 1.076E-06 | 0.05  |
| Ablim3        | 1.809E-03 | 0.27  |
| Pram1         | 1.861E-03 | 1.66  |
| Tpcn1         | 7.625E-03 | 0.63  |
| Slc24a6       | 2.204E-05 | 0.52  |
| Gng11         | 8.916E-03 | 0.57  |
| Mctp2         | 5.701E-03 | 1.69  |
| Gtf3c1        | 1.116E-02 | 1.59  |
| Cntrob        | 2.302E-04 | 2.33  |
| Troap         | 7.759E-06 | 5.10  |
| Pdxk          | 1.119E-06 | 0.37  |
| Arap1         | 2.644E-05 | 0.23  |
| Ank2          | 4.429E-04 | 0.41  |
| Ppp1r9a       | 6.866E-06 | 0.07  |
| Pwp2          | 3.778E-06 | 1.98  |
| 2410131K14Rik | 8.387E-03 | 1.66  |
| Abcc10        | 1.912E-02 | 1.83  |
| P2ry2         | 2.037E-02 | 1.63  |
| Smap2         | 4.013E-04 | 0.59  |
| Acsl3         | 7.970E-04 | 2.36  |
| Rangrf        | 2.266E-03 | 2.04  |
| Slc16a1       | 2.163E-03 | 2.36  |
| Cspg4         | 3.372E-02 | 0.63  |
| Itgbl1        | 1.657E-05 | 0.14  |
| Nup93         | 9.564E-03 | 1.62  |
| Ucp3          | 2.821E-04 | 0.11  |
| Rasgrp2       | 1.759E-06 | 0.37  |



|               |           |      |
|---------------|-----------|------|
| Fkbp1a        | 4.973E-02 | 0.60 |
| Inha          | 2.528E-03 | 3.52 |
| Mycbp2        | 5.295E-04 | 0.64 |
| Cdo1          | 1.701E-05 | 0.07 |
| C330027C09Rik | 4.558E-05 | 3.38 |
| Micall1       | 6.756E-04 | 1.66 |
| Dhrs7c        | 2.673E-04 | 0.02 |
| Npat          | 1.412E-04 | 1.69 |
| Lmo7          | 7.240E-03 | 0.46 |
| Pfkm          | 1.180E-07 | 0.09 |
| Gas7          | 1.299E-04 | 0.29 |
| Tbc1d4        | 1.399E-05 | 0.48 |
| Rnf125        | 5.842E-06 | 0.33 |
| Ybey          | 3.428E-06 | 1.53 |
| Slc22a15      | 5.770E-05 | 1.77 |
| Phldb2        | 5.008E-04 | 2.20 |
| Podxl2        | 1.790E-03 | 0.41 |
| Atp1a1        | 1.971E-03 | 2.21 |
| Dis3          | 7.539E-06 | 2.17 |
| Card10        | 1.330E-07 | 2.23 |
| Mgll          | 1.060E-04 | 0.06 |
| Kbtbd12       | 2.490E-06 | 0.03 |
| BC016579      | 2.106E-03 | 0.32 |
| Myh2          | 1.215E-04 | 0.01 |
| Tpsg1         | 1.878E-05 | 0.16 |
| Mamdc2        | 2.882E-03 | 0.17 |
| Ttc28         | 6.257E-03 | 0.54 |
| Eefsec        | 5.802E-03 | 1.64 |
| Rac2          | 7.278E-07 | 0.18 |
| Ttf2          | 1.978E-07 | 2.19 |
| Trim45        | 6.230E-03 | 2.03 |
| Hsf4          | 3.882E-02 | 2.05 |
| Duox1         | 5.583E-03 | 3.47 |
| Ptprm         | 3.577E-02 | 0.63 |
| Rpgrip1l      | 1.425E-02 | 1.72 |
| Noc4l         | 1.074E-04 | 1.87 |
| Ptprf         | 2.944E-02 | 1.91 |
| Mif           | 1.364E-03 | 1.88 |
| Fbxl8         | 1.605E-02 | 2.29 |
| Gstt2         | 2.764E-06 | 0.26 |
| Tnxb          | 1.518E-05 | 0.02 |
| Chst2         | 6.684E-06 | 4.50 |
| Pus7l         | 5.671E-05 | 2.32 |
| Usp37         | 2.516E-05 | 1.55 |
| Arhgap44      | 3.464E-04 | 0.42 |
| Agl           | 3.506E-05 | 0.38 |
| Nudt15        | 9.498E-04 | 1.94 |
| Snap91        | 2.210E-03 | 0.15 |
| Adamts15      | 1.101E-06 | 0.10 |
| Armxc1        | 1.599E-02 | 0.58 |
| Crif2         | 1.519E-02 | 0.65 |
| Tomm6         | 6.815E-04 | 1.73 |
| Catsper2      | 1.938E-03 | 1.89 |
| BC026585      | 2.205E-04 | 0.31 |
| Asprv1        | 3.443E-02 | 0.29 |
| Ttc7b         | 4.773E-03 | 0.61 |
| Casp4         | 4.506E-03 | 0.65 |
| Angptl1       | 4.789E-04 | 0.34 |
| Apol6         | 1.372E-03 | 0.15 |
| Myo6          | 1.505E-02 | 0.66 |
| Fa2h          | 5.528E-04 | 0.03 |
| Ndn           | 2.123E-05 | 0.13 |
| Rfwd3         | 1.344E-02 | 1.57 |
| Pank1         | 5.672E-03 | 0.34 |
| Zfp7          | 1.301E-04 | 2.01 |
| Gabrb3        | 3.672E-02 | 6.19 |
| Qsox1         | 7.117E-03 | 0.54 |
| Arhgap39      | 1.461E-04 | 0.57 |
| Fuk           | 4.925E-03 | 2.37 |
| Stard9        | 1.218E-04 | 0.25 |
| Smyd5         | 3.691E-03 | 1.61 |
| Akr1c14       | 3.433E-04 | 0.02 |
| Vav3          | 7.456E-03 | 1.56 |
| St18          | 1.052E-02 | 0.39 |
| Gadd45gip1    | 4.491E-03 | 1.66 |
| Mnd1          | 5.257E-03 | 2.07 |
| Recql4        | 2.330E-08 | 5.22 |
| Rpap2         | 1.555E-04 | 1.79 |
| Tlr13         | 4.468E-03 | 0.12 |
| Atp7a         | 3.839E-04 | 0.58 |
| Ephx4         | 3.730E-02 | 1.97 |
| Alg3          | 4.273E-06 | 1.99 |
| Tpsb2         | 9.625E-04 | 0.19 |
| Dnahc8        | 1.579E-03 | 2.58 |
| B3galt2       | 1.188E-02 | 0.57 |
| Ston1         | 1.770E-03 | 1.56 |
| Kif9          | 6.450E-05 | 0.35 |
| Cfhr2         | 1.389E-03 | 0.09 |
| Ccp110        | 1.037E-02 | 1.57 |
| Zdhhc15       | 2.252E-02 | 1.87 |
| Gucy1a3       | 2.489E-05 | 0.28 |
| Rbm34         | 6.671E-03 | 1.80 |
| Vhl           | 5.285E-03 | 1.84 |
| Aspm          | 2.498E-05 | 2.69 |
| Tnks1bp1      | 5.845E-03 | 1.64 |
| Zfp446        | 8.588E-04 | 1.81 |
| Slc16a2       | 3.836E-02 | 0.61 |



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|---------------|-----------|------|
| Rfc3          | 2.048E-06 | 2.11 |
| Ttc37         | 1.905E-05 | 1.59 |
| Kcnk1         | 1.268E-03 | 7.38 |
| Pqlc1         | 1.340E-05 | 1.76 |
| Fancd2        | 2.160E-03 | 3.20 |
| Cct2          | 8.459E-03 | 1.63 |
| Cd226         | 1.069E-03 | 0.44 |
| Rpap1         | 1.545E-02 | 1.59 |
| Ccdc17        | 3.930E-02 | 1.79 |
| Wbscr17       | 2.377E-04 | 0.19 |
| Lyl1          | 6.149E-07 | 0.13 |
| Phka1         | 2.069E-05 | 0.21 |
| 4632415K11Rik | 2.970E-03 | 1.68 |
| Ano7          | 4.832E-02 | 0.43 |
| Vav1          | 1.976E-05 | 0.32 |
| Bzrap1        | 1.707E-03 | 2.59 |
| 2310044G17Rik | 1.490E-04 | 0.45 |
| 2310007B03Rik | 4.973E-02 | 0.59 |
| Emid1         | 4.701E-04 | 2.54 |
| Irf2bpl       | 6.021E-03 | 1.64 |
| Faah          | 4.118E-04 | 0.15 |
| Rnf43         | 6.289E-03 | 1.68 |
| Lsm3          | 4.977E-05 | 1.85 |
| Chchd4        | 4.258E-04 | 1.96 |
| Polq          | 2.435E-06 | 4.18 |
| Usp54         | 3.189E-03 | 0.55 |
| Slc25a37      | 3.012E-02 | 2.74 |
| Exosc4        | 7.581E-08 | 1.70 |
| Zdhhc14       | 3.826E-04 | 0.32 |
| Batf          | 4.620E-06 | 0.31 |
| Jdp2          | 2.930E-02 | 0.65 |
| Ccdc15        | 1.811E-06 | 2.62 |
| Sdr42e1       | 1.351E-03 | 0.40 |
| Kif4          | 4.867E-08 | 3.93 |
| Iqsec1        | 3.636E-03 | 0.25 |
| Trim59        | 2.138E-06 | 3.47 |
| Exosc1        | 6.356E-05 | 1.89 |
| Brip1         | 1.277E-03 | 2.18 |
| Plcg2         | 2.816E-03 | 0.62 |
| Fam151b       | 1.369E-03 | 1.50 |
| Smc4          | 7.615E-06 | 1.93 |
| Ramp1         | 3.174E-05 | 0.19 |
| Skint2        | 6.437E-05 | 0.15 |
| Cpne2         | 1.492E-02 | 1.58 |
| Csta          | 3.737E-02 | 2.13 |
| Dak           | 8.203E-03 | 1.88 |
| Al661453      | 8.003E-04 | 2.05 |
| Zfp707        | 9.772E-06 | 1.76 |
| Tmem30b       | 2.062E-02 | 1.85 |
| Gbp8          | 4.565E-02 | 0.14 |
| Eda2r         | 4.950E-04 | 0.41 |
| Scara3        | 4.157E-06 | 0.09 |
| Caskin2       | 6.699E-04 | 1.81 |
| Uaca          | 2.495E-03 | 2.30 |
| Pcnxl4        | 1.605E-03 | 1.57 |
| Mad2l1bp      | 1.822E-05 | 1.66 |
| Zfp395        | 4.770E-02 | 1.85 |
| Ccp1          | 1.100E-05 | 0.50 |
| Ptpn13        | 6.229E-03 | 1.64 |
| 8430429K09Rik | 5.277E-05 | 2.21 |
| Slc41a2       | 1.618E-04 | 0.31 |
| Myo5a         | 8.738E-04 | 0.61 |
| 2700049A03Rik | 1.631E-03 | 1.81 |
| Pof1b         | 2.803E-02 | 0.61 |
| Chst11        | 2.563E-03 | 0.37 |
| Ppm1h         | 1.665E-04 | 0.30 |
| Mtrr          | 6.453E-06 | 1.54 |
| Setmar        | 9.781E-04 | 2.12 |
| Tiparp        | 8.976E-04 | 2.11 |
| Cd300ld       | 2.208E-04 | 0.28 |
| Ankrd12       | 1.170E-04 | 0.65 |
| Cd300a        | 9.917E-05 | 0.25 |
| Ythdc2        | 2.596E-03 | 1.71 |
| Cacna1a       | 2.474E-03 | 0.27 |
| Tmem109       | 7.842E-05 | 0.47 |
| Xpot          | 3.290E-05 | 1.70 |
| Tdg           | 5.492E-08 | 1.68 |
| Rnps1         | 3.481E-04 | 1.57 |
| Fam171a2      | 3.493E-02 | 1.83 |
| Prr7          | 1.271E-03 | 2.96 |
| Fras1         | 3.259E-03 | 7.49 |
| Gns           | 9.656E-05 | 0.31 |
| Grn           | 8.273E-03 | 0.59 |
| Ttyh2         | 1.590E-04 | 0.20 |
| Dgkh          | 1.249E-02 | 0.66 |
| Sirt6         | 5.525E-05 | 1.71 |
| Mast4         | 1.095E-03 | 1.89 |
| Tle6          | 2.330E-02 | 0.54 |
| Asb16         | 1.749E-03 | 2.26 |
| BC030867      | 9.790E-05 | 7.15 |
| Cd207         | 2.289E-04 | 0.26 |
| Gpsm3         | 5.001E-04 | 0.31 |
| Zfp661        | 2.064E-02 | 1.75 |
| Scn7a         | 5.555E-08 | 0.04 |
| Grip1         | 1.331E-05 | 4.34 |
| Nup54         | 3.074E-04 | 1.89 |
| Tespa1        | 9.790E-05 | 0.37 |



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|---------------|-----------|------|
| Art3          | 2.841E-02 | 0.50 |
| Plvap         | 4.972E-04 | 0.41 |
| Ttc21b        | 2.236E-03 | 2.12 |
| Mfsd12        | 1.365E-03 | 0.15 |
| BC031353      | 3.370E-02 | 0.63 |
| Ano8          | 1.223E-02 | 0.67 |
| Lrr1          | 4.748E-06 | 5.12 |
| Cactin        | 1.480E-05 | 1.68 |
| Filip1        | 1.282E-06 | 0.31 |
| Pip5k1c       | 8.568E-04 | 0.58 |
| Ncaph         | 4.106E-06 | 2.90 |
| Tjp3          | 4.164E-03 | 0.39 |
| Dhcr24        | 4.109E-03 | 0.31 |
| Arl4d         | 1.912E-03 | 3.53 |
| Tmem106a      | 4.690E-05 | 0.22 |
| Cebpa         | 1.051E-03 | 0.52 |
| 5031414D18Rik | 1.273E-03 | 0.55 |
| Vat1          | 1.274E-04 | 0.39 |
| Igsf6         | 2.066E-04 | 0.20 |
| Epgn          | 9.784E-04 | 6.04 |
| Ncapd3        | 1.566E-06 | 2.00 |
| Kri1          | 9.128E-05 | 1.61 |
| Rrp12         | 6.861E-03 | 1.59 |
| 1700020L24Rik | 3.994E-03 | 2.86 |
| Secisbp2l     | 1.153E-05 | 0.40 |
| Fam167a       | 4.116E-02 | 1.61 |
| Fam176a       | 3.015E-02 | 1.53 |
| Egln3         | 4.118E-05 | 4.25 |
| AW146020      | 2.017E-03 | 1.60 |
| Wdr78         | 1.181E-02 | 2.71 |
| Nubpl         | 2.667E-03 | 1.96 |
| Mitf          | 3.127E-06 | 0.16 |
| Zc3h12c       | 1.090E-05 | 2.11 |
| Kcne3         | 1.188E-03 | 2.90 |
| Fam124a       | 3.699E-05 | 0.33 |
| Tubg1         | 4.497E-06 | 2.46 |
| Arl6ip5       | 3.844E-05 | 0.44 |
| Leprot        | 3.257E-04 | 0.56 |
| Fam175a       | 1.590E-04 | 1.66 |
| Trim13        | 5.779E-03 | 1.78 |
| Eogt          | 1.796E-04 | 2.22 |
| Pcyt1b        | 7.064E-05 | 5.39 |
| Abi3bp        | 7.420E-05 | 0.27 |
| Helq          | 9.978E-04 | 1.51 |
| Pkig          | 7.430E-06 | 0.62 |
| Hpse          | 3.808E-07 | 0.28 |
| Tpbp          | 3.526E-03 | 1.66 |
| Ssc5d         | 8.224E-04 | 0.22 |
| Vps13c        | 8.380E-05 | 0.48 |
| G2e3          | 4.593E-05 | 1.93 |
| Sgcs          | 1.237E-05 | 0.03 |
| Khlh35        | 4.261E-02 | 1.67 |
| Lin54         | 3.248E-03 | 1.64 |
| Gnptab        | 1.208E-02 | 0.65 |
| Gdpcd5        | 7.596E-04 | 1.93 |
| Uchl4         | 4.079E-04 | 1.71 |
| Lzts2         | 1.143E-04 | 0.53 |
| Nup37         | 1.570E-05 | 2.91 |
| Ccl12         | 3.170E-04 | 0.23 |
| Pdzrn3        | 6.210E-04 | 0.31 |
| 4930524J08Rik | 4.269E-03 | 5.86 |
| Parpbbp       | 1.380E-06 | 4.82 |
| Adat3         | 1.154E-04 | 2.42 |
| 1810055G02Rik | 2.249E-03 | 1.72 |
| Ccl7          | 2.013E-02 | 0.55 |
| Ptplb         | 1.909E-02 | 0.61 |
| Shq1          | 8.180E-04 | 1.80 |
| Pmch          | 1.061E-03 | 3.76 |
| Ccl2          | 3.186E-02 | 0.57 |
| Dennd1a       | 1.496E-02 | 0.62 |
| Klf16         | 1.188E-04 | 2.31 |
| 2210018M11Rik | 2.863E-03 | 1.50 |
| Tmem98        | 2.254E-02 | 0.49 |
| Thyn1         | 1.191E-02 | 1.56 |
| Figl1         | 1.036E-04 | 3.00 |
| Tnni3         | 1.200E-02 | 3.93 |
| Cdcp1         | 8.617E-05 | 2.73 |
| Cox18         | 1.397E-05 | 1.76 |
| Aldh1b1       | 1.975E-03 | 0.53 |
| Pcdh17        | 4.331E-02 | 9.75 |
| Frmpd1        | 1.245E-02 | 0.42 |
| Midn          | 2.618E-03 | 1.53 |
| Grhpr         | 4.427E-08 | 2.65 |
| 1810020D17Rik | 1.619E-02 | 0.64 |
| Tnfsf9        | 7.450E-03 | 5.66 |
| Melk          | 6.833E-08 | 3.69 |
| Thrsp         | 1.226E-04 | 0.02 |
| Hmha1         | 1.710E-05 | 0.29 |
| Alg8          | 4.200E-05 | 2.41 |
| Dok3          | 5.552E-04 | 0.44 |
| Usp35         | 2.275E-04 | 0.55 |
| Wdr18         | 3.692E-07 | 1.59 |
| Bbs10         | 1.637E-02 | 1.75 |
| Tmem161b      | 5.207E-06 | 1.51 |
| Xylb          | 5.471E-03 | 4.14 |
| Mrps2         | 8.042E-04 | 1.72 |
| Ggta1         | 5.522E-03 | 1.67 |



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|---------------|-----------|-------|
| Cep19         | 1.145E-02 | 1.52  |
| Tk2           | 5.825E-04 | 0.66  |
| Polr3g        | 2.873E-03 | 1.65  |
| Lysmd3        | 8.984E-04 | 1.61  |
| Ddx11         | 9.327E-09 | 2.99  |
| lds           | 3.092E-02 | 0.63  |
| Tmprss11bnl   | 1.992E-02 | 14.73 |
| Paln          | 1.614E-05 | 0.52  |
| Pawr          | 2.688E-03 | 1.71  |
| Rnf126        | 2.135E-05 | 2.25  |
| Uba6          | 2.439E-03 | 1.59  |
| Dennd5a       | 1.204E-03 | 0.52  |
| Cd276         | 1.330E-04 | 2.11  |
| Myf6          | 2.447E-08 | 0.02  |
| Acss3         | 3.455E-05 | 0.05  |
| Tdp2          | 2.783E-02 | 1.96  |
| Apex1         | 7.377E-03 | 1.58  |
| Ddx26b        | 1.180E-03 | 0.64  |
| Fam65b        | 3.244E-03 | 0.53  |
| Tmtc2         | 1.990E-02 | 2.43  |
| Fam122b       | 3.339E-04 | 1.69  |
| Adamts12      | 2.015E-02 | 2.43  |
| 5031439G07Rik | 2.221E-03 | 0.45  |
| Dnajb5        | 7.714E-03 | 0.66  |
| Fmnl2         | 3.295E-02 | 2.20  |
| Ptpn23        | 4.775E-04 | 1.87  |
| Smug1         | 1.063E-04 | 1.55  |
| N28178        | 2.017E-02 | 0.29  |
| Slc2a6        | 1.414E-04 | 0.48  |
| Colec12       | 1.446E-04 | 0.25  |
| Mbnl3         | 8.741E-04 | 1.97  |
| Rfxank        | 3.643E-03 | 1.71  |
| Fam110c       | 2.218E-05 | 3.92  |
| Acaa1a        | 3.272E-03 | 0.65  |
| Surf6         | 4.160E-05 | 1.60  |
| Ccdc38        | 4.220E-03 | 2.97  |
| Fam69b        | 4.152E-03 | 2.13  |
| Rif1          | 4.153E-03 | 1.78  |
| Sh3bp4        | 5.730E-03 | 1.72  |
| BC027231      | 2.430E-03 | 1.51  |
| Znrd1as       | 1.518E-02 | 1.59  |
| Leap2         | 9.846E-03 | 3.18  |
| Ska1          | 2.869E-05 | 5.01  |
| Kctd1         | 2.903E-03 | 1.84  |
| 3632451O06Rik | 3.195E-03 | 0.51  |
| Gmip          | 4.651E-04 | 0.66  |
| Igfbp7        | 3.016E-03 | 0.49  |
| Noa1          | 4.763E-05 | 1.80  |
| Gramd1c       | 2.537E-02 | 0.55  |
| Zdhhc23       | 6.040E-03 | 2.11  |
| Srp72         | 7.206E-05 | 1.55  |
| Qsox2         | 1.567E-03 | 1.57  |
| Igslf10       | 1.231E-02 | 0.37  |
| P2ry12        | 9.726E-04 | 0.36  |
| P2ry13        | 1.036E-02 | 0.55  |
| Serbp1        | 1.328E-03 | 1.60  |
| P2ry14        | 4.085E-04 | 0.39  |
| Gilb1l2       | 1.793E-05 | 0.09  |
| Arsi          | 4.244E-04 | 0.21  |
| Tbcc          | 5.081E-03 | 1.55  |
| Npy1r         | 2.288E-05 | 0.41  |
| Lum           | 7.352E-04 | 0.18  |
| Arhgap26      | 3.086E-05 | 0.43  |
| Wtip          | 1.570E-06 | 2.27  |
| Megf11        | 1.919E-04 | 1.58  |
| 1-Mar         | 7.733E-06 | 0.26  |
| Tbc1d24       | 4.070E-04 | 0.64  |
| Rnf13         | 1.410E-05 | 0.57  |
| Rnf113a1      | 7.013E-04 | 1.71  |
| Adamts2       | 5.453E-04 | 0.30  |
| Sh3tc1        | 9.854E-04 | 0.46  |
| Fxyd1         | 2.460E-09 | 0.08  |
| H2-Aa         | 1.866E-04 | 0.20  |
| Eepd1         | 2.747E-08 | 0.37  |
| Rfxap         | 3.389E-06 | 1.78  |
| Etl4          | 5.623E-03 | 1.62  |
| Atp13a2       | 1.936E-05 | 0.23  |
| Clcn7         | 4.981E-04 | 0.57  |
| Nudt1         | 1.203E-03 | 1.67  |
| Cenpt         | 5.134E-05 | 2.55  |
| Aaas          | 1.179E-05 | 1.99  |
| Nop14         | 1.582E-04 | 1.89  |
| Micall2       | 1.785E-02 | 2.68  |
| Zscan12       | 8.868E-03 | 1.76  |
| Cuedc2        | 3.625E-03 | 0.48  |
| Dnajc12       | 4.492E-07 | 0.46  |
| Kif15         | 4.583E-07 | 3.55  |
| Anln          | 1.824E-04 | 3.51  |
| Klhl13        | 1.502E-05 | 0.09  |
| Jmjd4         | 1.602E-04 | 1.81  |
| Amdhd2        | 3.953E-04 | 0.48  |
| Topors        | 7.832E-03 | 1.50  |
| Tmem149       | 1.067E-02 | 0.50  |
| Lpar3         | 2.313E-02 | 0.58  |
| Pnpla7        | 5.671E-06 | 0.29  |
| Hspb6         | 3.307E-05 | 0.31  |
| Wnt4          | 3.393E-03 | 2.56  |



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|---------------|-----------|-------|
| BC053749      | 2.593E-02 | 1.98  |
| Smad6         | 7.118E-03 | 1.65  |
| Dna2          | 1.099E-04 | 1.57  |
| Phkb          | 3.448E-03 | 0.61  |
| Acaa2         | 5.984E-04 | 0.59  |
| C1qa          | 3.199E-05 | 0.18  |
| C1qc          | 4.382E-05 | 0.15  |
| Neto2         | 4.531E-02 | 3.04  |
| Fzd8          | 8.459E-06 | 1.98  |
| C1qb          | 3.203E-05 | 0.16  |
| Unc93b1       | 3.689E-05 | 0.16  |
| Zfp280c       | 8.458E-04 | 1.76  |
| 4921524J17Rik | 1.753E-02 | 1.69  |
| C130079G13Rik | 1.759E-02 | 0.29  |
| Bcor1         | 3.704E-04 | 1.68  |
| Anapc10       | 9.352E-03 | 1.64  |
| Asap3         | 6.261E-06 | 0.43  |
| Tenc1         | 7.137E-05 | 0.41  |
| Zfp113        | 3.023E-02 | 1.66  |
| Apln          | 1.139E-06 | 12.28 |
| Hk1           | 1.073E-03 | 1.51  |
| Tmem185b      | 6.488E-04 | 1.69  |
| Mmaa          | 1.775E-04 | 1.76  |
| Smpd1         | 3.340E-03 | 0.50  |
| Rbmx1         | 5.637E-04 | 1.94  |
| Scd1          | 4.166E-05 | 0.04  |
| Trmt12        | 1.884E-03 | 1.95  |
| Lrg1          | 1.507E-05 | 0.21  |
| Myom3         | 3.662E-02 | 0.64  |
| Arhgap10      | 1.838E-04 | 0.63  |
| Mgarp         | 4.658E-04 | 7.41  |
| E330009J07Rik | 3.102E-03 | 0.52  |
| Krt80         | 1.622E-02 | 0.50  |
| Grhl3         | 3.231E-02 | 1.72  |
| Cyb561d2      | 5.997E-03 | 1.53  |
| Islr          | 1.938E-03 | 0.26  |
| Thap1         | 3.665E-04 | 1.86  |
| Lipt1         | 3.062E-05 | 2.21  |
| Mospd3        | 3.507E-02 | 1.67  |
| Zfyve28       | 9.643E-05 | 0.18  |
| Fgf2          | 4.473E-03 | 0.24  |
| Spred3        | 6.524E-04 | 3.07  |
| Clic4         | 6.959E-03 | 0.55  |
| 1700055N04Rik | 2.812E-02 | 0.57  |
| D4Wsu53e      | 6.805E-03 | 0.61  |
| Gemin5        | 1.120E-04 | 1.72  |
| Ovol2         | 2.027E-03 | 7.17  |
| Ldlrap1       | 2.198E-03 | 1.91  |
| Lsm1          | 1.020E-03 | 1.72  |
| Man1c1        | 6.063E-05 | 0.22  |
| Tacc3         | 3.305E-06 | 3.67  |
| Phf16         | 2.235E-04 | 2.39  |
| Traf3ip3      | 3.825E-04 | 0.42  |
| Hand1         | 4.937E-02 | 11.07 |
| Map4k1        | 1.972E-03 | 0.49  |
| Slc9a7        | 5.094E-05 | 0.28  |
| Paqr7         | 6.167E-05 | 0.41  |
| Nov           | 9.959E-04 | 0.17  |
| Enpp1         | 1.039E-04 | 0.23  |
| Trmt6         | 8.601E-04 | 1.70  |
| Atp11b        | 7.666E-06 | 1.92  |
| Cnnm4         | 1.511E-03 | 1.58  |
| Tbc1d2b       | 3.408E-03 | 0.60  |
| Serpine1      | 4.573E-03 | 6.47  |
| Endod1        | 1.292E-02 | 0.61  |
| Slc30a1       | 5.486E-05 | 0.46  |
| Vnn1          | 1.849E-04 | 0.12  |
| Ints7         | 1.573E-04 | 1.58  |
| Klf10         | 7.562E-06 | 1.68  |
| 4930427A07Rik | 4.865E-05 | 3.19  |
| C330005M16Rik | 2.389E-02 | 0.46  |
| Dtl           | 2.190E-05 | 2.83  |
| Arhgef4       | 1.182E-03 | 1.92  |
| Samd4b        | 1.200E-02 | 1.59  |
| Bcdin3d       | 3.491E-06 | 2.15  |
| Mrpl47        | 2.250E-03 | 1.68  |
| Dlgap5        | 1.442E-04 | 2.46  |
| H2-DMb2       | 6.376E-04 | 0.42  |
| Wdhd1         | 3.717E-04 | 2.36  |
| BC022687      | 3.273E-04 | 1.88  |
| 1810019J16Rik | 4.398E-04 | 2.86  |
| Nme1          | 9.733E-03 | 1.56  |
| Lphn3         | 3.197E-04 | 0.17  |
| Tnfrsf23      | 3.344E-05 | 5.23  |
| Cdkn3         | 2.246E-05 | 3.43  |
| H2-DMa        | 1.254E-04 | 0.25  |
| Slc20a2       | 1.573E-03 | 2.05  |
| Cdkn1c        | 5.297E-04 | 0.02  |
| Atp8a1        | 7.702E-06 | 0.31  |
| Ahd1          | 3.473E-02 | 1.63  |
| Ddhd1         | 1.470E-05 | 0.27  |
| Prosapip1     | 1.216E-02 | 1.78  |
| Fermt2        | 3.791E-04 | 0.41  |
| Ckap2         | 1.616E-05 | 3.21  |
| Themis2       | 1.978E-03 | 0.32  |
| Mrps26        | 2.618E-05 | 1.58  |
| Phyhipl       | 7.909E-06 | 3.12  |



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|---------------|-----------|------|
| BC017647      | 2.679E-03 | 1.55 |
| Ptger2        | 8.258E-03 | 0.38 |
| Actr5         | 1.392E-02 | 1.54 |
| Slc16a9       | 2.520E-02 | 2.40 |
| Dzip1l        | 7.764E-04 | 1.95 |
| 3110057O12Rik | 3.682E-04 | 1.95 |
| Tgm2          | 3.751E-06 | 0.18 |
| 1110003E01Rik | 1.504E-05 | 0.58 |
| Iars          | 7.972E-05 | 1.55 |
| Egr2          | 3.231E-04 | 0.17 |
| Darc          | 1.633E-07 | 0.15 |
| Stk35         | 2.646E-04 | 1.59 |
| Dusp8         | 3.165E-03 | 2.12 |
| Pcdh18        | 5.188E-03 | 2.20 |
| Sirpa         | 1.652E-04 | 0.22 |
| Ankrd9        | 8.776E-03 | 2.17 |
| Bri3bp        | 1.347E-05 | 1.61 |
| Ankrd13b      | 2.852E-02 | 1.60 |
| Scarb1        | 4.848E-05 | 0.60 |
| Chchd5        | 9.276E-04 | 1.68 |
| Fgd3          | 2.663E-04 | 0.50 |
| Ccdc55        | 1.001E-03 | 1.57 |
| 1110007C09Rik | 1.444E-03 | 0.53 |
| Fam101a       | 3.925E-02 | 1.78 |
| Ninj1         | 2.387E-04 | 0.43 |
| Snn           | 1.385E-03 | 1.76 |
| Ccdc92        | 2.430E-03 | 3.19 |
| Wnk2          | 1.468E-02 | 2.06 |
| Rmi2          | 1.767E-02 | 1.59 |
| Ccdc138       | 1.217E-03 | 3.43 |
| 9630033F20Rik | 2.386E-03 | 1.52 |
| Ptpdc1        | 7.317E-03 | 1.52 |
| Rnmtl1        | 1.037E-04 | 1.63 |
| Haus6         | 1.993E-04 | 2.51 |
| 2010002N04Rik | 7.246E-06 | 3.36 |
| 2410066E13Rik | 7.637E-03 | 0.65 |
| Cdkn2aip      | 4.798E-03 | 1.67 |
| Hspb2         | 3.303E-05 | 0.17 |
| AW551984      | 3.986E-05 | 0.07 |
| Cdon          | 2.008E-04 | 0.57 |
| 4933403F05Rik | 7.365E-03 | 1.65 |
| D630037F22Rik | 3.919E-04 | 1.77 |
| Mphosph9      | 1.835E-02 | 1.61 |
| Camk4         | 3.280E-03 | 1.83 |
| Rbm24         | 2.864E-07 | 0.06 |
| Stox2         | 2.327E-02 | 1.62 |
| Cd84          | 1.028E-04 | 0.07 |
| 5033430I15Rik | 6.259E-05 | 4.32 |
| Plekhg6       | 4.216E-03 | 2.29 |
| Leprel1       | 4.784E-04 | 2.44 |
| Pde4dip       | 6.551E-09 | 0.23 |
| Ttc39b        | 1.110E-03 | 1.60 |
| Slc43a2       | 1.108E-03 | 0.40 |
| Slamf7        | 4.372E-04 | 0.11 |
| Scarf1        | 6.518E-04 | 0.38 |
| Rilp          | 8.908E-05 | 0.26 |
| Kcna7         | 4.969E-04 | 0.30 |
| Bend3         | 1.870E-07 | 2.76 |
| BC088983      | 4.891E-04 | 1.77 |
| Tlcd2         | 1.924E-04 | 0.30 |
| Ccdc111       | 5.335E-03 | 1.84 |
| F11r          | 6.440E-04 | 1.75 |
| Hrc           | 5.505E-07 | 0.04 |
| Aox4          | 1.014E-02 | 0.22 |
| Mical2        | 2.194E-03 | 0.55 |
| Ncapd2        | 1.138E-05 | 2.89 |
| Bcl9          | 4.455E-03 | 1.66 |
| Sema7a        | 3.202E-02 | 1.55 |
| Iffo1         | 5.442E-04 | 0.42 |
| Nop2          | 4.422E-07 | 2.23 |
| Ostm1         | 1.484E-04 | 0.60 |
| Snx25         | 7.897E-03 | 1.71 |
| Atg9b         | 3.812E-03 | 0.51 |
| Wdr36         | 3.174E-04 | 1.99 |
| Snx10         | 3.054E-03 | 0.52 |
| Spat2l        | 4.556E-03 | 2.13 |
| 1700066M21Rik | 6.899E-06 | 1.72 |
| Sesn1         | 1.433E-04 | 0.47 |
| Tsr1          | 2.675E-06 | 1.61 |
| Tcte2         | 3.099E-03 | 1.54 |
| Ankrd35       | 6.963E-03 | 0.49 |
| BC057079      | 5.983E-03 | 1.58 |
| Rbm8a         | 1.144E-05 | 1.66 |
| Trp53inp2     | 2.435E-04 | 0.41 |
| Ttk           | 6.234E-06 | 3.61 |
| Gpr162        | 2.396E-03 | 0.42 |
| Txnip         | 2.904E-06 | 0.21 |
| Pmepa1        | 3.709E-04 | 1.65 |
| Foxf2         | 1.612E-02 | 9.98 |
| Hfe2          | 4.761E-05 | 0.03 |
| Higd1a        | 7.421E-06 | 2.43 |
| Foxq1         | 9.455E-03 | 2.65 |
| Poli          | 2.218E-03 | 1.86 |
| Srcin1        | 8.616E-03 | 0.45 |
| Dennd2a       | 5.129E-04 | 0.16 |
| Fam70b        | 7.145E-04 | 0.09 |
| Olfml2b       | 1.339E-02 | 0.45 |



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| Nos1ap        | 5.648E-03 | 2.08  |
| Tfdp1         | 6.589E-07 | 2.17  |
| Socs7         | 1.657E-03 | 1.52  |
| Prr3          | 5.074E-03 | 1.52  |
| Rpf2          | 8.434E-04 | 1.99  |
| Jarid2        | 2.903E-04 | 2.62  |
| C1s           | 9.035E-04 | 0.40  |
| Rgs4          | 1.273E-02 | 0.61  |
| BC028528      | 1.557E-04 | 0.33  |
| Rad9b         | 5.455E-03 | 2.20  |
| Akap12        | 1.134E-02 | 0.61  |
| Tctn1         | 6.176E-03 | 1.53  |
| Gm9766        | 1.312E-03 | 0.46  |
| Atp6v0a4      | 2.415E-02 | 0.55  |
| Gng10         | 8.998E-04 | 0.52  |
| Dock10        | 3.746E-06 | 0.21  |
| Mcl1          | 7.433E-04 | 0.59  |
| Nfe2l1        | 4.664E-05 | 0.62  |
| Ensa          | 1.924E-04 | 0.64  |
| Med30         | 4.259E-03 | 1.54  |
| Tm6sf1        | 3.396E-05 | 0.17  |
| Lrrc56        | 1.829E-03 | 1.68  |
| Akr1d1        | 8.667E-03 | 5.19  |
| Ctss          | 2.256E-04 | 0.10  |
| Pold1         | 3.388E-04 | 2.30  |
| Fsd2          | 1.278E-05 | 0.05  |
| Lpar1         | 3.432E-04 | 0.09  |
| Mybpc2        | 9.433E-05 | 0.01  |
| Pak1ip1       | 2.967E-03 | 1.72  |
| Rtel1         | 5.209E-04 | 1.87  |
| Gmeb2         | 7.917E-04 | 1.63  |
| Txndc8        | 2.553E-02 | 12.44 |
| Fam63a        | 3.471E-04 | 0.67  |
| Akap2         | 8.251E-05 | 0.23  |
| Mboat1        | 2.880E-04 | 3.83  |
| Wdr26         | 8.809E-04 | 0.62  |
| Nudcd1        | 5.522E-03 | 2.19  |
| Angptl6       | 2.242E-03 | 1.86  |
| Elovl3        | 1.241E-03 | 0.03  |
| Nup205        | 8.289E-05 | 1.94  |
| Alpk3         | 8.676E-08 | 0.03  |
| 9130409I23Rik | 6.176E-03 | 0.13  |
| Ephx1         | 1.757E-04 | 0.28  |
| Sema6c        | 5.073E-04 | 0.38  |
| Smurf1        | 7.504E-04 | 1.92  |
| Gngt2         | 2.031E-04 | 0.22  |
| Ctnnal1       | 1.640E-03 | 1.65  |
| BC026590      | 2.023E-05 | 2.16  |
| Agbl3         | 2.971E-04 | 3.55  |
| Vars2         | 3.305E-02 | 1.66  |
| Gcnt1         | 6.749E-06 | 0.34  |
| Phb           | 2.033E-04 | 1.55  |
| Ythdf1        | 3.954E-04 | 1.57  |
| Itpkb         | 3.680E-06 | 0.36  |
| Bpgm          | 2.038E-02 | 1.75  |
| Man2a2        | 2.476E-05 | 0.53  |
| Ctu1          | 1.865E-03 | 1.56  |
| Fam117a       | 1.594E-05 | 0.32  |
| Irs2          | 2.215E-03 | 2.21  |
| Plcl2         | 1.008E-06 | 0.20  |
| Prc1          | 1.776E-05 | 3.09  |
| Cnst          | 3.626E-03 | 0.65  |
| Ecd3          | 5.890E-07 | 1.58  |
| Slco4a1       | 1.744E-02 | 3.74  |
| Pdk2          | 3.193E-05 | 0.31  |
| BC066135      | 3.071E-03 | 2.08  |
| 1700019L03Rik | 4.248E-02 | 1.90  |
| Tlr4          | 1.378E-06 | 0.25  |
| Pgcp          | 1.373E-05 | 0.14  |
| Siglec5       | 1.550E-02 | 0.34  |
| Arhgap18      | 1.401E-04 | 0.50  |
| St6galnac5    | 1.159E-07 | 0.16  |
| 2610034B18Rik | 3.807E-02 | 1.66  |
| Eme1          | 1.097E-05 | 2.86  |
| Anpep         | 3.101E-03 | 0.15  |
| Cpa4          | 2.361E-03 | 0.46  |
| Zfp503        | 9.532E-03 | 1.78  |
| Ss18l1        | 2.623E-03 | 1.72  |
| Rreb1         | 2.054E-02 | 1.53  |
| Sptlc3        | 1.194E-02 | 0.40  |
| Rsad1         | 1.112E-02 | 1.68  |
| Lsm14b        | 4.272E-04 | 1.64  |
| F13a1         | 8.504E-06 | 0.03  |
| Itga9         | 6.856E-04 | 0.42  |
| Gpr126        | 2.303E-02 | 0.53  |
| Taf4a         | 8.981E-03 | 1.58  |
| Prune2        | 3.845E-04 | 0.31  |
| Zc3hc1        | 2.421E-04 | 1.65  |
| Gipc2         | 4.780E-02 | 2.89  |
| Whrn          | 4.305E-03 | 2.93  |
| Fam102a       | 6.171E-04 | 1.55  |
| Akna          | 5.146E-05 | 0.34  |
| Naif1         | 2.053E-03 | 1.80  |
| AW209491      | 2.954E-03 | 1.77  |
| Fanci         | 4.629E-07 | 3.62  |
| Rbpj          | 2.562E-05 | 0.56  |
| Nlrc4         | 1.563E-04 | 0.31  |



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|---------------|-----------|------|
| 1110008P14Rik | 1.710E-02 | 0.63 |
| Orm1          | 1.327E-02 | 0.12 |
| Tbc1d25       | 2.042E-04 | 1.82 |
| Daglb         | 4.864E-05 | 0.19 |
| Metrn1        | 2.975E-04 | 0.56 |
| Rpl39l        | 1.851E-02 | 0.51 |
| Suv39h1       | 4.509E-05 | 2.27 |
| Isq20         | 6.758E-03 | 3.15 |
| Tgfb2         | 9.545E-03 | 1.92 |
| E130309D02Rik | 3.085E-06 | 1.66 |
| Lgi2          | 3.949E-03 | 4.48 |
| Rftn1         | 2.015E-04 | 0.22 |
| Rnf122        | 9.769E-03 | 1.88 |
| Atp6v0e2      | 1.989E-06 | 0.13 |
| C130074G19Rik | 2.095E-04 | 0.46 |
| Exosc2        | 8.785E-03 | 1.84 |
| Neil3         | 5.872E-06 | 2.65 |
| Wfs1          | 3.340E-03 | 0.09 |
| Prrx2         | 1.097E-02 | 0.53 |
| Nrtm          | 2.856E-02 | 0.48 |
| Dse           | 4.933E-03 | 0.66 |
| Znfx1         | 3.363E-02 | 0.53 |
| Rcan2         | 6.558E-03 | 0.34 |
| Rbms3         | 3.860E-02 | 0.52 |
| Prex1         | 4.026E-04 | 0.36 |
| Lonrf1        | 1.261E-02 | 2.15 |
| Mrpl12        | 1.872E-04 | 1.58 |
| Vasn          | 6.529E-03 | 0.61 |
| D2Wsu81e      | 7.984E-04 | 1.78 |
| Oxld1         | 9.322E-03 | 1.55 |
| Capsl         | 8.357E-04 | 3.07 |
| Mrps6         | 3.178E-04 | 1.51 |
| Lap3          | 1.749E-03 | 0.64 |
| Sdk1          | 2.579E-02 | 1.56 |
| 5730528L13Rik | 6.983E-04 | 3.09 |
| Ncoa7         | 3.979E-04 | 0.51 |
| Lmbrd2        | 4.031E-03 | 0.65 |
| Ldb2          | 8.374E-05 | 0.35 |
| Wdr34         | 2.553E-02 | 1.54 |
| Dock3         | 6.003E-03 | 4.22 |
| 2810408M09Rik | 4.788E-04 | 1.54 |
| Prkrip1       | 3.617E-02 | 1.69 |
| Alg2          | 4.680E-04 | 1.70 |
| Orai2         | 2.069E-04 | 2.70 |
| Exo1          | 3.889E-06 | 4.11 |
| Fbxl5         | 4.472E-04 | 2.58 |
| Alkbh4        | 5.320E-06 | 1.84 |
| Dnrtip2       | 5.086E-05 | 1.68 |
| Cc2d2a        | 2.524E-03 | 1.64 |
| Azi1          | 4.071E-06 | 2.20 |
| Kmo           | 2.506E-02 | 0.58 |
| Cercam        | 1.259E-02 | 0.64 |
| Zc3h10        | 7.145E-04 | 1.57 |
| Tbc1d2        | 1.318E-03 | 2.65 |
| Wdr70         | 1.432E-04 | 1.79 |
| Arhgap29      | 1.880E-03 | 0.57 |
| Zfp335        | 1.244E-05 | 1.64 |
| Mcph1         | 1.679E-04 | 1.96 |
| Endov         | 1.101E-03 | 1.62 |
| 4932438H23Rik | 1.393E-02 | 0.43 |
| Trim14        | 2.672E-02 | 0.61 |
| Neurl2        | 2.325E-03 | 0.46 |
| Txlnb         | 2.716E-07 | 0.06 |
| Fgl2          | 6.131E-06 | 0.12 |
| 4931408A02Rik | 9.390E-05 | 3.02 |
| Rhbdd2        | 2.924E-03 | 2.10 |
| Urb1          | 2.299E-04 | 1.53 |
| Pik3cd        | 2.821E-05 | 0.23 |
| Mrap          | 2.660E-05 | 0.06 |
| Hip1          | 4.234E-03 | 0.56 |
| Zc3h12d       | 6.533E-03 | 0.42 |
| Dtx4          | 1.975E-07 | 0.15 |
| Fam60a        | 3.929E-03 | 2.35 |
| Timeless      | 1.197E-03 | 2.41 |
| Ifi203        | 4.839E-02 | 0.57 |
| Ptger3        | 5.643E-04 | 0.31 |
| Saa3          | 6.383E-03 | 0.07 |
| Elavl1        | 4.595E-05 | 1.51 |
| Nup43         | 4.384E-06 | 2.24 |
| Tph1          | 2.384E-02 | 0.41 |
| Gjb6          | 1.852E-03 | 6.80 |
| Plcb2         | 1.687E-05 | 0.31 |
| Bub1b         | 2.227E-05 | 3.54 |
| Bmf           | 1.585E-03 | 0.46 |
| Klhdc5        | 7.849E-03 | 1.59 |
| Gramd1b       | 4.716E-06 | 0.23 |
| Mrps35        | 1.534E-04 | 1.85 |
| Cacna2d1      | 6.142E-07 | 0.14 |
| Gorab         | 3.600E-04 | 1.71 |
| Maob          | 1.466E-03 | 0.37 |
| 1700034J05Rik | 7.828E-03 | 1.60 |
| Fmo2          | 2.958E-03 | 0.05 |
| Fmo1          | 1.084E-06 | 0.19 |
| Arntl2        | 7.383E-05 | 2.61 |
| Tmem194       | 2.952E-04 | 1.76 |
| Cd209e        | 2.046E-02 | 0.05 |
| 2810417H13Rik | 4.380E-04 | 2.24 |



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|---------------|-----------|-------|
| Zfp704        | 2.039E-04 | 0.35  |
| Emp3          | 6.392E-05 | 0.17  |
| Gpr34         | 2.680E-04 | 0.38  |
| Tbc1d10c      | 9.749E-05 | 0.34  |
| Lrp1          | 5.677E-04 | 0.36  |
| Spata30       | 2.644E-02 | 1.50  |
| Sema3d        | 1.581E-02 | 0.23  |
| Nxph4         | 5.981E-06 | 14.89 |
| Dnm3          | 3.407E-05 | 0.34  |
| Bach2         | 6.753E-04 | 0.48  |
| Cdk6          | 1.377E-03 | 2.21  |
| Ndufa4l2      | 4.663E-04 | 5.75  |
| BC052040      | 3.605E-03 | 2.75  |
| Stac3         | 8.934E-07 | 0.23  |
| Cchcr1        | 4.179E-04 | 2.16  |
| Zfp770        | 3.368E-03 | 1.71  |
| Cul9          | 6.141E-05 | 0.37  |
| Il7           | 6.667E-03 | 0.45  |
| Fam102b       | 1.017E-02 | 0.50  |
| Arhgap9       | 4.764E-04 | 0.28  |
| Mars          | 1.353E-03 | 1.51  |
| Plekha4       | 7.003E-04 | 0.20  |
| Mterf         | 1.857E-03 | 1.77  |
| Pitpnc1       | 3.021E-03 | 1.80  |
| Ltb4r2        | 2.587E-03 | 3.11  |
| Gylt1b        | 1.747E-02 | 1.99  |
| Ppp1r15a      | 6.287E-03 | 1.68  |
| Rprd1a        | 5.175E-04 | 1.64  |
| Spns2         | 6.837E-03 | 0.54  |
| Mybbp1a       | 7.219E-05 | 1.79  |
| Gtpbp10       | 3.901E-02 | 1.54  |
| Blvrb         | 5.850E-05 | 0.38  |
| A330021E22Rik | 7.261E-03 | 4.07  |
| 9-Mar         | 3.033E-04 | 2.16  |
| Pvr           | 5.030E-05 | 2.15  |
| Tsfrn         | 1.196E-03 | 1.52  |
| Tlr8          | 1.085E-05 | 0.09  |
| Cblc          | 1.281E-02 | 1.67  |
| Gm885         | 2.415E-05 | 0.34  |
| Adam22        | 4.900E-03 | 0.37  |
| Pitpnm3       | 6.102E-04 | 4.42  |
| C3ar1         | 6.983E-05 | 0.13  |
| Gstm2         | 3.748E-05 | 0.31  |
| Rundc3b       | 1.649E-02 | 3.91  |
| Cd79b         | 5.991E-03 | 0.24  |
| Bace2         | 4.691E-02 | 1.53  |
| Apobec1       | 1.206E-04 | 0.27  |
| Tmem51        | 1.688E-04 | 1.94  |
| Gemin8        | 2.127E-03 | 1.79  |
| Dok4          | 5.001E-04 | 2.60  |
| Cyp2b23       | 2.009E-02 | 0.02  |
| BC048355      | 1.526E-03 | 3.29  |
| Effhd2        | 5.530E-03 | 0.60  |
| Clcf1         | 1.404E-03 | 5.41  |
| Sh3bgr        | 5.005E-03 | 0.15  |
| Phc1          | 1.958E-02 | 1.87  |
| Mthfd1l       | 1.812E-04 | 5.38  |
| Hmgn1         | 1.823E-03 | 1.55  |
| Tbl3          | 7.242E-04 | 1.61  |
| Apobec2       | 1.574E-04 | 0.02  |
| Cyp2s1        | 1.154E-02 | 7.45  |
| A930016O22Rik | 2.320E-02 | 0.03  |
| St8sia4       | 1.084E-04 | 0.20  |
| Sh3pxd2b      | 1.138E-02 | 0.65  |
| Creg1         | 1.766E-05 | 0.13  |
| Scamp5        | 2.507E-03 | 0.43  |
| Rcsd1         | 2.272E-10 | 0.21  |
| Ppp1r13l      | 2.422E-02 | 1.76  |
| Cd53          | 6.011E-06 | 0.20  |
| Siah1b        | 9.243E-07 | 2.83  |
| Lat2          | 1.525E-04 | 0.17  |
| C1qtnf4       | 2.658E-02 | 3.22  |
| Eml2          | 7.846E-03 | 2.16  |
| Tex264        | 4.638E-05 | 0.38  |
| Snrpd2        | 4.781E-04 | 1.52  |
| 4930579G18Rik | 4.946E-03 | 1.61  |
| Six5          | 3.659E-03 | 1.77  |
| Plekhh2       | 3.301E-02 | 0.56  |
| Reps2         | 1.193E-04 | 0.37  |
| Erf           | 2.606E-03 | 1.68  |
| Osbpl10       | 3.712E-04 | 3.38  |
| Wdr25         | 6.768E-04 | 1.97  |
| Gfer          | 3.453E-02 | 1.62  |
| Ccr6          | 4.123E-03 | 0.45  |
| Rnasek        | 6.892E-03 | 1.72  |
| Atp1a3        | 5.154E-03 | 0.04  |
| Slc16a11      | 8.367E-03 | 2.05  |
| Tet2          | 1.242E-03 | 1.54  |
| Rcc2          | 2.282E-03 | 1.68  |
| Mgl2          | 2.067E-05 | 0.06  |
| Cables1       | 4.630E-03 | 2.19  |
| Arhgef10l     | 2.271E-02 | 0.65  |
| Gm11992       | 2.984E-02 | 0.48  |
| Mill2         | 3.674E-05 | 0.16  |
| Abhd4         | 8.063E-07 | 0.60  |
| Cmtm8         | 1.884E-02 | 0.45  |
| Ramp3         | 2.507E-04 | 5.09  |



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|---------------|-----------|-------|
| Wdr43         | 1.652E-04 | 2.03  |
| Wwp1          | 4.854E-05 | 0.61  |
| Pif1          | 2.199E-06 | 4.74  |
| Fzd7          | 1.240E-02 | 0.60  |
| Rwdd2b        | 8.096E-05 | 1.85  |
| Elmo1         | 5.132E-07 | 0.27  |
| Iqsec2        | 2.568E-04 | 0.47  |
| Nbl1          | 2.337E-03 | 0.43  |
| Ripk2         | 3.986E-04 | 0.61  |
| Brca2         | 1.492E-04 | 3.13  |
| Otud3         | 1.790E-02 | 1.65  |
| Lonp1         | 1.075E-03 | 1.75  |
| Prkd2         | 9.270E-03 | 1.55  |
| Pla2g5        | 8.697E-03 | 0.25  |
| Rpusd1        | 1.610E-04 | 2.01  |
| Pla2g2d       | 2.674E-04 | 0.18  |
| Arhgap11a     | 4.654E-06 | 2.05  |
| Elov6         | 3.365E-03 | 0.10  |
| Rbbp8         | 1.300E-03 | 1.65  |
| Usp1          | 1.705E-04 | 1.54  |
| Dmxl2         | 7.406E-03 | 0.43  |
| Sox15         | 2.995E-05 | 7.18  |
| Gtf3c3        | 1.246E-03 | 1.51  |
| Slc7a1        | 2.006E-04 | 3.19  |
| Inhba         | 4.312E-02 | 4.98  |
| Ankrd42       | 1.238E-03 | 1.85  |
| Wrap53        | 4.480E-07 | 1.83  |
| Rap1gap       | 1.406E-03 | 2.63  |
| D19Bwg1357e   | 2.857E-02 | 1.61  |
| B4galnt3      | 3.707E-04 | 4.03  |
| Mdfic         | 2.752E-06 | 0.31  |
| Mettl18       | 4.354E-03 | 1.76  |
| BC055324      | 4.746E-05 | 2.58  |
| Pik3r1        | 1.109E-04 | 0.48  |
| Nthl1         | 3.279E-03 | 1.96  |
| Ccnb1         | 9.821E-04 | 3.83  |
| Cirh1a        | 2.681E-04 | 2.77  |
| Fam35a        | 5.364E-03 | 1.55  |
| Smpx          | 6.584E-05 | 0.01  |
| Syt15         | 2.251E-05 | 0.47  |
| Fam38b        | 3.695E-03 | 2.42  |
| Cep78         | 4.629E-03 | 1.76  |
| Kif14         | 6.490E-06 | 3.98  |
| Rrp9          | 6.052E-06 | 2.19  |
| H2-Ob         | 1.394E-02 | 0.54  |
| Sox5          | 6.927E-03 | 2.46  |
| Hspb8         | 3.086E-05 | 0.49  |
| Ptchd1        | 2.488E-03 | 0.16  |
| Serpina12     | 6.942E-03 | 0.31  |
| Camsap2       | 1.577E-03 | 2.20  |
| Prelp         | 4.872E-05 | 0.11  |
| Tmtc4         | 5.376E-04 | 1.83  |
| 5730559C18Rik | 9.608E-03 | 1.89  |
| Mmp1b         | 1.969E-03 | 25.93 |
| Mrps27        | 3.534E-05 | 1.81  |
| Kctd12b       | 4.552E-04 | 0.41  |
| Pnpla3        | 1.908E-03 | 0.38  |
| Slc39a11      | 3.167E-04 | 0.43  |
| Bbox1         | 1.938E-04 | 0.12  |
| Lrrc29        | 1.019E-02 | 2.11  |
| Bivm          | 3.243E-02 | 1.57  |
| Amot          | 3.458E-06 | 0.21  |
| Kcnj2         | 3.043E-02 | 0.59  |
| AK010878      | 1.395E-02 | 2.87  |
| Pi4ka         | 2.781E-05 | 0.58  |
| Coro2b        | 4.519E-04 | 0.29  |
| Pgm5          | 9.251E-05 | 0.25  |
| Gm13178       | 3.695E-03 | 0.03  |
| Pde3a         | 1.217E-02 | 0.53  |
| Utp15         | 2.683E-03 | 1.98  |
| Gpr155        | 1.853E-04 | 0.60  |
| Ydjc          | 3.003E-04 | 1.90  |
| Lad1          | 9.569E-04 | 1.98  |
| Abca9         | 2.059E-06 | 0.05  |
| Phlda3        | 2.430E-03 | 1.66  |
| Fam169a       | 1.503E-02 | 4.93  |
| Abca8a        | 4.156E-07 | 0.04  |
| Syt13         | 2.318E-03 | 0.49  |
| Pdcd7         | 5.626E-03 | 1.54  |
| Haus1         | 3.103E-06 | 2.23  |
| Mcm3          | 1.464E-05 | 2.23  |
| Shisa4        | 1.754E-06 | 0.17  |
| Wipi1         | 3.660E-03 | 1.81  |
| Dlx1          | 2.929E-04 | 7.76  |
| Metap1d       | 4.585E-03 | 1.57  |
| Tmco7         | 2.419E-03 | 2.64  |
| 2310008H04Rik | 1.846E-04 | 1.76  |
| Mettl8        | 3.689E-03 | 1.56  |
| Elmod1        | 6.355E-03 | 0.47  |
| Hnr           | 2.968E-02 | 0.34  |
| Rapgef5       | 4.640E-03 | 1.57  |
| Acacb         | 1.900E-06 | 0.13  |
| Ncapg2        | 1.807E-05 | 2.38  |
| Lce3b         | 4.203E-03 | 7.68  |
| Igsf3         | 1.858E-03 | 2.12  |
| Sln           | 3.414E-02 | 0.02  |
| Tmcc2         | 3.298E-03 | 0.60  |



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| Abhd14b       | 1.433E-06 | 0.42  |
| Arsb          | 1.240E-04 | 0.38  |
| 4933440N22Rik | 2.408E-02 | 1.87  |
| Lce1c         | 1.095E-03 | 0.23  |
| Kank3         | 1.650E-03 | 0.62  |
| 6230427J02Rik | 4.584E-04 | 1.54  |
| Vwa1          | 9.787E-06 | 2.43  |
| Lce1f         | 2.291E-03 | 0.44  |
| Rassf4        | 3.297E-05 | 0.10  |
| Cox10         | 9.940E-06 | 1.77  |
| Sprr2i        | 2.350E-02 | 12.19 |
| Cmklr1        | 2.194E-06 | 0.21  |
| Slc35f2       | 2.493E-02 | 1.92  |
| Abhd14a       | 1.352E-03 | 1.60  |
| Sprr2d        | 7.563E-03 | 6.44  |
| Zfand4        | 4.345E-03 | 2.17  |
| Bag2          | 4.710E-05 | 4.77  |
| Lyn           | 1.684E-04 | 0.33  |
| Tmc7          | 1.556E-06 | 7.76  |
| Adrbk2        | 1.201E-03 | 0.41  |
| Cilp          | 1.589E-04 | 0.04  |
| Sestd1        | 1.437E-03 | 0.49  |
| Pelo          | 5.475E-04 | 2.20  |
| Hsd3b7        | 3.891E-04 | 0.29  |
| Setd1a        | 1.802E-04 | 1.68  |
| S100a13       | 1.627E-04 | 0.51  |
| Prox2         | 1.653E-03 | 1.78  |
| Tnfrsf14      | 8.836E-03 | 0.42  |
| Ctf1          | 7.408E-03 | 2.32  |
| lkbke         | 8.931E-05 | 0.66  |
| Grap2         | 6.546E-03 | 0.50  |
| Gnl3          | 5.355E-04 | 1.65  |
| Gjb5          | 1.821E-02 | 0.53  |
| Gjb3          | 1.949E-04 | 0.35  |
| Slc5a10       | 4.353E-02 | 2.25  |
| Fam83g        | 4.762E-02 | 1.57  |
| Esm1          | 5.011E-05 | 17.69 |
| Tsen2         | 3.182E-03 | 1.53  |
| Dennd4b       | 1.731E-05 | 0.39  |
| Nfkbi1        | 2.765E-05 | 1.87  |
| Mfap4         | 2.494E-03 | 0.27  |
| Zfp532        | 6.302E-05 | 1.68  |
| Mybph         | 3.419E-02 | 0.42  |
| Dctpp1        | 6.985E-04 | 2.25  |
| Hoxd4         | 3.735E-05 | 0.41  |
| Tbc1d8b       | 5.290E-04 | 1.57  |
| Faim3         | 6.079E-04 | 6.66  |
| Abcb4         | 8.149E-04 | 0.35  |
| Tfap2e        | 2.873E-02 | 1.92  |
| Mustn1        | 1.440E-06 | 0.15  |
| Leo1          | 1.818E-05 | 1.90  |
| Clspn         | 2.386E-07 | 2.90  |
| Prdm10        | 1.277E-04 | 1.86  |
| Acn9          | 1.693E-02 | 1.78  |
| Sun2          | 1.458E-05 | 0.52  |
| Acot5         | 7.994E-03 | 0.11  |
| Gm16516       | 1.155E-02 | 1.59  |
| 4632404H12Rik | 2.273E-02 | 1.55  |
| lpo11         | 8.977E-03 | 1.67  |
| Hirip3        | 3.312E-04 | 3.15  |
| Pbxip1        | 7.182E-06 | 0.26  |
| Oscp1         | 2.102E-02 | 1.67  |
| Maff          | 1.351E-02 | 1.98  |
| Alkbh5        | 1.342E-04 | 1.63  |
| Wdr55         | 3.238E-04 | 1.86  |
| Dcst1         | 6.627E-04 | 2.09  |
| Zc3h12a       | 9.536E-03 | 2.01  |
| Npl           | 7.416E-03 | 0.49  |
| Jph1          | 5.573E-03 | 0.53  |
| Mapk6         | 1.927E-03 | 3.03  |
| Obfc1         | 1.574E-02 | 1.80  |
| Ppp1r3a       | 3.160E-07 | 0.01  |
| Trafd1        | 2.321E-02 | 0.62  |
| Wdr74         | 5.151E-03 | 1.65  |
| Ttc9          | 4.536E-04 | 4.29  |
| Apobr         | 1.069E-03 | 0.34  |
| Hebp1         | 6.515E-04 | 0.53  |
| Exog          | 9.374E-05 | 2.17  |
| 1700015E13Rik | 4.759E-03 | 3.05  |
| Gpr153        | 2.508E-02 | 0.54  |
| Hecw2         | 4.767E-05 | 1.70  |
| Mcts2         | 1.733E-03 | 1.59  |
| Gpr151        | 9.201E-05 | 2.68  |
| Flt3          | 3.660E-03 | 0.46  |
| Trim72        | 1.378E-07 | 0.20  |
| Serpinb6b     | 8.224E-03 | 0.52  |
| Trp53rk       | 1.389E-02 | 1.73  |
| Gm9776        | 3.208E-03 | 2.42  |
| Abra          | 1.861E-04 | 0.17  |
| Egflam        | 7.252E-03 | 0.51  |
| 9930038B18Rik | 2.342E-02 | 4.44  |
| Gng2          | 4.692E-05 | 0.40  |
| Klhl6         | 1.509E-04 | 0.44  |
| Tmem194b      | 4.695E-03 | 1.62  |
| Ptgir         | 1.227E-03 | 0.09  |
| Fam89a        | 4.929E-03 | 0.59  |
| Synpo         | 1.867E-03 | 1.69  |



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|---------------|-----------|-------|
| Il17re        | 9.574E-03 | 2.48  |
| Mmp1a         | 3.967E-02 | 47.82 |
| Hic1          | 3.152E-02 | 0.48  |
| Arl11         | 4.662E-05 | 0.13  |
| Lor           | 3.478E-03 | 0.33  |
| 4732471D19Rik | 6.571E-03 | 1.78  |
| Rfesd         | 3.563E-03 | 1.58  |
| Fam129c       | 3.252E-02 | 1.64  |
| Exoc3l        | 5.783E-06 | 4.56  |
| Pigv          | 4.417E-02 | 1.69  |
| Uevld         | 7.190E-03 | 1.51  |
| Gm5531        | 3.733E-02 | 2.26  |
| B3galnt1      | 2.782E-05 | 0.13  |
| Pcdhb19       | 1.002E-05 | 4.24  |
| Fbrs1         | 1.101E-03 | 1.55  |
| Rhbd12        | 3.670E-02 | 1.87  |
| A030009H04Rik | 1.392E-04 | 0.21  |
| Psap1         | 2.406E-04 | 0.14  |
| E130012A19Rik | 1.542E-04 | 8.97  |
| Pcdhb12       | 3.164E-02 | 2.85  |
| Gm9782        | 3.608E-03 | 4.46  |
| Gimap5        | 4.112E-03 | 0.54  |
| Pars2         | 4.496E-05 | 2.20  |
| Acpl2         | 5.304E-03 | 1.97  |
| Ecm2          | 4.271E-06 | 0.30  |
| Kcns3         | 8.293E-04 | 2.76  |
| Fam25c        | 6.110E-03 | 0.30  |
| Col6a6        | 7.636E-05 | 0.02  |
| B430306N03Rik | 2.663E-04 | 0.09  |
| Gm14492       | 4.160E-06 | 0.18  |
| Clec4a3       | 9.704E-06 | 0.12  |
| Zmym1         | 2.989E-03 | 1.80  |
| Slc36a4       | 2.124E-02 | 0.65  |
| S1pr2         | 2.273E-04 | 0.45  |
| Ccdc84        | 1.896E-04 | 1.57  |
| Ncmmap        | 1.576E-02 | 0.43  |
| Wdfy3         | 1.476E-04 | 0.60  |
| Naalad2       | 7.763E-05 | 0.33  |
| Ccrl2         | 2.220E-02 | 0.41  |
| Orai3         | 2.649E-05 | 0.43  |
| Cep164        | 3.164E-06 | 1.80  |
| 2900052L18Rik | 7.620E-03 | 1.90  |
| Gls2          | 9.666E-08 | 6.13  |
| Gpr133        | 1.078E-05 | 0.12  |
| Mrpl50        | 9.133E-04 | 1.69  |
| Pcdhb21       | 5.490E-06 | 4.26  |
| Rel12         | 4.999E-04 | 2.37  |
| Tmem20        | 3.643E-03 | 1.54  |
| Irf2bp1       | 4.625E-03 | 1.52  |
| Ccdc141       | 3.943E-04 | 0.29  |
| Als2cl        | 2.938E-03 | 1.90  |
| Krt13         | 2.830E-02 | 19.18 |
| Fmn1          | 5.247E-05 | 0.48  |
| Pcdhb14       | 6.949E-04 | 2.31  |
| Gpr22         | 3.016E-02 | 1.59  |
| S100a1        | 5.751E-05 | 0.13  |
| Lmod3         | 1.655E-05 | 0.02  |
| Ccdc166       | 1.853E-04 | 3.05  |
| 1810024B03Rik | 2.341E-02 | 2.33  |
| Nkrf          | 8.384E-07 | 2.43  |
| Naa38         | 1.988E-03 | 1.71  |
| Tnip3         | 3.078E-02 | 0.51  |
| Bcl2l15       | 1.822E-02 | 2.97  |
| Gpr146        | 4.414E-07 | 0.32  |
| Cdc25c        | 8.964E-08 | 4.34  |
| Vsig4         | 7.168E-05 | 0.07  |
| Dnajc21       | 4.560E-02 | 1.74  |
| Nhlrc1        | 5.401E-04 | 2.72  |
| Osbpl1a       | 5.144E-04 | 0.38  |
| Crb3          | 6.445E-03 | 1.61  |
| Cdkn2a        | 3.061E-02 | 1.81  |
| Mab21l3       | 7.753E-04 | 2.66  |
| 1700001O22Rik | 3.827E-02 | 2.48  |
| Cxcr7         | 1.767E-02 | 1.88  |
| Aplnr         | 3.504E-02 | 1.55  |
| Alkbh2        | 5.038E-04 | 2.54  |
| P2ry4         | 1.189E-03 | 0.21  |
| Tmem74b       | 4.143E-02 | 10.25 |
| Dsg2          | 6.371E-03 | 1.81  |
| Adig          | 5.192E-03 | 0.04  |
| Sptssa        | 7.030E-03 | 0.64  |
| Klk12         | 1.409E-02 | 7.45  |
| Zfp507        | 1.741E-03 | 1.58  |
| Rin3          | 4.179E-05 | 0.43  |
| Shisa2        | 4.726E-07 | 0.05  |
| Tnfaijp8l1    | 4.853E-02 | 1.61  |
| AB041803      | 7.133E-05 | 0.47  |
| Ascc1         | 1.557E-03 | 1.68  |
| Bod1          | 5.894E-04 | 1.71  |
| 9930012K11Rik | 1.138E-02 | 0.43  |
| Cage1         | 1.399E-02 | 2.18  |
| Acp1          | 4.797E-03 | 1.61  |
| Tlr7          | 3.270E-06 | 0.13  |
| Dnd1          | 4.011E-04 | 2.05  |
| Zbtb39        | 5.128E-04 | 1.75  |
| Cnrip1        | 1.554E-04 | 0.15  |
| Csrnp2        | 1.534E-05 | 2.11  |



|               |           |       |
|---------------|-----------|-------|
| Pard6b        | 2.968E-02 | 2.29  |
| Fzd1          | 9.376E-04 | 0.54  |
| Zfp612        | 1.316E-02 | 2.69  |
| Ly6k          | 4.230E-02 | 9.99  |
| Gm13749       | 1.848E-02 | 10.29 |
| Tmem201       | 3.976E-03 | 2.30  |
| Palb2         | 2.069E-05 | 2.78  |
| Slc38a6       | 2.571E-04 | 0.63  |
| Klk14         | 3.695E-02 | 6.58  |
| Defb1         | 1.060E-02 | 2.60  |
| Abca6         | 5.031E-07 | 0.05  |
| Trmt10c       | 3.832E-05 | 1.85  |
| AF251705      | 1.217E-04 | 0.19  |
| Shb           | 5.956E-03 | 1.81  |
| Tlr1          | 1.045E-03 | 0.35  |
| Lsm11         | 2.360E-06 | 2.47  |
| Ankrd50       | 2.015E-05 | 2.24  |
| Syt16         | 5.682E-04 | 20.59 |
| Rassf9        | 3.620E-03 | 0.23  |
| Klhl31        | 1.182E-05 | 0.02  |
| Mylk4         | 6.727E-03 | 0.05  |
| Pp2d1         | 1.925E-05 | 1.64  |
| Fbxo48        | 5.384E-07 | 4.71  |
| Napepld       | 2.645E-02 | 0.58  |
| E130304I02Rik | 1.572E-02 | 2.95  |
| Fzd5          | 3.585E-05 | 1.76  |
| Tubg2         | 9.070E-03 | 3.18  |
| Acer1         | 9.269E-03 | 0.40  |
| Lrln4         | 9.842E-04 | 2.66  |
| Kcng3         | 1.771E-02 | 6.32  |
| Pcdhb7        | 1.932E-02 | 2.82  |
| E130308A19Rik | 7.784E-05 | 2.17  |
| S1pr1         | 7.279E-04 | 0.57  |
| Arhgef37      | 1.262E-02 | 0.58  |
| Dmd           | 9.014E-05 | 0.38  |
| Rassf8        | 2.191E-02 | 0.25  |
| Pigw          | 6.139E-05 | 2.24  |
| AI467606      | 1.079E-04 | 0.20  |
| Shroom2       | 3.028E-04 | 2.56  |
| Nudt18        | 3.950E-02 | 1.61  |
| Hs6st1        | 2.150E-04 | 1.82  |
| Med26         | 4.960E-05 | 2.04  |
| Zfp574        | 4.414E-03 | 1.78  |
| Zfp691        | 2.842E-02 | 1.65  |
| Cenph         | 1.005E-03 | 3.60  |
| Insig1        | 1.641E-02 | 0.58  |
| Lhfp12        | 3.033E-04 | 0.08  |
| Sowahb        | 2.538E-02 | 2.92  |
| Fahd1         | 3.994E-02 | 1.55  |
| 5430407P10Rik | 9.092E-03 | 2.69  |
| Cenpe         | 1.046E-07 | 3.81  |
| Zfp423        | 1.677E-05 | 0.39  |
| Sh2d5         | 5.837E-05 | 21.93 |
| Tnfrsf26      | 3.501E-02 | 0.49  |
| Rbm15b        | 2.012E-06 | 1.53  |
| Tmem88        | 1.185E-02 | 1.54  |
| Cxcr4         | 1.747E-02 | 0.49  |
| Epcam         | 3.425E-03 | 0.38  |
| Trim39        | 1.121E-02 | 1.63  |
| 2810002D19Rik | 8.094E-03 | 2.00  |
| Lce3c         | 4.477E-03 | 5.95  |
| Niacr1        | 9.459E-04 | 2.03  |
| A930002H24Rik | 7.889E-05 | 5.28  |
| Sprr3         | 1.947E-02 | 71.11 |
| Krt14         | 7.321E-03 | 2.37  |
| Rnf113a2      | 1.727E-02 | 1.52  |
| Sprr4         | 1.825E-02 | 0.05  |
| Penk          | 4.774E-03 | 0.56  |
| Glb1          | 3.052E-03 | 0.61  |
| Zfp553        | 3.744E-04 | 1.95  |
| Esf1          | 2.333E-02 | 1.54  |
| Mtus1         | 1.228E-06 | 0.28  |
| Pcdhb10       | 1.116E-02 | 3.92  |
| Pid1          | 8.484E-05 | 0.16  |
| Smtnl2        | 2.122E-03 | 3.59  |
| Spred2        | 8.959E-07 | 2.32  |
| Pcdhb4        | 3.756E-02 | 3.24  |
| Mms22l        | 8.249E-05 | 2.28  |
| Tssc4         | 1.733E-04 | 1.68  |
| Zfp764        | 6.718E-03 | 1.72  |
| Fam179a       | 2.041E-02 | 2.71  |
| Ifitm10       | 8.209E-05 | 2.80  |
| Ptprcap       | 2.203E-03 | 0.49  |
| Serpinb9      | 2.858E-03 | 0.51  |
| A430105I19Rik | 8.933E-03 | 1.96  |
| Adra1a        | 5.923E-05 | 0.02  |
| 6330416G13Rik | 6.576E-05 | 0.36  |
| Clec14a       | 7.334E-04 | 0.53  |
| Sdpr          | 2.515E-05 | 0.17  |
| Ing1          | 3.326E-03 | 1.55  |
| C2cd2         | 2.044E-02 | 0.63  |
| Zfp830        | 2.497E-04 | 1.50  |
| Stard5        | 1.355E-03 | 0.50  |
| Fam26f        | 2.203E-02 | 0.19  |
| Sbsn          | 9.602E-03 | 0.45  |
| Tmem229b      | 1.913E-03 | 0.42  |
| Kcnrg         | 7.992E-03 | 1.97  |



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|---------------|-----------|-------|
| E2f8          | 6.897E-05 | 4.01  |
| Pcdhb20       | 1.132E-06 | 4.55  |
| Sprr2g        | 7.027E-03 | 7.09  |
| Pik3r6        | 4.036E-06 | 0.30  |
| Sprr2h        | 7.887E-05 | 4.81  |
| Usp27x        | 1.957E-04 | 2.15  |
| Tusc5         | 6.637E-05 | 0.14  |
| Ankle1        | 1.964E-05 | 4.55  |
| Stxbp6        | 4.207E-03 | 0.24  |
| Ccbe1         | 1.550E-02 | 0.35  |
| Ermp1         | 1.265E-02 | 0.62  |
| Slc25a23      | 7.402E-06 | 0.23  |
| Fam178b       | 2.761E-03 | 3.63  |
| Gm11223       | 9.570E-03 | 1.92  |
| Gjb2          | 1.083E-03 | 7.84  |
| Jrk           | 1.807E-04 | 2.20  |
| Pcdhb17       | 1.157E-03 | 2.61  |
| Rbp1          | 1.408E-02 | 2.00  |
| Yod1          | 4.594E-02 | 0.52  |
| 1700067K01Rik | 3.701E-02 | 2.04  |
| B430212C06Rik | 2.491E-03 | 2.26  |
| Ftsjd1        | 7.413E-04 | 2.15  |
| 5930403N24Rik | 1.011E-02 | 2.00  |
| Scn4b         | 2.172E-08 | 0.09  |
| C1qtnf2       | 1.928E-02 | 0.42  |
| Golph3l       | 3.882E-04 | 0.64  |
| Kctd4         | 1.347E-02 | 0.49  |
| Ar            | 9.987E-04 | 0.24  |
| Zfp526        | 1.441E-04 | 2.01  |
| Fam43a        | 3.305E-02 | 1.57  |
| Zfp319        | 1.507E-02 | 1.67  |
| Zfp518b       | 4.688E-03 | 1.70  |
| Lyrm4         | 3.280E-02 | 1.59  |
| Prr12         | 1.526E-03 | 1.67  |
| Ticrr         | 2.628E-06 | 4.77  |
| Bdh1          | 4.560E-04 | 1.51  |
| Gjb4          | 4.711E-04 | 0.31  |
| Zfp316        | 5.521E-04 | 1.60  |
| Coxc5         | 2.563E-02 | 0.66  |
| Tmem251       | 4.993E-03 | 1.53  |
| Lce1l         | 6.246E-04 | 0.23  |
| Tifa          | 8.277E-06 | 0.37  |
| 0610010O12Rik | 3.249E-03 | 0.58  |
| Kctd11        | 5.104E-03 | 1.57  |
| Gprc5a        | 2.571E-03 | 17.31 |
| Fam83h        | 1.234E-05 | 1.95  |
| Rhoj          | 6.009E-05 | 0.32  |
| 2410016O06Rik | 6.800E-06 | 1.78  |
| Ppp1r3b       | 7.881E-08 | 3.16  |
| Mpeg1         | 3.440E-04 | 0.08  |
| 3110062M04Rik | 2.166E-04 | 2.01  |
| Gchfr         | 3.305E-02 | 0.62  |
| Ddit4l        | 1.394E-02 | 0.16  |
| Fam187b       | 7.876E-03 | 2.05  |
| C230030N03Rik | 3.000E-04 | 3.20  |
| Fbl           | 4.343E-05 | 1.65  |
| Atxn1         | 2.256E-03 | 1.59  |
| Ltb4r1        | 1.494E-03 | 3.40  |
| Mars2         | 6.829E-05 | 1.97  |
| Spsb4         | 9.532E-04 | 0.14  |
| Zfp41         | 6.050E-05 | 1.85  |
| Mipol1        | 6.426E-03 | 2.47  |
| Pcdhb15       | 1.086E-04 | 3.54  |
| D030056L22Rik | 3.924E-03 | 1.66  |
| Tmem164       | 1.981E-05 | 0.47  |
| Cd24a         | 7.022E-03 | 1.88  |
| Zfp654        | 1.298E-04 | 1.56  |
| Tigd5         | 1.549E-06 | 2.12  |
| Neurl3        | 7.672E-03 | 0.53  |
| Dusp18        | 9.136E-04 | 0.20  |
| Fam185a       | 1.584E-02 | 1.67  |
| Ear11         | 2.940E-02 | 0.04  |
| Gm527         | 4.286E-03 | 2.48  |
| Hist1h2be     | 2.204E-03 | 1.85  |
| Sfn           | 1.497E-03 | 1.95  |
| Pcdhb13       | 1.776E-02 | 3.09  |
| Kcne4         | 6.446E-04 | 0.22  |
| B3gnt1        | 4.827E-03 | 1.62  |
| Ctdspl        | 2.005E-03 | 1.63  |
| Flrt2         | 1.046E-02 | 1.65  |
| Gpr68         | 1.332E-03 | 0.47  |
| Rexo1         | 2.996E-05 | 1.51  |
| Cmya5         | 1.721E-09 | 0.01  |
| Fam180a       | 1.198E-02 | 0.12  |
| Antxr1        | 9.784E-03 | 4.00  |
| Fam132b       | 5.745E-04 | 2.41  |
| A530099J19Rik | 1.503E-06 | 0.05  |
| Rnf152        | 4.445E-03 | 2.44  |
| Mis18bp1      | 2.582E-06 | 2.84  |
| Mmp10         | 9.257E-04 | 8.60  |
| Tyw3          | 8.108E-03 | 2.05  |
| Nxpe5         | 5.189E-05 | 0.11  |
| Zfp235        | 6.841E-03 | 1.58  |
| Fgfbp3        | 4.893E-02 | 1.66  |
| Tssk6         | 6.123E-03 | 2.93  |
| Trpt1         | 1.558E-02 | 1.56  |
| Gpr82         | 3.087E-04 | 1.59  |



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|---------------|-----------|-------|
| Zfp828        | 3.178E-03 | 1.65  |
| Fcgbp         | 1.828E-02 | 0.34  |
| Fbxo40        | 9.087E-06 | 0.10  |
| Rnf150        | 2.744E-04 | 0.23  |
| Zc3hav1l      | 8.815E-03 | 2.53  |
| Fancb         | 2.452E-04 | 1.90  |
| Lrrc49        | 5.506E-03 | 1.60  |
| Phf13         | 6.798E-03 | 1.68  |
| Sned1         | 2.763E-08 | 0.08  |
| 9330154K18Rik | 2.129E-02 | 1.71  |
| Trim16        | 1.674E-03 | 1.90  |
| Cdca4         | 9.926E-06 | 1.84  |
| Gimap6        | 1.001E-03 | 0.55  |
| A4galt        | 1.129E-03 | 0.29  |
| Ang2          | 7.478E-03 | 0.44  |
| Pcdhb16       | 1.503E-03 | 2.97  |
| 4933428G20Rik | 8.329E-03 | 1.95  |
| Prrg1         | 9.931E-04 | 0.47  |
| Timm8a1       | 7.446E-04 | 1.92  |
| Zfp473        | 5.335E-04 | 4.76  |
| Isg20l2       | 2.574E-07 | 1.56  |
| Tenn4         | 2.844E-03 | 2.16  |
| Lmod1         | 1.472E-02 | 0.54  |
| 4632415L05Rik | 1.285E-02 | 1.62  |
| Kctd12        | 5.244E-04 | 0.47  |
| Entpd1        | 6.064E-05 | 0.27  |
| Nat8l         | 1.081E-03 | 7.68  |
| Selplg        | 2.434E-05 | 0.27  |
| Efcab4a       | 4.146E-07 | 0.29  |
| Fbxo10        | 7.366E-04 | 1.72  |
| Rnf149        | 1.083E-03 | 0.58  |
| A930001N09Rik | 9.768E-05 | 0.57  |
| Ckap2l        | 1.237E-05 | 3.93  |
| Lhfp          | 1.285E-02 | 0.51  |
| Pcdhb18       | 6.017E-04 | 4.46  |
| Selrc1        | 4.486E-05 | 1.96  |
| Omd           | 9.837E-03 | 0.54  |
| Pdp2          | 9.713E-03 | 1.92  |
| Fgfbp1        | 8.593E-03 | 2.41  |
| F2r           | 3.898E-02 | 0.59  |
| Osr1          | 2.663E-04 | 0.14  |
| Gli2          | 8.974E-04 | 2.70  |
| B330016D10Rik | 8.507E-05 | 2.22  |
| Mlf1          | 2.408E-03 | 0.29  |
| Nupl2         | 8.055E-03 | 1.57  |
| 2210020M01Rik | 6.422E-03 | 0.64  |
| Ccdc57        | 2.827E-04 | 2.26  |
| Sprr1b        | 5.084E-03 | 3.18  |
| 6530418L21Rik | 1.117E-03 | 1.93  |
| Cxcr1         | 3.212E-03 | 0.07  |
| 8430408G22Rik | 2.278E-03 | 0.48  |
| Nrip1         | 1.989E-04 | 1.68  |
| Tyw5          | 9.291E-04 | 1.63  |
| Cxcr6         | 1.059E-03 | 0.47  |
| Amica1        | 5.890E-05 | 0.32  |
| Phldb1        | 5.249E-03 | 0.55  |
| Tmem252       | 4.379E-04 | 0.44  |
| Gm9828        | 2.398E-03 | 2.69  |
| Gm6377        | 5.175E-03 | 0.49  |
| Rhno1         | 5.935E-04 | 1.63  |
| Mex3d         | 1.418E-04 | 2.60  |
| Tbc1d12       | 1.688E-02 | 1.55  |
| Fndc9         | 8.305E-03 | 0.41  |
| Foxo3         | 1.836E-05 | 0.65  |
| Tmprss11f     | 8.942E-03 | 0.41  |
| Skint10       | 5.401E-04 | 0.23  |
| Serp1nb13     | 5.339E-03 | 0.28  |
| Pthlh         | 2.909E-03 | 34.75 |
| P2ry6         | 4.413E-06 | 0.26  |
| Slc35e4       | 2.511E-04 | 0.50  |
| Arhgap30      | 2.748E-05 | 0.20  |
| Cdk5r1        | 4.131E-03 | 2.13  |
| Rnf24         | 1.398E-03 | 1.68  |
| Efna5         | 2.104E-03 | 3.06  |
| Zfp689        | 1.947E-03 | 2.07  |
| Cdca2         | 8.285E-06 | 2.99  |
| Prex2         | 6.552E-04 | 0.53  |
| Atxn7l2       | 9.569E-07 | 2.31  |
| Ndnf          | 1.619E-04 | 0.15  |
| Clec4a1       | 6.291E-05 | 0.24  |
| Mterfd3       | 1.485E-03 | 1.60  |
| Armxc3        | 8.795E-06 | 0.29  |
| Bmyc          | 1.109E-02 | 1.83  |
| Ccr2          | 7.341E-05 | 0.17  |
| Agtr1a        | 3.470E-06 | 0.07  |
| C5ar1         | 8.758E-04 | 0.18  |
| Flg2          | 9.339E-04 | 0.08  |
| Nrap          | 1.001E-07 | 0.02  |
| Rgag4         | 4.372E-04 | 0.17  |
| Mblac1        | 3.853E-04 | 2.20  |
| Lix1l         | 2.511E-03 | 0.47  |
| Prmt6         | 1.588E-07 | 1.88  |
| Syt12         | 1.416E-02 | 1.58  |
| Setd8         | 6.662E-05 | 1.74  |
| Tenn2         | 1.486E-03 | 3.16  |
| Rarres1       | 2.550E-04 | 0.09  |
| Chchd10       | 4.480E-06 | 0.35  |



|               |           |        |
|---------------|-----------|--------|
| Aff4          | 4.579E-02 | 1.56   |
| Proser1       | 4.845E-03 | 1.62   |
| Htr1b         | 1.086E-04 | 3.85   |
| Cdc42ep1      | 4.907E-07 | 2.57   |
| Hist1h1a      | 6.638E-05 | 2.38   |
| Clip1         | 7.192E-05 | 0.59   |
| Polr1a        | 8.530E-05 | 1.70   |
| Aknad1        | 6.436E-04 | 3.81   |
| Zfa           | 2.909E-02 | 1.96   |
| Ccdc69        | 9.029E-05 | 0.39   |
| Lce1h         | 8.866E-04 | 0.30   |
| Zbtb45        | 8.208E-03 | 1.68   |
| Omg           | 4.891E-03 | 1.52   |
| Tifab         | 3.679E-04 | 0.33   |
| Zbtb5         | 1.233E-03 | 1.56   |
| Cyp2g1        | 1.420E-02 | 0.11   |
| Fam109b       | 4.115E-02 | 0.65   |
| Ucn2          | 2.050E-03 | 4.50   |
| Lig4          | 1.608E-04 | 2.19   |
| Prss46        | 1.367E-03 | 0.05   |
| Mmp12         | 5.576E-04 | 0.06   |
| Arhgap15      | 1.158E-05 | 0.23   |
| Zfp280b       | 2.193E-03 | 2.04   |
| Fzd4          | 1.993E-06 | 0.34   |
| Zbtb12        | 4.140E-03 | 1.97   |
| Ceacam19      | 2.522E-02 | 0.55   |
| Arl4c         | 8.316E-04 | 0.56   |
| Fam26e        | 1.050E-02 | 0.06   |
| Rlf           | 1.136E-03 | 1.55   |
| Mettl21d      | 1.630E-03 | 1.79   |
| Rasl11b       | 2.496E-02 | 0.53   |
| Slc35c1       | 3.100E-02 | 1.60   |
| H2afx         | 1.605E-03 | 3.36   |
| Lrrc4         | 2.218E-02 | 1.73   |
| Rpp38         | 1.262E-04 | 2.30   |
| Ccdc137       | 2.485E-04 | 1.77   |
| Glt1d1        | 6.981E-05 | 3.75   |
| Skint9        | 5.765E-04 | 0.11   |
| Lrrc25        | 3.426E-05 | 0.23   |
| Pitpnb        | 8.390E-05 | 1.72   |
| Amz1          | 5.383E-03 | 0.39   |
| Bex1          | 3.980E-03 | 0.07   |
| Agmo          | 3.173E-05 | 0.27   |
| Grrp1         | 1.872E-04 | 0.58   |
| Gsg2          | 1.541E-06 | 2.01   |
| F2rl3         | 3.290E-03 | 3.75   |
| Otop2         | 7.592E-03 | 7.23   |
| Pla2g4e       | 3.536E-02 | 1.61   |
| Cxcr3         | 1.087E-04 | 0.28   |
| Gja4          | 7.732E-05 | 1.55   |
| Heatr1        | 7.756E-06 | 1.69   |
| D8Erttd82e    | 1.887E-02 | 4.21   |
| Rictor        | 1.820E-02 | 1.54   |
| Synpo2        | 8.844E-08 | 0.11   |
| Ndufaf6       | 1.479E-04 | 2.07   |
| Lgals3        | 3.182E-04 | 0.29   |
| Sprr1a        | 3.764E-02 | 1.59   |
| Kif7          | 3.593E-02 | 1.83   |
| Tcf19         | 1.520E-06 | 2.27   |
| Mrgprb2       | 4.108E-07 | 0.09   |
| Krt78         | 4.211E-02 | 0.47   |
| Hyls1         | 1.101E-06 | 2.49   |
| Mmp13         | 8.409E-07 | 9.49   |
| Fam78a        | 3.621E-03 | 0.44   |
| 1700019N12Rik | 2.433E-02 | 4.79   |
| Sprr2f        | 6.368E-03 | 19.25  |
| Tmem150c      | 5.479E-03 | 2.98   |
| Vstm4         | 2.486E-05 | 0.26   |
| Ccdc75        | 1.966E-03 | 1.50   |
| 2310061I04Rik | 5.003E-03 | 1.71   |
| Ftl1          | 1.253E-04 | 0.15   |
| 4932442E05Rik | 1.162E-02 | 1.67   |
| Zbtb26        | 1.235E-02 | 1.90   |
| Plekha2       | 7.686E-05 | 0.18   |
| Ptges         | 3.411E-04 | 2.40   |
| Defb6         | 5.492E-03 | 0.04   |
| Tmem37        | 1.261E-04 | 0.23   |
| Ccdc126       | 2.442E-02 | 1.61   |
| B3galt6       | 1.186E-03 | 1.97   |
| Hist1h2ba     | 2.873E-02 | 2.38   |
| Muc15         | 3.270E-02 | 0.48   |
| Tmem125       | 2.704E-03 | 2.48   |
| Clrn3         | 2.029E-03 | 126.82 |
| Tatdn1        | 4.380E-03 | 1.66   |
| Ankrd37       | 7.291E-03 | 3.09   |
| P2ry10        | 1.473E-03 | 0.51   |
| 4933403G14Rik | 2.577E-02 | 3.10   |
| Sgms2         | 2.788E-02 | 0.51   |
| Hist2h2bb     | 1.202E-03 | 2.07   |
| Gja1          | 6.755E-05 | 4.61   |
| D330012F22Rik | 7.677E-07 | 2.28   |
| Hs3st1        | 1.689E-02 | 4.67   |
| Zfp11         | 2.320E-04 | 1.64   |
| Olfr11        | 1.137E-06 | 0.05   |
| Gprc5c        | 1.816E-07 | 0.07   |
| Mb21d2        | 7.947E-06 | 2.18   |
| 4930579K19Rik | 3.795E-02 | 2.55   |



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|---------------|-----------|-------|
| Gm4847        | 1.456E-02 | 0.08  |
| Mblac2        | 3.456E-02 | 1.54  |
| Camk2n2       | 1.392E-02 | 3.44  |
| Adnp          | 1.042E-03 | 1.96  |
| Cited1        | 1.623E-03 | 71.00 |
| Eml5          | 5.377E-03 | 1.53  |
| Rpusd3        | 6.088E-04 | 1.99  |
| Fam174a       | 9.413E-06 | 0.60  |
| Gpr183        | 1.898E-03 | 0.58  |
| Ercc6l        | 1.561E-05 | 4.15  |
| Tceanc        | 2.152E-03 | 2.00  |
| Fam83a        | 4.109E-05 | 2.54  |
| Gen1          | 6.702E-06 | 4.36  |
| Msrb3         | 2.791E-04 | 0.21  |
| 4930422G04Rik | 3.570E-05 | 2.36  |
| 1500011K16Rik | 1.935E-03 | 1.55  |
| Pcdh19        | 3.800E-03 | 0.44  |
| Nup160        | 3.159E-03 | 1.78  |
| 2900026A02Rik | 1.493E-02 | 1.61  |
| Zfp52         | 1.060E-03 | 2.06  |
| Rab11fip5     | 5.253E-03 | 0.60  |
| Plekhn3       | 1.416E-06 | 0.45  |
| Spryd4        | 6.493E-05 | 1.58  |
| Zfp46         | 4.288E-02 | 1.60  |
| Ncald         | 2.570E-05 | 0.26  |
| Kif18b        | 1.381E-05 | 4.22  |
| Flrt3         | 5.484E-04 | 2.93  |
| Plagl2        | 2.175E-02 | 1.60  |
| Bbs12         | 7.201E-04 | 2.24  |
| Spn           | 4.732E-04 | 0.37  |
| Ufsp1         | 7.974E-03 | 1.73  |
| Siglech       | 1.481E-02 | 0.47  |
| Wdfy4         | 2.056E-05 | 0.11  |
| Arhgef39      | 6.326E-06 | 3.27  |
| Rps19bp1      | 2.614E-04 | 1.64  |
| Mical3        | 3.090E-03 | 1.62  |
| B3gnt2        | 2.284E-02 | 1.60  |
| AU021092      | 2.731E-03 | 1.55  |
| Dcun1d4       | 3.756E-02 | 1.70  |
| Senp8         | 4.486E-04 | 2.25  |
| BC068281      | 2.503E-02 | 1.58  |
| Rinl          | 1.045E-03 | 0.44  |
| Ttn           | 2.777E-08 | 0.01  |
| 1100001G20Rik | 4.717E-04 | 0.08  |
| Mest          | 1.642E-04 | 4.73  |
| Cd209f        | 9.855E-06 | 0.01  |
| Sox6          | 4.210E-02 | 1.76  |
| Spats2        | 1.235E-05 | 1.88  |
| 5031410I06Rik | 3.655E-02 | 21.45 |
| Prdm9         | 1.468E-02 | 1.52  |
| Erich1        | 1.370E-03 | 1.61  |
| Lax1          | 3.535E-03 | 0.49  |
| Btla          | 3.390E-06 | 0.27  |
| Slc6a7        | 9.295E-05 | 0.03  |
| Pfdn4         | 1.754E-03 | 1.89  |
| Pard3b        | 7.228E-07 | 0.14  |
| Dock8         | 1.697E-07 | 0.35  |
| Rgs14         | 7.109E-05 | 0.40  |
| Rasal3        | 6.811E-04 | 0.29  |
| Gm9869        | 9.187E-04 | 3.56  |
| Ppap2c        | 3.778E-04 | 1.83  |
| Gm650         | 1.620E-02 | 1.87  |
| Pld4          | 6.727E-05 | 0.17  |
| 1700084E18Rik | 2.085E-02 | 3.34  |
| Gm13476       | 3.640E-05 | 0.20  |
| Zfp622        | 4.362E-03 | 1.65  |
| Fpr2          | 1.637E-03 | 0.34  |
| 5330438D12Rik | 3.713E-07 | 2.39  |
| Cdc42se2      | 3.207E-04 | 0.53  |
| Doc2a         | 4.625E-05 | 3.23  |
| Ankrd44       | 1.032E-06 | 0.28  |
| 9930013L23Rik | 1.076E-04 | 3.26  |
| 1700109F18Rik | 4.182E-02 | 0.59  |
| Actn2         | 1.856E-04 | 0.02  |
| Lrrc33        | 7.303E-08 | 0.17  |
| Ccdc171       | 1.998E-02 | 1.92  |
| 2610001J05Rik | 1.571E-02 | 1.55  |
| Prmt1         | 3.863E-03 | 2.03  |
| Bmpr1b        | 8.565E-05 | 6.29  |
| Zfp961        | 3.137E-04 | 2.08  |
| Atp6v1a       | 6.744E-03 | 0.61  |
| C130026I21Rik | 2.554E-04 | 0.27  |
| Cherp         | 1.758E-04 | 2.10  |
| Nav2          | 4.850E-02 | 2.01  |
| Robo2         | 1.598E-02 | 2.16  |
| Nup188        | 8.304E-03 | 1.56  |
| Pbx1          | 4.072E-03 | 1.75  |
| Magi3         | 1.253E-04 | 2.39  |
| Gan           | 7.754E-03 | 0.50  |
| D930048N14Rik | 6.652E-03 | 1.52  |
| Hist1h1d      | 1.618E-04 | 2.34  |
| Asap2         | 2.717E-03 | 2.73  |
| 5830454E08Rik | 2.425E-02 | 2.20  |
| Gm9887        | 3.228E-03 | 2.17  |
| 5430435G22Rik | 5.240E-04 | 0.25  |
| Zfp608        | 5.035E-04 | 0.39  |
| Repin1        | 1.393E-05 | 0.27  |



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|---------------|-----------|-------|
| A630001G21Rik | 9.493E-03 | 0.32  |
| 4833418N17Rik | 1.647E-04 | 5.72  |
| 1700030K09Rik | 1.190E-03 | 2.12  |
| Nup107        | 5.566E-04 | 2.12  |
| Cysl1r1       | 2.735E-05 | 0.29  |
| Sae1          | 9.050E-04 | 1.56  |
| Junb          | 5.800E-04 | 1.98  |
| Reep1         | 6.881E-03 | 3.83  |
| Prkcb         | 3.347E-06 | 0.20  |
| Ubxn8         | 5.356E-05 | 1.95  |
| Lamb2         | 4.118E-04 | 0.48  |
| Prkg1         | 1.342E-03 | 0.39  |
| Arhgef15      | 1.200E-03 | 2.13  |
| Mrpl35        | 8.059E-04 | 1.96  |
| Cyp2f2        | 1.198E-06 | 0.01  |
| Uba2          | 1.569E-04 | 1.55  |
| Aph1c         | 2.437E-04 | 0.27  |
| Jam2          | 2.516E-06 | 0.32  |
| Clec12a       | 5.101E-07 | 0.11  |
| 9230110C19Rik | 1.744E-02 | 1.97  |
| Lins          | 1.465E-04 | 1.96  |
| Socs3         | 9.288E-05 | 1.89  |
| Rnf26         | 7.138E-05 | 1.98  |
| Fes           | 7.554E-06 | 0.33  |
| Gpr21         | 9.872E-03 | 1.63  |
| Bcl3          | 8.996E-03 | 1.65  |
| Gm9897        | 9.870E-03 | 1.75  |
| Dand5         | 2.660E-02 | 1.82  |
| Aldh1a1       | 4.243E-04 | 0.20  |
| Ddx10         | 5.468E-05 | 1.87  |
| Pom121        | 2.279E-04 | 2.86  |
| Slamf8        | 1.020E-03 | 0.11  |
| Phgdh         | 5.514E-05 | 1.66  |
| Cbx7          | 2.497E-05 | 0.43  |
| Hunk          | 4.909E-03 | 8.55  |
| Kdm3a         | 4.681E-03 | 1.74  |
| Tnfaip6       | 3.824E-03 | 0.17  |
| Tcf4          | 2.512E-04 | 0.51  |
| Nrd1          | 8.471E-03 | 0.61  |
| Cstf2t        | 4.461E-04 | 0.41  |
| 3110082I17Rik | 5.874E-06 | 2.07  |
| Ier2          | 2.238E-03 | 1.59  |
| Tll1          | 1.251E-02 | 3.73  |
| Plxnb1        | 1.402E-04 | 2.47  |
| Krt42         | 3.489E-03 | 4.16  |
| 2700023E23Rik | 2.503E-05 | 1.64  |
| BC048403      | 2.130E-04 | 1.89  |
| Dpep2         | 4.041E-04 | 0.18  |
| Mast1         | 1.491E-02 | 1.57  |
| Nebi          | 6.729E-03 | 0.40  |
| Dusp7         | 6.671E-08 | 3.06  |
| Tmem39b       | 3.788E-03 | 2.24  |
| Oas1f         | 1.160E-04 | 0.16  |
| Exoc6         | 2.639E-04 | 0.56  |
| Grwd1         | 5.954E-06 | 2.27  |
| H2-T24        | 1.482E-02 | 0.36  |
| Nanp          | 1.097E-03 | 1.81  |
| Pde5a         | 8.350E-03 | 1.97  |
| Mill1         | 1.171E-02 | 0.52  |
| Klk13         | 4.447E-02 | 3.13  |
| A930004D18Rik | 9.067E-05 | 2.81  |
| Skida1        | 2.075E-02 | 2.29  |
| 1810037I17Rik | 1.460E-02 | 1.65  |
| Slc25a40      | 6.286E-03 | 1.55  |
| Skp2          | 7.347E-03 | 1.59  |
| Adm2          | 3.925E-03 | 17.19 |
| 4831426I19Rik | 1.673E-05 | 0.37  |
| O3far1        | 9.120E-03 | 0.15  |
| Ifi205        | 5.452E-06 | 0.08  |
| Sprr2k        | 2.832E-02 | 21.74 |
| Fra10ac1      | 7.984E-03 | 1.53  |
| Fgfr3         | 6.103E-04 | 2.51  |
| Lifr          | 9.855E-06 | 0.36  |
| A630033H20Rik | 4.465E-03 | 0.28  |
| Taf4b         | 1.050E-04 | 3.11  |
| Lce3a         | 4.797E-02 | 6.50  |
| Zfp747        | 1.227E-04 | 1.74  |
| 4930517O19Rik | 8.451E-04 | 5.26  |
| Slfn5         | 2.238E-05 | 0.25  |
| Syt15         | 3.254E-03 | 5.72  |
| Vsnl1         | 1.146E-02 | 4.75  |
| Tmem62        | 2.123E-03 | 0.48  |
| Gm14461       | 1.671E-05 | 0.04  |
| Pla2r1        | 4.505E-03 | 0.49  |
| Gm9949        | 8.485E-03 | 1.53  |
| Xlr           | 3.392E-03 | 0.42  |
| Slc8a1        | 5.054E-05 | 0.29  |
| Mmnn1         | 1.594E-06 | 0.13  |
| Ano9          | 4.672E-04 | 0.32  |
| Emcn          | 9.569E-05 | 2.41  |
| Adam10        | 8.290E-05 | 1.73  |
| Ankrd24       | 4.962E-03 | 1.58  |
| Hmgb2         | 2.494E-04 | 2.26  |
| MsrA          | 1.911E-03 | 0.56  |
| Set           | 8.699E-03 | 2.06  |
| Cadm4         | 8.970E-03 | 3.21  |
| Elp6          | 3.361E-06 | 2.26  |



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| Rnd1          | 7.716E-03 | 2.08 |
| Tmem158       | 7.080E-04 | 3.01 |
| Zfp667        | 3.210E-03 | 0.46 |
| Kcnmb4        | 1.873E-02 | 5.84 |
| Zfp174        | 1.754E-06 | 1.93 |
| Gm9958        | 1.098E-02 | 2.10 |
| 9130008F23Rik | 4.208E-05 | 4.38 |
| Nt5c1a        | 2.458E-02 | 4.50 |
| Agap1         | 2.194E-03 | 0.58 |
| Cntn1         | 1.597E-02 | 8.33 |
| Smyd1         | 2.008E-05 | 0.04 |
| Sprr2e        | 3.856E-02 | 6.05 |
| Pdlim1        | 1.450E-03 | 1.74 |
| Cgrrf1        | 2.857E-03 | 0.59 |
| Klf2          | 4.779E-03 | 0.43 |
| C1ra          | 1.581E-05 | 0.31 |
| 2900002K06Rik | 1.035E-02 | 2.22 |
| Zfp101        | 5.581E-04 | 1.76 |
| Ntrk2         | 5.172E-07 | 0.17 |
| 9330161L09Rik | 3.837E-02 | 1.71 |
| Mrfap1        | 3.927E-02 | 1.58 |
| Zfp93         | 1.262E-04 | 2.38 |
| Pgbd1         | 1.692E-02 | 5.54 |
| Tns1          | 1.680E-05 | 0.21 |
| Fat2          | 3.000E-03 | 2.63 |
| Snupn         | 1.671E-05 | 1.77 |
| Slc6a2        | 4.784E-02 | 0.26 |
| Gm9968        | 5.583E-04 | 0.52 |
| Atp10b        | 7.198E-04 | 0.25 |
| Cd47          | 1.543E-05 | 0.65 |
| Pprc1         | 1.134E-02 | 1.58 |
| Epm2a         | 4.418E-06 | 0.46 |
| Zcchc24       | 6.585E-05 | 0.31 |
| Lair1         | 4.242E-03 | 0.30 |
| Zfp459        | 6.081E-03 | 1.61 |
| Cdca7         | 1.528E-03 | 2.19 |
| B4galnt4      | 6.969E-04 | 2.42 |
| Hmcn2         | 1.020E-04 | 0.11 |
| Gpc3          | 1.149E-02 | 0.31 |
| Mettl4        | 4.565E-03 | 1.68 |
| Rras2         | 1.430E-05 | 3.01 |
| Ghr           | 1.946E-05 | 0.51 |
| Gemin6        | 3.504E-04 | 2.87 |
| Myh8          | 3.171E-02 | 0.03 |
| Abcd2         | 2.036E-06 | 0.05 |
| Tcf7l1        | 2.555E-02 | 0.26 |
| Fmnl1         | 1.055E-03 | 0.45 |
| Dnaaf3        | 4.054E-02 | 3.56 |
| Gsdmc3        | 4.673E-02 | 3.75 |
| 1700034H15Rik | 3.707E-03 | 0.56 |
| Zfp1          | 5.806E-03 | 1.87 |
| Abhd16b       | 1.095E-02 | 3.73 |
| Fancm         | 2.540E-04 | 1.80 |
| Tmem150a      | 1.310E-03 | 0.61 |
| Gm14137       | 1.424E-02 | 0.60 |
| Skint4        | 6.609E-03 | 0.45 |
| Cldn23        | 3.103E-02 | 0.42 |
| Fut2          | 3.096E-02 | 0.52 |
| Irs1          | 1.425E-05 | 0.36 |
| Nod2          | 1.077E-02 | 1.99 |
| Clca1         | 2.826E-02 | 0.43 |
| S100a8        | 2.733E-03 | 3.91 |
| Fam105a       | 9.963E-04 | 0.60 |
| S100a9        | 1.180E-03 | 4.64 |
| Eif3b         | 1.640E-05 | 1.66 |
| Lipm          | 1.968E-02 | 0.51 |
| St3gal5       | 1.201E-02 | 0.65 |
| B4galt6       | 2.142E-05 | 0.27 |
| Ticam2        | 2.061E-06 | 0.10 |
| AI504432      | 1.263E-03 | 0.53 |
| Rdh9          | 2.636E-03 | 0.22 |
| Col8a2        | 1.883E-02 | 0.33 |
| Snx32         | 1.306E-05 | 0.27 |
| Npm3          | 3.401E-04 | 1.79 |
| Pard6g        | 1.544E-05 | 1.89 |
| Cars2         | 2.337E-04 | 1.61 |
| Cep70         | 1.384E-02 | 1.53 |
| Dennd1b       | 1.977E-04 | 0.49 |
| Prr9          | 1.975E-02 | 3.17 |
| Ms4a4b        | 1.579E-03 | 0.31 |
| Usp39         | 1.763E-03 | 1.68 |
| 1810011O10Rik | 6.645E-05 | 2.16 |
| Myh1          | 6.003E-03 | 0.01 |
| Lig1          | 1.480E-04 | 2.18 |
| Adap1         | 1.737E-02 | 0.59 |
| Slit3         | 2.765E-05 | 0.31 |
| Tgoln1        | 2.182E-06 | 0.59 |
| Stk30         | 3.369E-02 | 1.69 |
| Zbtb25        | 1.637E-03 | 1.60 |
| Cd248         | 2.738E-03 | 0.43 |
| Foxk1         | 4.684E-03 | 1.84 |
| Ptafr         | 2.948E-05 | 0.15 |
| Ccdc18        | 2.048E-06 | 3.75 |
| Mpz           | 7.467E-03 | 0.06 |
| Lrrc48        | 2.277E-02 | 1.97 |
| Fry           | 4.134E-03 | 0.61 |
| Ppp1r14b      | 1.567E-03 | 1.61 |



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| Dsg3          | 8.013E-06 | 3.91  |
| Apol8         | 2.836E-03 | 2.99  |
| 4930572J05Rik | 7.836E-05 | 2.88  |
| Prelid2       | 8.212E-04 | 7.25  |
| Elmod3        | 1.388E-03 | 1.52  |
| Gm13199       | 4.761E-03 | 1.93  |
| Nfil3         | 7.383E-06 | 1.76  |
| Ttc26         | 3.435E-02 | 1.92  |
| Gulp1         | 4.924E-04 | 0.25  |
| Gadl1         | 5.840E-03 | 0.33  |
| Glipr1        | 2.840E-04 | 0.29  |
| Usp13         | 1.591E-05 | 0.14  |
| Jmjd6         | 3.694E-05 | 2.18  |
| Ces1d         | 2.010E-05 | 0.01  |
| Ide           | 4.791E-02 | 0.57  |
| Myh4          | 9.830E-03 | 0.01  |
| Skap1         | 5.449E-05 | 0.28  |
| Ero1lb        | 8.454E-05 | 0.46  |
| Ebf1          | 2.304E-08 | 0.17  |
| Npm1          | 2.084E-02 | 1.77  |
| Trim12c       | 2.347E-02 | 0.63  |
| Atpbd4        | 7.464E-04 | 1.81  |
| AB124611      | 8.821E-05 | 0.31  |
| Mettl15       | 6.969E-03 | 1.91  |
| Snrg          | 2.616E-04 | 1.72  |
| Arhgap24      | 1.607E-04 | 0.45  |
| Cep170        | 5.526E-05 | 0.45  |
| Whsc1         | 4.762E-03 | 1.52  |
| Lypd3         | 1.299E-02 | 1.82  |
| Fam136a       | 2.395E-02 | 1.92  |
| Pus7          | 1.011E-02 | 1.69  |
| Trim30d       | 4.972E-02 | 0.55  |
| Lmcd1         | 5.336E-05 | 0.11  |
| Lce1a1        | 1.341E-03 | 0.26  |
| Gnai1         | 1.117E-02 | 2.78  |
| Gapdh         | 1.667E-02 | 1.85  |
| Pkn1          | 9.865E-06 | 0.23  |
| Sh3rf2        | 4.370E-02 | 0.66  |
| Lepr          | 7.594E-04 | 0.50  |
| Prt3          | 1.671E-04 | 0.17  |
| Ankrd29       | 8.078E-04 | 2.59  |
| Cyb5d2        | 3.056E-04 | 1.50  |
| Ddx49         | 6.180E-04 | 1.56  |
| 1700007G11Rik | 4.025E-02 | 13.84 |
| Zfp119a       | 2.929E-03 | 1.55  |
| Camk2b        | 4.892E-06 | 0.13  |
| Gm10033       | 5.279E-03 | 1.79  |
| Gsta2         | 1.773E-02 | 4.66  |
| Fgf18         | 1.309E-02 | 13.48 |
| Sema3b        | 1.703E-03 | 0.34  |
| Skint11       | 4.400E-02 | 0.52  |
| Adtrp         | 1.069E-02 | 0.47  |
| Palld         | 1.833E-02 | 1.60  |
| Nfam1         | 3.290E-06 | 0.18  |
| Gstm1         | 1.075E-04 | 0.12  |
| Gm5431        | 3.800E-03 | 0.37  |
| Zfp846        | 1.434E-04 | 1.70  |
| Kcnh1         | 4.141E-02 | 3.53  |
| Tspan7        | 1.243E-03 | 0.54  |
| Esp1          | 1.590E-07 | 2.71  |
| Krt6a         | 3.622E-03 | 2.93  |
| Abce1         | 1.198E-03 | 1.88  |
| Hist1h2bg     | 2.410E-03 | 1.71  |
| Rrp1b         | 2.705E-03 | 1.72  |
| Zfp82         | 3.808E-04 | 3.00  |
| Rnf207        | 7.277E-03 | 3.49  |
| Gpc6          | 2.047E-04 | 0.24  |
| Gm5801        | 3.587E-03 | 2.44  |
| Gda           | 4.311E-05 | 0.52  |
| Samd12        | 3.927E-04 | 7.62  |
| Gcap14        | 6.653E-04 | 0.56  |
| Fcer1g        | 4.189E-05 | 0.14  |
| Lin9          | 9.962E-04 | 1.72  |
| Hist1h1b      | 8.955E-04 | 2.43  |
| Cds2          | 5.737E-03 | 0.64  |
| Nap1l1        | 2.287E-03 | 1.67  |
| Col13a1       | 3.066E-07 | 7.28  |
| Lilrb3        | 6.507E-05 | 0.08  |
| Zfp708        | 1.508E-05 | 1.94  |
| Deaf1         | 2.042E-04 | 1.54  |
| C1qtnf3       | 3.825E-02 | 0.43  |
| Fam57b        | 1.274E-03 | 0.22  |
| Vwa8          | 8.402E-06 | 0.49  |
| Hnrnpa3       | 1.382E-03 | 1.75  |
| Gm5506        | 4.932E-04 | 2.04  |
| Rad51l1       | 4.718E-04 | 3.20  |
| Fcgr4         | 9.985E-03 | 0.15  |
| Ifitm6        | 1.200E-02 | 0.53  |
| Nap1l4        | 7.370E-04 | 1.63  |
| Zfp945        | 2.628E-04 | 0.61  |
| Pde1a         | 5.185E-07 | 0.13  |
| Mtfmt         | 6.550E-05 | 1.59  |
| Lep           | 4.970E-04 | 0.04  |
| Olf494        | 3.471E-02 | 0.10  |
| R74862        | 2.564E-05 | 2.46  |
| Hist1h3f      | 3.084E-04 | 2.39  |
| Slc27a4       | 5.750E-03 | 0.55  |



|               |           |       |
|---------------|-----------|-------|
| Tonsl         | 9.227E-06 | 2.50  |
| Csf2ra        | 1.187E-03 | 0.25  |
| Nkapl         | 1.647E-03 | 3.06  |
| Fxyd2         | 3.080E-03 | 0.06  |
| Actg2         | 1.076E-02 | 2.42  |
| B3gnt8        | 1.421E-03 | 1.79  |
| Nhs           | 5.512E-04 | 3.39  |
| Fcgr3         | 1.784E-04 | 0.10  |
| Znhit1        | 2.501E-03 | 1.55  |
| Trp53         | 5.215E-03 | 1.53  |
| Gm16218       | 4.715E-03 | 2.20  |
| Calcr1        | 7.859E-04 | 0.55  |
| Cdh24         | 2.612E-04 | 3.20  |
| Flot1         | 2.831E-03 | 0.62  |
| Nrm           | 3.180E-06 | 2.27  |
| AU019823      | 8.235E-06 | 1.58  |
| Kprp          | 1.244E-02 | 0.51  |
| Zfp341        | 7.916E-04 | 2.50  |
| Zfp422        | 8.847E-04 | 0.44  |
| Zfp930        | 3.029E-04 | 1.85  |
| Dsc3          | 6.618E-04 | 1.70  |
| Mug1          | 8.311E-05 | 0.03  |
| Grb2          | 1.004E-03 | 0.62  |
| 9430015G10Rik | 2.362E-03 | 1.90  |
| Taok2         | 6.645E-03 | 1.65  |
| Chpt1         | 5.996E-07 | 0.33  |
| Kif13b        | 4.780E-03 | 0.63  |
| Alox5ap       | 1.361E-04 | 0.16  |
| Rp2h          | 7.136E-04 | 0.60  |
| Hist1h4a      | 2.247E-03 | 1.81  |
| Sip1          | 7.080E-05 | 2.00  |
| Atp8b4        | 4.667E-07 | 0.24  |
| Arrb2         | 2.464E-04 | 0.39  |
| Pyroxd2       | 1.856E-03 | 0.20  |
| Alyref2       | 4.040E-02 | 1.58  |
| Ppih          | 3.229E-03 | 1.89  |
| Zfp941        | 1.567E-02 | 3.94  |
| Calm5         | 2.760E-03 | 0.33  |
| C030014I23Rik | 6.976E-04 | 1.82  |
| Sntb1         | 1.051E-03 | 0.13  |
| Kng2          | 5.531E-03 | 0.11  |
| Tor3a         | 6.659E-04 | 0.42  |
| Ces4a         | 4.948E-04 | 0.04  |
| H2-Eb1        | 3.919E-04 | 0.22  |
| Ifitm2        | 1.018E-04 | 0.57  |
| Layn          | 4.609E-04 | 0.15  |
| Eno3          | 2.365E-06 | 0.03  |
| Pla2g16       | 1.490E-04 | 0.27  |
| Hist1h4c      | 1.039E-02 | 2.04  |
| Cd302         | 4.372E-05 | 0.19  |
| Gmfg          | 3.069E-06 | 0.18  |
| B2m           | 1.738E-02 | 0.51  |
| Ube2s         | 3.802E-05 | 1.75  |
| Zbtb40        | 8.030E-03 | 1.89  |
| Acyp2         | 3.643E-05 | 0.32  |
| Csmd1         | 1.104E-03 | 0.05  |
| Trmt61a       | 2.029E-03 | 1.61  |
| Slc4a4        | 2.489E-07 | 0.12  |
| Rrs1          | 2.502E-06 | 2.09  |
| Cdh3          | 2.584E-04 | 3.97  |
| Mcpt4         | 1.801E-06 | 0.11  |
| Gapdhs        | 4.747E-02 | 2.26  |
| Retnla        | 4.768E-02 | 0.01  |
| Prpc          | 1.066E-06 | 0.43  |
| Blnk          | 1.779E-06 | 0.42  |
| Maml3         | 2.440E-03 | 1.58  |
| Spink12       | 1.727E-03 | 5.31  |
| Fnip2         | 2.762E-03 | 0.49  |
| H2-K1         | 1.710E-02 | 0.59  |
| Exosc5        | 8.817E-03 | 1.53  |
| Taok3         | 8.969E-05 | 0.40  |
| Cxcl12        | 5.773E-09 | 0.04  |
| Phf5a         | 3.175E-06 | 1.52  |
| Acvr2b        | 1.086E-02 | 1.94  |
| Krt79         | 6.623E-04 | 0.03  |
| Efcab4b       | 1.198E-04 | 0.26  |
| Obscn         | 6.025E-05 | 0.02  |
| Snrpa         | 1.728E-05 | 1.57  |
| Hist1h4d      | 4.213E-02 | 1.79  |
| Sox21         | 6.187E-03 | 2.05  |
| Krt5          | 3.852E-02 | 2.38  |
| Cep128        | 4.470E-03 | 1.59  |
| C1qtnf7       | 2.457E-05 | 0.05  |
| Wdr61         | 1.506E-04 | 1.62  |
| Mdc1          | 2.806E-02 | 1.51  |
| U2af1         | 6.333E-04 | 1.75  |
| Med9          | 1.257E-05 | 1.54  |
| Tnnt3         | 8.293E-05 | 0.01  |
| Ext1          | 3.766E-02 | 1.74  |
| Kalrn         | 8.428E-03 | 0.42  |
| Mospd2        | 5.243E-06 | 0.45  |
| Cfd           | 5.145E-05 | 0.00  |
| Myl1          | 9.698E-05 | 0.01  |
| Ces2c         | 2.297E-02 | 17.58 |
| Suc1g2        | 1.146E-04 | 1.58  |
| Inadl         | 2.207E-04 | 1.88  |
| Sphk1         | 1.010E-04 | 0.44  |



|               |           |       |
|---------------|-----------|-------|
| Ccdc62        | 2.050E-03 | 2.05  |
| Zscan20       | 2.184E-02 | 1.54  |
| Olfr492       | 4.529E-02 | 0.03  |
| Flot2         | 1.294E-03 | 0.59  |
| Iah1          | 3.149E-04 | 0.67  |
| Pgk1          | 3.749E-03 | 2.40  |
| Lmnb2         | 1.648E-06 | 1.80  |
| Trim54        | 5.358E-07 | 0.02  |
| Btbd3         | 1.193E-02 | 1.76  |
| Zfp119b       | 2.584E-03 | 1.54  |
| Il28ra        | 4.893E-03 | 2.03  |
| Tgif2         | 3.551E-03 | 2.10  |
| 2700097O09Rik | 4.712E-04 | 2.10  |
| Cks2          | 1.507E-05 | 3.04  |
| Opcml         | 1.977E-06 | 0.02  |
| Rpp25         | 9.323E-03 | 6.12  |
| Gm10115       | 1.417E-06 | 0.03  |
| Cytl1         | 1.490E-06 | 0.02  |
| Serpib2       | 3.101E-02 | 2.01  |
| Hist1h3g      | 3.823E-02 | 2.68  |
| Nsl1          | 6.124E-06 | 1.53  |
| Ncr1          | 1.872E-02 | 0.14  |
| Cys1          | 1.205E-02 | 0.29  |
| Cnr2          | 4.620E-05 | 0.33  |
| Lilrb4        | 4.097E-05 | 0.16  |
| Kcnj15        | 1.315E-02 | 2.56  |
| Ncs1          | 5.714E-03 | 1.82  |
| 1110001A16Rik | 2.413E-03 | 1.58  |
| Cav3          | 3.672E-05 | 0.02  |
| Hist1h2bk     | 3.322E-02 | 2.09  |
| Kcnc3         | 1.252E-02 | 7.47  |
| Zfp599        | 1.004E-05 | 3.91  |
| I7Rn6         | 2.831E-05 | 1.83  |
| Hist1h3d      | 1.187E-02 | 2.68  |
| Ces2f         | 3.877E-02 | 3.21  |
| Impdh2        | 2.061E-04 | 1.71  |
| Klhl24        | 5.945E-03 | 0.61  |
| Acadm         | 2.553E-07 | 0.48  |
| Cfl2          | 1.959E-03 | 0.59  |
| 9130023H24Rik | 2.595E-06 | 1.67  |
| A430107O13Rik | 4.162E-06 | 0.16  |
| Nrg1          | 9.815E-03 | 10.15 |
| 2010204K13Rik | 4.463E-03 | 7.55  |
| Hist1h2ak     | 6.437E-03 | 2.58  |
| Ing2          | 1.420E-03 | 2.41  |
| Lrrc40        | 2.217E-03 | 1.82  |
| Mapk3         | 1.476E-03 | 0.65  |
| Kif1b         | 7.519E-05 | 0.58  |
| Calml3        | 1.245E-02 | 0.35  |
| Rps4y2        | 1.940E-02 | 0.43  |
| Hspb11        | 5.826E-03 | 1.78  |
| Cd300lb       | 3.391E-04 | 0.07  |
| Nol7          | 2.413E-02 | 1.68  |
| Ldha          | 6.300E-03 | 2.06  |
| B230325K18Rik | 3.792E-03 | 1.57  |
| Ptpla         | 2.339E-06 | 2.31  |
| Zfp35         | 1.021E-05 | 1.73  |
| Tmem117       | 2.069E-04 | 3.59  |
| 1190007I07Rik | 3.660E-03 | 2.54  |
| Krr1          | 1.387E-03 | 1.65  |
| Alg11         | 1.578E-03 | 1.74  |
| Bcl9l         | 1.293E-03 | 1.99  |
| Zfp947        | 3.480E-03 | 1.72  |
| Ube2d2b       | 2.106E-03 | 1.75  |
| D630045J12Rik | 1.078E-03 | 3.28  |
| 1700112E06Rik | 4.143E-05 | 0.35  |
| 2010109I03Rik | 4.935E-02 | 1.78  |
| Eno1          | 2.704E-04 | 1.95  |
| Aox1          | 6.035E-03 | 0.52  |
| Gm10134       | 1.999E-04 | 0.19  |
| Glyat         | 2.259E-04 | 17.45 |
| Hist2h2ab     | 1.974E-03 | 2.24  |
| Mapk15        | 5.794E-04 | 3.39  |
| Gm13939       | 1.544E-02 | 2.34  |
| S100a7a       | 6.662E-03 | 10.03 |
| Prpf38a       | 5.581E-04 | 1.69  |
| Hspbp1        | 4.355E-03 | 1.52  |
| Alms1         | 2.618E-02 | 1.80  |
| Rnf183        | 5.121E-03 | 3.94  |
| Slc24a3       | 3.082E-02 | 1.82  |
| Ptcd3         | 1.323E-04 | 1.71  |
| Rpl7l1        | 3.623E-03 | 1.63  |
| Klk1          | 2.402E-02 | 0.52  |
| Srrm4         | 3.239E-02 | 3.15  |
| Pepd          | 8.514E-07 | 0.44  |
| Nr6a1         | 1.244E-02 | 2.14  |
| Wibg          | 5.921E-04 | 1.81  |
| Gpn1          | 9.523E-05 | 1.72  |
| Trerf1        | 1.077E-02 | 1.63  |
| lpcef1        | 3.455E-05 | 0.41  |
| Fbln2         | 1.440E-02 | 0.45  |
| Cnnm2         | 2.271E-04 | 2.20  |
| Hcst          | 3.365E-04 | 0.24  |
| Cadm2         | 3.960E-03 | 0.06  |
| Rhox8         | 1.760E-04 | 1.95  |
| Zfp69         | 1.269E-03 | 2.08  |
| Hist1h2bh     | 1.767E-02 | 2.19  |



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|-----------------|-----------|----------|
| Ano6            | 5.946E-04 | 0.62     |
| Ifi2711         | 2.226E-03 | 0.59     |
| Gsdma3          | 1.244E-02 | 0.05     |
| Paqr9           | 1.269E-02 | 2.95     |
| Gm5414          | 1.398E-02 | 3.46     |
| Gimap8          | 2.350E-04 | 0.58     |
| Hvcn1           | 5.554E-04 | 0.14     |
| Tank            | 1.427E-04 | 0.61     |
| Aox3            | 5.079E-05 | 0.04     |
| Lrrc51          | 1.586E-04 | 1.51     |
| mt-Nd5          | 2.829E-02 | 1.52     |
| Sepp1           | 4.769E-07 | 0.05     |
| U6              | 1.117E-02 | 23611.24 |
| SNORA5          | 1.753E-02 | 4.84     |
| SNORA13         | 2.566E-02 | 1.65     |
| Snora41         | 1.417E-02 | 3.57     |
| SNORA1          | 4.365E-02 | 1.65     |
| Telomerase-vert | 3.703E-03 | 4.43     |
| U3              | 1.318E-02 | 3.24     |
| Snora43         | 1.197E-03 | 2.83     |
| U1              | 4.122E-02 | 5.25     |
| U1              | 3.160E-02 | 8.05     |
| U2              | 3.775E-02 | 4.68     |
| SNORA32         | 8.676E-03 | 3.66     |
| U6              | 1.117E-02 | 23611.24 |
| SNORA71         | 4.998E-02 | 2.15     |
| SNORA25         | 2.246E-02 | 3.18     |
| U3              | 1.482E-02 | 3.81     |
| SNORA25         | 1.392E-03 | 3.02     |
| U1              | 4.323E-02 | 5.30     |
| SNORA67         | 4.747E-02 | 1.74     |
| U3              | 4.423E-02 | 1.62     |
| n-R5s185        | 4.026E-02 | 2.03     |
| SNORA72         | 3.743E-02 | 2.65     |
| U1              | 1.566E-02 | 7.99     |
| Tacc1           | 3.038E-05 | 0.26     |
| Cd209b          | 2.663E-06 | 0.01     |
| 2610305D13Rik   | 8.927E-03 | 0.49     |
| Dhrs3           | 1.527E-05 | 0.21     |
| Med18           | 5.976E-03 | 1.51     |
| Gm1976          | 1.178E-03 | 2.64     |
| Gm12866         | 4.576E-02 | 6.28     |
| Adamts11        | 7.259E-06 | 0.18     |
| Prpf4           | 2.307E-05 | 1.82     |
| Fkbp15          | 3.461E-05 | 0.66     |
| Slc31a2         | 1.634E-04 | 0.59     |
| AY512931        | 3.734E-04 | 0.50     |
| 2510046G10Rik   | 4.660E-02 | 2.23     |
| Trim12a         | 4.457E-02 | 0.60     |
| Vps37b          | 2.344E-03 | 2.75     |
| Serpina3c       | 1.664E-05 | 0.07     |
| Serpina3b       | 7.691E-03 | 0.04     |
| Serpina1a       | 1.869E-03 | 0.35     |
| Akap13          | 2.434E-06 | 0.38     |
| Rdh11           | 7.176E-03 | 0.45     |
| Ttc32           | 9.790E-03 | 1.72     |
| Fbxl18          | 4.625E-04 | 1.61     |
| Wdr35           | 5.717E-04 | 1.70     |
| Pilrb2          | 4.914E-03 | 0.48     |
| Pilrb1          | 1.267E-02 | 0.52     |
| Zbtb16          | 6.290E-03 | 0.14     |
| Cyp2b19         | 6.289E-05 | 0.25     |
| Fxyd6           | 4.156E-04 | 0.30     |
| Rnasel          | 1.010E-02 | 0.61     |
| Ecsit           | 1.376E-04 | 1.59     |
| Hmcn1           | 7.575E-05 | 0.20     |
| Ptpv            | 4.446E-02 | 0.56     |
| Bub3            | 6.967E-03 | 1.59     |
| Serpina7        | 6.399E-03 | 0.17     |
| Polr1c          | 6.851E-03 | 1.51     |
| Igj             | 8.578E-04 | 0.01     |
| Mrgpra4         | 6.596E-05 | 0.18     |
| H2-T23          | 2.226E-02 | 0.56     |
| Lgi1            | 1.536E-03 | 9.43     |
| Ppp1r3c         | 7.201E-06 | 0.02     |
| Rps25-ps1       | 1.146E-02 | 2.31     |
| Lyar            | 1.008E-04 | 2.29     |
| B3galt4         | 9.279E-06 | 1.54     |
| Zfp763          | 9.349E-03 | 1.69     |
| Hist1h4j        | 2.942E-04 | 2.33     |
| Klra3           | 5.606E-04 | 0.05     |
| Dgat2l6         | 2.134E-03 | 0.04     |
| Ankrd23         | 1.975E-04 | 0.18     |
| Gm10220         | 2.605E-02 | 21.66    |
| Lpar5           | 6.607E-05 | 2.75     |
| BC003965        | 7.624E-07 | 1.70     |
| Xlr4b           | 1.364E-03 | 0.36     |
| Pi15            | 4.139E-04 | 8.07     |
| Myl9            | 9.724E-03 | 0.45     |
| Pex26           | 2.950E-05 | 2.10     |
| Cxx1a           | 1.652E-02 | 0.66     |
| Zfp948          | 6.465E-04 | 1.76     |
| Mllt4           | 3.051E-03 | 0.50     |
| Tcp1            | 9.765E-03 | 1.52     |
| Cenpm           | 2.670E-05 | 3.42     |
| Ccdc134         | 1.344E-04 | 1.55     |
| Cst7            | 6.586E-03 | 0.49     |



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|----------------|-----------|-------|
| Ndufaf2        | 2.747E-03 | 1.72  |
| Macrocl2       | 6.570E-03 | 1.93  |
| Lgals1         | 1.241E-03 | 0.17  |
| Pdxp           | 4.910E-06 | 2.59  |
| Gm6723         | 3.740E-02 | 2.70  |
| Il2rb          | 8.145E-03 | 0.42  |
| Ccdc48         | 2.417E-03 | 0.17  |
| Shroom4        | 3.434E-02 | 1.66  |
| Cma2           | 3.415E-02 | 7.90  |
| Dok1           | 3.545E-04 | 0.42  |
| Gml            | 2.295E-02 | 3.21  |
| Cep152         | 1.168E-04 | 1.98  |
| Rpl34-ps1      | 1.594E-02 | 2.68  |
| Hemt1          | 3.007E-02 | 4.24  |
| Myoz1          | 1.524E-05 | 0.01  |
| Finc           | 6.339E-05 | 0.09  |
| Trp53i11       | 4.234E-04 | 2.38  |
| Psrc1          | 1.412E-02 | 0.65  |
| Sort1          | 1.334E-05 | 0.36  |
| Ptprz1         | 4.204E-03 | 12.91 |
| Il3ra          | 9.964E-04 | 0.41  |
| Col28a1        | 2.189E-03 | 0.21  |
| Hist1h2ac      | 2.338E-02 | 2.00  |
| Sf3b4          | 2.472E-04 | 1.67  |
| Cgn            | 2.401E-02 | 0.49  |
| Lce3f          | 2.189E-02 | 5.00  |
| Lce1j          | 6.643E-04 | 0.27  |
| Lce1i          | 1.123E-03 | 0.23  |
| Lce1e          | 3.370E-03 | 0.35  |
| Lce1a2         | 1.570E-02 | 0.21  |
| Msto1          | 5.793E-08 | 1.58  |
| Urm1           | 6.812E-03 | 1.52  |
| Fgfr1op        | 2.702E-03 | 1.62  |
| Zfp72          | 9.140E-04 | 2.01  |
| 4930451E10Rik  | 8.644E-03 | 3.15  |
| Hist1h3a       | 9.110E-03 | 2.33  |
| Hist1h2bf      | 1.897E-02 | 2.08  |
| Hist1h2ac      | 1.982E-04 | 2.92  |
| Hist1h2ae      | 1.178E-04 | 2.60  |
| Hist1h3e       | 6.663E-04 | 2.44  |
| Hist1h4f       | 2.306E-04 | 2.19  |
| Hist1h2bj      | 4.280E-02 | 2.49  |
| Hist1h2br      | 1.889E-04 | 2.07  |
| Hist1h4m       | 2.679E-04 | 2.01  |
| Hist1h2bp      | 1.855E-04 | 2.22  |
| Hist1h3c       | 1.272E-02 | 2.53  |
| Hist1h3h       | 1.937E-02 | 2.31  |
| Ctxn3          | 6.323E-05 | 0.01  |
| Lyz1           | 3.966E-05 | 0.06  |
| Lyz2           | 1.504E-04 | 0.05  |
| Tspear         | 1.840E-02 | 4.34  |
| Cd300lh        | 5.280E-04 | 0.10  |
| Gm11710        | 8.981E-05 | 0.12  |
| Tmem100        | 8.114E-05 | 0.18  |
| Wfdc17         | 3.109E-05 | 0.11  |
| Sfn9           | 2.905E-05 | 2.61  |
| Gm10277        | 4.070E-03 | 1.98  |
| Fbp1           | 5.458E-04 | 0.15  |
| Ahnak          | 9.170E-04 | 0.64  |
| 4930438A08Rik  | 1.057E-02 | 0.39  |
| 9930111J21Rik2 | 2.301E-03 | 0.38  |
| 9930111J21Rik1 | 1.675E-03 | 0.36  |
| Ccdc99         | 7.035E-07 | 3.18  |
| Fam196b        | 2.773E-06 | 0.24  |
| Fcho1          | 9.059E-04 | 0.45  |
| Sp140          | 4.300E-03 | 0.59  |
| Sp110          | 7.994E-03 | 0.36  |
| Fat1           | 7.428E-04 | 1.97  |
| Mfhas1         | 3.896E-06 | 1.83  |
| 4930581F22Rik  | 5.478E-03 | 1.53  |
| Mmp27          | 3.941E-03 | 0.27  |
| Ccnd1          | 2.486E-03 | 2.87  |
| Prss36         | 8.732E-03 | 1.60  |
| Ampd1          | 1.442E-02 | 0.20  |
| Nlrp1b         | 6.698E-05 | 0.32  |
| Cyp3a57        | 2.119E-03 | 0.05  |
| Zfp498         | 1.345E-04 | 1.64  |
| Mesdc1         | 1.936E-03 | 1.52  |
| Adamts13       | 3.791E-03 | 0.45  |
| Ndn12          | 1.052E-04 | 2.04  |
| Mrgprb1        | 3.703E-07 | 0.10  |
| Mn1            | 2.422E-02 | 0.59  |
| Fv1            | 7.593E-04 | 1.92  |
| Vsig10l        | 3.817E-02 | 1.80  |
| Gm13177        | 1.814E-03 | 0.05  |
| Btbd8          | 5.017E-03 | 2.66  |
| Utp3           | 1.229E-03 | 1.64  |
| Sars2          | 3.571E-06 | 1.84  |
| Eid2b          | 2.138E-03 | 1.61  |
| Pla2g4d        | 6.654E-03 | 8.01  |
| Gltscr1        | 2.454E-02 | 1.73  |
| 6330408A02Rik  | 4.699E-03 | 1.59  |
| Skint3         | 2.408E-03 | 0.36  |
| Rabepk         | 2.156E-03 | 1.86  |
| Gm6313         | 3.979E-02 | 1.72  |
| Ccl19          | 1.708E-04 | 0.06  |
| Sdr16c6        | 1.159E-03 | 0.12  |



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|---------------|-----------|-------|
| Camkmt        | 3.624E-02 | 1.59  |
| Rasgrp3       | 1.264E-05 | 1.73  |
| Zfp827        | 6.460E-04 | 2.11  |
| Ptges3        | 8.586E-04 | 1.74  |
| Nr2c2ap       | 3.864E-04 | 1.53  |
| Gm10311       | 1.168E-03 | 1.87  |
| 1700029J07Rik | 3.890E-03 | 2.61  |
| Mboat4        | 4.222E-03 | 4.74  |
| Serpina1d     | 1.018E-02 | 0.34  |
| Serpina1b     | 6.797E-04 | 0.24  |
| Naip5         | 1.268E-04 | 0.43  |
| Zfp213        | 5.288E-03 | 1.76  |
| G630090E17Rik | 2.347E-02 | 1.75  |
| C1qtnf9       | 9.162E-06 | 0.22  |
| Mcpt9         | 1.220E-02 | 42.28 |
| 1110002L01Rik | 4.273E-02 | 1.56  |
| Ccnb1ip1      | 4.156E-04 | 3.82  |
| Zfp777        | 1.389E-03 | 1.96  |
| Hist1h2ai     | 2.021E-03 | 2.63  |
| Gprin2        | 3.997E-04 | 0.12  |
| Klrg2         | 5.145E-03 | 2.46  |
| 3425401B19Rik | 9.929E-06 | 0.02  |
| Nt5dc2        | 2.695E-04 | 3.38  |
| Cebpd         | 2.451E-03 | 0.47  |
| Tut1          | 6.245E-04 | 1.52  |
| Ints5         | 9.050E-04 | 1.72  |
| Lrrn4cl       | 6.384E-04 | 0.41  |
| Zbtb3         | 1.156E-03 | 1.97  |
| Snx29         | 4.889E-08 | 0.40  |
| Gm960         | 2.943E-02 | 2.09  |
| Csf2rb        | 8.706E-05 | 0.25  |
| Csf2rb2       | 3.799E-05 | 0.31  |
| Ncf4          | 8.633E-05 | 0.22  |
| Zhx2          | 6.013E-04 | 1.90  |
| Ccdc112       | 3.730E-03 | 2.13  |
| Fndc1         | 1.779E-03 | 0.36  |
| 6720489N17Rik | 9.226E-03 | 1.98  |
| Ccnf          | 1.556E-06 | 3.45  |
| Klf12         | 1.734E-03 | 4.18  |
| Dppa2         | 7.746E-03 | 0.36  |
| Nanos1        | 2.306E-02 | 2.35  |
| Fam84b        | 1.989E-04 | 2.79  |
| Slc39a2       | 7.438E-04 | 0.14  |
| Gm7489        | 8.214E-06 | 12.38 |
| 5930412G12Rik | 7.195E-03 | 2.22  |
| Ear2          | 4.185E-04 | 0.08  |
| Ear1          | 2.055E-03 | 0.05  |
| Gm10382       | 1.912E-02 | 1.69  |
| Slfn10-ps     | 1.395E-02 | 2.12  |
| 1810012P15Rik | 3.266E-03 | 2.23  |
| Adam1a        | 4.725E-02 | 1.59  |
| Gm6288        | 3.195E-04 | 5.66  |
| Gm10393       | 2.084E-04 | 0.15  |
| 1500011B03Rik | 5.636E-04 | 1.53  |
| Myo18b        | 1.753E-09 | 0.03  |
| Gm6712        | 3.081E-02 | 1.62  |
| 5430403G16Rik | 1.237E-02 | 1.53  |
| Ahnak2        | 1.798E-04 | 0.36  |
| AW555464      | 1.390E-02 | 1.53  |
| Tmprss11a     | 3.459E-02 | 8.12  |
| Sod3          | 1.820E-05 | 0.10  |
| Acot1         | 4.718E-04 | 0.14  |
| Adam4         | 3.385E-03 | 1.62  |
| Gm4787        | 6.765E-03 | 2.06  |
| Oip5          | 1.536E-05 | 4.72  |
| Vamp5         | 2.317E-05 | 0.38  |
| Lrrc61        | 2.253E-03 | 0.46  |
| Vma21         | 1.667E-03 | 1.52  |
| Gm12000       | 2.071E-03 | 0.35  |
| 2500004C02Rik | 1.711E-04 | 1.82  |
| Gm10485       | 6.700E-03 | 0.29  |
| Gm14636       | 4.740E-02 | 0.66  |
| Nudt11        | 2.172E-03 | 4.06  |
| C030034I22Rik | 2.480E-03 | 1.94  |
| C920025E04Rik | 4.921E-02 | 1.68  |
| H2-Q6         | 3.208E-02 | 0.52  |
| H2-D1         | 1.237E-02 | 0.60  |
| Lst1          | 7.096E-04 | 0.32  |
| C4b           | 3.885E-06 | 0.02  |
| H2-Ab1        | 9.414E-04 | 0.27  |
| Gm4924        | 4.650E-04 | 2.10  |
| Arhgdig       | 3.384E-02 | 2.74  |
| Wdr90         | 7.781E-04 | 2.16  |
| Mosc2         | 3.340E-05 | 0.54  |
| Gm16067       | 5.005E-03 | 2.35  |
| Ifi204        | 1.568E-03 | 0.34  |
| Al607873      | 1.001E-02 | 0.44  |
| Gm10521       | 7.443E-04 | 0.12  |
| Cep76         | 3.338E-05 | 1.99  |
| Ppp1r12b      | 4.359E-06 | 0.60  |
| Pcdhb22       | 1.317E-06 | 3.40  |
| Gm1614        | 1.330E-02 | 0.60  |
| Gm10548       | 1.086E-02 | 3.73  |
| C130036L24Rik | 5.911E-04 | 2.55  |
| Gm10552       | 2.126E-03 | 0.47  |
| Gm10564       | 1.332E-02 | 3.01  |
| Apitd1        | 4.230E-04 | 2.80  |



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|---------------|-----------|-------|
| Gm10565       | 3.671E-03 | 2.58  |
| 5730409E04Rik | 1.467E-03 | 0.55  |
| Kti12         | 4.749E-05 | 1.94  |
| Efcab7        | 1.359E-02 | 1.69  |
| Alg6          | 8.800E-04 | 1.68  |
| Fam196a       | 1.370E-05 | 1.81  |
| 8030451A03Rik | 8.571E-03 | 2.28  |
| Mup11         | 6.378E-03 | 0.02  |
| Mup7          | 4.297E-02 | 0.03  |
| Al427809      | 2.968E-03 | 0.13  |
| B430319F04Rik | 1.591E-03 | 3.34  |
| AA474408      | 2.624E-03 | 2.13  |
| Gm13305       | 2.712E-04 | 0.24  |
| Gm13306       | 9.738E-03 | 0.33  |
| Gm13304       | 1.869E-04 | 0.17  |
| Il11ra1       | 3.374E-04 | 0.26  |
| Ggh           | 1.085E-03 | 0.41  |
| Ttpa          | 6.912E-03 | 1.74  |
| Kbtbd5        | 2.548E-06 | 0.03  |
| Exoc8         | 7.768E-03 | 1.56  |
| 4930520O04Rik | 9.912E-07 | 2.63  |
| Gm10615       | 9.591E-04 | 1.83  |
| Mlycd         | 1.172E-04 | 0.49  |
| Snrnp40       | 3.702E-03 | 1.61  |
| Ntf5          | 1.720E-04 | 3.76  |
| 4930513N10Rik | 2.819E-02 | 2.52  |
| Zfp319        | 3.451E-02 | 1.58  |
| Klk5          | 2.464E-02 | 0.49  |
| Plekhf1       | 5.963E-04 | 0.50  |
| Gm10639       | 1.132E-02 | 10.77 |
| Znhit6        | 1.141E-04 | 2.21  |
| Gsta1         | 5.893E-03 | 20.04 |
| Adh1          | 2.892E-05 | 0.10  |
| Dnajb14       | 2.415E-05 | 0.54  |
| Gm10643       | 2.034E-02 | 2.17  |
| Cox7a1        | 7.016E-06 | 0.04  |
| Zfp568        | 1.313E-02 | 1.59  |
| Gramd2        | 5.825E-05 | 4.55  |
| Amy1          | 9.531E-07 | 0.14  |
| Phldb3        | 3.247E-03 | 1.64  |
| Gm6166        | 1.682E-02 | 2.74  |
| Zfp94         | 2.657E-02 | 1.72  |
| Zfp109        | 3.526E-04 | 1.82  |
| Gm10658       | 3.461E-03 | 2.03  |
| Ovgp1         | 1.388E-04 | 2.38  |
| AA386476      | 3.654E-02 | 1.79  |
| Gpr77         | 1.471E-02 | 1.67  |
| Al429214      | 3.683E-02 | 1.57  |
| Hist2h3b      | 9.416E-03 | 2.42  |
| Zfp628        | 5.925E-03 | 1.93  |
| 2610203C20Rik | 3.876E-05 | 2.33  |
| Gm14548       | 1.224E-04 | 0.08  |
| 2310001H18Rik | 2.087E-02 | 3.75  |
| Spc24         | 6.042E-04 | 1.78  |
| Mex3a         | 4.821E-03 | 2.78  |
| Zfp558        | 3.911E-02 | 2.24  |
| Cass4         | 2.101E-02 | 0.54  |
| Mocs3         | 1.749E-04 | 2.55  |
| Fam65c        | 6.481E-03 | 0.63  |
| 1500012F01Rik | 3.153E-06 | 1.67  |
| Lekr1         | 3.147E-06 | 2.02  |
| 4931440P22Rik | 1.966E-02 | 2.14  |
| 4930449A18Rik | 2.199E-03 | 0.03  |
| Gm10728       | 2.185E-04 | 1.71  |
| Zfp850        | 3.406E-02 | 2.29  |
| 1700034I23Rik | 2.316E-02 | 2.23  |
| Gm10731       | 4.728E-02 | 2.58  |
| Gm826         | 6.735E-05 | 6.66  |
| Arhgap40      | 7.266E-03 | 0.43  |
| Cpne1         | 1.579E-03 | 1.63  |
| 6430550D23Rik | 3.520E-02 | 1.53  |
| Eif2s2        | 2.739E-03 | 1.69  |
| Pde4d         | 1.202E-04 | 0.64  |
| Zcchc3        | 2.389E-02 | 3.42  |
| Gm10749       | 3.324E-02 | 2.03  |
| Thbd          | 8.735E-03 | 3.13  |
| Ism1          | 3.875E-04 | 0.06  |
| Plxnc1        | 5.538E-06 | 0.35  |
| Hspa12b       | 1.853E-04 | 0.54  |
| Slc4a11       | 1.962E-03 | 3.80  |
| Gm10762       | 2.691E-02 | 1.93  |
| Gm10767       | 4.925E-02 | 2.27  |
| BC025920      | 8.146E-04 | 2.72  |
| Zfp934        | 2.572E-04 | 1.75  |
| Ctla2b        | 3.189E-05 | 0.25  |
| Spata5l1      | 9.681E-03 | 1.62  |
| Lcmt2         | 8.658E-03 | 1.87  |
| B3galt5       | 2.692E-02 | 3.31  |
| 5430417L22Rik | 4.507E-05 | 1.78  |
| Fam122a       | 4.107E-02 | 1.61  |
| Pak6          | 1.137E-03 | 2.68  |
| Fibin         | 2.893E-04 | 0.14  |
| AW112010      | 2.711E-02 | 0.29  |
| 4631405J19Rik | 2.064E-02 | 14.94 |
| Prdm11        | 1.091E-02 | 2.11  |
| 4833423E24Rik | 1.848E-02 | 1.99  |
| Znhit2        | 3.526E-03 | 1.51  |



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| Ccdc58        | 8.999E-06 | 2.23   |
| Heg1          | 1.917E-04 | 0.32   |
| Gm10818       | 1.140E-03 | 1.68   |
| Cenpw         | 6.514E-04 | 4.54   |
| Pde11a        | 4.575E-02 | 0.36   |
| Ttc30a1       | 8.436E-03 | 1.75   |
| Wipf1         | 2.486E-05 | 0.28   |
| Aldh3b2       | 1.360E-02 | 0.60   |
| H60b          | 1.661E-02 | 0.21   |
| Kbtbd10       | 1.629E-07 | 0.13   |
| Gm5465        | 5.897E-04 | 3.12   |
| Gm13375       | 1.541E-02 | 1.72   |
| Aarsd1        | 5.464E-04 | 1.59   |
| Gm17151       | 2.387E-03 | 2.08   |
| Gm12359       | 9.112E-03 | 1.84   |
| 6330403L08Rik | 3.432E-03 | 2.30   |
| Nrbp2         | 1.330E-03 | 1.59   |
| B130006D01Rik | 2.253E-03 | 1.59   |
| 2300005B03Rik | 4.252E-03 | 0.09   |
| Gm11545       | 1.039E-02 | 2.78   |
| Vimp          | 4.382E-03 | 0.64   |
| Selm          | 2.219E-04 | 0.28   |
| Msrb1         | 8.220E-04 | 0.58   |
| Gpx4          | 2.305E-02 | 0.61   |
| U4            | 2.855E-02 | 5.65   |
| BC100451      | 6.689E-05 | 0.31   |
| 2700094K13Rik | 8.341E-07 | 2.95   |
| Gm20730       | 2.011E-02 | 0.02   |
| Igkv2-137     | 6.459E-03 | 0.02   |
| Igkv1-131     | 3.567E-03 | 0.06   |
| Igkv15-103    | 1.966E-02 | 0.02   |
| Igkv19-93     | 5.984E-03 | 0.01   |
| Igkv1-88      | 8.184E-03 | 0.10   |
| Igkv4-86      | 4.882E-02 | 0.06   |
| Igkv4-80      | 2.894E-02 | 0.01   |
| Igkv4-79      | 2.137E-03 | 0.04   |
| Igkv4-74      | 4.413E-02 | 0.02   |
| Igkv4-70      | 3.191E-02 | 0.00   |
| Igkv4-61      | 4.417E-03 | 0.03   |
| Igkv4-57      | 1.096E-02 | 0.00   |
| Igkv4-56      | 5.664E-03 | 0.02   |
| Igkv12-46     | 1.200E-02 | 0.02   |
| Igkv5-39      | 4.365E-03 | 0.00   |
| Igkv6-32      | 1.687E-02 | 0.03   |
| Igkv8-24      | 1.469E-02 | 0.03   |
| Igkv6-20      | 4.329E-02 | 0.01   |
| Igkv6-13      | 1.292E-02 | 0.01   |
| Igkv3-10      | 1.760E-03 | 0.02   |
| Igkv3-7       | 1.502E-02 | 0.00   |
| Igkc          | 2.572E-03 | 0.02   |
| Ighg2c        | 5.508E-03 | 0.02   |
| Ighm          | 3.038E-04 | 0.13   |
| Ighv2-6-8     | 2.121E-02 | 0.02   |
| Ighv7-1       | 1.644E-02 | 0.06   |
| Ighv7-2       | 2.091E-02 | 0.11   |
| Ighv14-4      | 1.513E-02 | 0.03   |
| Ighv3-6       | 2.294E-03 | 0.02   |
| Ighv6-6       | 6.756E-03 | 0.00   |
| Ighv1-30      | 2.118E-02 | 0.00   |
| Ighv1-18      | 2.715E-02 | 0.03   |
| Ighv8-12      | 1.322E-02 | 0.02   |
| Tcrg-C1       | 3.997E-02 | 0.24   |
| Tcrg-C2       | 1.688E-02 | 0.36   |
| Trgv2         | 2.150E-02 | 0.35   |
| Tcrg-C        | 3.876E-02 | 0.36   |
| Trac          | 1.426E-02 | 0.46   |
| Iglv1         | 2.185E-02 | 0.02   |
| Iglc2         | 1.502E-02 | 0.03   |
| Iglv3         | 1.549E-02 | 0.13   |
| SNORA66       | 1.718E-02 | 2.28   |
| SNORA42       | 6.782E-03 | 102.57 |
| SNORA42       | 3.685E-03 | 7.40   |
| SNORA27       | 2.742E-02 | 2.62   |
| SNORA3        | 4.241E-02 | 1.94   |
| SNORA40       | 1.166E-02 | 50.01  |
| Snord17       | 6.130E-05 | 0.50   |
| F630028O10Rik | 8.420E-06 | 0.19   |
| Capns2        | 1.396E-02 | 0.54   |
| Dnm3os        | 1.782E-03 | 0.42   |
| F8a           | 8.196E-03 | 1.59   |
| AW011738      | 3.510E-03 | 2.09   |
| 1190007F08Rik | 1.321E-03 | 0.38   |
| Sarnp         | 2.060E-03 | 1.54   |
| 2310042D19Rik | 7.633E-03 | 0.65   |
| A930039A15Rik | 3.876E-04 | 0.24   |
| Gm13157       | 1.319E-05 | 0.34   |
| Gm13212       | 6.021E-08 | 0.22   |
| Gm438         | 2.763E-03 | 0.07   |
| Gm436         | 1.139E-03 | 0.03   |
| Gm13124       | 1.295E-03 | 0.04   |
| Aadacl3       | 8.483E-04 | 0.09   |
| Aunip         | 4.410E-09 | 5.19   |
| Nkain1        | 2.707E-02 | 1.84   |
| 2210404O09Rik | 2.107E-03 | 1.68   |
| Dear1         | 1.242E-02 | 1.87   |
| Bnip3         | 8.025E-04 | 3.88   |
| E430018J23Rik | 1.247E-03 | 1.93   |



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| AU022252      | 1.955E-03 | 1.77 |
| Gm5901        | 4.708E-02 | 1.63 |
| Tomt          | 2.388E-04 | 1.75 |
| Aoc2          | 4.908E-03 | 2.07 |
| Psme3         | 4.542E-04 | 1.64 |
| Lce1d         | 1.743E-03 | 0.29 |
| Fam174b       | 1.775E-03 | 0.49 |
| Mup19         | 4.580E-02 | 0.03 |
| Mup18         | 7.431E-03 | 0.02 |
| Mup10         | 8.657E-03 | 0.02 |
| Mup2          | 4.298E-02 | 0.04 |
| D030028A08Rik | 5.981E-05 | 1.61 |
| Gm2002        | 4.824E-03 | 0.30 |
| Haus5         | 6.422E-05 | 2.31 |
| Zfp566        | 4.377E-04 | 2.13 |
| Evi2a         | 6.662E-07 | 0.21 |
| Rad54b        | 4.560E-05 | 3.14 |
| Eif5a         | 1.425E-02 | 1.54 |
| Gm6746        | 4.957E-04 | 2.84 |
| Hist3h2a      | 2.960E-02 | 1.89 |
| Gm14412       | 1.555E-02 | 2.57 |
| Dpm1          | 4.042E-02 | 1.54 |
| 2410002O22Rik | 4.996E-03 | 1.71 |
| Cpt1b         | 2.853E-05 | 0.21 |
| Taf9          | 1.371E-02 | 1.68 |
| Naip6         | 9.419E-04 | 0.27 |
| Naip2         | 6.500E-05 | 0.30 |
| Gm12033       | 3.190E-02 | 4.08 |
| Wdr92         | 4.179E-06 | 1.79 |
| C030006K11Rik | 3.891E-03 | 1.53 |
| Samd1         | 4.363E-02 | 1.58 |
| Serpina3j     | 2.037E-03 | 0.01 |
| Serpina1c     | 9.822E-03 | 0.39 |
| Ly6c1         | 3.576E-02 | 0.53 |
| D130040H23Rik | 3.319E-04 | 0.43 |
| Fastkd5       | 1.018E-03 | 1.66 |
| Cyp4v3        | 1.181E-04 | 0.21 |
| Jrkl          | 2.175E-04 | 1.82 |
| Pms2          | 1.040E-03 | 1.78 |
| Capn3         | 1.822E-02 | 0.57 |
| Gm4204        | 9.386E-03 | 3.58 |
| A130010J15Rik | 4.596E-04 | 1.72 |
| Tlr5          | 1.607E-03 | 0.48 |
| Cd209g        | 6.339E-05 | 0.01 |
| Gzmc          | 4.349E-03 | 0.31 |
| Ccr5          | 1.269E-03 | 0.43 |
| Itpr1p        | 1.760E-02 | 1.57 |
| Slco1a6       | 1.916E-05 | 4.82 |
| Tmem233       | 1.017E-03 | 0.05 |
| Clec7a        | 9.716E-04 | 0.09 |
| Rab9          | 1.912E-04 | 0.63 |
| Gm5077        | 4.869E-04 | 0.45 |
| Ccrl1         | 2.054E-02 | 0.51 |
| Gm11110       | 2.140E-03 | 3.64 |
| Ms4a6c        | 2.459E-04 | 0.34 |
| Tceal7        | 1.666E-03 | 0.02 |
| St6galnac4    | 2.132E-05 | 0.27 |
| Tmprss11g     | 3.829E-02 | 9.02 |
| Gm7609        | 1.340E-02 | 0.38 |
| Utp14b        | 5.223E-04 | 2.20 |
| Sssca1        | 4.640E-03 | 2.02 |
| Nhs12         | 9.469E-04 | 0.30 |
| Phyhd1        | 6.523E-06 | 0.27 |
| 6530402F18Rik | 3.269E-02 | 2.15 |
| Gm11131       | 3.091E-02 | 1.89 |
| H2-DMb1       | 6.728E-04 | 0.32 |
| Kifc1         | 4.626E-05 | 3.26 |
| Haus3         | 1.841E-04 | 2.20 |
| Tmem182       | 4.160E-07 | 0.01 |
| C1qtnf5       | 7.512E-03 | 0.36 |
| Gm1975        | 5.816E-03 | 2.60 |
| Gm5483        | 3.766E-02 | 2.87 |
| Clec2l        | 4.628E-04 | 3.16 |
| 9230102O04Rik | 1.402E-02 | 2.80 |
| Gm13219       | 1.109E-02 | 3.75 |
| Ankrd39       | 2.251E-04 | 1.74 |
| Sehl1         | 2.656E-04 | 1.76 |
| Hspa14        | 2.590E-03 | 2.33 |
| Tm4sf19       | 1.434E-03 | 0.03 |
| Fam71f2       | 7.228E-03 | 7.07 |
| Rab26         | 4.763E-05 | 2.85 |
| 2610203C22Rik | 8.810E-03 | 0.62 |
| Gm15846       | 3.163E-03 | 1.84 |
| Gm16073       | 4.895E-02 | 1.64 |
| Gm17235       | 8.851E-04 | 2.03 |
| Gm14239       | 1.361E-04 | 1.71 |
| SNORA50       | 1.487E-02 | 7.10 |
| Gm12564       | 2.159E-05 | 2.80 |
| Rps2-ps9      | 8.809E-03 | 1.86 |
| Gm15661       | 1.409E-02 | 1.96 |
| Gm15613       | 2.986E-02 | 1.59 |
| Gm8731        | 2.719E-02 | 2.31 |
| Gm11442       | 7.266E-04 | 2.44 |
| Gm9159        | 4.611E-02 | 2.01 |
| Gm15760       | 4.987E-02 | 3.59 |
| Gm12529       | 2.121E-03 | 1.69 |
| Rpl30-ps3     | 3.167E-02 | 3.28 |



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|---------------|-----------|-------|
| Gm15739       | 1.319E-03 | 1.76  |
| Gm16061       | 3.953E-02 | 2.85  |
| Hist2h3c2     | 2.168E-02 | 2.53  |
| Gm13899       | 6.685E-04 | 1.96  |
| Rps12-ps26    | 8.722E-04 | 4.01  |
| BC022960      | 7.136E-05 | 5.07  |
| Gm15497       | 9.601E-03 | 1.68  |
| Gm14425       | 1.610E-02 | 2.03  |
| Gm12551       | 2.352E-03 | 0.08  |
| Gm11935       | 3.331E-02 | 1.71  |
| Cyp2j12       | 1.024E-02 | 0.04  |
| Gm11517       | 1.672E-02 | 1.63  |
| Gm11653       | 1.519E-03 | 2.31  |
| Gm12275       | 4.567E-02 | 1.78  |
| Gm16071       | 1.440E-04 | 2.09  |
| Gm15694       | 1.952E-02 | 2.21  |
| Gm13608       | 9.484E-03 | 1.65  |
| Gm13689       | 3.597E-03 | 1.62  |
| Gm15368       | 4.973E-02 | 1.56  |
| Gm15560       | 8.696E-04 | 2.21  |
| Gm12924       | 9.414E-03 | 2.39  |
| Slc48a1       | 1.190E-03 | 0.54  |
| Gm13717       | 6.134E-03 | 3.00  |
| Gm12192       | 1.661E-03 | 1.78  |
| Gm12926       | 1.433E-03 | 1.93  |
| Gm15953       | 2.261E-03 | 2.32  |
| Gm16210       | 1.529E-02 | 2.04  |
| Gm13423       | 1.153E-02 | 2.70  |
| Gm15922       | 1.700E-02 | 0.23  |
| Gm12959       | 3.638E-02 | 2.03  |
| Fzd10         | 1.515E-02 | 1.78  |
| Gm15931       | 4.379E-03 | 0.10  |
| Gm12852       | 4.777E-02 | 1.59  |
| Gm15549       | 3.255E-02 | 1.75  |
| Gm15152       | 4.648E-02 | 3.37  |
| Dnmt3l-ps1    | 4.842E-03 | 2.39  |
| Gm15539       | 1.877E-02 | 1.54  |
| Gm14212       | 2.653E-03 | 2.12  |
| Gm11719       | 1.453E-03 | 3.15  |
| Gm15231       | 1.770E-02 | 3.21  |
| Gm13862       | 2.986E-02 | 7.64  |
| Gm12312       | 2.631E-02 | 2.52  |
| Gm14276       | 4.472E-03 | 2.65  |
| Gm15994       | 3.970E-03 | 2.04  |
| Gm14382       | 1.369E-04 | 2.39  |
| Gm16074       | 1.728E-02 | 4.79  |
| Gm15547       | 1.307E-02 | 2.26  |
| Pisd-ps1      | 8.977E-04 | 0.49  |
| Btc           | 2.924E-02 | 0.30  |
| Gm11955       | 2.451E-02 | 2.81  |
| Gm12363       | 5.834E-03 | 1.96  |
| Gm12741       | 2.543E-03 | 1.59  |
| Gm15480       | 1.058E-02 | 2.14  |
| Gm11688       | 1.565E-02 | 2.12  |
| Gm13591       | 4.061E-02 | 2.30  |
| Gm13349       | 4.423E-02 | 1.55  |
| Gm15580       | 3.139E-03 | 3.30  |
| Gm12058       | 1.137E-03 | 6.22  |
| Gm12566       | 1.280E-02 | 0.40  |
| Gm11366       | 2.944E-03 | 5.83  |
| Gm14001       | 1.161E-02 | 2.39  |
| Gm13258       | 1.724E-02 | 14.54 |
| Gm12774       | 2.903E-02 | 1.71  |
| Gm12987       | 2.375E-04 | 1.95  |
| Rpl31-ps5     | 1.758E-02 | 4.06  |
| Gm9308        | 1.474E-02 | 0.17  |
| Gm13193       | 1.697E-03 | 4.20  |
| Gm15741       | 3.561E-02 | 0.49  |
| Gm13204       | 2.729E-02 | 1.64  |
| Gm11440       | 4.142E-02 | 2.05  |
| Cyp2j8        | 3.257E-03 | 0.04  |
| Rps13-ps6     | 1.511E-02 | 17.20 |
| 2810453106Rik | 2.711E-02 | 1.71  |
| Gm15531       | 1.587E-05 | 0.05  |
| Gm12917       | 2.883E-03 | 2.56  |
| Gm13511       | 6.909E-05 | 2.96  |
| D11Bhm181e    | 2.731E-02 | 3.53  |
| Gm14780       | 1.518E-05 | 2.50  |
| Gm11969       | 8.495E-03 | 1.93  |
| Gm13406       | 9.072E-03 | 2.78  |
| Ctsf          | 3.427E-03 | 0.47  |
| Gm11693       | 2.106E-03 | 2.14  |
| Gm13156       | 4.786E-02 | 1.77  |
| Gm11652       | 1.397E-02 | 2.38  |
| Gm12035       | 1.872E-03 | 1.92  |
| Gm13666       | 1.464E-02 | 1.98  |
| Gm15538       | 4.799E-03 | 1.82  |
| Gm15798       | 1.303E-02 | 1.92  |
| Gm11699       | 7.349E-04 | 0.07  |
| Gm2986        | 3.339E-04 | 2.17  |
| Gm13543       | 1.699E-03 | 2.48  |
| Gm13033       | 3.451E-04 | 5.02  |
| Gm15712       | 1.253E-02 | 0.57  |
| Gm15696       | 6.865E-03 | 1.86  |
| Gm11761       | 3.056E-04 | 2.55  |
| Plk-ps1       | 9.116E-03 | 1.62  |
| Gm15842       | 1.177E-02 | 1.79  |



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| Gm11483       | 3.065E-02 | 0.53  |
| Gm13786       | 4.558E-02 | 1.52  |
| Rps10-ps4     | 1.428E-04 | 3.72  |
| Gm12607       | 1.951E-02 | 4.78  |
| Gm7645        | 1.064E-02 | 1.98  |
| Gm15844       | 3.244E-02 | 2.44  |
| Gm14000       | 5.890E-03 | 3.95  |
| Gm12516       | 4.573E-02 | 1.76  |
| Gm14734       | 4.962E-02 | 6.13  |
| Gm11926       | 3.323E-04 | 3.26  |
| Gm8145        | 3.249E-02 | 0.59  |
| Gm6654        | 1.483E-03 | 1.97  |
| Gm15550       | 1.500E-02 | 1.80  |
| Znf41-ps      | 5.634E-05 | 0.61  |
| 2610024D14Rik | 4.128E-03 | 0.65  |
| AA413626      | 1.191E-02 | 1.75  |
| Gm11576       | 3.051E-03 | 5.21  |
| Gm11870       | 3.153E-04 | 1.75  |
| U4            | 3.086E-02 | 0.20  |
| 7SK           | 2.900E-02 | 2.51  |
| 7SK           | 1.836E-02 | 1.74  |
| U2            | 2.893E-03 | 10.95 |
| 7SK           | 7.820E-03 | 0.23  |
| 4930564G21Rik | 1.200E-04 | 3.72  |
| A430104N18Rik | 6.472E-05 | 0.26  |
| Gm17216       | 1.251E-02 | 1.68  |
| Gm16278       | 7.820E-06 | 2.33  |
| Ccdc85c       | 2.238E-04 | 3.74  |
| Gm14471       | 3.427E-03 | 2.13  |
| Gm17477       | 2.557E-03 | 1.63  |
| Gm15230       | 4.335E-03 | 3.83  |
| Gm5724        | 1.059E-03 | 11.58 |
| Dlx1as        | 8.070E-04 | 3.61  |
| Gm16194       | 3.141E-02 | 0.54  |
| B430010I23Rik | 9.849E-04 | 0.50  |
| Gm16260       | 3.911E-02 | 9.49  |
| BC021767      | 3.888E-02 | 0.54  |
| Gm13399       | 4.092E-04 | 1.60  |
| Gm12977       | 2.422E-03 | 2.76  |
| Gm5860        | 6.447E-03 | 2.13  |
| 4933421O10Rik | 5.504E-03 | 1.50  |
| Gm15927       | 9.982E-03 | 3.13  |
| Gm15834       | 8.333E-05 | 2.61  |
| A430071A18Rik | 1.417E-02 | 1.63  |
| Gm15635       | 2.261E-03 | 0.05  |
| Gm16288       | 4.779E-02 | 2.68  |
| Gm16070       | 5.662E-03 | 10.44 |
| Gm12609       | 2.896E-03 | 3.32  |
| Mir22hg       | 3.779E-03 | 0.56  |
| Gm11496       | 1.232E-03 | 4.36  |
| C130046K22Rik | 3.485E-03 | 2.23  |
| Gm11974       | 6.481E-05 | 1.68  |
| Gm10785       | 2.848E-02 | 1.64  |
| 1700064E03Rik | 4.025E-04 | 2.56  |
| Al838599      | 2.941E-04 | 0.08  |
| Gm12603       | 3.526E-03 | 15.63 |
| Gm13507       | 3.528E-03 | 2.63  |
| 6330418K02Rik | 7.265E-03 | 1.62  |
| Gm11713       | 4.437E-02 | 2.50  |
| BC046401      | 4.838E-03 | 2.10  |
| 4930430E12Rik | 1.831E-03 | 0.18  |
| Gm13684       | 7.446E-04 | 2.10  |
| Rps13-ps3     | 2.191E-02 | 2.48  |
| 3010003L21Rik | 5.233E-06 | 4.13  |
| Gm13480       | 6.440E-05 | 2.31  |
| Gm11647       | 3.494E-02 | 2.72  |
| Gm14508       | 7.508E-04 | 2.40  |
| 4930551L18Rik | 1.748E-02 | 3.34  |
| 9430008C03Rik | 2.383E-02 | 2.00  |
| C530005A16Rik | 2.095E-04 | 2.21  |
| 4930483C13Rik | 6.957E-05 | 4.33  |
| Gm16001       | 5.062E-04 | 2.41  |
| Gm16320       | 2.238E-04 | 6.80  |
| Trmt61b       | 8.885E-03 | 1.86  |
| Gm14023       | 3.175E-03 | 2.50  |
| Gm12868       | 4.050E-04 | 8.06  |
| 4930538E20Rik | 3.509E-02 | 2.02  |
| A730017L22Rik | 3.093E-04 | 2.07  |
| Gm13053       | 3.953E-02 | 2.08  |
| Gm15868       | 3.906E-06 | 2.10  |
| D630032N06Rik | 6.648E-03 | 3.76  |
| Gm9855        | 1.565E-04 | 2.21  |
| Gm16153       | 4.792E-03 | 1.64  |
| 2700086A05Rik | 3.782E-02 | 2.15  |
| 4921531C22Rik | 4.312E-02 | 1.58  |
| Gm15736       | 3.901E-03 | 0.19  |
| Gm7854        | 2.706E-03 | 2.07  |
| Gm11641       | 1.705E-03 | 2.83  |
| 5430405H02Rik | 7.443E-06 | 2.01  |
| Gm13536       | 2.705E-02 | 0.28  |
| Gm15412       | 2.421E-02 | 2.45  |
| 4930443B20Rik | 2.481E-03 | 2.47  |
| Gm13563       | 9.647E-04 | 2.35  |
| 2310050B05Rik | 2.071E-06 | 0.06  |
| Gm15640       | 8.693E-03 | 2.95  |
| Gm15624       | 3.433E-02 | 1.54  |
| Gm12158       | 1.121E-04 | 0.20  |



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| Gm13092       | 1.984E-02 | 3.26  |
| Gm15414       | 3.979E-03 | 2.86  |
| Zfp703        | 1.485E-02 | 1.82  |
| Gm4285        | 1.293E-02 | 1.55  |
| Gm14540       | 1.578E-02 | 1.80  |
| Gm12750       | 2.546E-05 | 2.87  |
| 2010012P19Rik | 1.004E-05 | 0.17  |
| Gm11604       | 4.693E-02 | 2.42  |
| Gm15601       | 3.125E-04 | 0.41  |
| Gm13421       | 2.868E-04 | 4.62  |
| Gm2788        | 1.775E-02 | 4.30  |
| Gm15706       | 1.615E-02 | 2.89  |
| 4833417C18Rik | 1.564E-05 | 1.87  |
| Gm16045       | 1.443E-02 | 2.20  |
| Gm15797       | 3.163E-05 | 2.03  |
| Gm13708       | 3.607E-02 | 0.51  |
| Gm13391       | 8.967E-05 | 0.20  |
| Gm14206       | 4.454E-03 | 7.66  |
| Gm13827       | 2.775E-03 | 2.54  |
| Gm13609       | 1.367E-02 | 1.53  |
| Gm16170       | 3.459E-02 | 1.54  |
| Gm15513       | 1.218E-06 | 0.11  |
| Gm11716       | 9.667E-03 | 0.48  |
| 2700033N17Rik | 4.287E-03 | 2.09  |
| Gm16310       | 2.108E-02 | 1.88  |
| Gm12932       | 7.745E-03 | 3.05  |
| Gm13830       | 7.252E-06 | 3.92  |
| Gm13705       | 3.171E-02 | 2.36  |
| Gm15563       | 2.352E-03 | 2.12  |
| 1810019D21Rik | 3.973E-02 | 1.71  |
| Gm16144       | 5.906E-03 | 1.59  |
| Gm15559       | 4.661E-04 | 3.31  |
| Gm15645       | 3.659E-04 | 1.82  |
| Gm13362       | 2.952E-02 | 2.57  |
| Gm14091       | 1.589E-02 | 4.27  |
| Gm11722       | 1.527E-02 | 1.76  |
| 4933431K23Rik | 6.962E-06 | 5.15  |
| Gm11457       | 2.797E-03 | 4.00  |
| Gm16172       | 1.586E-03 | 1.93  |
| Gm12264       | 2.284E-03 | 2.13  |
| Gm13648       | 8.481E-03 | 1.99  |
| Gm12002       | 4.197E-03 | 0.26  |
| C030005K06Rik | 4.182E-03 | 1.82  |
| 4930562D21Rik | 8.491E-06 | 2.99  |
| Gm12064       | 7.172E-03 | 4.54  |
| Gm11831       | 2.331E-02 | 1.93  |
| 4921530L18Rik | 1.707E-02 | 3.42  |
| Gm11592       | 2.972E-02 | 2.66  |
| Gm16023       | 9.230E-04 | 1.71  |
| Gm12867       | 3.042E-03 | 6.27  |
| Gm15247       | 2.357E-03 | 3.63  |
| Gm15848       | 4.413E-02 | 1.89  |
| Al427809      | 4.978E-03 | 0.21  |
| Gm17029       | 3.243E-02 | 2.00  |
| Gm15751       | 1.622E-02 | 1.59  |
| Gm13562       | 1.776E-03 | 1.98  |
| E130102H24Rik | 2.189E-03 | 0.57  |
| Gm15675       | 4.459E-04 | 0.39  |
| Gm16618       | 2.560E-04 | 2.75  |
| B230206H07Rik | 2.296E-04 | 2.08  |
| Lce6a         | 4.461E-04 | 0.15  |
| Gm7809        | 4.401E-02 | 2.56  |
| Gm15672       | 7.073E-05 | 3.39  |
| Gm11365       | 2.412E-02 | 2.13  |
| 1600002D24Rik | 7.122E-03 | 11.56 |
| Gm12207       | 4.082E-02 | 1.97  |
| Gm15489       | 5.647E-03 | 5.15  |
| Gm12248       | 1.019E-02 | 0.15  |
| Gm16314       | 1.223E-04 | 3.33  |
| 4933431E20Rik | 1.360E-03 | 0.45  |
| 4930443O20Rik | 2.442E-02 | 2.41  |
| Gm12981       | 3.465E-03 | 2.48  |
| Gm13889       | 4.884E-04 | 0.29  |
| A230103J11Rik | 4.682E-03 | 1.97  |
| Gm16295       | 4.302E-03 | 3.12  |
| Gm11948       | 3.488E-05 | 1.97  |
| 2810442I21Rik | 4.643E-04 | 4.11  |
| Gm11721       | 3.829E-04 | 1.84  |
| Gm12505       | 4.863E-02 | 3.47  |
| Nctc1         | 5.699E-09 | 0.03  |
| Al662270      | 1.723E-05 | 0.23  |
| Gm16093       | 2.867E-02 | 1.67  |
| Gm11714       | 4.626E-04 | 2.73  |
| Gm12655       | 4.414E-02 | 1.74  |
| A930001C03Rik | 2.251E-02 | 1.82  |
| Gm16096       | 5.602E-04 | 1.94  |
| Gm15545       | 8.738E-04 | 1.82  |
| Gm12454       | 6.627E-04 | 4.73  |
| Gm6483        | 4.149E-02 | 1.68  |
| Gm15246       | 1.337E-05 | 5.18  |
| Skint6        | 1.541E-02 | 0.16  |
| Gm15261       | 9.803E-05 | 0.11  |
| 2810408I11Rik | 7.318E-05 | 4.43  |
| Gm16062       | 2.195E-02 | 1.58  |
| 2610035D17Rik | 7.731E-08 | 3.00  |
| Gm15726       | 4.583E-02 | 2.22  |
| Gm12349       | 3.669E-03 | 9.84  |



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| D330023K18Rik | 3.743E-03 | 1.57  |
| Gm15317       | 1.172E-02 | 2.73  |
| Gm11946       | 1.495E-03 | 2.02  |
| Gm15884       | 3.161E-03 | 2.89  |
| 1700047K16Rik | 1.375E-04 | 1.67  |
| 4930404I05Rik | 7.497E-03 | 1.62  |
| Gm13710       | 2.811E-02 | 0.41  |
| BC042782      | 1.872E-03 | 2.43  |
| BC065397      | 1.524E-04 | 2.37  |
| Gm15892       | 1.648E-03 | 3.22  |
| AV099323      | 3.436E-02 | 5.78  |
| Gm16323       | 4.819E-02 | 0.47  |
| Gm12971       | 3.541E-03 | 1.94  |
| Gm13999       | 6.086E-03 | 3.67  |
| 2810001G20Rik | 1.537E-02 | 1.51  |
| Gm16091       | 2.997E-03 | 1.62  |
| Gm16141       | 1.705E-02 | 3.79  |
| Gm14389       | 2.182E-03 | 0.27  |
| 9830144P21Rik | 1.000E-02 | 3.12  |
| Gm15830       | 1.485E-02 | 2.20  |
| Gm13427       | 1.731E-03 | 3.32  |
| C030037D09Rik | 5.010E-04 | 4.44  |
| Gm16174       | 1.189E-02 | 1.60  |
| BC039771      | 1.634E-03 | 1.75  |
| Zfp111        | 1.473E-05 | 1.70  |
| Gm15050       | 8.105E-04 | 3.35  |
| Gm15051       | 3.602E-05 | 3.64  |
| Gm12606       | 2.778E-03 | 2.32  |
| Gm11724       | 3.318E-02 | 2.69  |
| C330006A16Rik | 1.277E-03 | 1.55  |
| Gm15845       | 4.038E-07 | 5.87  |
| Gm15674       | 1.732E-03 | 0.38  |
| Gm11940       | 1.709E-03 | 0.37  |
| Gm15283       | 4.598E-05 | 4.16  |
| SNORA74       | 2.232E-02 | 1.71  |
| 7SK           | 4.367E-02 | 2.91  |
| snoU13        | 1.227E-02 | 0.02  |
| SNORA61       | 2.244E-02 | 6.10  |
| 7SK           | 1.507E-02 | 0.51  |
| snoU109       | 1.040E-02 | 3.71  |
| 7SK           | 2.420E-02 | 1.67  |
| 7SK           | 1.032E-02 | 2.08  |
| SNORA48       | 2.415E-02 | 2.23  |
| U1            | 1.124E-03 | 5.27  |
| SCARNA7       | 9.433E-05 | 0.60  |
| SNORA50       | 4.480E-02 | 20.11 |
| U1            | 4.978E-02 | 2.46  |
| 1700058P15Rik | 2.149E-02 | 1.74  |
| Gm2862        | 1.476E-02 | 2.29  |
| Fcor          | 7.974E-05 | 0.20  |
| Tnfsf13       | 1.945E-06 | 0.11  |
| Gp49a         | 5.948E-05 | 0.20  |
| Cbx6          | 1.102E-03 | 0.36  |
| Gm11711       | 7.684E-05 | 0.11  |
| Mir17hg       | 1.052E-03 | 2.82  |
| Clec2f-ps     | 4.093E-04 | 6.42  |
| Gm16552       | 1.159E-02 | 1.70  |
| Ier5l         | 1.561E-03 | 2.65  |
| Skint1        | 4.788E-03 | 0.55  |
| Rdh1          | 2.694E-03 | 0.25  |
| 1700028K03Rik | 4.899E-03 | 2.09  |
| Gm16138       | 1.396E-04 | 2.59  |
| A530032D15Rik | 1.688E-02 | 0.47  |
| Gm15853       | 4.936E-02 | 1.87  |
| Gm16184       | 4.076E-02 | 2.25  |
| Gm15664       | 1.221E-02 | 9.75  |
| Bcl2a1b       | 4.325E-04 | 0.24  |
| Gm4117        | 2.934E-04 | 2.32  |
| Pira2         | 1.134E-04 | 0.08  |
| Gm20459       | 6.718E-03 | 0.58  |
| Gm16137       | 9.538E-07 | 3.72  |
| Ugt1a1        | 1.084E-04 | 0.17  |
| Flt3l         | 7.912E-03 | 0.62  |
| Gm16006       | 2.541E-02 | 2.23  |
| Gm16147       | 9.108E-03 | 0.49  |
| Srpx          | 7.855E-04 | 0.28  |
| Abhd12b       | 1.798E-02 | 0.28  |
| Ugt1a7c       | 2.048E-03 | 0.51  |
| Ear10         | 3.520E-03 | 0.09  |
| Gm16161       | 2.623E-02 | 1.98  |
| AU015336      | 4.459E-04 | 2.28  |
| Tepp          | 3.440E-02 | 2.01  |
| Tmem189       | 2.167E-04 | 0.55  |
| Gm16315       | 4.548E-02 | 0.62  |
| Cfb           | 1.189E-06 | 0.10  |
| Gm4524        | 5.049E-05 | 3.17  |
| Eif4ebp3      | 5.231E-03 | 1.60  |
| Mndal         | 1.148E-02 | 0.28  |
| Gm17296       | 1.834E-03 | 2.06  |
| Gm17034       | 7.022E-03 | 4.52  |
| 1700071M16Rik | 1.870E-02 | 0.40  |
| 2310050C09Rik | 5.166E-04 | 0.19  |
| 9130221H12Rik | 1.594E-04 | 1.73  |
| 2810055G20Rik | 2.701E-05 | 0.36  |
| 4930523C07Rik | 9.856E-04 | 0.46  |
| Gm17096       | 1.464E-03 | 2.09  |
| Efna5         | 2.599E-02 | 3.57  |



|               |           |       |
|---------------|-----------|-------|
| Gypc          | 3.085E-03 | 0.40  |
| Gm5538        | 1.855E-03 | 0.04  |
| Gm20731       | 1.150E-03 | 2.08  |
| Tex9          | 1.457E-06 | 1.53  |
| Gm20425       | 3.966E-02 | 0.56  |
| Zfp493        | 1.267E-02 | 2.66  |
| Gm8378        | 5.586E-03 | 1.96  |
| Gm17213       | 3.519E-05 | 3.17  |
| Gm17201       | 1.913E-02 | 1.92  |
| Gm3235        | 2.558E-02 | 1.69  |
| Klh133        | 2.009E-04 | 0.14  |
| 1700092M07Rik | 8.431E-03 | 4.91  |
| Ccdc71l       | 1.179E-02 | 1.88  |
| Gm17251       | 6.588E-03 | 1.64  |
| Gm17300       | 1.813E-03 | 2.16  |
| 9330020H09Rik | 1.202E-04 | 2.45  |
| Gm17105       | 5.463E-03 | 2.54  |
| 5830462119Rik | 3.699E-04 | 2.05  |
| Gm5633        | 1.958E-03 | 3.28  |
| 4921509A06Rik | 2.773E-02 | 3.07  |
| Gm3604        | 4.570E-04 | 1.66  |
| Gm20390       | 6.335E-03 | 1.66  |
| Vgll3         | 6.455E-04 | 0.39  |
| Gm17430       | 1.538E-03 | 0.11  |
| Fth-ps2       | 7.625E-03 | 2.13  |
| Gm17214       | 3.016E-02 | 3.52  |
| Flg           | 2.455E-02 | 0.37  |
| Col6a5        | 1.440E-03 | 0.01  |
| Gcnt4         | 2.772E-02 | 0.46  |
| Hist2h4       | 8.977E-05 | 1.92  |
| Gm2895        | 9.504E-05 | 25.03 |
| Gm17084       | 4.849E-02 | 0.51  |
| 2610021A01Rik | 9.083E-04 | 1.58  |
| Gm6548        | 1.040E-02 | 1.79  |
| Gm6211        | 1.973E-03 | 7.85  |
| Cyp4f17       | 1.568E-02 | 2.45  |
| Gm17092       | 3.925E-03 | 3.09  |
| Lsm5          | 2.138E-04 | 2.18  |
| H2-Q2         | 3.353E-02 | 3.33  |
| Yy2           | 3.779E-03 | 1.51  |
| D17H6S56E-5   | 1.331E-02 | 1.92  |
| Sco2          | 1.499E-03 | 2.70  |
| Gm17022       | 8.205E-03 | 1.71  |
| Gm4707        | 3.329E-03 | 1.59  |
| 1700099I09Rik | 2.166E-04 | 2.21  |
| Gm17354       | 5.342E-04 | 1.50  |
| E130317F20Rik | 1.021E-03 | 2.69  |
| Gbp11         | 2.198E-02 | 0.24  |
| Bend4         | 7.577E-03 | 2.27  |
| Fancf         | 1.264E-04 | 2.34  |
| Gcom1         | 4.533E-02 | 0.18  |
| 4930515G01Rik | 1.130E-04 | 2.33  |
| Gm20471       | 4.516E-03 | 0.40  |
| Gm20470       | 1.012E-02 | 2.03  |
| 1110038B12Rik | 2.183E-04 | 2.30  |
| Gm4433        | 2.391E-02 | 1.70  |
| Gm20540       | 2.744E-02 | 1.64  |
| 4930518C09Rik | 1.974E-02 | 0.27  |
| Hspe1-ps3     | 4.917E-02 | 2.06  |
| Gm20535       | 3.179E-02 | 3.17  |
| Gm4189        | 5.275E-03 | 3.07  |
| Gm20456       | 1.069E-03 | 2.24  |
| Gm18343       | 4.181E-03 | 2.63  |
| Gm17907       | 4.582E-04 | 1.76  |
| Gm20418       | 2.723E-02 | 8.51  |
| Gm20475       | 2.123E-02 | 0.04  |
| Gm20544       | 7.644E-03 | 3.03  |
| Ly6g6c        | 1.325E-03 | 0.45  |
| Gm20427       | 1.304E-03 | 2.14  |
| Gm20442       | 1.545E-02 | 8.65  |
| 9130230N09Rik | 8.759E-04 | 2.63  |
| 7SK           | 1.207E-03 | 3.64  |
| Metazoa_SRP   | 2.964E-02 | 12.26 |
| AC165250.1    | 3.047E-02 | 4.04  |
| Gm20702       | 6.158E-03 | 2.41  |
| Lrch4         | 1.603E-02 | 0.66  |
| AA465934      | 7.651E-03 | 1.72  |
| Gm20699       | 8.588E-03 | 1.51  |
| Gm20695       | 1.159E-02 | 3.32  |
| A730085K08Rik | 5.711E-03 | 1.99  |
| Gm19357       | 2.092E-03 | 1.93  |
| Elf4e3        | 4.524E-02 | 1.52  |
| Gm20667       | 5.837E-04 | 4.66  |
| Hist2h3c1     | 1.076E-02 | 3.02  |
| CAA01154301.1 | 3.768E-04 | 2.35  |
| Bcl2a1a       | 9.615E-04 | 0.35  |
| AC140374.1    | 1.580E-02 | 0.03  |
| SNORA25       | 3.836E-02 | 2.91  |
| AC074329.1    | 1.354E-02 | 0.03  |
| Gm5784        | 4.153E-02 | 1.55  |
| SNORA17       | 1.118E-03 | 0.03  |
| EVI2B         | 1.601E-05 | 0.35  |
| AC073565.1    | 3.948E-03 | 0.07  |
| AC156953.1    | 6.664E-03 | 0.04  |
| Ccl21b        | 2.491E-04 | 0.18  |
| Gm4767        | 3.124E-03 | 1.90  |
| AC164609.1    | 2.130E-02 | 0.07  |



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|---------------|-----------|---------|
| Gm15921       | 3.385E-03 | 2.03    |
| AC155333.1    | 1.261E-02 | 0.01    |
| AC153855.1    | 1.033E-02 | 0.00    |
| RPP14         | 3.794E-03 | 1.80    |
| AC160985.1    | 1.925E-02 | 0.02    |
| AC090887.1    | 1.362E-02 | 0.01    |
| Hist1h2ao     | 5.331E-04 | 2.49    |
| AC153614.1    | 2.213E-02 | 0.04    |
| AC073590.2    | 2.543E-02 | 0.02    |
| AC139157.1    | 3.748E-03 | 3.92    |
| AC122260.1    | 3.561E-02 | 0.04    |
| AC159715.1    | 2.928E-02 | 0.04    |
| AC174597.1    | 8.640E-03 | 0.03    |
| AC155333.2    | 1.234E-02 | 0.02    |
| AC100927.1    | 2.655E-02 | 1.55    |
| AC171501.1    | 3.687E-03 | 0.06    |
| 2700090003Rik | 1.993E-02 | 2.07    |
| AC079273.2    | 4.652E-02 | 0.07    |
| AC158361.2    | 3.069E-02 | 0.40    |
| AC073565.5    | 1.192E-02 | 0.04    |
| AC079181.1    | 4.014E-02 | 0.01    |
| Gm20382       | 1.768E-03 | 3.26    |
| Ccl21a        | 2.520E-06 | 0.12    |
| 1600014C23Rik | 1.363E-02 | 145.86  |
| Gm5416        | 2.375E-03 | 7.87    |
| AC122322.1    | 6.272E-04 | 0.03    |
| AC140374.2    | 6.650E-03 | 0.04    |
| AC074329.4    | 2.208E-02 | 0.03    |
| AC153855.2    | 1.524E-02 | 0.01    |
| PLAC9         | 2.845E-04 | 0.16    |
| AL805896.1    | 4.380E-02 | 6180.44 |
| AC122260.2    | 2.676E-02 | 0.03    |
| AC120404.1    | 2.841E-02 | 0.00    |
| ZFP936        | 8.332E-03 | 2.11    |
| Gm3944        | 2.660E-02 | 2.48    |
| AC155333.3    | 3.708E-03 | 0.01    |
| AC158361.3    | 2.856E-02 | 0.37    |
| AC160982.1    | 4.309E-03 | 0.02    |
| Edaradd       | 1.081E-02 | 1.87    |
| AC079181.2    | 2.437E-03 | 0.04    |
| AC079181.3    | 4.269E-02 | 0.05    |
| AC073939.2    | 3.927E-03 | 0.05    |
| AW146154      | 6.753E-04 | 2.51    |
| AC160985.3    | 7.813E-03 | 0.02    |
| Gm9944        | 3.298E-03 | 0.08    |
| KRT6A         | 5.192E-03 | 4.10    |
| Zfp799        | 5.964E-03 | 1.56    |
| AC090887.3    | 4.474E-02 | 0.01    |
| Gm12407       | 6.499E-03 | 0.12    |
| Plac9         | 3.902E-04 | 0.16    |
| AC169518.1    | 1.426E-07 | 0.19    |
| U6            | 3.941E-02 | 8.59    |
| AC153928.1    | 2.567E-03 | 0.00    |
| AC090887.4    | 3.650E-02 | 0.02    |
| AC087166.3    | 5.195E-03 | 0.06    |
| A630023A22Rik | 1.340E-02 | 3.47    |
| AC122260.3    | 2.417E-02 | 0.00    |
| U1            | 3.911E-02 | 6.51    |
| AC073939.3    | 2.925E-02 | 0.00    |
| Gm15682       | 2.507E-03 | 3.44    |
| AC090843.3    | 4.381E-03 | 0.02    |
| CR536618.1    | 1.804E-02 | 2.09    |
| Noc2l         | 1.004E-02 | 1.77    |
| AC160985.5    | 4.140E-02 | 0.03    |
| AC073563.2    | 3.072E-03 | 0.08    |
| AC090887.5    | 3.851E-02 | 0.02    |
| AC158672.2    | 1.164E-02 | 0.04    |
| AC156953.3    | 1.942E-02 | 0.04    |
| Gm2004        | 2.214E-02 | 2.90    |
| RP24-69M8.3   | 1.148E-02 | 2.04    |
| Ccl21c        | 9.419E-04 | 0.21    |
| AC153612.3    | 1.636E-02 | 0.03    |
| U1            | 4.278E-02 | 5.35    |
| AC153615.2    | 1.111E-02 | 0.02    |
| AC240744.2    | 1.715E-02 | 1.95    |
| Sirpb1a       | 4.934E-03 | 0.46    |
| AC158672.3    | 3.471E-02 | 0.03    |
| AC079181.4    | 3.111E-02 | 0.07    |
| AC090887.6    | 2.244E-02 | 0.01    |
| AC079181.5    | 1.406E-02 | 0.01    |
| AC073561.5    | 1.028E-02 | 0.01    |
| Zfp97         | 1.785E-02 | 1.54    |
| 2610528A11Rik | 5.811E-03 | 3.07    |
| Hist4h4       | 6.595E-04 | 2.04    |
| SYNE1         | 1.105E-02 | 0.41    |
| A630095N17Rik | 8.582E-03 | 4.78    |
| U6            | 2.816E-02 | 4.00    |
| Cmtm4         | 1.106E-02 | 1.83    |
| Ptrhd1        | 2.851E-04 | 1.78    |
| U1            | 4.201E-02 | 3.51    |
| AC124758.1    | 3.303E-03 | 0.02    |
| Samd11        | 1.008E-03 | 2.37    |
| AC155333.4    | 4.571E-03 | 0.02    |
| AC160473.5    | 1.462E-02 | 0.08    |
| MOAP1         | 4.159E-03 | 2.04    |
| AC073563.4    | 8.583E-03 | 0.03    |
| AC090887.7    | 3.149E-02 | 0.02    |



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| AC160990.5    | 1.303E-02 | 0.07 |
| Cdkn2d        | 1.821E-05 | 2.20 |
| AC120404.2    | 1.789E-02 | 0.02 |
| AC090887.8    | 4.372E-02 | 0.01 |
| AC073561.6    | 4.158E-02 | 0.04 |
| AC122918.1    | 3.949E-02 | 0.04 |
| AC171501.3    | 3.562E-02 | 0.03 |
| Bcl2a1d       | 1.578E-02 | 0.32 |
| AC158672.4    | 7.955E-03 | 0.02 |
| Gm10591       | 2.048E-03 | 0.22 |
| AC131065.1    | 1.727E-03 | 2.45 |
| Gm7694        | 6.380E-03 | 2.87 |
| GM5849        | 4.135E-03 | 0.04 |
| AC079273.4    | 6.232E-03 | 0.01 |
| U6            | 3.120E-02 | 6.17 |
| AC160985.6    | 1.144E-02 | 0.00 |
| Mup15         | 2.571E-02 | 0.03 |
| SNORA17       | 2.545E-02 | 0.19 |
| AC153928.3    | 2.456E-02 | 0.01 |
| Tmem181c-ps   | 2.177E-02 | 2.27 |
| AC073563.5    | 6.570E-03 | 0.00 |
| Hist1h2bm     | 7.904E-03 | 2.44 |
| Ccl27b        | 4.464E-04 | 0.28 |
| AC158673.1    | 3.197E-02 | 0.01 |
| AC153855.3    | 7.102E-03 | 0.03 |
| Gm4767        | 2.783E-03 | 1.93 |
| AC158361.6    | 1.936E-02 | 0.41 |
| AC130841.1    | 1.891E-02 | 1.81 |
| AC131761.2    | 1.554E-03 | 1.65 |
| mmu-mir-29b-2 | 3.224E-03 | 0.57 |
| AC110382.1    | 6.467E-05 | 8.46 |
| RP23-251i6.1  | 2.761E-02 | 0.47 |
| AC163623.1    | 3.183E-02 | 1.57 |
| AC153516.1    | 2.080E-03 | 1.72 |
| AC127433.1    | 2.383E-03 | 1.90 |
| AC163357.1    | 5.257E-04 | 6.81 |
| AC172623.1    | 1.318E-02 | 1.63 |
| CT025649.1    | 6.720E-03 | 3.47 |
| AC124998.1    | 2.213E-04 | 1.64 |
| AC079443.1    | 1.768E-03 | 2.11 |
| AC115880.1    | 3.990E-03 | 3.76 |
| AC156618.1    | 1.724E-03 | 1.72 |
| AC122371.1    | 1.939E-03 | 2.52 |
| AC140326.1    | 4.148E-04 | 2.32 |
| AC142103.1    | 2.386E-03 | 2.35 |
| AL732311.1    | 1.234E-04 | 1.81 |
| AL589650.1    | 1.457E-06 | 2.29 |
| CT010439.1    | 2.009E-02 | 1.82 |
| AC099934.1    | 5.490E-03 | 1.54 |
| AL663030.1    | 1.639E-02 | 2.12 |
| AC133646.1    | 6.884E-06 | 2.54 |
| AC141882.1    | 3.099E-04 | 1.67 |
| AL672219.1    | 4.927E-05 | 2.30 |
| AC132304.1    | 9.639E-04 | 7.46 |
| AC125483.1    | 4.091E-03 | 5.46 |
| AC163677.1    | 1.260E-02 | 1.75 |
| AC131759.1    | 1.268E-04 | 1.52 |
| AC120136.1    | 1.306E-04 | 1.97 |
| AC122200.1    | 2.983E-04 | 2.09 |
| AC154015.1    | 1.728E-02 | 2.26 |
| AL672278.1    | 3.851E-02 | 1.60 |
| AC158975.1    | 4.680E-03 | 1.84 |
| AL627104.1    | 2.024E-03 | 1.87 |
| AC101790.1    | 5.046E-03 | 3.91 |
| AL732490.1    | 8.089E-04 | 3.42 |
| AC151989.1    | 7.047E-03 | 2.05 |
| AC117663.1    | 2.269E-04 | 2.01 |
| RP23-399i8.10 | 3.721E-02 | 2.44 |
| AC025794.1    | 1.514E-03 | 1.78 |
| CT025673.1    | 7.012E-03 | 1.55 |
| AL672246.2    | 8.839E-03 | 1.57 |
| AC092094.1    | 5.076E-04 | 2.02 |
| AC112688.1    | 2.080E-04 | 2.41 |
| AC161166.1    | 3.039E-02 | 1.90 |
| CT033751.2    | 8.222E-04 | 2.20 |
| AC137156.1    | 8.630E-04 | 1.71 |
| AARSD1        | 2.817E-05 | 3.03 |
| AC149052.1    | 1.605E-02 | 1.76 |
| AC167537.1    | 6.574E-03 | 2.04 |
| AC121121.1    | 1.123E-05 | 2.16 |
| AL603843.1    | 6.882E-03 | 1.83 |
| mmu-mir-1839  | 2.082E-03 | 0.62 |
| AC158608.1    | 2.491E-04 | 1.71 |
| AC140333.2    | 8.002E-04 | 2.48 |
| AC124550.1    | 1.078E-02 | 1.85 |
| AC122247.1    | 8.352E-04 | 2.53 |
| AC148011.1    | 4.042E-03 | 0.49 |
| Tnfrsf12      | 4.282E-04 | 0.12 |
| AC166827.1    | 4.171E-02 | 1.64 |
| AC020971.1    | 6.461E-03 | 2.87 |
| AC144852.1    | 1.345E-06 | 2.25 |
| AC132406.1    | 8.825E-03 | 2.10 |
| AL591113.1    | 3.548E-03 | 1.74 |
| AC099930.1    | 2.866E-03 | 1.79 |
| AC122881.1    | 2.638E-02 | 2.39 |
| RP24-547D11.3 | 3.698E-02 | 0.09 |
| AC129082.1    | 1.085E-04 | 3.52 |



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| AC110567.1    | 3.855E-04 | 2.32  |
| AC154200.1    | 1.298E-03 | 2.01  |
| AC116739.1    | 8.710E-03 | 2.19  |
| AC131692.1    | 4.879E-03 | 2.62  |
| AL731670.1    | 6.103E-03 | 2.18  |
| AC152453.2    | 6.346E-03 | 1.88  |
| AC161165.1    | 1.692E-05 | 1.68  |
| RP23-285C18.2 | 8.034E-03 | 0.44  |
| AC124550.2    | 2.947E-04 | 3.54  |
| AC163637.1    | 1.467E-04 | 3.10  |
| AL450399.2    | 1.571E-04 | 3.46  |
| AC158898.2    | 2.743E-04 | 1.96  |
| D330020A13RIK | 5.493E-03 | 6.59  |
| AC119214.1    | 3.378E-04 | 3.37  |
| RP23-73F23.2  | 9.579E-03 | 1.84  |
| RP23-268C9.2  | 1.122E-03 | 1.58  |
| AC159277.2    | 1.913E-02 | 1.99  |
| mmu-mir-706   | 2.528E-03 | 1.82  |
| AC087541.3    | 8.227E-04 | 1.76  |
| AC162384.1    | 1.579E-03 | 2.61  |
| AC098726.2    | 1.869E-03 | 1.55  |
| RP24-547D11.5 | 4.238E-04 | 0.11  |
| AC154660.1    | 2.186E-04 | 0.60  |
| AC113124.1    | 3.396E-02 | 1.55  |
| AC124191.1    | 9.489E-03 | 1.54  |
| AC113309.1    | 2.862E-02 | 1.73  |
| 4921514A10RIK | 3.014E-02 | 1.97  |
| AC126942.1    | 1.010E-02 | 1.69  |
| AC123702.1    | 4.722E-04 | 2.48  |
| AC122397.1    | 2.041E-03 | 6.14  |
| BX537302.1    | 2.925E-03 | 2.94  |
| AC140410.1    | 1.870E-03 | 1.85  |
| AC164614.1    | 3.440E-02 | 1.61  |
| AC161602.1    | 1.504E-02 | 0.42  |
| AC130277.1    | 6.157E-03 | 1.90  |
| RP24-547D11.2 | 1.067E-02 | 0.27  |
| AC127314.1    | 3.266E-03 | 0.35  |
| RP23-111M12.1 | 1.317E-03 | 3.26  |
| CT030166.1    | 2.416E-04 | 0.34  |
| AC164612.1    | 2.397E-04 | 3.99  |
| AC124461.1    | 4.639E-03 | 1.57  |
| AC123834.1    | 1.531E-07 | 4.56  |
| AC114655.2    | 4.860E-02 | 12.24 |
| AC121821.1    | 1.191E-03 | 1.78  |
| AC107744.1    | 9.260E-06 | 2.32  |
| AC121499.1    | 2.027E-03 | 1.60  |
| AL607108.1    | 3.948E-03 | 5.17  |
| AC125169.1    | 1.015E-04 | 2.83  |
| AC122273.1    | 1.489E-06 | 1.93  |
| AC108434.1    | 6.797E-03 | 1.92  |
| mmu-mir-205   | 1.183E-02 | 2.42  |
| AL844859.1    | 4.145E-02 | 2.14  |
| AL772401.1    | 2.443E-04 | 0.42  |
| AC135354.1    | 1.168E-02 | 2.08  |
| 4932427H20RIK | 4.696E-03 | 2.34  |
| AC116484.1    | 5.863E-03 | 1.71  |
| AC158928.1    | 1.587E-04 | 1.57  |
| AC123699.1    | 3.071E-02 | 1.60  |
| AC147987.1    | 1.297E-06 | 3.25  |
| AC109232.1    | 1.239E-03 | 5.25  |
| AC129574.1    | 8.881E-03 | 2.61  |
| AC102862.2    | 6.790E-04 | 2.99  |
| AC136147.1    | 1.378E-02 | 13.14 |



gene signature CHR-SCC

| Gene     | p-value   | fold change<br>SCC/CHR |
|----------|-----------|------------------------|
| Cdc45    | 4.830E-03 | 2.24                   |
| Scmh1    | 5.618E-03 | 1.74                   |
| Wnt3     | 3.974E-02 | 0.46                   |
| Wnt9a    | 1.198E-02 | 3.95                   |
| Pih1d2   | 1.628E-02 | 2.10                   |
| Ccnd2    | 3.347E-03 | 0.54                   |
| Sifn4    | 2.687E-02 | 2.69                   |
| Tspan32  | 1.750E-03 | 0.45                   |
| Clec2g   | 1.464E-02 | 0.48                   |
| Gmpr     | 6.885E-06 | 0.46                   |
| Itgb2    | 6.423E-03 | 0.29                   |
| Hddc2    | 1.878E-03 | 2.00                   |
| Tpd52l1  | 1.132E-02 | 1.83                   |
| Pemt     | 4.692E-02 | 1.75                   |
| Bcl6b    | 1.825E-04 | 2.30                   |
| Clec10a  | 2.296E-05 | 0.10                   |
| Arvcf    | 4.393E-03 | 0.58                   |
| Fap      | 1.510E-02 | 0.55                   |
| Cttnbp2  | 5.273E-05 | 0.36                   |
| Pparg    | 2.323E-06 | 0.13                   |
| 1-Sep    | 1.867E-02 | 0.65                   |
| Acvrl1   | 9.405E-03 | 0.64                   |
| Itga5    | 3.135E-02 | 1.72                   |
| Adora3   | 2.107E-03 | 0.52                   |
| Hnrnpd   | 3.957E-05 | 1.76                   |
| Gm2a     | 1.926E-03 | 0.51                   |
| Myo18a   | 2.040E-04 | 0.56                   |
| Cd52     | 7.476E-03 | 0.47                   |
| Kat2b    | 5.981E-04 | 0.51                   |
| Dnmt3l   | 4.752E-02 | 2.17                   |
| Polr3d   | 1.001E-03 | 1.52                   |
| Pxmp4    | 2.479E-04 | 0.37                   |
| Gnb1l    | 6.151E-05 | 2.20                   |
| Nsun5    | 4.767E-04 | 1.64                   |
| Top1mt   | 1.263E-02 | 1.88                   |
| Nhp2     | 2.344E-02 | 1.55                   |
| Mfsd10   | 7.756E-07 | 1.66                   |
| Cfp      | 2.541E-02 | 0.50                   |
| Uhrf1    | 2.380E-04 | 2.23                   |
| Hpn      | 8.960E-04 | 0.41                   |
| Ckb      | 1.922E-04 | 0.10                   |
| Efnb2    | 1.236E-03 | 0.39                   |
| Rrp15    | 2.331E-02 | 1.75                   |
| Rnd2     | 3.868E-03 | 0.64                   |
| Cnn1     | 6.395E-03 | 2.27                   |
| Ube2c    | 5.632E-06 | 3.87                   |
| Col18a1  | 2.347E-03 | 1.77                   |
| Slc19a1  | 1.339E-03 | 2.30                   |
| Kpnb1    | 2.425E-04 | 1.57                   |
| Tubb6    | 2.674E-04 | 2.49                   |
| Pax9     | 4.688E-05 | 25.03                  |
| Irx2     | 2.048E-03 | 0.44                   |
| Itga3    | 9.194E-03 | 4.81                   |
| Sgca     | 8.319E-04 | 0.39                   |
| Foxm1    | 6.305E-07 | 2.56                   |
| Tubb5    | 5.127E-05 | 1.55                   |
| Elf2     | 4.028E-03 | 1.61                   |
| Fkbp10   | 1.995E-02 | 2.10                   |
| Tcea3    | 1.233E-06 | 0.22                   |
| Stk38l   | 8.567E-05 | 1.66                   |
| Akr1b3   | 4.227E-02 | 1.54                   |
| Gstt1    | 5.518E-05 | 0.22                   |
| Ddx18    | 1.097E-02 | 1.75                   |
| Ubl3     | 1.980E-04 | 0.62                   |
| Gramd3   | 2.577E-04 | 0.58                   |
| Eef1e1   | 1.096E-02 | 2.25                   |
| Il16     | 1.745E-04 | 0.46                   |
| Naglu    | 8.884E-03 | 0.48                   |
| Smo      | 4.147E-07 | 1.83                   |
| Pwp1     | 2.251E-03 | 1.57                   |
| Lrp3     | 6.450E-03 | 0.52                   |
| Aif1l    | 9.277E-04 | 0.23                   |
| Cpa3     | 1.164E-05 | 0.19                   |
| Nfix     | 1.157E-02 | 0.65                   |
| Slc1a5   | 3.798E-03 | 0.57                   |
| Sipa1l2  | 3.870E-05 | 2.02                   |
| Blvra    | 3.903E-03 | 0.66                   |
| Pdzd4    | 8.637E-03 | 0.65                   |
| Srpk3    | 2.109E-02 | 0.67                   |
| Cd3g     | 1.392E-04 | 0.39                   |
| Spag5    | 6.196E-07 | 3.13                   |
| Foxn1    | 9.019E-03 | 2.28                   |
| Unc119   | 3.432E-03 | 0.64                   |
| Ccne1    | 2.026E-02 | 3.85                   |
| Celf2    | 9.427E-05 | 0.30                   |
| Nr1h3    | 7.093E-04 | 0.37                   |
| Ddb2     | 2.373E-03 | 1.55                   |
| Sfp1l    | 1.125E-02 | 0.48                   |
| Napsa    | 1.911E-04 | 0.44                   |
| Paxip1   | 3.135E-05 | 1.72                   |
| Rmnd5a   | 3.691E-04 | 0.59                   |
| Ppm1j    | 2.370E-02 | 1.53                   |
| Ppard    | 1.471E-03 | 2.35                   |
| Metrn    | 2.057E-02 | 1.83                   |
| Dbf4     | 1.211E-04 | 3.27                   |
| Abhd3    | 1.291E-03 | 0.24                   |
| Snrpd1   | 5.636E-05 | 1.56                   |
| Rpl3l    | 1.018E-07 | 0.16                   |
| Slc9a3r2 | 2.706E-02 | 0.55                   |
| Scin     | 4.754E-04 | 0.50                   |
| Dennd1c  | 1.201E-02 | 0.58                   |
| Lcp2     | 2.203E-02 | 0.56                   |
| Cse1l    | 8.913E-04 | 1.57                   |
| Jag2     | 5.488E-03 | 2.12                   |
| Nudt14   | 8.815E-04 | 1.80                   |



|          |           |       |
|----------|-----------|-------|
| Top3a    | 2.969E-04 | 1.52  |
| Qtrt1    | 3.737E-03 | 1.99  |
| Plin4    | 1.177E-06 | 0.10  |
| Chaf1a   | 2.369E-05 | 2.46  |
| Mcm2     | 2.100E-04 | 2.36  |
| Tpra1    | 4.215E-05 | 0.57  |
| Nab1     | 9.366E-04 | 1.58  |
| Cd97     | 5.485E-03 | 0.47  |
| Arrdc2   | 8.258E-04 | 0.66  |
| Cd36     | 2.846E-04 | 0.09  |
| Apoe     | 3.909E-05 | 0.27  |
| Elf3     | 2.219E-04 | 5.60  |
| Lipe     | 2.179E-03 | 0.43  |
| Ebi3     | 1.164E-02 | 0.58  |
| Fkbp11   | 1.627E-02 | 2.06  |
| Pld3     | 1.471E-04 | 0.35  |
| Etv3     | 3.905E-03 | 0.63  |
| St8sia6  | 5.780E-03 | 0.40  |
| Fcgrt    | 3.313E-03 | 0.43  |
| Timm50   | 1.071E-02 | 1.56  |
| Phyhip   | 2.525E-02 | 0.20  |
| Inmt     | 1.855E-02 | 0.00  |
| Dusp3    | 4.075E-02 | 0.61  |
| Dgcr14   | 2.269E-04 | 1.50  |
| Ier3     | 8.559E-04 | 2.96  |
| Ercc1    | 1.187E-03 | 1.80  |
| Cyp17a1  | 2.998E-04 | 0.08  |
| Homer3   | 1.800E-05 | 2.77  |
| Cp       | 2.568E-03 | 0.43  |
| Crot     | 1.150E-03 | 0.53  |
| Insig2   | 5.274E-04 | 0.31  |
| Klf20a   | 3.216E-06 | 2.98  |
| Dnase2a  | 5.921E-05 | 0.53  |
| Syce2    | 3.322E-03 | 3.69  |
| Nob1     | 1.294E-03 | 1.86  |
| Ruvbl2   | 1.241E-02 | 2.23  |
| Il7r     | 3.023E-03 | 0.24  |
| Zfp81    | 1.067E-02 | 1.55  |
| Mmd      | 1.006E-03 | 0.59  |
| Fam162a  | 6.776E-03 | 2.42  |
| Gstm5    | 1.687E-02 | 0.48  |
| Stat5a   | 7.244E-04 | 0.66  |
| Ppan     | 1.216E-03 | 1.94  |
| Trmt10a  | 2.159E-03 | 2.00  |
| Psap     | 4.255E-03 | 0.39  |
| Atn1     | 9.172E-03 | 1.71  |
| Ptpn6    | 6.095E-04 | 0.50  |
| Cul3     | 2.977E-03 | 0.64  |
| Il11     | 3.336E-03 | 1.89  |
| Ralb     | 3.317E-05 | 1.86  |
| Gab2     | 1.068E-02 | 0.56  |
| Ndrg2    | 1.074E-05 | 0.26  |
| Sgce     | 2.044E-02 | 0.59  |
| Slbp     | 4.990E-04 | 1.61  |
| Aqp1     | 3.382E-03 | 0.57  |
| Ly9      | 4.839E-04 | 0.24  |
| Emr1     | 2.304E-04 | 0.37  |
| Pgf      | 8.932E-04 | 8.58  |
| Grap     | 8.196E-05 | 0.47  |
| Mapk13   | 2.744E-03 | 0.53  |
| Srpk1    | 1.130E-04 | 0.45  |
| Nes      | 5.065E-03 | 3.99  |
| Thop1    | 2.566E-03 | 0.64  |
| Matk     | 3.434E-02 | 0.43  |
| Rasa4    | 5.809E-03 | 0.54  |
| Sgsh     | 3.350E-05 | 0.67  |
| Sh2b2    | 4.185E-03 | 1.62  |
| Wisp1    | 4.918E-03 | 3.47  |
| Ndrg1    | 1.274E-03 | 3.79  |
| Man2b1   | 4.366E-02 | 0.54  |
| Klf5     | 3.295E-04 | 2.22  |
| Spc25    | 7.659E-05 | 2.44  |
| Ripk4    | 3.431E-03 | 1.66  |
| Prlr     | 1.410E-03 | 0.22  |
| Cadm3    | 1.666E-04 | 0.23  |
| Casp14   | 3.771E-02 | 0.46  |
| Mlxipl   | 1.095E-04 | 0.17  |
| Tbl2     | 3.029E-03 | 1.87  |
| Mcm5     | 1.129E-03 | 2.88  |
| Pafah1b3 | 3.083E-03 | 1.82  |
| Il27ra   | 1.045E-03 | 0.52  |
| Asf1b    | 3.020E-04 | 2.92  |
| Ddx39    | 1.838E-05 | 1.81  |
| Igf1r    | 1.666E-03 | 1.54  |
| Trim28   | 2.980E-04 | 1.51  |
| Adcy9    | 7.551E-05 | 0.50  |
| Mef2c    | 6.814E-03 | 0.56  |
| Pcyt1a   | 6.821E-04 | 0.63  |
| Tmod4    | 4.686E-06 | 0.22  |
| Mthfd2   | 3.914E-02 | 1.94  |
| Kit      | 6.541E-03 | 0.52  |
| Pvalb    | 3.340E-03 | 0.06  |
| Tfap4    | 3.219E-02 | 1.94  |
| Ranbp1   | 1.674E-03 | 1.81  |
| Cd247    | 1.822E-02 | 0.62  |
| Gata6    | 2.597E-03 | 0.24  |
| Rsl1d1   | 1.512E-03 | 1.73  |
| Reep5    | 4.546E-03 | 0.56  |
| Nr2c1    | 3.008E-04 | 1.62  |
| Itgae    | 3.418E-04 | 0.34  |
| Ctns     | 4.916E-03 | 0.57  |
| P2rx5    | 1.849E-03 | 0.55  |
| Tuft1    | 4.479E-03 | 0.57  |
| Typr1    | 4.101E-03 | 0.27  |
| Upk3bl   | 3.170E-02 | 21.16 |
| Eps8l1   | 5.549E-05 | 0.25  |
| Prss16   | 4.528E-03 | 5.32  |
| Susd2    | 1.193E-05 | 0.09  |



|           |           |       |
|-----------|-----------|-------|
| Ggt5      | 3.602E-04 | 0.36  |
| Crip2     | 2.641E-03 | 0.47  |
| Crip1     | 3.730E-03 | 0.33  |
| Tek       | 2.594E-04 | 0.54  |
| Cdc20     | 1.334E-03 | 3.02  |
| Adamts4   | 2.112E-03 | 5.49  |
| Pfdn2     | 1.369E-02 | 1.69  |
| Srm       | 2.976E-02 | 1.97  |
| Epha2     | 1.394E-05 | 2.09  |
| Actn3     | 9.536E-03 | 0.19  |
| Pdk1      | 1.038E-02 | 2.06  |
| Ptbp1     | 2.655E-03 | 1.51  |
| Rundc3a   | 3.449E-02 | 2.51  |
| Gtf2h1    | 2.771E-05 | 1.59  |
| Hfe       | 1.849E-02 | 0.59  |
| Aplp1     | 1.741E-03 | 2.38  |
| Pola1     | 1.424E-03 | 2.00  |
| Gmnn      | 4.933E-04 | 2.55  |
| Cdk4      | 7.731E-05 | 1.65  |
| Mettl1    | 7.122E-03 | 1.68  |
| Saal1     | 2.647E-04 | 1.70  |
| Krt23     | 2.902E-04 | 0.22  |
| Sulf2     | 2.022E-04 | 0.39  |
| Leprel4   | 3.924E-02 | 2.15  |
| Lsm2      | 9.676E-04 | 1.87  |
| Pole      | 9.919E-05 | 3.03  |
| Atp1a2    | 1.008E-06 | 0.23  |
| Casq1     | 2.217E-04 | 0.17  |
| Stx1a     | 1.211E-04 | 2.54  |
| Scube2    | 2.055E-03 | 0.25  |
| Dennd2c   | 6.419E-05 | 1.68  |
| Mark3     | 3.224E-04 | 1.80  |
| Mc5r      | 5.196E-04 | 0.07  |
| Tinf2     | 1.417E-03 | 1.73  |
| Rad51c    | 6.299E-03 | 2.74  |
| Dio2      | 2.943E-02 | 0.49  |
| Ankrd26   | 9.784E-04 | 1.63  |
| Hnrnpa0   | 3.317E-06 | 1.57  |
| Ift43     | 1.854E-02 | 1.50  |
| Tcap      | 1.004E-05 | 0.15  |
| Ctsd      | 1.533E-04 | 0.36  |
| Hmgcl1    | 2.053E-04 | 11.07 |
| Fhl2      | 9.764E-04 | 2.13  |
| Clstn3    | 4.018E-03 | 0.06  |
| Lass4     | 4.767E-04 | 0.10  |
| Tle1      | 1.422E-02 | 0.66  |
| Elk3      | 2.751E-03 | 2.19  |
| Rdh13     | 5.525E-06 | 0.55  |
| Nutf2     | 7.299E-03 | 1.70  |
| Fut1      | 5.417E-04 | 0.28  |
| Mgst1     | 8.970E-05 | 0.34  |
| Nfib      | 2.661E-04 | 0.50  |
| Rbfox1    | 1.629E-02 | 0.50  |
| Cd163     | 1.082E-02 | 0.39  |
| Hdac5     | 5.611E-05 | 0.58  |
| Rarres2   | 1.138E-02 | 0.43  |
| Syn2      | 1.689E-02 | 0.35  |
| Fpgs      | 3.125E-05 | 2.13  |
| Sardh     | 5.677E-03 | 0.42  |
| G0s2      | 8.551E-03 | 0.45  |
| Bcr       | 5.203E-03 | 1.52  |
| Wnt3a     | 3.772E-03 | 5.48  |
| Kdsr      | 1.359E-03 | 0.59  |
| Aldh3a2   | 9.637E-04 | 0.46  |
| Ifrd2     | 1.153E-02 | 2.07  |
| Tnfrsf13b | 2.012E-02 | 0.59  |
| Raver1    | 2.456E-04 | 1.65  |
| Tmem86a   | 9.886E-04 | 0.53  |
| Mettl16   | 2.208E-03 | 1.60  |
| Psen2     | 3.235E-04 | 0.35  |
| Plcd1     | 6.214E-03 | 1.67  |
| Tnfrsf22  | 3.815E-07 | 2.61  |
| Phlda2    | 2.037E-02 | 2.46  |
| Kdelr3    | 2.055E-02 | 1.79  |
| Mcoln2    | 1.166E-02 | 0.42  |
| Panx3     | 1.447E-03 | 0.04  |
| Adssl1    | 1.194E-05 | 0.29  |
| Odc1      | 9.266E-03 | 4.65  |
| Pabpc4    | 6.097E-04 | 1.63  |
| Exoc3l2   | 3.710E-03 | 1.68  |
| Dhdh      | 1.915E-05 | 0.37  |
| Pgam1     | 1.677E-05 | 1.81  |
| Tjap1     | 4.156E-03 | 1.57  |
| Nanog     | 1.592E-04 | 2.47  |
| Steap4    | 3.428E-03 | 0.25  |
| Kif11     | 3.554E-04 | 2.36  |
| Rpa3      | 3.776E-03 | 1.62  |
| Mkl1      | 2.439E-02 | 2.19  |
| Retn      | 8.159E-05 | 0.07  |
| Podn11    | 2.970E-03 | 3.99  |
| Enkd1     | 4.750E-02 | 2.58  |
| Card14    | 3.466E-04 | 0.25  |
| DI6H22S68 | 3.913E-04 | 0.61  |
| Cad       | 1.008E-04 | 1.99  |
| Tnfaip8l2 | 8.334E-03 | 0.44  |
| Ly6g6e    | 3.868E-02 | 0.52  |
| 1500003OC | 4.062E-05 | 0.50  |
| Mertk     | 6.582E-03 | 0.33  |
| Mrps25    | 1.120E-03 | 1.55  |
| Csf1      | 8.882E-03 | 0.60  |
| Kif1a     | 7.846E-04 | 0.33  |
| 2310061C1 | 7.890E-03 | 1.50  |
| Dll1      | 3.617E-03 | 2.42  |
| Slc9a5    | 6.168E-05 | 4.41  |
| Stc1      | 1.564E-05 | 4.21  |
| Tppp3     | 3.399E-02 | 0.39  |
| E2f4      | 3.873E-04 | 1.81  |
| Naf1      | 5.506E-04 | 2.40  |



|           |           |       |
|-----------|-----------|-------|
| Yes1      | 6.700E-04 | 1.63  |
| Tsen15    | 6.760E-03 | 1.54  |
| Gata2     | 8.683E-05 | 0.54  |
| Entpd2    | 2.748E-04 | 0.36  |
| Clic3     | 2.874E-03 | 0.44  |
| Aldh1a3   | 4.892E-02 | 5.54  |
| Sirt2     | 7.869E-04 | 0.64  |
| Nolc1     | 4.753E-03 | 2.03  |
| Hmgb3     | 7.974E-05 | 2.22  |
| Mtap2     | 7.944E-05 | 0.34  |
| Cyp2j9    | 2.147E-03 | 0.65  |
| Abca1     | 3.497E-03 | 0.47  |
| Sash1     | 2.065E-03 | 0.62  |
| Zdhhc12   | 4.386E-02 | 1.64  |
| Cybb      | 1.582E-02 | 0.35  |
| Pcolce2   | 1.123E-03 | 0.29  |
| Cd48      | 4.159E-05 | 0.34  |
| Fam116b   | 8.367E-03 | 1.95  |
| Cd83      | 9.330E-04 | 0.24  |
| Gzmb      | 4.932E-02 | 3.54  |
| Gzmf      | 4.068E-02 | 5.40  |
| C4a       | 1.536E-03 | 0.27  |
| Notch4    | 7.772E-05 | 2.26  |
| Ppt2      | 3.215E-03 | 0.66  |
| Hivep2    | 1.155E-02 | 1.60  |
| Itga2     | 6.864E-03 | 3.35  |
| Lpl       | 4.869E-05 | 0.12  |
| Lama5     | 3.215E-03 | 2.03  |
| Steap1    | 4.107E-02 | 16.58 |
| Steap2    | 4.009E-03 | 5.21  |
| Awat1     | 1.545E-03 | 0.05  |
| Anxa9     | 1.055E-04 | 0.18  |
| Plekho1   | 1.169E-02 | 0.49  |
| Eps8      | 2.171E-02 | 0.51  |
| Fcrls     | 4.033E-03 | 0.38  |
| Ncapg     | 3.328E-05 | 3.23  |
| Gatsl2    | 2.565E-04 | 1.77  |
| Ncf1      | 1.783E-02 | 0.37  |
| Lrrc27    | 2.285E-02 | 0.53  |
| Lbp       | 4.714E-03 | 0.36  |
| Fli1      | 5.447E-03 | 0.60  |
| Diexf     | 2.643E-02 | 1.51  |
| Hsd11b1   | 3.592E-02 | 0.50  |
| H2-M3     | 3.046E-02 | 0.57  |
| Lonrf3    | 3.035E-03 | 0.41  |
| Ctsz      | 4.481E-03 | 0.36  |
| H2-M2     | 1.223E-02 | 0.49  |
| Eef1a2    | 6.846E-05 | 0.23  |
| Lnx2      | 2.472E-04 | 1.78  |
| Il19      | 4.648E-02 | 12.18 |
| Dyrk3     | 2.779E-02 | 2.90  |
| Foxred2   | 5.336E-04 | 0.46  |
| Cmah      | 7.421E-03 | 2.11  |
| Ttil12    | 7.497E-04 | 1.64  |
| Etaa1     | 6.283E-03 | 1.53  |
| Matn4     | 1.523E-03 | 0.23  |
| Brca1     | 1.376E-03 | 2.69  |
| Gsdma     | 2.196E-04 | 0.29  |
| Tnnc2     | 1.637E-04 | 0.15  |
| Cd300lg   | 1.639E-03 | 0.58  |
| Vtn       | 6.432E-04 | 0.42  |
| Traf4     | 7.614E-03 | 2.19  |
| Aldoc     | 8.896E-04 | 1.77  |
| Stac2     | 1.691E-02 | 0.35  |
| Plxdc1    | 2.104E-03 | 0.42  |
| Timp2     | 6.761E-03 | 0.46  |
| Cdc6      | 9.704E-03 | 2.43  |
| Suz12     | 1.686E-04 | 1.55  |
| Atad5     | 1.706E-05 | 2.15  |
| Tns4      | 1.234E-02 | 1.76  |
| Rhbdl3    | 5.882E-04 | 0.41  |
| Serinc3   | 4.008E-05 | 0.55  |
| Birc5     | 2.494E-05 | 3.30  |
| Afmid     | 1.092E-02 | 1.60  |
| Wfdc2     | 3.557E-02 | 90.96 |
| Etv4      | 5.844E-04 | 4.10  |
| Mmp9      | 1.033E-03 | 5.53  |
| Pltp      | 7.676E-05 | 0.28  |
| Ctsa      | 1.035E-06 | 0.40  |
| Jph2      | 4.775E-03 | 0.52  |
| Mybl2     | 6.008E-04 | 2.80  |
| Eya2      | 8.971E-03 | 0.49  |
| Ddx27     | 2.079E-03 | 1.63  |
| Cyth4     | 5.911E-03 | 0.43  |
| Rac3      | 4.958E-03 | 3.22  |
| Ints2     | 4.896E-04 | 1.66  |
| Ikzf3     | 2.780E-02 | 0.58  |
| Uchl5     | 1.990E-02 | 1.67  |
| Pmp22     | 4.888E-05 | 0.24  |
| Zcchc10   | 2.236E-03 | 2.47  |
| Ksr1      | 3.313E-03 | 0.60  |
| Anxa6     | 6.028E-03 | 0.57  |
| Kpna2     | 1.578E-05 | 2.21  |
| Cuedc1    | 7.832E-03 | 1.58  |
| Shroom1   | 5.863E-03 | 5.87  |
| 8-Sep     | 1.019E-03 | 0.62  |
| Myo1b     | 4.213E-05 | 2.04  |
| Ypel2     | 4.313E-04 | 0.56  |
| Nol11     | 8.975E-04 | 1.69  |
| C1qbp     | 7.203E-03 | 1.78  |
| Trpv2     | 3.973E-03 | 0.41  |
| Pcgf2     | 1.665E-03 | 1.58  |
| Trim37    | 2.862E-03 | 1.69  |
| Slc2a4    | 1.137E-05 | 0.36  |
| 2810408A1 | 1.677E-02 | 1.89  |
| Acadvl    | 3.724E-05 | 0.63  |
| G3bp1     | 9.234E-04 | 1.56  |
| Tada2a    | 4.184E-05 | 1.79  |



|           |           |      |
|-----------|-----------|------|
| lkzf1     | 1.608E-03 | 0.47 |
| BC096441  | 1.717E-02 | 0.43 |
| Cd68      | 1.375E-03 | 0.26 |
| Acs1      | 2.981E-05 | 0.37 |
| Lsp1      | 2.688E-02 | 0.58 |
| Myh11     | 2.980E-04 | 0.37 |
| Unc45b    | 2.665E-03 | 0.45 |
| Pnpla5    | 1.398E-03 | 0.05 |
| Mrpl45    | 3.609E-03 | 1.64 |
| Mb        | 6.381E-03 | 0.22 |
| P4ha2     | 3.787E-03 | 1.68 |
| Alox12e   | 8.347E-04 | 0.05 |
| Arrb1     | 3.524E-03 | 0.57 |
| Sart3     | 4.765E-03 | 1.55 |
| Sifn3     | 3.781E-02 | 3.00 |
| Nars2     | 1.899E-03 | 1.64 |
| Plod1     | 2.856E-02 | 1.55 |
| Mfsd3     | 2.091E-03 | 1.89 |
| Dnase1l1  | 2.597E-02 | 0.57 |
| Aldh3a1   | 1.114E-02 | 0.08 |
| Scrn1     | 1.973E-03 | 0.38 |
| BC005537  | 9.176E-04 | 0.65 |
| Scn1b     | 5.350E-05 | 0.44 |
| Atp6v1e1  | 5.805E-05 | 0.57 |
| Chtf18    | 5.305E-05 | 3.17 |
| Ahr       | 1.056E-03 | 0.57 |
| 2610027L1 | 4.694E-03 | 1.72 |
| Atp6v0a1  | 7.591E-04 | 0.54 |
| Psmc3ip   | 2.812E-03 | 2.73 |
| Aoc3      | 2.213E-02 | 0.60 |
| Sec14l4   | 9.668E-04 | 0.06 |
| Tlcd1     | 6.507E-03 | 0.53 |
| Gyg       | 1.916E-05 | 0.34 |
| Slc6a8    | 8.194E-03 | 0.65 |
| Pdk4      | 3.006E-02 | 0.22 |
| Sema6a    | 2.521E-04 | 0.24 |
| Lyst      | 7.107E-05 | 0.45 |
| Esr1      | 4.708E-04 | 0.43 |
| Syne1     | 5.453E-03 | 0.58 |
| Fbxo5     | 4.049E-04 | 2.05 |
| Frk       | 7.586E-04 | 1.92 |
| Trdn      | 1.213E-05 | 0.26 |
| Trmt11    | 2.695E-04 | 1.89 |
| Lrp11     | 1.520E-03 | 2.30 |
| Adat2     | 1.357E-03 | 1.79 |
| Pex3      | 3.841E-03 | 0.56 |
| Mical1    | 5.767E-03 | 0.61 |
| Slc16a10  | 3.181E-04 | 0.42 |
| Fyn       | 1.250E-02 | 0.66 |
| Tube1     | 2.438E-03 | 2.42 |
| Prep      | 1.788E-05 | 2.06 |
| D10Bwg13  | 4.204E-02 | 0.31 |
| Hebp2     | 1.231E-03 | 0.42 |
| Smpdl3a   | 2.846E-06 | 0.31 |
| Fabp7     | 4.773E-04 | 0.17 |
| Pkib      | 9.973E-06 | 0.24 |
| Echdc1    | 3.424E-03 | 0.34 |
| Ccdc59    | 1.192E-05 | 1.53 |
| Lama2     | 2.397E-03 | 0.39 |
| P4ha1     | 4.990E-04 | 1.62 |
| Zwint     | 5.638E-04 | 1.71 |
| Dcn       | 4.464E-05 | 0.21 |
| 2310015B2 | 5.187E-03 | 0.36 |
| Cdk1      | 1.339E-04 | 3.19 |
| Poc1b     | 3.973E-03 | 1.62 |
| Tmpo      | 1.546E-04 | 1.64 |
| Sgk1      | 7.217E-04 | 0.62 |
| Arg1      | 8.617E-03 | 9.44 |
| Nedd1     | 1.062E-04 | 1.97 |
| Fam54a    | 6.089E-04 | 2.16 |
| Moxd1     | 8.661E-03 | 1.64 |
| Vnn3      | 4.930E-03 | 0.08 |
| Gm872     | 1.373E-03 | 4.15 |
| Hal       | 4.610E-06 | 0.12 |
| Snrpf     | 1.933E-03 | 1.92 |
| Tmcc3     | 2.904E-05 | 0.58 |
| Ccdc41    | 5.948E-05 | 1.74 |
| Cry1      | 4.837E-02 | 1.63 |
| Btbd11    | 1.107E-04 | 2.61 |
| Timp3     | 1.749E-03 | 0.49 |
| Mybpc1    | 2.326E-04 | 0.25 |
| Slc5a8    | 1.263E-03 | 0.40 |
| Mypn      | 8.874E-05 | 0.34 |
| Pbld1     | 1.118E-03 | 1.64 |
| Ddx21     | 5.197E-05 | 1.65 |
| Supv3l1   | 7.319E-04 | 1.61 |
| H2afy2    | 3.832E-02 | 2.01 |
| Sgpl1     | 1.748E-05 | 0.40 |
| Pcbd1     | 2.733E-02 | 0.58 |
| Slc29a3   | 6.930E-03 | 0.63 |
| 4632428NC | 4.407E-03 | 0.44 |
| Slc16a7   | 3.775E-06 | 0.26 |
| Lrig3     | 1.957E-04 | 0.41 |
| Ddit4     | 8.020E-04 | 4.04 |
| Pno1      | 8.654E-03 | 1.80 |
| Plek      | 1.269E-02 | 0.42 |
| Srgap1    | 4.133E-02 | 0.66 |
| Pcsk4     | 1.351E-02 | 2.13 |
| Peli1     | 3.156E-05 | 0.51 |
| Slc1a4    | 4.434E-02 | 2.34 |
| Dock2     | 2.274E-04 | 0.33 |
| Gamt      | 9.777E-04 | 0.44 |
| Meis1     | 2.941E-02 | 1.57 |
| 1700058G1 | 1.533E-02 | 8.82 |
| Cnot2     | 5.026E-04 | 1.56 |
| Cobl      | 2.832E-03 | 0.19 |
| Snrpd3    | 2.980E-03 | 1.60 |
| E2f7      | 2.585E-05 | 6.08 |



|            |           |       |
|------------|-----------|-------|
| Osbpl8     | 2.493E-03 | 0.58  |
| Phlda1     | 2.127E-03 | 6.22  |
| Sf3a2      | 1.524E-02 | 1.75  |
| Mdm1       | 2.613E-02 | 1.51  |
| Jsrp1      | 1.451E-04 | 0.24  |
| Irak3      | 3.783E-04 | 0.46  |
| 4930404N1  | 3.750E-03 | 0.28  |
| Fzr1       | 9.360E-06 | 1.74  |
| Txnrd1     | 1.332E-03 | 0.57  |
| Aldh1l2    | 5.085E-04 | 3.38  |
| Adarb1     | 7.664E-04 | 2.75  |
| Appl2      | 4.485E-05 | 0.54  |
| Slc36a2    | 6.609E-05 | 0.23  |
| Stk10      | 1.611E-03 | 0.51  |
| Pfkf       | 1.949E-05 | 2.60  |
| Pex13      | 1.182E-02 | 0.51  |
| Xpo1       | 4.931E-04 | 1.53  |
| Cpeb4      | 1.642E-05 | 0.52  |
| Shc2       | 3.530E-02 | 0.56  |
| Spnb2      | 2.550E-03 | 0.66  |
| Fgf22      | 1.933E-03 | 0.29  |
| Nudcd2     | 4.354E-03 | 1.54  |
| Hmmr       | 3.276E-05 | 2.80  |
| Cyflp2     | 1.466E-06 | 0.34  |
| Sgcd       | 2.060E-04 | 0.39  |
| Rnf130     | 8.925E-03 | 0.63  |
| Ltc4s      | 4.075E-04 | 0.40  |
| Phf15      | 1.128E-02 | 0.66  |
| Pdlim4     | 5.146E-03 | 0.34  |
| Cdkl3      | 7.340E-03 | 1.64  |
| Cdkn2aipnl | 1.368E-03 | 1.61  |
| Itk        | 4.038E-03 | 0.51  |
| Upp1       | 2.821E-02 | 16.26 |
| Hus1       | 2.591E-03 | 2.22  |
| Pttg1      | 8.398E-05 | 2.18  |
| Tns3       | 4.078E-02 | 0.65  |
| Btg2       | 1.091E-02 | 0.67  |
| Gatsl3     | 6.218E-03 | 2.02  |
| Igfbp3     | 1.754E-04 | 6.12  |
| Myo1g      | 8.971E-04 | 0.33  |
| Guk1       | 5.607E-04 | 0.46  |
| Efemp1     | 4.263E-03 | 0.35  |
| Pold2      | 3.957E-02 | 1.91  |
| Pgam2      | 4.238E-07 | 0.17  |
| Xbp1       | 2.459E-05 | 0.62  |
| Ska2       | 6.618E-04 | 1.90  |
| Prr11      | 2.943E-06 | 2.69  |
| Smg8       | 3.648E-03 | 1.64  |
| Tubd1      | 1.794E-02 | 1.51  |
| Mrp122     | 3.187E-02 | 1.51  |
| Znhit3     | 1.584E-02 | 1.65  |
| Shmt1      | 2.523E-02 | 1.54  |
| Elac2      | 1.579E-03 | 1.61  |
| Pctp       | 9.334E-04 | 0.16  |
| Twistnb    | 1.798E-04 | 1.55  |
| Atp6v1c2   | 2.797E-04 | 0.10  |
| Pik3cg     | 1.320E-03 | 0.52  |
| Tspan13    | 1.117E-03 | 0.55  |
| Fam49a     | 3.563E-05 | 0.54  |
| Lpin1      | 8.881E-07 | 0.33  |
| Nrcam      | 1.404E-04 | 0.29  |
| Fam84a     | 2.773E-04 | 0.40  |
| Fam20a     | 3.431E-03 | 3.28  |
| Fkbp1b     | 1.124E-02 | 0.57  |
| Id2        | 7.268E-04 | 0.54  |
| Mboat2     | 9.142E-04 | 0.29  |
| Dus4l      | 7.332E-03 | 1.79  |
| Rrm2       | 3.016E-07 | 2.58  |
| Grhl1      | 3.457E-02 | 0.64  |
| Efr3b      | 8.748E-03 | 0.40  |
| Dnmt3a     | 8.847E-04 | 0.29  |
| Ddx52      | 9.480E-04 | 1.90  |
| Hnf1b      | 3.209E-02 | 32.58 |
| Taf15      | 1.604E-03 | 1.68  |
| Ace        | 1.085E-03 | 0.36  |
| Mmp28      | 5.543E-03 | 1.94  |
| Mettl2     | 8.112E-03 | 1.55  |
| Nle1       | 6.263E-04 | 1.97  |
| Ftsj3      | 3.140E-03 | 1.52  |
| Adap2      | 6.612E-03 | 0.50  |
| Nup85      | 2.481E-04 | 1.70  |
| Itgb4      | 2.561E-03 | 2.85  |
| Acocx1     | 1.113E-06 | 0.48  |
| Tsen54     | 3.318E-03 | 1.55  |
| Llg12      | 1.195E-03 | 1.54  |
| Camkk1     | 4.387E-04 | 0.45  |
| P2rx1      | 5.001E-03 | 0.45  |
| Atp2a3     | 3.781E-07 | 0.34  |
| Txndc17    | 2.763E-05 | 1.84  |
| Fam64a     | 9.765E-04 | 3.19  |
| Cygb       | 6.571E-05 | 0.29  |
| 1810032OC  | 5.305E-03 | 1.65  |
| Dhrs13     | 2.228E-03 | 2.72  |
| Coro6      | 2.711E-02 | 0.57  |
| Tmigd1     | 2.465E-02 | 7.23  |
| Nxn        | 6.499E-04 | 1.86  |
| Fam101b    | 9.610E-03 | 1.99  |
| Rph3al     | 1.433E-02 | 2.02  |
| Cacna1g    | 2.362E-02 | 3.03  |
| Lrrc59     | 1.308E-02 | 1.60  |
| Tac4       | 5.773E-03 | 0.22  |
| Scrn2      | 2.067E-02 | 1.77  |
| Cacnb1     | 3.214E-04 | 0.48  |
| Aurkb      | 2.810E-08 | 2.63  |
| Ctc1       | 1.154E-03 | 1.56  |
| Pfas       | 1.907E-03 | 1.51  |
| Pik3r5     | 5.594E-04 | 0.25  |
| Ntn1       | 1.585E-02 | 0.55  |



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|-----------|-----------|-------|
| Myh3      | 3.569E-02 | 17.08 |
| Top2a     | 1.474E-04 | 2.55  |
| Kat2a     | 1.610E-03 | 1.73  |
| Lsm12     | 2.814E-04 | 1.73  |
| Ccdc43    | 3.210E-03 | 1.54  |
| Higd1b    | 1.504E-02 | 1.62  |
| Eftud2    | 4.272E-03 | 1.64  |
| Dcald     | 1.058E-03 | 1.63  |
| Plcd3     | 1.843E-02 | 1.74  |
| Coch      | 1.361E-05 | 0.13  |
| Dnaaf2    | 5.004E-04 | 1.64  |
| Pole2     | 4.262E-03 | 2.05  |
| Pnn       | 1.359E-04 | 1.53  |
| Galc      | 2.184E-03 | 0.35  |
| Polr2h    | 1.884E-02 | 1.53  |
| Mbip      | 1.096E-05 | 1.67  |
| Gstz1     | 3.637E-03 | 0.53  |
| 2700073G1 | 5.076E-03 | 1.71  |
| Nova1     | 1.767E-04 | 0.25  |
| Mthfd1    | 1.335E-04 | 1.78  |
| Sgpp1     | 5.879E-05 | 0.37  |
| Nin       | 1.071E-02 | 0.63  |
| Bdkrb2    | 3.171E-04 | 3.33  |
| Serpina3n | 4.538E-04 | 0.36  |
| Dhrs7     | 2.024E-03 | 0.45  |
| Hif1a     | 7.173E-04 | 2.69  |
| Snapc1    | 1.039E-04 | 2.09  |
| Elf2s1    | 1.987E-04 | 1.72  |
| Plek2     | 3.313E-02 | 1.79  |
| Erh       | 1.793E-05 | 1.79  |
| Slc10a1   | 1.408E-02 | 1.72  |
| Mta1      | 6.396E-03 | 1.60  |
| Gtpbp4    | 1.094E-02 | 1.59  |
| Tdp1      | 6.036E-03 | 1.55  |
| Lgmn      | 2.738E-02 | 0.59  |
| Pitrm1    | 7.270E-04 | 1.72  |
| Chga      | 1.266E-03 | 0.24  |
| Asb2      | 1.436E-03 | 0.32  |
| Akr1c18   | 9.357E-05 | 0.25  |
| Rgs6      | 1.617E-02 | 0.07  |
| Acot2     | 3.472E-04 | 0.32  |
| Aldh6a1   | 1.980E-03 | 0.48  |
| Vash1     | 8.542E-04 | 2.80  |
| Ccnk      | 1.462E-03 | 1.56  |
| Hhip1     | 5.539E-03 | 2.99  |
| Evl       | 1.675E-02 | 0.57  |
| Hsp90aa1  | 2.590E-05 | 2.08  |
| Cinp      | 3.938E-03 | 1.55  |
| Kif26a    | 4.195E-03 | 3.44  |
| Gpr137b   | 5.995E-03 | 0.39  |
| Gli3      | 4.436E-03 | 2.16  |
| Aoah      | 1.816E-02 | 0.61  |
| Trim27    | 3.062E-03 | 1.68  |
| Gpld1     | 5.415E-03 | 0.51  |
| Irf4      | 1.891E-02 | 0.47  |
| Tfap2a    | 1.339E-03 | 1.84  |
| Gcnt2     | 1.807E-02 | 0.65  |
| Tbc1d7    | 8.633E-03 | 1.60  |
| Ccdc90a   | 4.264E-05 | 0.63  |
| Id4       | 4.338E-04 | 0.25  |
| Susd3     | 7.342E-03 | 0.58  |
| Ogn       | 2.660E-04 | 0.24  |
| Cenpp     | 1.610E-04 | 2.26  |
| Nol8      | 2.844E-03 | 1.73  |
| Wrnip1    | 3.689E-03 | 1.65  |
| Pxdc1     | 1.422E-04 | 2.65  |
| Ly86      | 7.414E-03 | 0.49  |
| Riok1     | 1.153E-04 | 1.54  |
| Snrrp48   | 1.037E-04 | 1.78  |
| Fbp2      | 2.059E-04 | 0.15  |
| Syk       | 8.620E-03 | 0.41  |
| Ror2      | 1.991E-02 | 2.18  |
| Sfxn1     | 7.587E-05 | 1.51  |
| Ctsl      | 2.206E-03 | 0.40  |
| Mxd3      | 1.487E-02 | 1.85  |
| Prelid1   | 1.183E-04 | 1.51  |
| Pdlim7    | 7.468E-05 | 1.69  |
| Ddx41     | 1.103E-03 | 1.55  |
| Fastkd3   | 1.690E-03 | 1.79  |
| Dapk1     | 8.049E-03 | 0.54  |
| Slc6a19   | 8.943E-03 | 0.09  |
| Trip13    | 2.840E-03 | 4.45  |
| Cep72     | 1.914E-03 | 2.26  |
| Ahrr      | 7.390E-03 | 0.38  |
| Mctp1     | 1.192E-03 | 0.39  |
| Ankrd32   | 4.089E-04 | 1.57  |
| Med10     | 2.759E-05 | 1.72  |
| Lpcat1    | 1.185E-02 | 1.95  |
| Ckmt2     | 1.179E-03 | 0.14  |
| Cd180     | 1.845E-03 | 0.32  |
| Marveld2  | 2.065E-02 | 0.47  |
| Smn1      | 3.741E-03 | 1.85  |
| Rgnef     | 2.841E-03 | 2.41  |
| Hexb      | 7.283E-04 | 0.51  |
| Iqgap2    | 6.446E-06 | 0.32  |
| Pde8b     | 3.730E-03 | 0.55  |
| Jmy       | 2.360E-02 | 0.63  |
| Dimt1     | 6.875E-03 | 1.68  |
| Elovl7    | 7.767E-04 | 0.26  |
| Depdc1b   | 1.291E-03 | 2.10  |
| Dhfr      | 2.941E-03 | 2.25  |
| Rasgrf2   | 3.010E-03 | 0.51  |
| Cenpk     | 1.819E-03 | 2.44  |
| Emb       | 5.070E-03 | 0.49  |
| Slc4a7    | 4.757E-04 | 2.71  |
| Ptprg     | 2.056E-02 | 1.61  |
| Acox2     | 1.508E-03 | 0.09  |
| Il6st     | 2.658E-05 | 0.45  |



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|-----------|-----------|-------|
| Dusp13    | 3.337E-04 | 0.37  |
| Ldb3      | 1.778E-06 | 0.16  |
| Nid2      | 2.865E-04 | 2.11  |
| Dnajc9    | 3.685E-03 | 1.51  |
| Txndc16   | 1.151E-02 | 0.64  |
| Ero1l     | 2.293E-02 | 2.17  |
| Rnase4    | 1.785E-05 | 0.44  |
| Rnase6    | 3.608E-03 | 0.38  |
| Hac1l     | 4.581E-02 | 0.30  |
| Asb14     | 1.518E-05 | 0.41  |
| Plrf7     | 3.935E-03 | 1.87  |
| Gaintl2   | 1.066E-05 | 0.18  |
| Dph3      | 4.858E-04 | 1.56  |
| Oxnad1    | 2.918E-05 | 1.92  |
| Ctsb      | 8.375E-04 | 0.37  |
| Prkcd     | 2.349E-02 | 0.65  |
| Pinx1     | 3.654E-03 | 1.60  |
| Ska3      | 7.030E-05 | 3.58  |
| Wnt5a     | 3.700E-03 | 5.20  |
| Lcp1      | 1.095E-02 | 0.43  |
| Nufip1    | 2.157E-02 | 1.88  |
| Epsti1    | 1.786E-02 | 0.52  |
| Tnfsf11   | 2.454E-02 | 4.50  |
| 1190002H2 | 1.211E-03 | 0.50  |
| Diap3     | 3.799E-04 | 2.28  |
| Scara5    | 1.207E-04 | 0.13  |
| Pbk       | 2.355E-04 | 2.38  |
| Esco2     | 7.995E-03 | 2.16  |
| Clu       | 5.479E-05 | 0.30  |
| Ephx2     | 2.963E-06 | 0.19  |
| Dpysl2    | 9.555E-03 | 0.53  |
| Adamdec1  | 2.531E-02 | 24.67 |
| Bora      | 1.411E-04 | 2.42  |
| Pdlim2    | 3.693E-02 | 0.62  |
| Sorbs3    | 2.658E-03 | 0.51  |
| Hr        | 3.338E-02 | 0.47  |
| Bmp1      | 1.159E-02 | 2.19  |
| Dok2      | 7.529E-03 | 0.40  |
| Uchl3     | 1.456E-02 | 1.56  |
| Ednrb     | 3.617E-02 | 0.55  |
| Scel      | 7.851E-05 | 0.28  |
| Dct       | 6.934E-03 | 0.30  |
| Tgds      | 1.393E-04 | 1.54  |
| Nup155    | 1.157E-04 | 1.86  |
| Gdnf      | 5.192E-03 | 4.18  |
| Fyb       | 4.287E-03 | 0.53  |
| Dab2      | 9.533E-03 | 0.51  |
| Rem2      | 5.185E-03 | 5.80  |
| Haus4     | 4.349E-04 | 1.83  |
| Jub       | 8.720E-05 | 1.95  |
| C6        | 8.406E-03 | 0.23  |
| Drosha    | 1.608E-03 | 1.59  |
| Pdzd2     | 7.531E-03 | 0.61  |
| Npr3      | 4.526E-02 | 0.43  |
| Fitm1     | 2.133E-05 | 0.19  |
| Cideb     | 3.252E-04 | 2.35  |
| Ripk3     | 8.961E-03 | 2.32  |
| Cma1      | 4.106E-05 | 0.17  |
| Mcpt2     | 3.679E-02 | 44.58 |
| Atp12a    | 3.093E-02 | 0.05  |
| Cmb1      | 9.044E-09 | 0.14  |
| Tars      | 9.611E-04 | 1.58  |
| Brix1     | 7.950E-03 | 1.89  |
| Ank       | 2.625E-05 | 0.44  |
| Fam134b   | 6.023E-05 | 0.37  |
| Pabpc1    | 5.229E-03 | 1.63  |
| Grhl2     | 1.576E-02 | 1.72  |
| Lrp12     | 2.531E-03 | 0.49  |
| Angpt1    | 2.677E-02 | 0.66  |
| Utp23     | 3.905E-02 | 1.61  |
| Rad21     | 1.288E-02 | 1.53  |
| Shcbp1    | 2.562E-04 | 3.62  |
| Pop1      | 1.162E-03 | 1.95  |
| Khdrbs3   | 1.032E-02 | 0.53  |
| Eny2      | 1.091E-02 | 1.50  |
| Sybu      | 6.601E-03 | 0.38  |
| Myc       | 6.764E-04 | 1.92  |
| Klhl38    | 4.199E-07 | 0.13  |
| Fbxo32    | 4.792E-05 | 0.25  |
| Atad2     | 1.801E-02 | 1.55  |
| Has2      | 5.442E-03 | 2.47  |
| Mtbp      | 9.308E-03 | 1.85  |
| Sla       | 1.121E-02 | 0.58  |
| Fam49b    | 1.538E-03 | 1.90  |
| Ppara     | 3.738E-04 | 0.28  |
| Gtse1     | 2.181E-02 | 3.12  |
| L3mbtl2   | 3.547E-02 | 1.54  |
| Syng1     | 4.618E-04 | 0.19  |
| Deptor    | 8.039E-04 | 0.57  |
| Dsc1      | 2.009E-03 | 2.65  |
| Enpp2     | 2.895E-04 | 0.33  |
| Csnk1e    | 3.270E-05 | 0.51  |
| Parvb     | 4.380E-02 | 0.63  |
| C1qtnf6   | 2.254E-02 | 2.48  |
| Naga      | 2.126E-03 | 0.59  |
| 3-Sep     | 7.899E-06 | 0.14  |
| Slc38a2   | 2.463E-03 | 2.13  |
| Rpap3     | 2.077E-02 | 1.58  |
| Rapgef3   | 2.427E-02 | 2.50  |
| Desi1     | 5.060E-03 | 0.56  |
| Polr3h    | 4.754E-02 | 1.76  |
| Vdr       | 6.280E-04 | 0.52  |
| Nckap1l   | 1.685E-03 | 0.36  |
| Ppp1r1a   | 1.859E-05 | 0.13  |
| Trp63     | 1.224E-02 | 1.65  |
| Cldn1     | 2.116E-04 | 0.26  |
| Mgmn1     | 2.322E-03 | 0.66  |
| Srl       | 2.996E-05 | 0.41  |



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|----------|-----------|------|
| Hes1     | 1.130E-02 | 1.53 |
| Tmem44   | 3.622E-04 | 1.88 |
| Apod     | 1.862E-04 | 0.16 |
| Fam203a  | 2.831E-02 | 2.10 |
| Bop1     | 1.094E-02 | 1.57 |
| Scrib    | 4.064E-02 | 1.52 |
| Pyclr    | 2.136E-02 | 1.64 |
| Gplhbp1  | 2.322E-04 | 3.35 |
| Slurp1   | 9.176E-04 | 0.03 |
| Arc      | 7.727E-03 | 3.86 |
| Ptk2     | 6.406E-03 | 1.52 |
| Rabl2    | 2.413E-03 | 2.14 |
| Yaf2     | 1.499E-02 | 1.94 |
| Alcam    | 1.454E-03 | 0.21 |
| Cd96     | 5.536E-03 | 0.50 |
| Cd200    | 4.332E-02 | 0.47 |
| Cd200r1  | 2.971E-04 | 0.25 |
| Mcm4     | 2.577E-04 | 2.18 |
| Snai2    | 8.966E-05 | 2.54 |
| Qtrtd1   | 3.797E-02 | 1.56 |
| Zbtb20   | 5.785E-06 | 0.40 |
| Cmss1    | 1.504E-02 | 2.25 |
| Tmem45a  | 2.141E-05 | 0.22 |
| Fgd4     | 5.657E-04 | 0.35 |
| Yars2    | 8.550E-03 | 1.67 |
| Arhgap31 | 3.167E-03 | 0.56 |
| Umps     | 1.926E-02 | 1.64 |
| Abcc5    | 7.490E-05 | 0.41 |
| Hcls1    | 3.497E-02 | 0.61 |
| Ccdc14   | 1.089E-02 | 1.81 |
| Ece2     | 3.926E-03 | 1.57 |
| Cxad     | 2.758E-03 | 0.52 |
| Adipoq   | 5.897E-05 | 0.06 |
| Rfc4     | 7.083E-04 | 2.32 |
| Robo1    | 1.387E-02 | 1.74 |
| St6gal1  | 3.888E-04 | 0.44 |
| Adamts5  | 3.187E-04 | 0.48 |
| Ildr1    | 1.163E-02 | 0.19 |
| Cd86     | 1.699E-02 | 0.66 |
| Pros1    | 4.616E-04 | 0.61 |
| Chaf1b   | 1.708E-02 | 1.89 |
| Dopey2   | 6.052E-06 | 0.50 |
| Itns1    | 5.485E-04 | 0.51 |
| Ifngr2   | 4.104E-03 | 0.54 |
| Il10rb   | 8.111E-04 | 0.50 |
| Synj1    | 1.209E-02 | 0.65 |
| Mis18a   | 6.419E-03 | 1.85 |
| Enah     | 2.946E-02 | 3.64 |
| Fmnl3    | 2.628E-03 | 1.58 |
| Racgap1  | 1.717E-03 | 2.42 |
| Gpd1     | 1.605E-05 | 0.11 |
| Lass5    | 5.716E-03 | 0.53 |
| Slc11a2  | 5.154E-03 | 0.59 |
| Cela1    | 1.016E-02 | 0.44 |
| Krt18    | 1.428E-02 | 8.96 |
| Csad     | 6.714E-03 | 0.65 |
| Igfbp6   | 6.784E-03 | 0.45 |
| Calcoco1 | 4.192E-06 | 0.43 |
| Rtnn     | 3.105E-02 | 1.51 |
| Rgn      | 5.754E-04 | 0.09 |
| Mospd1   | 6.678E-04 | 0.41 |
| Cxcl13   | 3.044E-02 | 0.38 |
| Abcc1    | 1.075E-02 | 0.64 |
| Fhl1     | 2.735E-03 | 0.41 |
| Rfc2     | 1.642E-04 | 1.64 |
| Prmt5    | 1.512E-02 | 1.97 |
| Tmem52   | 1.493E-07 | 0.12 |
| Vwa5a    | 1.659E-06 | 0.50 |
| Serping1 | 8.321E-03 | 0.47 |
| Guca2a   | 3.247E-03 | 0.26 |
| Acy1     | 1.307E-03 | 1.75 |
| Cd4      | 1.577E-02 | 0.42 |
| Ube2j2   | 1.115E-02 | 1.53 |
| Ache     | 2.205E-02 | 0.44 |
| Dtwd1    | 6.729E-03 | 1.73 |
| Wfdc1    | 3.532E-06 | 0.18 |
| Poc1a    | 4.168E-04 | 3.06 |
| Trip6    | 1.109E-06 | 2.46 |
| Tmem176a | 5.060E-03 | 0.63 |
| Nfatc4   | 3.324E-02 | 1.93 |
| Tpi1     | 9.660E-04 | 1.60 |
| Cdca3    | 7.367E-06 | 2.68 |
| Fam132a  | 2.632E-03 | 0.42 |
| Rps6ka2  | 2.359E-03 | 0.51 |
| Park2    | 7.080E-05 | 0.32 |
| Agpat4   | 1.064E-04 | 0.34 |
| Mpc1     | 2.227E-04 | 0.47 |
| Thbs2    | 2.064E-02 | 2.79 |
| Smoc2    | 1.064E-02 | 0.62 |
| Pkmyt1   | 1.763E-03 | 2.01 |
| Flywh2   | 2.218E-03 | 2.19 |
| Gpr115   | 4.025E-03 | 0.49 |
| Cenpq    | 3.712E-04 | 2.63 |
| Satb1    | 7.254E-03 | 0.56 |
| Sgol1    | 7.447E-06 | 2.76 |
| Slc29a1  | 2.144E-04 | 0.39 |
| Vegfa    | 1.331E-04 | 3.22 |
| Polh     | 3.477E-04 | 1.53 |
| Clic5    | 5.861E-04 | 0.46 |
| Enpp5    | 4.427E-05 | 0.29 |
| Enpp4    | 1.654E-02 | 0.61 |
| Ptk7     | 2.956E-03 | 2.38 |
| Bysl     | 3.426E-05 | 1.57 |
| Tfeb     | 1.810E-03 | 0.54 |
| Foxp4    | 4.209E-05 | 1.94 |
| Trem2    | 3.201E-03 | 0.22 |
| Ppil1    | 6.323E-04 | 2.08 |
| Pi16     | 4.999E-04 | 0.30 |



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|-----------|-----------|-------|
| Fgd2      | 2.673E-03 | 0.47  |
| Abcg1     | 1.317E-03 | 0.36  |
| Slc37a1   | 4.402E-02 | 0.66  |
| Wdr4      | 4.904E-05 | 1.64  |
| Epb4.1l3  | 4.294E-02 | 1.96  |
| Myom1     | 9.783E-08 | 0.21  |
| Clip4     | 1.974E-02 | 0.54  |
| Lbh       | 2.932E-03 | 0.52  |
| Dpy30     | 4.612E-03 | 1.56  |
| Ttc27     | 1.403E-02 | 1.57  |
| Cyp1b1    | 3.808E-03 | 0.51  |
| Srsf7     | 5.924E-04 | 1.52  |
| Prss41    | 2.063E-02 | 2.32  |
| Abca3     | 1.406E-03 | 0.54  |
| Dnase1l2  | 4.260E-05 | 0.22  |
| C3        | 7.714E-05 | 0.23  |
| Hn1l      | 1.807E-04 | 1.86  |
| Nme4      | 4.641E-03 | 1.77  |
| Rgs11     | 1.438E-02 | 2.18  |
| Itfg3     | 1.887E-06 | 0.37  |
| Snrpc     | 5.232E-05 | 1.51  |
| Fkbp5     | 3.223E-02 | 0.54  |
| Tmem178   | 6.015E-04 | 0.08  |
| Thumpd2   | 4.919E-03 | 1.57  |
| Pkdcc     | 4.477E-02 | 0.54  |
| Polr2d    | 5.690E-04 | 1.50  |
| Celf4     | 1.038E-02 | 2.81  |
| Slc39a6   | 2.682E-03 | 1.58  |
| Adamts10  | 9.044E-03 | 0.59  |
| Myo1f     | 1.977E-03 | 0.29  |
| Kifc5b    | 1.217E-05 | 2.61  |
| Dtna      | 9.847E-04 | 0.49  |
| Dsc2      | 2.241E-03 | 11.91 |
| Spat24    | 1.891E-02 | 1.78  |
| 2010001Ml | 2.750E-02 | 0.37  |
| C2        | 3.738E-02 | 0.53  |
| Epb4.1l4a | 3.407E-02 | 1.56  |
| Tslp      | 4.546E-02 | 9.54  |
| Bin1      | 3.991E-03 | 0.54  |
| Lims2     | 1.280E-03 | 0.52  |
| Npc1      | 2.652E-03 | 0.65  |
| Zfp521    | 1.656E-03 | 0.60  |
| Lama3     | 3.464E-03 | 3.52  |
| Cabyr     | 1.385E-02 | 0.50  |
| Nr3c1     | 5.985E-04 | 0.66  |
| Mrps18b   | 1.975E-03 | 1.52  |
| Pcdh12    | 4.131E-06 | 2.86  |
| H2-M5     | 7.914E-05 | 0.09  |
| Gabbr1    | 5.070E-03 | 0.61  |
| Myot      | 9.389E-07 | 0.20  |
| 4833403l1 | 1.440E-02 | 0.42  |
| Hbegf     | 2.994E-04 | 3.24  |
| Hsd17b4   | 2.349E-05 | 0.50  |
| 2310002L1 | 3.253E-02 | 68.32 |
| Sec11c    | 1.195E-03 | 0.65  |
| Pmaip1    | 4.072E-03 | 2.74  |
| Impa2     | 1.607E-02 | 1.55  |
| Cidea     | 5.054E-03 | 0.19  |
| Ppic      | 4.581E-02 | 1.65  |
| Cep192    | 4.131E-03 | 1.51  |
| Lmnb1     | 1.923E-04 | 1.94  |
| Slc27a6   | 3.548E-04 | 0.40  |
| Cd74      | 7.747E-03 | 0.45  |
| Camk2a    | 2.211E-04 | 0.34  |
| Csf1r     | 4.914E-03 | 0.43  |
| Psat1     | 2.627E-03 | 2.07  |
| Cndp2     | 2.958E-03 | 0.56  |
| Cyb5      | 6.574E-05 | 0.45  |
| Incenp    | 7.189E-05 | 2.38  |
| Fth1      | 3.424E-02 | 0.51  |
| Rab3il1   | 1.487E-02 | 0.52  |
| Tmem138   | 2.737E-05 | 1.94  |
| Ms4a4d    | 4.624E-03 | 0.52  |
| Ms4a2     | 2.101E-02 | 0.47  |
| Lpxn      | 9.926E-05 | 0.32  |
| Pcsk5     | 4.158E-02 | 2.95  |
| Ms4a8a    | 9.961E-03 | 0.42  |
| Ccd86     | 3.141E-02 | 1.74  |
| Fen1      | 8.017E-04 | 2.14  |
| Ppp2r5b   | 1.057E-02 | 1.70  |
| Lipa      | 1.019E-03 | 0.23  |
| Sac3d1    | 2.420E-02 | 1.69  |
| Cdca5     | 8.683E-03 | 3.78  |
| Tnfrsf25  | 6.682E-04 | 0.46  |
| Kif20b    | 2.354E-04 | 3.32  |
| Rpp30     | 1.601E-02 | 1.69  |
| Ankrd1    | 1.394E-02 | 4.82  |
| Mlana     | 1.399E-07 | 0.09  |
| Slc25a45  | 1.194E-03 | 0.58  |
| Ighmbp2   | 4.477E-04 | 1.52  |
| Polia2    | 7.531E-03 | 1.69  |
| Chka      | 1.421E-03 | 2.01  |
| Banf1     | 6.058E-03 | 1.59  |
| Cst6      | 8.663E-03 | 0.08  |
| Pacs1     | 1.144E-04 | 1.59  |
| Doc2g     | 9.954E-03 | 1.79  |
| Rin1      | 1.822E-04 | 2.13  |
| Aldh3b1   | 4.258E-02 | 0.57  |
| Asah2     | 6.498E-04 | 0.38  |
| Slc29a2   | 2.091E-03 | 3.96  |
| Pcx       | 8.961E-05 | 0.33  |
| Cpt1a     | 5.813E-04 | 0.59  |
| Ctsw      | 1.953E-03 | 0.45  |
| Fosl1     | 1.486E-05 | 6.26  |
| Rps6ka4   | 7.520E-03 | 1.80  |
| Fermt3    | 2.117E-02 | 0.57  |
| Rcor2     | 1.177E-02 | 4.15  |
| Lgals12   | 4.829E-07 | 0.19  |



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| Pdcd4     | 2.116E-02 | 0.61 |
| Gpam      | 3.542E-05 | 0.32 |
| Acsf5     | 9.906E-04 | 0.61 |
| Hhex      | 2.395E-02 | 0.58 |
| Cep55     | 1.809E-05 | 3.86 |
| Rbp4      | 3.446E-05 | 0.17 |
| Noc3l     | 6.150E-04 | 1.71 |
| Hells     | 1.452E-03 | 2.50 |
| Pik3ap1   | 3.492E-03 | 0.46 |
| Slit1     | 7.943E-03 | 6.40 |
| Add3      | 2.476E-04 | 0.54 |
| Trim8     | 4.362E-03 | 1.58 |
| Taf5      | 1.610E-02 | 1.68 |
| Pcgf6     | 3.453E-04 | 2.03 |
| Col17a1   | 6.787E-03 | 2.21 |
| Sfr1      | 3.197E-02 | 2.41 |
| Gsto1     | 1.939E-02 | 4.92 |
| Dclre1a   | 9.721E-03 | 1.58 |
| Abli1     | 3.347E-03 | 0.63 |
| Hspa12a   | 4.012E-06 | 0.30 |
| Slc18a2   | 1.069E-04 | 0.61 |
| Bnc1      | 7.942E-04 | 3.42 |
| Ppp1r27   | 5.574E-03 | 0.27 |
| Alyref    | 5.146E-03 | 1.84 |
| Pycr1     | 3.163E-04 | 1.94 |
| Myadml2   | 4.399E-04 | 0.35 |
| Fasn      | 1.937E-03 | 0.61 |
| Arhgap19  | 1.870E-02 | 1.89 |
| Zdhhc16   | 5.345E-05 | 1.67 |
| Rfng      | 3.781E-02 | 2.09 |
| Slc16a3   | 3.199E-03 | 4.05 |
| Cd7       | 2.737E-02 | 0.42 |
| Sectm1a   | 1.204E-03 | 0.26 |
| Rab40b    | 2.133E-02 | 0.59 |
| Pi4k2a    | 1.419E-04 | 0.65 |
| Got1      | 6.426E-06 | 0.47 |
| Entpd7    | 7.209E-05 | 1.63 |
| Cpn1      | 4.702E-03 | 8.65 |
| Cwf19l1   | 1.782E-03 | 1.77 |
| Scd3      | 2.283E-02 | 0.15 |
| Sema4g    | 3.392E-02 | 0.62 |
| Sufu      | 1.055E-03 | 1.51 |
| Hexa      | 6.828E-04 | 0.37 |
| Adpgk     | 1.410E-03 | 1.57 |
| Fyco1     | 2.120E-05 | 0.53 |
| Ribc1     | 2.914E-02 | 4.42 |
| Fgd1      | 1.529E-02 | 2.49 |
| Dnase1l3  | 4.931E-03 | 0.56 |
| Sat1      | 5.862E-03 | 1.56 |
| Acot9     | 1.377E-04 | 1.55 |
| Itgb8     | 4.668E-04 | 0.21 |
| Gdf11     | 2.710E-03 | 1.97 |
| Cdk2      | 1.360E-05 | 1.70 |
| Pa2g4     | 8.738E-04 | 1.59 |
| Esy1      | 4.939E-03 | 0.51 |
| Baiap2    | 4.410E-03 | 0.63 |
| Aatk      | 3.616E-02 | 0.51 |
| Il23a     | 1.952E-03 | 5.15 |
| 2310003HC | 1.343E-02 | 1.59 |
| Prim1     | 4.934E-04 | 2.07 |
| Shmt2     | 3.117E-04 | 2.62 |
| Pstpip2   | 1.763E-02 | 0.53 |
| Xrcc6bp1  | 1.845E-02 | 1.83 |
| Zfp511    | 5.309E-03 | 1.68 |
| Cyp2e1    | 3.282E-03 | 0.20 |
| Cox8b     | 1.209E-06 | 0.14 |
| 1600016N2 | 3.817E-03 | 2.28 |
| Lrdd      | 1.002E-02 | 1.94 |
| Pnpla2    | 4.062E-05 | 0.27 |
| Gusb      | 3.831E-03 | 0.41 |
| Phkg1     | 1.070E-02 | 0.22 |
| Slc15a1   | 2.009E-03 | 0.17 |
| Tk1       | 3.310E-04 | 2.20 |
| Cpeb1     | 8.710E-04 | 0.38 |
| Tma16     | 9.067E-03 | 1.90 |
| Phf6      | 8.115E-04 | 1.54 |
| Ccd51     | 1.338E-03 | 2.51 |
| Col7a1    | 8.471E-03 | 3.28 |
| Rps6ka6   | 8.946E-04 | 0.18 |
| Alox5     | 3.151E-05 | 0.38 |
| 8-Mar     | 4.833E-06 | 0.50 |
| Wdr73     | 1.439E-02 | 1.76 |
| Sdc3      | 4.814E-02 | 0.55 |
| Il6       | 3.032E-02 | 2.44 |
| Agbl1     | 3.480E-03 | 0.23 |
| Plk4      | 4.442E-05 | 2.61 |
| Itih5     | 1.902E-04 | 0.16 |
| Clec3b    | 1.460E-04 | 0.15 |
| Slco3a1   | 6.216E-05 | 0.31 |
| Rassf3    | 3.980E-05 | 0.34 |
| Itgb1     | 3.848E-03 | 1.73 |
| Nrp1      | 2.055E-03 | 0.46 |
| Heatr2    | 1.627E-03 | 2.06 |
| Get4      | 8.106E-04 | 1.55 |
| Nop16     | 4.742E-03 | 1.90 |
| Thoc3     | 4.980E-03 | 1.72 |
| Hk3       | 1.335E-03 | 0.20 |
| Smad7     | 2.433E-03 | 1.89 |
| Aasdhppt  | 2.279E-03 | 1.60 |
| Rb1cc1    | 6.557E-03 | 0.63 |
| Mybl1     | 1.102E-02 | 2.02 |
| Terf1     | 1.749E-03 | 1.58 |
| Paqr8     | 4.524E-05 | 0.40 |
| Gsta3     | 1.024E-05 | 0.17 |
| Klf7      | 7.504E-04 | 2.52 |
| Adam23    | 1.408E-03 | 0.51 |
| Nrp2      | 3.852E-02 | 0.60 |
| 9430016HC | 8.919E-04 | 1.56 |



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|-----------|-----------|-------|
| Rftn2     | 1.010E-02 | 1.78  |
| Hspd1     | 1.204E-02 | 1.54  |
| Slc40a1   | 2.403E-05 | 0.26  |
| Icos      | 2.800E-02 | 0.59  |
| Cd28      | 3.958E-02 | 0.59  |
| Wdr12     | 4.752E-03 | 1.53  |
| Nop58     | 1.294E-03 | 1.96  |
| Orc2      | 4.546E-04 | 1.89  |
| Sgol2     | 1.719E-03 | 4.01  |
| Kdelc1    | 1.156E-03 | 1.57  |
| Tex30     | 1.530E-02 | 1.92  |
| 150001501 | 4.352E-03 | 17.51 |
| Il18r1    | 2.018E-02 | 0.58  |
| Pdcl3     | 1.001E-05 | 1.53  |
| Pms1      | 1.191E-02 | 1.75  |
| Mstn      | 1.174E-02 | 0.03  |
| Inpp4a    | 2.887E-03 | 0.62  |
| Sema4c    | 1.484E-04 | 2.44  |
| Ptpn18    | 1.910E-03 | 0.52  |
| Prim2     | 5.338E-05 | 1.98  |
| Wnt10a    | 9.151E-04 | 2.20  |
| Cyp27a1   | 3.842E-07 | 0.25  |
| Rqcd1     | 3.955E-04 | 1.51  |
| Slc11a1   | 4.995E-03 | 0.30  |
| Cxcr2     | 3.992E-02 | 1.52  |
| Xrcc5     | 1.888E-04 | 1.84  |
| Atic      | 6.045E-03 | 1.74  |
| Bard1     | 1.158E-04 | 2.62  |
| Ptprn     | 3.784E-03 | 15.32 |
| Des       | 8.353E-03 | 0.55  |
| Sp100     | 1.049E-02 | 0.41  |
| Ncl       | 1.558E-04 | 1.93  |
| Farsb     | 8.341E-03 | 1.52  |
| Serpine2  | 4.583E-02 | 2.19  |
| Ngef      | 3.579E-05 | 6.82  |
| Gpr35     | 1.625E-03 | 1.94  |
| Dtymk     | 1.740E-02 | 1.64  |
| Inpp5d    | 8.748E-03 | 0.55  |
| Serpinc8  | 8.727E-04 | 0.46  |
| Cln8      | 4.824E-06 | 0.48  |
| Tnfrsf11a | 1.534E-04 | 0.38  |
| Gin1      | 7.834E-03 | 1.61  |
| Gpr39     | 1.107E-03 | 10.11 |
| Mcm6      | 1.315E-02 | 1.62  |
| Rgs18     | 4.015E-05 | 0.24  |
| Rgs1      | 1.029E-03 | 0.14  |
| Rgs2      | 4.042E-05 | 0.41  |
| Cfh       | 5.002E-03 | 0.38  |
| Mki67ip   | 1.539E-02 | 1.64  |
| Dbi       | 1.867E-02 | 0.60  |
| Steap3    | 2.268E-03 | 0.46  |
| Ptprc     | 5.000E-03 | 0.49  |
| Cd55      | 1.451E-02 | 0.46  |
| Ddx59     | 4.490E-02 | 1.86  |
| Cacna1s   | 3.233E-05 | 0.25  |
| Tmem9     | 7.966E-03 | 1.57  |
| Tnnt2     | 9.449E-04 | 8.87  |
| Il24      | 1.537E-02 | 9.26  |
| Ube2t     | 1.399E-03 | 3.09  |
| Slc45a3   | 7.527E-04 | 0.23  |
| Cdk18     | 1.319E-02 | 0.35  |
| Atp2b4    | 7.051E-04 | 0.41  |
| Glul      | 1.179E-04 | 0.30  |
| Lamc2     | 1.428E-02 | 3.32  |
| Ncf2      | 1.490E-02 | 0.43  |
| Rgl1      | 2.417E-04 | 0.32  |
| Adck3     | 9.090E-05 | 0.35  |
| Cdc42bpa  | 1.866E-02 | 1.91  |
| Ahctf1    | 3.251E-02 | 1.61  |
| Kif26b    | 2.359E-02 | 2.05  |
| Mnda      | 2.083E-02 | 0.61  |
| Uck2      | 1.035E-03 | 1.98  |
| Mpzl1     | 1.578E-05 | 2.19  |
| Mpc2      | 7.135E-03 | 0.62  |
| Dpt       | 3.416E-04 | 0.25  |
| Nme7      | 1.611E-02 | 1.71  |
| Atp1b1    | 8.176E-04 | 0.20  |
| F5        | 1.434E-03 | 0.41  |
| Sele      | 1.471E-02 | 0.47  |
| Soat1     | 1.315E-04 | 0.31  |
| Nphs2     | 9.994E-03 | 7.01  |
| Ptpn14    | 1.388E-02 | 0.58  |
| Cenpf     | 2.388E-02 | 2.36  |
| Mark1     | 1.054E-02 | 0.52  |
| Nek2      | 2.173E-03 | 3.30  |
| Atf3      | 2.395E-03 | 0.24  |
| Batf3     | 1.493E-02 | 0.54  |
| Lamb3     | 3.052E-03 | 3.99  |
| Olah      | 4.182E-03 | 0.04  |
| Suv39h2   | 6.408E-03 | 2.17  |
| Dclre1c   | 3.091E-04 | 0.61  |
| Fam107b   | 3.873E-04 | 0.59  |
| Frmf4a    | 4.452E-04 | 0.54  |
| Dusp12    | 7.592E-03 | 1.60  |
| Mcm10     | 9.592E-04 | 3.21  |
| Optn      | 1.907E-03 | 0.60  |
| Ddr2      | 5.644E-04 | 0.47  |
| Nuf2      | 8.305E-05 | 3.36  |
| Mgst3     | 3.740E-04 | 0.51  |
| Myoc      | 3.237E-04 | 0.06  |
| Cenpl     | 1.162E-02 | 1.82  |
| Mrc1      | 5.735E-03 | 0.36  |
| Tnn       | 3.623E-02 | 5.02  |
| Vim       | 8.058E-03 | 0.37  |
| Pip4k2a   | 9.912E-04 | 0.61  |
| Plxdc2    | 6.601E-05 | 0.39  |
| Orc4      | 3.174E-04 | 1.54  |
| Prkcq     | 1.236E-04 | 0.28  |



|            |           |       |
|------------|-----------|-------|
| Mastl      | 7.606E-05 | 2.64  |
| Pdss1      | 5.393E-03 | 0.50  |
| Apbb1ip    | 2.506E-03 | 0.38  |
| St6galnac6 | 2.953E-02 | 0.58  |
| Lcn2       | 2.648E-02 | 0.29  |
| Gbgt1      | 1.958E-02 | 0.56  |
| Cytip      | 1.950E-02 | 0.64  |
| Acvr1c     | 3.187E-04 | 0.12  |
| Crat       | 7.342E-06 | 0.32  |
| Fam73b     | 2.689E-03 | 0.65  |
| Zeb2       | 9.305E-04 | 0.38  |
| Phf19      | 3.544E-03 | 2.59  |
| Gsn        | 9.427E-07 | 0.21  |
| Stom       | 2.715E-04 | 2.49  |
| Dab2ip     | 7.104E-04 | 2.03  |
| Grb14      | 5.380E-03 | 0.40  |
| Gca        | 1.208E-03 | 0.32  |
| Strbp      | 6.162E-05 | 1.59  |
| Wdr5       | 1.857E-05 | 1.51  |
| Card9      | 1.824E-03 | 0.56  |
| Neb        | 4.421E-06 | 0.28  |
| 2010317E2  | 3.259E-04 | 2.61  |
| Uap1l1     | 2.057E-03 | 0.55  |
| Itgb6      | 6.364E-03 | 1.78  |
| Zmynd19    | 1.304E-04 | 2.18  |
| Ly75       | 2.717E-02 | 0.62  |
| Il1f5      | 1.622E-02 | 0.30  |
| Il1f8      | 2.773E-02 | 0.51  |
| Hnmt       | 2.201E-04 | 0.43  |
| Dapl1      | 1.389E-02 | 0.31  |
| Pkp4       | 3.269E-05 | 1.98  |
| Gaint3     | 1.984E-04 | 2.90  |
| Nup35      | 2.079E-03 | 1.78  |
| Dusp19     | 8.844E-04 | 1.63  |
| Ssfa2      | 3.423E-04 | 0.47  |
| Itga4      | 1.766E-03 | 0.48  |
| Slc25a12   | 5.206E-04 | 0.66  |
| Hat1       | 1.843E-03 | 1.75  |
| Stk39      | 4.684E-02 | 1.69  |
| Ssrp1      | 1.276E-04 | 1.50  |
| Dhrs9      | 1.950E-04 | 0.61  |
| Slc43a3    | 7.104E-04 | 0.49  |
| Smtnl1     | 2.318E-03 | 0.30  |
| Clp1       | 3.819E-03 | 1.54  |
| Med19      | 5.540E-05 | 1.59  |
| Chrna1     | 4.311E-02 | 1.52  |
| Itga6      | 2.474E-04 | 2.56  |
| Kif18a     | 4.842E-05 | 2.90  |
| Slc12a6    | 6.773E-04 | 0.64  |
| Lpcat4     | 2.802E-02 | 2.79  |
| Ccdc34     | 2.301E-04 | 1.87  |
| B230118HC  | 2.472E-02 | 0.66  |
| Depdc7     | 3.003E-04 | 2.23  |
| Cat        | 6.694E-04 | 0.50  |
| Pamr1      | 3.160E-03 | 0.27  |
| Hsd17b12   | 1.752E-02 | 0.63  |
| Sema6d     | 1.151E-06 | 2.46  |
| Slc28a2    | 2.203E-05 | 0.39  |
| Duoxa1     | 3.176E-04 | 2.51  |
| Sord       | 1.827E-04 | 0.52  |
| Mdk        | 2.952E-02 | 1.98  |
| Lrp4       | 1.545E-02 | 0.59  |
| Jag1       | 1.780E-02 | 2.34  |
| 2210009G2  | 2.904E-03 | 1.72  |
| Ubox5      | 2.706E-04 | 1.63  |
| Ptptra     | 1.037E-06 | 0.59  |
| Nusap1     | 3.696E-05 | 2.31  |
| Dll4       | 3.271E-06 | 3.68  |
| Adam33     | 6.610E-04 | 0.40  |
| Siglec1    | 2.873E-03 | 0.20  |
| Rad51      | 3.278E-04 | 2.46  |
| Rpusd2     | 1.499E-03 | 1.83  |
| Casc5      | 2.536E-05 | 3.03  |
| Cdc25b     | 8.131E-05 | 2.32  |
| D2Ertd750k | 5.488E-06 | 3.23  |
| Rassf2     | 1.608E-03 | 0.41  |
| Gpcpd1     | 5.147E-03 | 0.51  |
| Fam98b     | 5.558E-06 | 1.70  |
| Mcm8       | 1.396E-04 | 2.37  |
| Fermt1     | 1.388E-03 | 2.30  |
| Bmp2       | 1.236E-03 | 2.70  |
| Mrps5      | 1.696E-02 | 1.55  |
| Bub1       | 5.367E-05 | 4.32  |
| Acox1      | 1.623E-02 | 0.09  |
| Fbln7      | 1.159E-03 | 0.21  |
| Zc3h8      | 4.894E-03 | 2.11  |
| Polr1b     | 9.977E-04 | 1.70  |
| Slc20a1    | 5.361E-04 | 2.25  |
| Tgm3       | 1.108E-02 | 4.99  |
| Nop56      | 5.774E-04 | 2.08  |
| Bfsp1      | 7.918E-07 | 5.61  |
| 843040610i | 2.520E-03 | 2.37  |
| Cd93       | 4.235E-02 | 0.57  |
| Cst3       | 2.967E-03 | 0.52  |
| Acss1      | 6.260E-04 | 0.25  |
| Gins1      | 4.956E-03 | 2.64  |
| Snph       | 5.937E-03 | 0.27  |
| Angpt4     | 1.481E-02 | 0.30  |
| Tbc1d20    | 5.470E-05 | 0.64  |
| Tpx2       | 3.812E-06 | 2.81  |
| Mylk2      | 3.025E-06 | 0.12  |
| Snta1      | 1.987E-07 | 0.44  |
| Aurka      | 8.132E-05 | 3.52  |
| Cstf1      | 1.202E-03 | 1.60  |
| Pkia       | 4.255E-06 | 0.23  |
| Pag1       | 6.111E-03 | 0.65  |
| Pck1       | 4.744E-03 | 0.06  |
| Fabp12     | 8.880E-03 | 14.04 |



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|-----------|-----------|-------|
| Snx16     | 4.349E-02 | 0.58  |
| Nfatc2    | 3.121E-05 | 0.33  |
| Zfp64     | 3.682E-04 | 2.09  |
| Car3      | 5.550E-05 | 0.11  |
| Zbtb46    | 3.862E-04 | 0.57  |
| Ahcy      | 2.189E-03 | 1.91  |
| Map1lc3a  | 3.463E-05 | 0.32  |
| Acss2     | 6.400E-03 | 0.51  |
| Gss       | 6.768E-05 | 1.69  |
| Procr     | 4.574E-04 | 3.68  |
| Dsn1      | 1.769E-05 | 1.84  |
| Rbl1      | 6.130E-04 | 1.84  |
| Src       | 3.282E-04 | 1.96  |
| Ctnnb1    | 6.426E-04 | 1.52  |
| Fam83d    | 1.303E-05 | 3.60  |
| Wisp2     | 3.986E-02 | 0.50  |
| Gnb4      | 6.983E-03 | 0.61  |
| Nceh1     | 1.430E-03 | 0.44  |
| Ect2      | 2.880E-05 | 2.49  |
| Acad9     | 3.013E-03 | 0.39  |
| Anxa5     | 2.717E-04 | 0.47  |
| Ccna2     | 2.109E-07 | 2.75  |
| Spata5    | 7.827E-04 | 1.51  |
| Aadac     | 1.310E-03 | 0.10  |
| P2ry1     | 2.944E-02 | 1.59  |
| Schip1    | 2.718E-03 | 1.59  |
| Nmd3      | 2.313E-03 | 1.54  |
| Bche      | 1.516E-04 | 0.07  |
| Ppid      | 2.056E-03 | 1.81  |
| Pfn2      | 8.769E-04 | 0.42  |
| Mme       | 4.490E-04 | 0.41  |
| Gmps      | 4.485E-06 | 1.53  |
| Shox2     | 3.247E-02 | 0.52  |
| Dclre1b   | 6.444E-03 | 1.51  |
| Ngf       | 1.594E-03 | 1.84  |
| Casq2     | 6.822E-03 | 1.91  |
| Cd2       | 2.711E-04 | 0.37  |
| Tbx15     | 2.811E-03 | 0.49  |
| Hsd3b6    | 8.194E-03 | 0.06  |
| Hmgcs2    | 1.316E-03 | 0.15  |
| Notch2    | 6.030E-04 | 0.63  |
| Stxbp3a   | 3.707E-04 | 0.66  |
| Gpsm2     | 2.712E-02 | 1.52  |
| Sypl2     | 7.613E-05 | 0.34  |
| Dram2     | 1.435E-04 | 0.61  |
| Ddx20     | 7.960E-06 | 1.80  |
| S100a11   | 3.145E-03 | 1.66  |
| Lce1m     | 4.268E-04 | 0.04  |
| Crt1      | 2.766E-02 | 0.57  |
| Lce1g     | 1.152E-02 | 0.37  |
| Lce1b     | 1.468E-03 | 0.15  |
| Sprr2j-ps | 2.821E-02 | 23.78 |
| Npr1      | 4.121E-04 | 0.40  |
| Creb3l4   | 3.780E-03 | 2.29  |
| Pmvk      | 9.094E-03 | 0.60  |
| Sass6     | 1.839E-04 | 1.78  |
| Larp7     | 1.260E-04 | 1.63  |
| Hadh      | 3.096E-02 | 0.66  |
| Trim2     | 5.364E-03 | 0.48  |
| Sfrp2     | 3.545E-02 | 2.35  |
| Casp6     | 9.624E-04 | 1.82  |
| Gar1      | 3.098E-05 | 2.24  |
| Ctso      | 8.234E-04 | 0.51  |
| Gstcd     | 7.260E-04 | 1.78  |
| Enpep     | 1.849E-04 | 0.14  |
| Dkk2      | 2.209E-03 | 0.36  |
| Kcnq5     | 4.956E-02 | 2.85  |
| Efna3     | 7.784E-03 | 0.24  |
| Cks1b     | 3.536E-04 | 2.76  |
| Pmf1      | 6.344E-05 | 2.17  |
| Iqgap3    | 1.518E-05 | 2.19  |
| Gpatch4   | 4.252E-04 | 1.95  |
| Cd1d1     | 9.597E-04 | 0.43  |
| Fmo5      | 1.299E-02 | 0.43  |
| Nudt17    | 2.817E-03 | 0.12  |
| Ctsk      | 7.388E-05 | 0.30  |
| Mettl14   | 1.185E-03 | 1.55  |
| Bnip1     | 1.259E-02 | 0.62  |
| Bcar3     | 7.151E-04 | 2.84  |
| Abcd3     | 2.724E-03 | 0.45  |
| Tmem56    | 3.686E-03 | 0.06  |
| Rorc      | 5.737E-03 | 0.47  |
| Tspan5    | 8.878E-05 | 0.64  |
| Mttp      | 4.556E-04 | 3.28  |
| Depdc1a   | 1.021E-05 | 4.22  |
| Cth       | 5.531E-03 | 3.84  |
| Lphn2     | 1.202E-05 | 0.36  |
| Rpf1      | 9.987E-04 | 1.74  |
| Ddah1     | 6.905E-03 | 3.58  |
| Cyr61     | 1.022E-02 | 2.05  |
| Col24a1   | 3.988E-02 | 2.66  |
| Cryz      | 7.325E-04 | 1.65  |
| Trp53inp1 | 5.241E-03 | 0.55  |
| Ccne2     | 1.722E-02 | 2.47  |
| Fam92a    | 1.271E-04 | 1.82  |
| Decr1     | 1.213E-03 | 0.54  |
| Sdr16c5   | 5.001E-04 | 0.29  |
| Atp6v0d2  | 1.609E-03 | 0.15  |
| Odf2l     | 7.781E-05 | 1.63  |
| Ndufaf4   | 2.453E-02 | 1.53  |
| Clca2     | 2.829E-05 | 0.12  |
| Rragd     | 5.154E-07 | 0.23  |
| 3110043O2 | 7.565E-04 | 0.65  |
| Smc2      | 1.398E-03 | 2.69  |
| Polr1e    | 1.544E-02 | 1.83  |
| Exosc3    | 4.711E-02 | 1.53  |
| 1300002K0 | 1.984E-02 | 0.32  |
| 5830415F0 | 2.591E-02 | 1.91  |



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|-----------|-----------|------|
| Anp32b    | 2.800E-04 | 2.13 |
| Nans      | 8.628E-03 | 1.69 |
| Col15a1   | 4.865E-02 | 0.64 |
| Tex10     | 1.004E-02 | 1.56 |
| Tmeff1    | 8.607E-03 | 3.48 |
| Dhc1      | 3.531E-03 | 5.82 |
| Tnc       | 2.204E-02 | 3.60 |
| Txn1      | 1.061E-02 | 2.24 |
| Svep1     | 1.339E-02 | 0.51 |
| Pappa     | 2.149E-03 | 3.85 |
| Hsd12     | 3.674E-02 | 0.66 |
| Smx30     | 1.407E-03 | 0.60 |
| Slc46a2   | 7.899E-04 | 0.05 |
| Alad      | 8.044E-03 | 0.52 |
| 2310002L0 | 9.109E-03 | 0.41 |
| Zdhhc21   | 3.646E-02 | 1.52 |
| Tmem38b   | 6.494E-04 | 0.64 |
| Nol6      | 4.534E-03 | 1.51 |
| Sit1      | 2.518E-03 | 0.40 |
| Car9      | 3.272E-03 | 4.31 |
| Tpm2      | 9.904E-03 | 0.58 |
| Gba2      | 2.402E-02 | 0.58 |
| Npr2      | 1.949E-02 | 0.65 |
| Reck      | 1.290E-03 | 0.46 |
| Plin2     | 1.050E-04 | 0.31 |
| Ptplad2   | 7.238E-03 | 0.61 |
| Ppap2b    | 1.610E-05 | 0.34 |
| Prkaa2    | 2.303E-04 | 0.29 |
| Sgjp1     | 6.459E-05 | 1.70 |
| Ak4       | 3.990E-02 | 2.50 |
| Cachd1    | 1.341E-03 | 0.45 |
| Artn      | 2.363E-02 | 7.25 |
| Dph2      | 3.957E-02 | 1.66 |
| B4galt2   | 4.614E-03 | 1.72 |
| Slc5a9    | 1.605E-02 | 0.44 |
| Bend5     | 2.196E-02 | 4.34 |
| Cdkn2c    | 2.037E-02 | 0.65 |
| Usp1      | 1.304E-03 | 1.60 |
| Ift74     | 1.617E-02 | 1.56 |
| Laptm5    | 2.411E-03 | 0.38 |
| Orc1      | 2.466E-03 | 3.11 |
| Tnfrsf1b  | 2.473E-02 | 0.49 |
| Podn      | 4.808E-03 | 0.52 |
| Scp2      | 4.766E-04 | 0.48 |
| Magoh     | 1.148E-02 | 1.62 |
| Lrp8      | 9.973E-05 | 3.85 |
| Tmem48    | 1.627E-02 | 2.11 |
| Kcnq4     | 1.738E-02 | 2.55 |
| Ctps      | 1.657E-04 | 2.27 |
| Slc2a1    | 2.379E-03 | 3.74 |
| Fuca1     | 1.066E-04 | 0.65 |
| Kif2c     | 5.721E-05 | 3.13 |
| Elf2b3    | 6.704E-03 | 1.53 |
| Mutyh     | 2.114E-02 | 2.02 |
| Nasp      | 7.058E-03 | 1.64 |
| Rad54l    | 3.674E-03 | 2.35 |
| Mknk1     | 1.870E-03 | 0.66 |
| Cyp4b1    | 8.007E-05 | 0.19 |
| Pdzk1p1   | 1.104E-02 | 0.49 |
| Stil      | 2.653E-04 | 2.95 |
| Ebna1bp2  | 3.092E-02 | 1.67 |
| Mrto4     | 9.588E-03 | 1.76 |
| Pla2g2f   | 3.323E-05 | 0.14 |
| Pla2g2e   | 2.143E-04 | 0.23 |
| Pink1     | 8.526E-07 | 0.42 |
| Kif17     | 6.386E-03 | 7.71 |
| Ptpn12    | 8.778E-04 | 1.70 |
| Fabp3     | 8.505E-04 | 0.23 |
| Tinag1    | 3.794E-03 | 2.53 |
| Tmem54    | 8.048E-03 | 0.62 |
| Adc       | 1.092E-02 | 1.94 |
| Ccdc28b   | 3.746E-03 | 0.65 |
| Tmem50a   | 1.872E-05 | 0.65 |
| Trim63    | 2.016E-05 | 0.27 |
| Extl1     | 5.768E-03 | 0.45 |
| Zfp593    | 1.257E-02 | 2.34 |
| Cnksr1    | 2.687E-03 | 2.08 |
| Syt11     | 1.396E-03 | 0.52 |
| Cdca8     | 5.575E-04 | 3.05 |
| Rpa2      | 5.950E-03 | 1.65 |
| Yrdc      | 1.018E-02 | 1.59 |
| Inpp5b    | 6.907E-04 | 0.63 |
| Rcc1      | 3.759E-03 | 2.12 |
| Plekhh2   | 4.265E-03 | 0.61 |
| Cdk14     | 3.047E-04 | 0.45 |
| Kcnab2    | 9.523E-03 | 0.51 |
| Xrcc2     | 8.751E-06 | 2.02 |
| Nol9      | 3.411E-02 | 1.52 |
| Smardc3   | 7.858E-04 | 0.51 |
| Zbtb48    | 1.895E-02 | 1.73 |
| Abcb1b    | 1.593E-02 | 2.01 |
| Car6      | 6.007E-03 | 0.15 |
| Dffa      | 2.811E-03 | 0.65 |
| Cas21     | 1.015E-03 | 0.46 |
| Nos3      | 2.330E-04 | 1.91 |
| H6pd      | 1.054E-02 | 0.64 |
| Ctnnbip1  | 8.580E-04 | 0.33 |
| Angptl7   | 9.290E-03 | 0.56 |
| Fam126a   | 1.271E-07 | 1.82 |
| Agtrap    | 1.497E-02 | 0.62 |
| Orc5      | 1.092E-03 | 1.68 |
| Dnajc2    | 2.765E-03 | 1.85 |
| Dffb      | 2.575E-02 | 1.79 |
| Lrrc47    | 2.388E-02 | 1.53 |
| Prkcz     | 3.145E-02 | 1.70 |
| Plch2     | 7.636E-03 | 1.69 |
| 2810405K0 | 7.503E-03 | 0.48 |
| Mib2      | 2.598E-03 | 0.66 |



|            |           |      |
|------------|-----------|------|
| Tnfrsf4    | 8.889E-03 | 0.63 |
| Pacrgl     | 1.458E-03 | 1.63 |
| Gpr125     | 1.528E-02 | 0.49 |
| Sorcs2     | 3.666E-03 | 2.88 |
| Htra3      | 6.468E-03 | 0.43 |
| Acx3       | 2.394E-05 | 0.42 |
| Rgs12      | 6.809E-03 | 1.75 |
| Pcdh7      | 4.197E-04 | 3.30 |
| Ppp2r2c    | 8.384E-05 | 0.18 |
| Plb1       | 2.289E-03 | 0.40 |
| Rbks       | 1.862E-02 | 1.61 |
| Ppm1g      | 3.193E-04 | 1.65 |
| Krtcap3    | 3.274E-03 | 1.67 |
| Pgm1       | 9.414E-05 | 1.57 |
| Cenpa      | 3.445E-05 | 2.26 |
| Pi4k2b     | 4.787E-06 | 1.71 |
| Slc34a2    | 2.548E-02 | 0.47 |
| Sel1l3     | 2.731E-02 | 0.39 |
| Rfc1       | 1.132E-03 | 1.52 |
| Tada2b     | 2.441E-04 | 1.52 |
| Grpel1     | 7.780E-03 | 1.52 |
| Tec        | 1.703E-03 | 0.55 |
| Ln timer   | 1.516E-02 | 0.52 |
| Ppat       | 9.030E-03 | 2.42 |
| Cenpc1     | 1.280E-05 | 1.53 |
| Stap1      | 8.539E-04 | 0.18 |
| Glmn       | 1.484E-03 | 1.99 |
| Cdc7       | 6.625E-03 | 1.93 |
| Tgfb3      | 1.477E-04 | 0.41 |
| Hsd17b11   | 8.162E-03 | 0.43 |
| Enoph1     | 6.429E-03 | 1.63 |
| Rasgef1b   | 2.750E-05 | 0.40 |
| Prkg2      | 2.214E-03 | 5.36 |
| Bmp3       | 1.623E-04 | 4.25 |
| Tesc       | 1.509E-02 | 0.22 |
| Nos1       | 6.880E-05 | 0.10 |
| Rfc5       | 1.055E-03 | 1.51 |
| Pf4        | 5.720E-03 | 0.38 |
| Mthfd2l    | 6.327E-04 | 1.91 |
| Ereg       | 1.206E-02 | 0.62 |
| Areg       | 4.613E-03 | 3.50 |
| Cxcl3      | 3.188E-02 | 4.61 |
| Shroom3    | 2.768E-02 | 2.11 |
| Ccng2      | 2.686E-02 | 1.75 |
| Tctn2      | 1.563E-02 | 2.00 |
| Eif2b1     | 2.186E-03 | 1.52 |
| Rilpl2     | 2.665E-03 | 0.40 |
| Naaa       | 1.123E-03 | 0.53 |
| Kntc1      | 2.362E-03 | 2.52 |
| Sdad1      | 2.073E-03 | 1.68 |
| Ran        | 7.393E-04 | 1.74 |
| Gbas       | 2.592E-05 | 0.59 |
| Psmc9      | 1.725E-03 | 1.52 |
| Cct6a      | 7.873E-04 | 1.84 |
| Aldh2      | 2.489E-06 | 0.43 |
| P2rx7      | 1.521E-03 | 0.54 |
| P2rx4      | 3.097E-03 | 0.50 |
| Anxa3      | 9.575E-03 | 1.87 |
| Pde6b      | 2.072E-02 | 2.33 |
| P2rx2      | 9.235E-05 | 0.19 |
| Ddx51      | 6.707E-05 | 1.70 |
| Pus1       | 4.072E-04 | 2.05 |
| Gpc2       | 9.426E-03 | 3.44 |
| Cit        | 6.438E-04 | 2.05 |
| Chek2      | 1.116E-04 | 2.07 |
| Srsf9      | 4.500E-04 | 1.67 |
| Psmg3      | 2.609E-03 | 1.50 |
| Tes        | 3.759E-02 | 1.66 |
| Mad1l1     | 1.116E-02 | 2.03 |
| Fscn1      | 5.685E-07 | 2.85 |
| Ung        | 8.889E-03 | 2.01 |
| Rbm19      | 8.396E-03 | 1.54 |
| 1110008J0: | 1.166E-02 | 1.54 |
| Rasa1      | 8.426E-04 | 0.42 |
| Aimp2      | 7.632E-03 | 1.57 |
| Polr1d     | 3.090E-04 | 1.70 |
| Flt1       | 2.014E-04 | 2.17 |
| Slc46a3    | 5.084E-07 | 0.39 |
| Tfpi2      | 9.526E-03 | 3.58 |
| Limk1      | 8.618E-03 | 1.95 |
| Eln        | 1.409E-02 | 0.42 |
| Hyal4      | 3.680E-03 | 0.29 |
| Lmod2      | 2.677E-03 | 0.36 |
| Lrwd1      | 7.958E-04 | 1.76 |
| Ephb4      | 1.194E-03 | 2.22 |
| Mcm7       | 7.129E-04 | 1.82 |
| Asns       | 5.773E-04 | 2.00 |
| Dlx5       | 1.624E-02 | 2.79 |
| Pon3       | 2.322E-04 | 0.53 |
| Akr1b8     | 2.199E-04 | 2.68 |
| Irf5       | 2.432E-03 | 0.56 |
| Ahcyl2     | 8.749E-03 | 1.56 |
| Adcyap1r1  | 1.837E-03 | 0.22 |
| NT5c3      | 2.134E-04 | 0.31 |
| Tmem209    | 4.384E-06 | 1.65 |
| Tsga14     | 1.483E-03 | 1.83 |
| Tmem176b   | 6.990E-04 | 0.56 |
| Gpnmb      | 1.276E-03 | 0.10 |
| Npy        | 7.451E-03 | 0.10 |
| Nfe2l3     | 5.737E-03 | 0.53 |
| Cbx3       | 1.615E-04 | 1.60 |
| Hoxa1      | 1.806E-03 | 5.77 |
| Clcn1      | 4.453E-03 | 0.43 |
| Ephb6      | 7.327E-03 | 0.47 |
| Mad2l1     | 2.885E-05 | 2.78 |
| Tbxas1     | 1.449E-02 | 0.39 |
| Anxa4      | 1.864E-03 | 0.55 |
| Tgfa       | 2.079E-03 | 2.57 |



|           |           |       |
|-----------|-----------|-------|
| Cct7      | 1.280E-04 | 1.53  |
| Lrig1     | 4.060E-03 | 0.42  |
| Kbtbd8    | 3.287E-02 | 1.66  |
| Wdr54     | 6.357E-03 | 1.95  |
| D6Mm5e    | 3.126E-02 | 4.15  |
| Arhgap25  | 1.952E-03 | 0.24  |
| Rab43     | 5.767E-03 | 0.60  |
| Frm4b     | 4.250E-03 | 0.65  |
| Gm20696   | 4.014E-02 | 0.58  |
| Ch1       | 2.034E-03 | 0.66  |
| Ruvbl1    | 8.968E-03 | 1.98  |
| Plxna1    | 2.484E-02 | 0.64  |
| Klf15     | 6.544E-05 | 0.41  |
| Slc41a3   | 7.218E-05 | 0.50  |
| Nup210    | 4.741E-03 | 0.58  |
| Wnt7a     | 2.044E-02 | 15.57 |
| Tmem43    | 1.277E-03 | 0.60  |
| Bhlhe40   | 1.818E-02 | 1.58  |
| Slc6a12   | 1.380E-02 | 0.14  |
| A2m       | 3.196E-02 | 38.93 |
| Gdf3      | 5.907E-03 | 0.54  |
| Tmcc1     | 3.118E-05 | 0.54  |
| Zfp248    | 2.554E-02 | 1.63  |
| Clec4b1   | 1.303E-04 | 0.22  |
| Clec4a2   | 3.132E-04 | 0.39  |
| Cd69      | 3.713E-02 | 0.61  |
| Clec2d    | 1.664E-04 | 0.56  |
| Gabarapl1 | 3.171E-07 | 0.35  |
| Adipor2   | 2.081E-04 | 0.62  |
| Mgp       | 7.570E-03 | 0.21  |
| Arhgdib   | 2.913E-03 | 0.66  |
| Ptpro     | 1.566E-04 | 0.30  |
| Strap     | 1.518E-03 | 1.52  |
| Ldhd      | 3.906E-05 | 0.18  |
| Rad18     | 1.339E-04 | 2.12  |
| Sspn      | 7.838E-03 | 0.55  |
| Bhlhe41   | 9.217E-03 | 0.28  |
| Lrmp      | 2.264E-04 | 0.37  |
| Ogg1      | 1.236E-03 | 1.57  |
| Camk1     | 4.619E-03 | 0.52  |
| Cidec     | 1.345E-04 | 0.05  |
| Med21     | 1.871E-04 | 1.67  |
| Far2      | 2.118E-03 | 0.12  |
| Tmtc1     | 1.257E-03 | 0.44  |
| Caprin2   | 8.926E-03 | 1.55  |
| Dennd5b   | 8.476E-04 | 2.02  |
| Timp4     | 9.293E-05 | 0.08  |
| Rad51ap1  | 2.581E-04 | 2.87  |
| Tspan9    | 1.262E-02 | 1.51  |
| Ckm       | 6.684E-04 | 0.09  |
| Rtn2      | 8.598E-07 | 0.26  |
| Vasp      | 2.714E-03 | 1.57  |
| Dmwd      | 1.147E-02 | 1.73  |
| Pop4      | 2.700E-02 | 1.51  |
| Lilra6    | 1.591E-03 | 0.32  |
| Ttyh1     | 4.362E-04 | 1.95  |
| Tmem238   | 1.083E-02 | 3.04  |
| Sbk2      | 3.688E-03 | 0.18  |
| Zdhhc13   | 1.412E-04 | 2.09  |
| Cyp2b10   | 3.323E-02 | 0.38  |
| Lypd5     | 1.879E-02 | 0.51  |
| C23005211 | 1.192E-04 | 1.90  |
| Slc7a10   | 2.671E-03 | 0.11  |
| Gas2      | 3.092E-04 | 2.25  |
| Snrpa1    | 1.097E-02 | 2.06  |
| Pcsk6     | 2.649E-06 | 0.21  |
| Tarsl2    | 2.568E-02 | 0.61  |
| Mphosph1  | 2.118E-03 | 1.55  |
| Blm       | 4.461E-04 | 3.05  |
| Sema4b    | 1.821E-03 | 1.67  |
| Pex11a    | 2.238E-03 | 0.43  |
| Plin1     | 1.973E-04 | 0.07  |
| Synn      | 2.554E-06 | 0.26  |
| Lrrc28    | 2.133E-03 | 0.33  |
| Tyropb    | 2.167E-03 | 0.39  |
| 2200002D0 | 4.786E-02 | 1.73  |
| Rasgrp4   | 1.350E-04 | 0.43  |
| Ryr1      | 8.123E-05 | 0.30  |
| Fbxo17    | 1.823E-02 | 2.62  |
| Mfge8     | 9.027E-03 | 0.28  |
| Mrps11    | 4.131E-03 | 1.51  |
| Syt12     | 1.023E-02 | 0.51  |
| Me3       | 3.131E-07 | 0.46  |
| Zfand6    | 6.798E-03 | 0.63  |
| 463243411 | 1.761E-02 | 2.86  |
| Xylt1     | 5.770E-03 | 0.53  |
| Mylpf     | 8.072E-03 | 0.23  |
| Klf22     | 4.381E-06 | 3.00  |
| Ino80e    | 1.879E-03 | 1.63  |
| Klk10     | 4.347E-02 | 2.12  |
| Aldoa     | 8.748E-04 | 0.57  |
| Plekhhb1  | 9.922E-04 | 0.60  |
| Gdpd3     | 1.007E-02 | 0.57  |
| Coro1a    | 1.130E-02 | 0.54  |
| Sult1a1   | 3.581E-07 | 0.14  |
| Klk7      | 5.994E-04 | 0.33  |
| Nupr1     | 2.874E-04 | 0.47  |
| Nfatc2ip  | 6.285E-03 | 1.58  |
| Lipt2     | 2.801E-02 | 1.89  |
| Atp2a1    | 5.415E-09 | 0.10  |
| Slco2b1   | 6.844E-07 | 0.18  |
| Myh14     | 2.336E-03 | 0.46  |
| Lat       | 1.263E-05 | 0.35  |
| Dgat2     | 4.332E-05 | 0.38  |
| Nsmce1    | 3.307E-03 | 1.86  |
| Jmjd5     | 3.332E-03 | 2.08  |
| Slc5a11   | 6.501E-03 | 0.06  |
| Parva     | 5.894E-03 | 1.75  |



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|-----------|-----------|------|
| Micalcl   | 4.842E-04 | 0.40 |
| Dkk3      | 3.269E-02 | 1.70 |
| Trat1     | 1.391E-03 | 0.25 |
| Tgfb11    | 1.890E-02 | 1.96 |
| Cox6a2    | 1.934E-05 | 0.27 |
| Itgax     | 1.452E-02 | 0.29 |
| Adm       | 2.661E-03 | 3.79 |
| Dkk11     | 1.998E-04 | 0.17 |
| Fus       | 8.388E-04 | 1.52 |
| Cd37      | 3.502E-04 | 0.30 |
| Prss8     | 6.456E-04 | 0.39 |
| 913001902 | 5.561E-04 | 1.64 |
| Bcat2     | 1.567E-05 | 0.41 |
| Rgs10     | 2.935E-04 | 0.44 |
| Fgfr2     | 4.977E-02 | 1.86 |
| Tacc2     | 2.639E-03 | 0.65 |
| Acadsb    | 2.910E-04 | 0.65 |
| 2010110P0 | 6.704E-05 | 0.15 |
| Plk1      | 1.246E-03 | 3.59 |
| Ears2     | 8.752E-03 | 1.54 |
| Scnn1b    | 1.106E-02 | 0.58 |
| Cdr2      | 7.853E-03 | 0.58 |
| Mrpl17    | 3.538E-04 | 1.53 |
| Rrp8      | 8.039E-06 | 1.63 |
| Tmem159   | 8.785E-05 | 0.39 |
| Eri2      | 8.256E-04 | 1.87 |
| Acsm3     | 4.002E-03 | 0.35 |
| Lhpp      | 7.879E-05 | 0.23 |
| Zranb1    | 7.500E-03 | 0.64 |
| Ctbp2     | 3.647E-04 | 1.60 |
| Rrm1      | 2.271E-05 | 1.99 |
| Art1      | 6.323E-05 | 0.25 |
| Mki67     | 5.623E-05 | 1.90 |
| Tnni2     | 2.886E-05 | 0.16 |
| Syt8      | 2.729E-04 | 5.99 |
| Sash3     | 4.963E-03 | 0.50 |
| RbmX2     | 1.575E-04 | 2.10 |
| 2610018G0 | 1.333E-03 | 2.80 |
| Slc9a9    | 1.538E-05 | 0.32 |
| Arhgef6   | 2.418E-04 | 0.37 |
| Fgf13     | 2.521E-02 | 0.50 |
| Praf2     | 1.009E-02 | 1.88 |
| Hdac6     | 5.334E-06 | 1.67 |
| Was       | 3.198E-03 | 0.49 |
| Wdr13     | 5.197E-05 | 0.64 |
| Rpgr      | 7.656E-03 | 1.76 |
| Heph      | 6.801E-04 | 0.40 |
| Ophn1     | 4.003E-05 | 0.43 |
| Stard8    | 8.869E-05 | 0.28 |
| Efnb1     | 4.920E-04 | 2.34 |
| Awat2     | 9.081E-03 | 0.07 |
| Srpx2     | 2.598E-02 | 2.24 |
| Cstf2     | 4.020E-03 | 1.65 |
| Xkrx      | 1.393E-02 | 0.31 |
| Cenpi     | 1.869E-05 | 3.61 |
| Btk       | 2.588E-04 | 0.44 |
| Gla       | 9.466E-03 | 0.45 |
| Chrd1     | 6.849E-05 | 0.24 |
| Pak3      | 9.794E-04 | 0.22 |
| Gpr64     | 4.349E-02 | 2.25 |
| Map3k15   | 6.411E-03 | 2.31 |
| Itgb1bp2  | 2.127E-03 | 0.51 |
| Mtm1      | 4.140E-04 | 0.59 |
| Gpm6b     | 1.271E-02 | 0.55 |
| Hccs      | 5.443E-04 | 1.58 |
| Arhgap6   | 2.599E-03 | 0.29 |
| Abcd1     | 3.562E-03 | 0.49 |
| Piga      | 9.124E-04 | 2.19 |
| Asb11     | 3.957E-06 | 0.28 |
| Dusp9     | 1.252E-03 | 4.90 |
| Renbp     | 1.467E-02 | 0.53 |
| Dkc1      | 6.899E-04 | 2.06 |
| Plp1      | 1.773E-02 | 0.58 |
| Psmc10    | 1.658E-02 | 1.56 |
| Tsc22d3   | 1.664E-03 | 0.26 |
| Morc4     | 1.208E-02 | 2.89 |
| Rnf128    | 1.088E-02 | 0.30 |
| Mcf2l     | 6.104E-03 | 0.47 |
| Gas6      | 2.791E-04 | 0.33 |
| 2410022L0 | 3.380E-02 | 1.60 |
| Myom2     | 7.077E-06 | 0.22 |
| Angpt2    | 9.752E-05 | 2.12 |
| Adrb3     | 1.624E-02 | 0.36 |
| Elf4ebp1  | 2.180E-03 | 1.90 |
| Cd209a    | 8.805E-04 | 0.13 |
| Cd209d    | 2.476E-04 | 0.11 |
| Tnfsf13b  | 2.600E-03 | 0.45 |
| Rab20     | 3.940E-02 | 1.91 |
| Ptpn7     | 5.386E-03 | 0.57 |
| Ankrd10   | 2.464E-05 | 1.64 |
| Dlc1      | 1.141E-02 | 0.64 |
| Eri1      | 6.893E-04 | 1.69 |
| Plat      | 3.884E-02 | 1.74 |
| Ank1      | 1.752E-02 | 0.50 |
| Tenm3     | 1.247E-02 | 4.78 |
| Dctd      | 9.527E-03 | 2.80 |
| Rwdd4a    | 1.517E-03 | 1.59 |
| Ash2l     | 1.021E-03 | 1.59 |
| Mak16     | 1.656E-03 | 1.66 |
| Gsr       | 3.421E-02 | 1.91 |
| Gtf2e2    | 7.938E-04 | 1.81 |
| Rbpms     | 3.634E-02 | 2.45 |
| Sc4mol    | 2.725E-02 | 0.55 |
| Sap30     | 7.682E-03 | 2.18 |
| Hpgd      | 5.741E-03 | 0.37 |
| Ednra     | 9.525E-03 | 1.79 |
| Nr3c2     | 1.624E-05 | 0.37 |
| Casp3     | 1.952E-03 | 1.83 |



|           |           |       |
|-----------|-----------|-------|
| Mlf1ip    | 1.341E-02 | 2.15  |
| Slc25a4   | 1.967E-04 | 0.61  |
| Pdlim3    | 7.148E-03 | 0.48  |
| Sh3rf1    | 1.278E-05 | 2.00  |
| Adcy7     | 1.505E-03 | 0.40  |
| Gins3     | 4.365E-04 | 2.02  |
| Orc6      | 1.396E-02 | 2.41  |
| Tecr      | 2.220E-03 | 0.58  |
| Tbc1d9    | 2.509E-02 | 0.60  |
| Ili5      | 1.349E-04 | 0.43  |
| Smarca5   | 2.139E-03 | 1.50  |
| Hp        | 1.625E-03 | 0.28  |
| Dhodh     | 5.988E-03 | 1.57  |
| Ii34      | 1.325E-03 | 0.50  |
| Nudt21    | 1.410E-03 | 1.62  |
| Cenpn     | 7.808E-04 | 3.54  |
| Cdyl2     | 1.485E-03 | 1.75  |
| Mt2       | 2.591E-02 | 2.34  |
| Mt1       | 5.601E-03 | 1.82  |
| Ccl22     | 2.351E-03 | 0.22  |
| Ciapi1    | 1.340E-03 | 1.54  |
| Gpr56     | 4.497E-02 | 0.61  |
| Mmp15     | 2.122E-03 | 2.42  |
| Tmem38a   | 5.370E-07 | 0.20  |
| Slc27a1   | 2.122E-05 | 0.39  |
| Cotl1     | 2.532E-03 | 1.74  |
| Mast3     | 1.358E-05 | 0.63  |
| Ifi30     | 2.708E-03 | 0.57  |
| Mphosph6  | 1.264E-03 | 2.05  |
| Cdh5      | 6.015E-04 | 1.97  |
| Ces2g     | 4.284E-03 | 3.54  |
| Fam96b    | 8.220E-03 | 1.72  |
| Rrad      | 3.446E-03 | 3.14  |
| Ces2e     | 2.114E-04 | 5.78  |
| Tradd     | 2.356E-05 | 1.86  |
| Pla2g15   | 6.391E-03 | 0.52  |
| Smpd3     | 4.055E-02 | 0.52  |
| Has3      | 1.413E-03 | 6.22  |
| Nip7      | 1.980E-02 | 1.53  |
| Mre11a    | 1.556E-03 | 1.53  |
| Heph1l    | 9.355E-04 | 0.28  |
| Taf1d     | 7.555E-04 | 1.66  |
| Kars      | 1.385E-03 | 1.64  |
| Adat1     | 4.624E-02 | 1.51  |
| Gabara12  | 8.259E-03 | 0.58  |
| Cfdp1     | 1.800E-03 | 1.64  |
| Bcar1     | 4.888E-05 | 1.79  |
| Wdr59     | 1.925E-03 | 1.52  |
| Arv1      | 2.285E-02 | 1.84  |
| 2310022B0 | 4.981E-02 | 1.54  |
| 2810004N2 | 2.402E-04 | 1.71  |
| Egln1     | 3.271E-02 | 1.54  |
| Trpc6     | 8.514E-04 | 2.52  |
| Dcun1d5   | 1.262E-03 | 1.61  |
| Usp2      | 9.579E-06 | 0.36  |
| Pvrl1     | 2.083E-02 | 1.76  |
| Oaf       | 5.260E-03 | 2.65  |
| Pou2f3    | 4.312E-04 | 0.21  |
| Clmp      | 1.006E-02 | 0.49  |
| Dcps      | 6.138E-03 | 1.61  |
| Tirap     | 3.272E-03 | 2.25  |
| Abhd12    | 1.966E-05 | 0.66  |
| Acat1     | 3.070E-03 | 0.66  |
| Cryab     | 4.232E-02 | 0.50  |
| 2310030GC | 4.723E-03 | 1.88  |
| Dixdc1    | 1.097E-03 | 2.48  |
| Bco2      | 3.099E-02 | 3.30  |
| Tagln     | 1.917E-02 | 2.21  |
| Mpxl2     | 2.063E-03 | 2.11  |
| Cd3e      | 2.616E-02 | 0.57  |
| Pus3      | 1.014E-02 | 1.52  |
| Chek1     | 1.528E-03 | 3.18  |
| Slc37a2   | 1.432E-07 | 0.26  |
| Robo4     | 3.149E-04 | 1.68  |
| Mcam      | 6.111E-04 | 1.97  |
| Pin1      | 1.966E-02 | 1.60  |
| Scg3      | 9.719E-04 | 0.10  |
| Lysmd2    | 2.561E-02 | 1.53  |
| Rsl24d1   | 5.602E-04 | 1.65  |
| Ccnb2     | 2.223E-05 | 2.64  |
| Cgln1     | 2.863E-03 | 0.60  |
| Rora      | 1.327E-03 | 0.40  |
| Kif23     | 2.073E-03 | 2.18  |
| Ankk1     | 4.386E-02 | 18.96 |
| Elovl4    | 1.073E-03 | 0.24  |
| Nnmt      | 8.222E-03 | 0.40  |
| Paqr5     | 1.173E-02 | 0.44  |
| Thsd4     | 1.180E-02 | 2.39  |
| Pkm       | 1.191E-04 | 1.66  |
| Nrg4      | 3.958E-04 | 0.40  |
| Cyp1a1    | 1.352E-04 | 0.06  |
| Rcn2      | 3.188E-04 | 1.63  |
| Cyp11a1   | 9.533E-05 | 0.27  |
| Tspan3    | 1.213E-05 | 2.99  |
| Stra6     | 1.379E-03 | 34.99 |
| Col12a1   | 7.731E-03 | 3.84  |
| Gsta4     | 2.567E-02 | 31.62 |
| Elovl5    | 3.331E-04 | 0.46  |
| Mlip      | 1.372E-03 | 0.42  |
| Adamts7   | 3.409E-03 | 3.62  |
| Tpm1      | 2.655E-03 | 0.47  |
| Plscr2    | 7.333E-04 | 0.48  |
| Car12     | 1.288E-02 | 2.02  |
| Plod2     | 2.076E-02 | 2.90  |
| Parp16    | 2.619E-03 | 1.78  |
| Tipin     | 8.736E-04 | 1.82  |
| Snapc5    | 5.784E-04 | 0.65  |
| Zwilch    | 1.061E-04 | 3.10  |



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|-----------|-----------|------|
| Ube2cbp   | 4.551E-03 | 1.98 |
| Me1       | 2.284E-03 | 0.40 |
| Nt5e      | 4.669E-02 | 1.80 |
| Tgfb2     | 1.449E-02 | 0.65 |
| Clstn2    | 2.108E-03 | 4.71 |
| Nmnat3    | 2.058E-03 | 1.60 |
| Mrps22    | 4.102E-02 | 1.52 |
| Pik3cb    | 4.429E-05 | 0.58 |
| Cdc25a    | 3.087E-04 | 2.28 |
| Nme6      | 1.215E-03 | 1.79 |
| Ptgs2     | 1.869E-06 | 6.16 |
| Nradd     | 5.140E-03 | 1.63 |
| Hhat1     | 7.075E-05 | 0.27 |
| Pccb      | 9.844E-05 | 0.64 |
| Slco2a1   | 1.500E-02 | 1.86 |
| Srprb     | 3.958E-04 | 1.56 |
| Trf       | 1.508E-03 | 0.28 |
| Topbp1    | 7.844E-05 | 2.03 |
| Acpp      | 1.282E-04 | 0.30 |
| Nudt16    | 1.042E-02 | 0.45 |
| Mst1r     | 6.644E-03 | 1.66 |
| Traip     | 5.693E-04 | 4.14 |
| Slc25a20  | 1.182E-04 | 0.61 |
| Thsd7a    | 2.229E-05 | 0.27 |
| Chsy1     | 3.741E-03 | 1.93 |
| Pygm      | 7.657E-06 | 0.10 |
| Crebl2    | 4.777E-05 | 0.54 |
| 3-Mar     | 4.984E-05 | 0.33 |
| Pon2      | 6.335E-03 | 0.65 |
| Lmo2      | 2.561E-05 | 0.31 |
| Mdfi      | 2.337E-03 | 2.28 |
| Mansc1    | 3.198E-04 | 0.21 |
| Folr2     | 1.648E-03 | 0.28 |
| Abilm3    | 2.130E-02 | 0.46 |
| Tpcn1     | 5.687E-03 | 0.63 |
| Heyl      | 2.575E-02 | 3.25 |
| Slc24a6   | 1.353E-04 | 0.55 |
| Cntrob    | 1.683E-03 | 1.77 |
| Troap     | 9.281E-04 | 3.67 |
| Pdxk      | 1.528E-04 | 0.51 |
| Arap1     | 2.906E-03 | 0.47 |
| Ppp1r9a   | 2.079E-04 | 0.26 |
| Pwp2      | 1.161E-03 | 1.89 |
| Smap2     | 1.972E-04 | 0.59 |
| Arhgef17  | 1.454E-02 | 1.68 |
| Acsf3     | 1.244E-03 | 2.13 |
| Rangrf    | 2.580E-02 | 1.76 |
| Slc16a1   | 8.488E-04 | 1.70 |
| Itgbl1    | 3.398E-03 | 0.40 |
| Ucp3      | 4.731E-04 | 0.16 |
| Rasgrp2   | 1.723E-03 | 0.55 |
| Inha      | 3.371E-03 | 2.40 |
| Nfatc1    | 2.229E-04 | 0.62 |
| Cdo1      | 2.857E-05 | 0.11 |
| C330027C0 | 2.035E-04 | 2.96 |
| Dhrs7c    | 4.075E-04 | 0.07 |
| Npat      | 1.623E-03 | 1.54 |
| Pfkm      | 8.114E-07 | 0.20 |
| Gas7      | 3.884E-04 | 0.44 |
| Tbc1d4    | 2.600E-05 | 0.48 |
| Apmap     | 5.487E-03 | 0.66 |
| Rnf125    | 1.838E-02 | 0.65 |
| Phldb2    | 5.991E-03 | 2.00 |
| Atp1a1    | 2.044E-02 | 1.76 |
| Dis3      | 2.067E-03 | 2.26 |
| Card10    | 9.162E-03 | 1.91 |
| Mgil      | 1.445E-04 | 0.08 |
| Kbtbd12   | 8.379E-05 | 0.25 |
| Mxt1      | 3.031E-05 | 1.51 |
| BC016579  | 3.838E-04 | 0.16 |
| Myh2      | 6.126E-03 | 0.31 |
| Tpsg1     | 1.425E-05 | 0.19 |
| Mamdc2    | 2.159E-02 | 0.41 |
| Rac2      | 7.464E-04 | 0.43 |
| Ttf2      | 9.978E-05 | 1.83 |
| Hsf4      | 1.578E-02 | 2.30 |
| Duox1     | 3.335E-04 | 3.25 |
| Noc4l     | 7.744E-03 | 1.88 |
| Mif       | 3.321E-03 | 1.66 |
| Fbxl8     | 6.902E-06 | 1.84 |
| Gstt2     | 5.416E-04 | 0.53 |
| Tnxb      | 4.139E-05 | 0.10 |
| Chst2     | 1.648E-04 | 4.13 |
| Pus7l     | 2.196E-02 | 1.90 |
| Palmd     | 2.661E-02 | 0.58 |
| Agl       | 8.622E-05 | 0.41 |
| Nudt15    | 8.469E-03 | 1.75 |
| Snap91    | 1.555E-03 | 0.11 |
| Adamts15  | 3.555E-03 | 0.41 |
| Asprv1    | 2.820E-02 | 0.24 |
| Apol6     | 1.693E-02 | 0.38 |
| Myo6      | 9.758E-03 | 0.60 |
| Fa2h      | 6.766E-04 | 0.05 |
| Igf2bp2   | 1.007E-03 | 3.71 |
| Ndn       | 1.428E-02 | 0.54 |
| Rfwd3     | 6.733E-04 | 1.60 |
| Pank1     | 3.011E-03 | 0.28 |
| Ddx19b    | 9.226E-04 | 1.54 |
| Zfp7      | 6.150E-03 | 1.71 |
| Gabrb3    | 4.295E-03 | 6.94 |
| Ucp2      | 3.922E-03 | 0.49 |
| Arhgap39  | 1.147E-04 | 0.61 |
| Fuk       | 1.740E-04 | 1.84 |
| Stard9    | 4.097E-03 | 0.47 |
| Akr1c14   | 6.085E-04 | 0.08 |
| Adra2a    | 1.648E-02 | 3.97 |
| Egr3      | 7.606E-04 | 0.41 |
| St18      | 2.251E-02 | 0.47 |



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|------------|-----------|------|
| Gadd45gip: | 2.960E-02 | 1.54 |
| Mnd1       | 5.040E-03 | 1.79 |
| Recql4     | 4.253E-03 | 3.95 |
| Rpap2      | 5.987E-04 | 1.68 |
| Tlr13      | 3.619E-02 | 0.38 |
| Atp7a      | 5.487E-04 | 0.63 |
| Alg3       | 2.330E-03 | 1.65 |
| Tpsb2      | 9.237E-03 | 0.42 |
| B3galt2    | 4.960E-02 | 0.66 |
| Klf9       | 3.812E-04 | 0.46 |
| Ppargc1b   | 3.601E-03 | 0.60 |
| Cflr2      | 2.668E-02 | 0.40 |
| Gucy1a3    | 5.785E-04 | 0.49 |
| Rbm34      | 2.101E-03 | 1.79 |
| Aspm       | 4.255E-03 | 2.58 |
| 2310014L1  | 7.655E-03 | 0.44 |
| Rfc3       | 2.766E-03 | 2.10 |
| Kcnk1      | 3.352E-03 | 5.65 |
| Fancd2     | 2.482E-04 | 2.21 |
| Cct2       | 3.824E-05 | 1.57 |
| Cd226      | 2.554E-03 | 0.45 |
| Lyl1       | 1.631E-04 | 0.34 |
| Phka1      | 2.900E-04 | 0.38 |
| Ano7       | 1.766E-03 | 0.18 |
| Tspan8     | 4.345E-04 | 0.31 |
| 2310044G1  | 1.398E-04 | 0.45 |
| 2310007B0  | 7.766E-04 | 0.31 |
| Emid1      | 3.341E-03 | 1.93 |
| Faah       | 2.115E-04 | 0.10 |
| Lsm3       | 1.824E-02 | 1.64 |
| Chchd4     | 8.339E-04 | 1.72 |
| Loxl2      | 4.159E-02 | 1.96 |
| Polq       | 6.819E-04 | 3.04 |
| Usp54      | 1.487E-03 | 0.53 |
| Slc25a37   | 3.149E-05 | 2.51 |
| Exosc4     | 2.784E-02 | 1.70 |
| Batf       | 6.136E-03 | 0.57 |
| Traf3ip1   | 1.114E-02 | 1.53 |
| Fhod3      | 3.342E-02 | 2.28 |
| Ccdc15     | 4.224E-04 | 1.99 |
| Sdr42e1    | 4.280E-03 | 0.36 |
| Kif4       | 2.779E-05 | 2.92 |
| Iqsec1     | 2.004E-02 | 0.38 |
| Trim59     | 1.727E-05 | 2.69 |
| Exosc1     | 3.934E-03 | 1.86 |
| Brip1      | 1.825E-03 | 2.09 |
| Smc4       | 7.642E-05 | 1.74 |
| Ramp1      | 1.393E-04 | 0.28 |
| Skint2     | 4.185E-05 | 0.12 |
| Dak        | 1.197E-04 | 1.63 |
| Al661453   | 7.245E-03 | 1.59 |
| Lif        | 4.435E-02 | 2.71 |
| Gcsh       | 7.151E-04 | 1.61 |
| Pkd2       | 1.438E-02 | 1.74 |
| Scara3     | 6.451E-03 | 0.43 |
| Caskin2    | 4.211E-03 | 1.55 |
| Uaca       | 7.934E-04 | 2.35 |
| Edil3      | 4.588E-02 | 4.09 |
| Gjc1       | 3.265E-02 | 1.68 |
| Zfyve9     | 8.596E-03 | 0.65 |
| Ccpg1      | 9.472E-04 | 0.62 |
| Ptpn13     | 1.562E-03 | 1.81 |
| Exph5      | 1.867E-02 | 0.63 |
| 8430429K0  | 3.403E-03 | 1.56 |
| Slc41a2    | 8.182E-03 | 0.51 |
| Myo5a      | 4.648E-03 | 0.63 |
| 2700049A0  | 3.673E-02 | 1.50 |
| Pof1b      | 1.430E-02 | 0.55 |
| Ppm1h      | 2.968E-03 | 0.47 |
| Tiparp     | 3.833E-04 | 1.67 |
| Cd300a     | 5.548E-04 | 0.37 |
| Cacna1a    | 1.598E-02 | 0.47 |
| Tmem109    | 1.073E-03 | 0.55 |
| Xpot       | 6.280E-05 | 1.71 |
| Tdg        | 6.481E-05 | 1.53 |
| Sema3f     | 1.116E-02 | 1.79 |
| Gns        | 2.790E-03 | 0.49 |
| Ttyh2      | 1.461E-03 | 0.37 |
| Sirt6      | 2.842E-05 | 1.65 |
| Mast4      | 1.825E-03 | 1.71 |
| Tle6       | 1.270E-02 | 0.42 |
| 1700006J1  | 3.931E-02 | 5.38 |
| BC030867   | 1.087E-04 | 4.89 |
| Cd207      | 6.062E-06 | 0.08 |
| Gpsm3      | 2.662E-02 | 0.55 |
| Unc13a     | 9.254E-03 | 2.97 |
| Scn7a      | 1.669E-05 | 0.23 |
| Grip1      | 1.625E-04 | 3.75 |
| Nrip3      | 9.314E-03 | 0.40 |
| Nup54      | 1.732E-04 | 2.11 |
| Tespa1     | 1.212E-05 | 0.39 |
| Ttc21b     | 6.849E-03 | 2.07 |
| Mfsd12     | 4.082E-03 | 0.24 |
| BC031353   | 7.811E-03 | 0.51 |
| Ano8       | 8.147E-04 | 0.50 |
| Lrr1       | 1.251E-03 | 3.48 |
| Cactin     | 6.052E-04 | 1.56 |
| Ncaph      | 3.797E-05 | 2.31 |
| Tjp3       | 5.125E-04 | 0.26 |
| Dhcr24     | 3.404E-03 | 0.29 |
| Arl4d      | 3.509E-02 | 2.20 |
| Tmem106a   | 9.491E-04 | 0.36 |
| Cebpa      | 5.911E-05 | 0.49 |
| 5031414D1  | 1.574E-02 | 0.60 |
| Vat1       | 2.641E-04 | 0.44 |
| Igsf6      | 8.912E-03 | 0.44 |
| Epgn       | 4.671E-04 | 4.39 |
| Ncapd3     | 7.913E-04 | 1.62 |



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|-----------|-----------|-------|
| Creb3l3   | 5.467E-03 | 2.50  |
| Eef2k     | 8.616E-03 | 0.63  |
| 1700020L2 | 8.927E-03 | 2.31  |
| Secisbp2l | 6.154E-05 | 0.46  |
| Egln3     | 3.092E-02 | 2.32  |
| Mitf      | 2.560E-05 | 0.26  |
| Zc3h12c   | 6.895E-03 | 1.80  |
| Kcne3     | 1.382E-03 | 3.60  |
| Fam124a   | 4.544E-05 | 0.34  |
| Tubg1     | 1.221E-03 | 2.20  |
| Arl6ip5   | 1.693E-03 | 0.57  |
| Fam175a   | 1.369E-03 | 1.70  |
| Trim13    | 4.794E-03 | 1.74  |
| Eogt      | 1.995E-04 | 1.81  |
| Pcytlb    | 1.060E-02 | 3.25  |
| Hpse      | 2.386E-05 | 0.37  |
| Vps13c    | 1.776E-03 | 0.58  |
| Gze3      | 1.139E-04 | 1.70  |
| Sgcg      | 8.304E-04 | 0.33  |
| Klhl35    | 3.890E-02 | 1.70  |
| Gdpc5     | 8.855E-03 | 1.71  |
| Uchl4     | 4.219E-02 | 1.51  |
| Lzts2     | 1.868E-04 | 0.63  |
| Nup37     | 2.838E-04 | 2.79  |
| Parpbb    | 1.757E-07 | 4.38  |
| Adat3     | 3.188E-02 | 2.10  |
| 1810055Gc | 5.553E-05 | 2.07  |
| Ptplb     | 6.828E-03 | 0.48  |
| Shq1      | 1.160E-02 | 1.55  |
| Pmch      | 1.074E-02 | 2.62  |
| Klf16     | 8.217E-03 | 2.06  |
| Thyn1     | 3.076E-02 | 1.59  |
| Figlnl    | 1.210E-04 | 3.02  |
| Tgfb1     | 1.794E-02 | 1.68  |
| Cdcp1     | 9.662E-06 | 2.41  |
| Cox18     | 8.996E-04 | 1.56  |
| Frmpd1    | 7.552E-04 | 0.24  |
| Grhpr     | 2.616E-03 | 1.83  |
| Tnfsf9    | 4.340E-03 | 4.40  |
| Melk      | 1.257E-03 | 2.83  |
| Thrsp     | 1.569E-04 | 0.05  |
| Hmha1     | 2.189E-02 | 0.58  |
| Alg8      | 1.682E-03 | 1.87  |
| Mrps2     | 3.031E-05 | 1.65  |
| Ggta1     | 2.454E-03 | 1.51  |
| Acta2     | 1.603E-02 | 2.12  |
| Tk2       | 9.545E-04 | 0.67  |
| Lysmd3    | 1.121E-04 | 1.68  |
| Ddx11     | 4.247E-04 | 2.10  |
| Ids       | 1.393E-02 | 0.53  |
| Tmprss11b | 4.219E-03 | 20.97 |
| Pawr      | 7.838E-05 | 1.65  |
| Rnf126    | 1.379E-03 | 1.78  |
| Uba6      | 6.264E-05 | 1.81  |
| Cd276     | 1.590E-04 | 2.57  |
| Myf6      | 9.149E-03 | 0.54  |
| Acss3     | 1.448E-04 | 0.18  |
| Tdp2      | 1.136E-03 | 1.67  |
| Apex1     | 6.144E-03 | 1.74  |
| Ddx26b    | 4.787E-02 | 0.61  |
| Zfp57     | 1.159E-03 | 2.13  |
| 5031439Gc | 6.888E-03 | 0.52  |
| Fmnl2     | 4.838E-05 | 1.92  |
| Ptpn23    | 2.997E-04 | 1.67  |
| N28178    | 1.660E-02 | 0.26  |
| Arl5a     | 6.657E-04 | 0.61  |
| Colec12   | 1.607E-02 | 0.56  |
| Mbn13     | 4.760E-04 | 1.94  |
| Fam110c   | 6.658E-07 | 3.42  |
| Acaa1a    | 2.831E-04 | 0.62  |
| Prickle1  | 1.732E-02 | 1.60  |
| Ccdc38    | 1.486E-02 | 2.26  |
| Ng23      | 2.510E-02 | 0.39  |
| Fam69b    | 5.082E-03 | 1.75  |
| Rif1      | 1.057E-03 | 1.73  |
| Sh3bp4    | 1.857E-03 | 1.56  |
| Ska1      | 1.309E-03 | 2.97  |
| Gmip      | 8.787E-04 | 0.63  |
| Pnpla8    | 8.249E-03 | 0.66  |
| Macrocl   | 1.468E-03 | 0.59  |
| Noa1      | 1.683E-02 | 1.58  |
| Gramd1c   | 5.736E-03 | 0.36  |
| P2ry14    | 1.478E-03 | 0.49  |
| Glb1l2    | 2.060E-05 | 0.08  |
| Npy1r     | 4.554E-05 | 0.45  |
| Arhgap26  | 1.094E-02 | 0.66  |
| Wtip      | 1.556E-05 | 2.24  |
| 1-Mar     | 2.189E-02 | 0.57  |
| Rnf13     | 9.101E-04 | 0.66  |
| Sh3tc1    | 1.319E-03 | 0.44  |
| Lgi4      | 1.130E-02 | 0.65  |
| Fxyd1     | 1.397E-05 | 0.33  |
| H2-Aa     | 5.670E-03 | 0.44  |
| Eepd1     | 4.924E-07 | 0.43  |
| Atp13a2   | 1.806E-03 | 0.40  |
| Clcn7     | 1.522E-03 | 0.58  |
| Cenpt     | 2.716E-03 | 2.26  |
| Nop14     | 4.631E-03 | 1.70  |
| Micall2   | 4.905E-02 | 3.10  |
| Zscan12   | 4.590E-03 | 1.68  |
| Dnajc12   | 1.183E-03 | 0.60  |
| Kif15     | 1.488E-05 | 2.89  |
| Anln      | 2.205E-04 | 2.63  |
| Jmjd4     | 1.813E-03 | 1.52  |
| Tmem149   | 3.079E-03 | 0.45  |
| Lpar3     | 6.029E-05 | 0.21  |
| Pnpla7    | 1.334E-03 | 0.49  |
| Mcoln3    | 2.743E-02 | 0.15  |



|            |           |      |
|------------|-----------|------|
| Hspb6      | 2.033E-04 | 0.43 |
| Wnt4       | 4.305E-03 | 2.02 |
| Phkb       | 2.825E-03 | 0.61 |
| Acaa2      | 6.593E-04 | 0.51 |
| C1qc       | 3.603E-02 | 0.54 |
| Neto2      | 1.165E-02 | 3.54 |
| Unc93b1    | 1.024E-02 | 0.50 |
| Ttc7       | 1.758E-03 | 0.66 |
| 4921524J1: | 1.345E-04 | 1.85 |
| C130079G1  | 7.481E-03 | 0.17 |
| Zdnhc9     | 1.731E-03 | 0.62 |
| Asap3      | 4.385E-03 | 0.67 |
| Tenc1      | 1.026E-03 | 0.54 |
| Apln       | 2.726E-05 | 9.67 |
| Tmem185b   | 1.044E-03 | 1.52 |
| Inhbb      | 3.074E-03 | 1.66 |
| Smpd1      | 2.803E-03 | 0.51 |
| Rbmxl1     | 1.599E-04 | 1.91 |
| Scd1       | 6.909E-05 | 0.08 |
| Lrg1       | 1.451E-02 | 0.58 |
| Ralgapa2   | 4.810E-03 | 0.64 |
| Aff3       | 6.249E-03 | 0.57 |
| Arhgap10   | 3.758E-04 | 0.60 |
| E330009J0: | 6.674E-04 | 0.41 |
| Krt80      | 9.855E-04 | 0.39 |
| Thap1      | 2.357E-02 | 1.74 |
| Lipt1      | 5.178E-03 | 1.58 |
| Zfyve28    | 1.290E-03 | 0.33 |
| Spred3     | 1.334E-03 | 3.12 |
| Clic4      | 1.898E-02 | 0.60 |
| 1700055NC  | 2.084E-03 | 0.40 |
| D4Wsu53e   | 5.809E-03 | 0.62 |
| Gemin5     | 3.336E-03 | 1.52 |
| Ovol2      | 4.084E-05 | 3.14 |
| Ldlrap1    | 1.406E-03 | 1.62 |
| Lsm1       | 1.962E-03 | 1.50 |
| Man1c1     | 3.619E-03 | 0.44 |
| Tacc3      | 6.184E-05 | 3.41 |
| Phf16      | 1.695E-03 | 1.95 |
| Hand1      | 2.613E-02 | 8.94 |
| Slc9a7     | 7.422E-04 | 0.42 |
| Paqr7      | 6.167E-05 | 0.44 |
| Pafah2     | 4.558E-02 | 0.66 |
| Hhat       | 7.200E-03 | 1.67 |
| Trmt6      | 5.939E-03 | 1.67 |
| Spon2      | 1.049E-02 | 0.46 |
| Atp11b     | 3.072E-03 | 1.83 |
| Serpine1   | 1.368E-03 | 4.81 |
| Endod1     | 4.043E-02 | 0.65 |
| Slc30a1    | 4.764E-06 | 0.43 |
| Vnn1       | 8.483E-04 | 0.21 |
| Arid5a     | 3.650E-02 | 1.58 |
| Ints7      | 2.512E-02 | 1.52 |
| 4930427A0  | 2.182E-06 | 2.51 |
| C330005M:  | 2.150E-02 | 0.49 |
| Dtl        | 1.419E-03 | 2.67 |
| Slc2a12    | 6.118E-03 | 0.24 |
| Samd4b     | 3.976E-05 | 1.52 |
| Bcdin3d    | 2.276E-02 | 1.55 |
| Dlgap5     | 1.882E-05 | 2.47 |
| H2-DMb2    | 3.353E-04 | 0.45 |
| Plekhg2    | 2.684E-02 | 1.54 |
| Vash2      | 4.931E-02 | 1.87 |
| Wdhd1      | 1.484E-04 | 2.49 |
| BC022687   | 2.659E-05 | 1.79 |
| 181001911: | 2.690E-03 | 2.15 |
| Nme1       | 4.954E-03 | 1.57 |
| Lphn3      | 4.039E-03 | 0.35 |
| Tnfrsf23   | 1.040E-04 | 4.94 |
| Spag1      | 3.133E-03 | 0.47 |
| Cdkn3      | 4.044E-04 | 3.06 |
| H2-DMa     | 1.309E-02 | 0.50 |
| Slc20a2    | 3.532E-05 | 2.02 |
| Gpr160     | 1.007E-03 | 0.54 |
| Cdkn1c     | 6.425E-04 | 0.05 |
| Esyt3      | 1.076E-02 | 0.56 |
| Atp8a1     | 9.337E-05 | 0.44 |
| Aspg       | 2.466E-02 | 0.51 |
| Ddhd1      | 1.198E-04 | 0.39 |
| Fam13a     | 1.396E-02 | 0.30 |
| Cisd1      | 4.334E-03 | 0.64 |
| Gnpnat1    | 2.991E-04 | 1.65 |
| Ckap2      | 2.915E-03 | 2.47 |
| Themis2    | 3.728E-02 | 0.56 |
| Dzip1l     | 2.307E-02 | 1.70 |
| Iars       | 3.002E-05 | 1.55 |
| Egr2       | 6.628E-04 | 0.19 |
| Darc       | 9.624E-07 | 0.30 |
| Wdr19      | 3.465E-03 | 1.53 |
| Sirpa      | 6.610E-03 | 0.44 |
| Ankrd9     | 3.111E-02 | 1.85 |
| Ccdc55     | 7.205E-04 | 1.53 |
| Fam101a    | 9.900E-03 | 2.56 |
| Ninj1      | 3.434E-03 | 0.63 |
| Snn        | 2.482E-05 | 1.84 |
| Acer2      | 2.738E-02 | 0.48 |
| Ccdc138    | 4.179E-03 | 2.36 |
| Dennd4c    | 4.825E-05 | 0.57 |
| Rnmtl1     | 1.866E-02 | 1.60 |
| Haus6      | 1.946E-03 | 2.19 |
| Dexi       | 1.930E-03 | 0.64 |
| Nod1       | 4.180E-02 | 0.66 |
| 2010002NC  | 3.579E-04 | 2.74 |
| 2410066E1  | 1.004E-02 | 0.64 |
| Camk4      | 5.962E-03 | 1.50 |
| Rbm24      | 1.478E-03 | 0.42 |
| Cd84       | 1.971E-03 | 0.26 |
| 503343011: | 2.648E-02 | 2.14 |



|            |           |      |
|------------|-----------|------|
| Spon1      | 3.772E-02 | 2.25 |
| Plekhhg6   | 2.784E-02 | 1.93 |
| Pde4dip    | 9.417E-07 | 0.38 |
| Slc43a2    | 3.098E-03 | 0.51 |
| Slamf7     | 7.699E-04 | 0.17 |
| Rilp       | 7.121E-04 | 0.38 |
| Kcna7      | 3.923E-04 | 0.33 |
| Bend3      | 1.613E-04 | 2.21 |
| BC088983   | 1.684E-03 | 1.52 |
| Tlcd2      | 2.364E-04 | 0.33 |
| F11r       | 3.624E-02 | 1.79 |
| Hrc        | 1.022E-05 | 0.20 |
| Aox4       | 4.591E-03 | 0.14 |
| Ncapd2     | 1.213E-05 | 2.18 |
| Hoxa5      | 4.100E-02 | 1.60 |
| Sema7a     | 1.489E-02 | 3.04 |
| Iffo1      | 1.939E-02 | 0.61 |
| Nop2       | 2.041E-04 | 1.92 |
| Wdr36      | 8.638E-05 | 1.70 |
| Spats2l    | 3.879E-03 | 2.77 |
| Sesn1      | 8.915E-04 | 0.47 |
| Tsr1       | 7.056E-04 | 1.62 |
| Ankrd35    | 3.640E-04 | 0.32 |
| Pcp4l1     | 3.265E-02 | 0.53 |
| Trp53inp2  | 1.935E-04 | 0.39 |
| Ttk        | 5.090E-04 | 3.09 |
| Txnip      | 4.884E-05 | 0.34 |
| Pmepa1     | 1.915E-02 | 1.75 |
| Hfe2       | 1.553E-03 | 0.31 |
| Higd1a     | 4.083E-02 | 1.72 |
| Foxq1      | 5.656E-03 | 2.00 |
| Srcin1     | 2.026E-04 | 0.17 |
| Dennd2a    | 6.193E-03 | 0.38 |
| Fam70b     | 7.520E-03 | 0.33 |
| Tfdp1      | 1.558E-05 | 1.86 |
| Rplf2      | 1.711E-02 | 1.98 |
| Jarid2     | 7.998E-05 | 2.25 |
| Car14      | 1.058E-02 | 0.66 |
| Osbpl7     | 1.259E-04 | 1.61 |
| BC028528   | 8.807E-03 | 0.58 |
| Gm9766     | 5.711E-04 | 0.50 |
| Atp6v0a4   | 9.464E-03 | 0.40 |
| Dock10     | 1.888E-05 | 0.32 |
| Tm6sf1     | 2.844E-04 | 0.32 |
| Ctss       | 1.710E-02 | 0.40 |
| Pold1      | 3.358E-04 | 2.30 |
| Fsd2       | 9.788E-05 | 0.22 |
| Lpar1      | 1.827E-02 | 0.42 |
| Mybpc2     | 3.356E-04 | 0.13 |
| Pak1ip1    | 5.079E-03 | 1.51 |
| Rtel1      | 1.315E-05 | 1.85 |
| Pbx3       | 1.406E-03 | 1.63 |
| Akap2      | 1.113E-03 | 0.42 |
| Mboat1     | 8.735E-03 | 2.78 |
| Nudcd1     | 4.320E-03 | 2.04 |
| Elovl3     | 1.529E-03 | 0.05 |
| Nup205     | 1.371E-04 | 1.59 |
| Alpk3      | 3.350E-04 | 0.39 |
| 913040912: | 4.687E-03 | 0.10 |
| Ephx1      | 7.130E-04 | 0.32 |
| Sema6c     | 9.672E-03 | 0.56 |
| Smurf1     | 1.650E-03 | 1.61 |
| Gngt2      | 1.654E-02 | 0.51 |
| BC026590   | 2.814E-03 | 1.81 |
| Agbl3      | 3.116E-02 | 2.53 |
| Vars2      | 9.697E-05 | 1.72 |
| Gcnt1      | 1.374E-02 | 0.59 |
| Phb        | 7.897E-03 | 1.62 |
| Itpkb      | 1.269E-05 | 0.40 |
| Bpgm       | 5.920E-04 | 1.69 |
| Fam117a    | 1.031E-03 | 0.49 |
| Plcl2      | 1.229E-04 | 0.38 |
| Prc1       | 2.178E-07 | 2.54 |
| Cnst       | 6.633E-04 | 0.55 |
| Slco4a1    | 1.194E-02 | 4.14 |
| Pdk2       | 8.766E-04 | 0.43 |
| Tlr4       | 3.264E-02 | 0.62 |
| Pgcp       | 2.374E-04 | 0.34 |
| Arhgap18   | 2.325E-04 | 0.53 |
| St6galnac5 | 8.310E-03 | 0.53 |
| 261003481  | 1.485E-03 | 1.62 |
| Eme1       | 4.531E-04 | 2.85 |
| Anpep      | 7.816E-03 | 0.25 |
| Cpa4       | 1.405E-03 | 0.39 |
| Zfp503     | 2.616E-02 | 1.84 |
| Sptlc3     | 3.860E-03 | 0.28 |
| F13a1      | 1.276E-04 | 0.19 |
| Gpr126     | 2.235E-06 | 0.27 |
| Gipc2      | 3.236E-02 | 3.38 |
| Whrn       | 1.656E-02 | 2.49 |
| Akna       | 6.564E-03 | 0.54 |
| Fanci      | 2.058E-04 | 2.62 |
| Nlrc4      | 3.025E-02 | 0.63 |
| 1110008P1  | 2.346E-02 | 0.62 |
| Orm1       | 9.595E-03 | 0.07 |
| Daglb      | 3.098E-04 | 0.31 |
| Metrl1     | 3.421E-04 | 0.60 |
| Il18       | 1.550E-03 | 0.36 |
| Suv39h1    | 1.406E-03 | 2.21 |
| Isg20      | 8.234E-03 | 1.61 |
| Tgfb2      | 9.841E-04 | 1.96 |
| Lgi2       | 1.983E-03 | 3.25 |
| Megf9      | 4.809E-02 | 0.64 |
| Rftn1      | 3.735E-02 | 0.57 |
| Atp6v0e2   | 2.767E-04 | 0.34 |
| C130074G1  | 2.207E-04 | 0.52 |
| Exosc2     | 1.450E-03 | 1.65 |
| Sectm1b    | 2.413E-03 | 0.31 |



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|-----------|-----------|------|
| Ppl       | 1.378E-02 | 0.65 |
| Wfs1      | 6.954E-03 | 0.18 |
| Nrtn      | 1.494E-03 | 0.27 |
| Znfx1     | 4.935E-02 | 0.56 |
| Cdsn      | 3.959E-02 | 0.59 |
| Cyp7b1    | 3.793E-02 | 2.81 |
| Ncam1     | 1.201E-02 | 3.38 |
| Prex1     | 3.311E-02 | 0.60 |
| D2Wsu81e  | 3.138E-03 | 1.67 |
| 5730528L1 | 2.497E-05 | 2.98 |
| Ncoa7     | 1.474E-03 | 0.62 |
| Lmbrd2    | 1.630E-03 | 0.63 |
| Plekkg5   | 1.996E-04 | 0.60 |
| Prkrip1   | 2.714E-03 | 1.58 |
| Orai2     | 1.065E-04 | 2.69 |
| Exo1      | 4.083E-03 | 3.92 |
| Fbx15     | 9.619E-06 | 2.40 |
| Alkbh4    | 3.009E-03 | 1.50 |
| Dnttip2   | 4.507E-06 | 1.82 |
| Azi1      | 2.906E-02 | 1.64 |
| Kmo       | 3.182E-02 | 0.66 |
| Tbc1d2    | 1.643E-03 | 1.97 |
| Myf6b     | 1.852E-02 | 2.51 |
| Mcph1     | 6.186E-04 | 1.69 |
| Neur12    | 1.561E-02 | 0.64 |
| Heca      | 1.159E-03 | 0.63 |
| Lrrc17    | 1.661E-02 | 2.32 |
| Txlnb     | 4.584E-06 | 0.22 |
| Fgl2      | 4.514E-04 | 0.36 |
| 4931408A0 | 2.090E-02 | 3.23 |
| Cited2    | 1.943E-03 | 0.62 |
| Spsb1     | 2.201E-03 | 2.25 |
| Coq10a    | 1.918E-04 | 0.58 |
| Rhbdd2    | 3.075E-03 | 1.81 |
| Pik3cd    | 9.278E-03 | 0.50 |
| Plcb4     | 1.489E-04 | 0.65 |
| Mrap      | 1.510E-04 | 0.16 |
| Dtx4      | 3.939E-04 | 0.45 |
| Fam60a    | 7.670E-04 | 2.01 |
| Timeless  | 4.684E-04 | 2.02 |
| Ptger3    | 3.991E-03 | 0.41 |
| Nup43     | 7.602E-03 | 2.13 |
| Gjb6      | 1.950E-02 | 6.64 |
| Plcb2     | 4.326E-03 | 0.53 |
| Bub1b     | 6.148E-05 | 2.74 |
| Bmf       | 2.695E-03 | 0.66 |
| Gramd1b   | 6.489E-03 | 0.49 |
| Cacna2d1  | 8.666E-04 | 0.46 |
| Gorab     | 1.435E-03 | 1.83 |
| Gpr176    | 1.523E-02 | 2.31 |
| Maob      | 6.285E-06 | 0.24 |
| Fmo2      | 5.926E-03 | 0.14 |
| Fmo1      | 8.296E-05 | 0.39 |
| Arntl2    | 1.043E-03 | 2.55 |
| 2810417H1 | 5.466E-03 | 1.77 |
| Zfp704    | 1.659E-03 | 0.50 |
| Emp3      | 1.884E-03 | 0.39 |
| Gpr34     | 1.660E-03 | 0.49 |
| Tbc1d10c  | 7.633E-03 | 0.52 |
| Lrp1      | 1.859E-02 | 0.54 |
| Sema3d    | 2.109E-02 | 0.28 |
| Nxph4     | 2.062E-02 | 8.99 |
| Dnm3      | 1.726E-04 | 0.45 |
| Cdk6      | 2.405E-06 | 2.14 |
| Ndufa4l2  | 4.670E-02 | 2.89 |
| BC052040  | 6.821E-03 | 1.77 |
| Stac3     | 1.414E-06 | 0.32 |
| Cchcr1    | 7.856E-04 | 1.89 |
| Slc25a24  | 3.277E-03 | 1.84 |
| Fam102b   | 3.445E-02 | 0.62 |
| Arhgap9   | 6.756E-03 | 0.44 |
| Plekha4   | 1.125E-02 | 0.45 |
| Pitpnc1   | 1.490E-02 | 1.86 |
| Ltb4r2    | 2.968E-03 | 2.03 |
| Spns2     | 5.326E-03 | 0.59 |
| Sgms1     | 1.969E-04 | 0.66 |
| Mybbp1a   | 1.414E-03 | 1.70 |
| Gtpbp10   | 4.685E-03 | 1.71 |
| Blvrb     | 7.929E-04 | 0.48 |
| A330021E2 | 8.039E-03 | 9.32 |
| 9-Mar     | 1.307E-03 | 1.71 |
| Pvr       | 3.377E-03 | 2.04 |
| Tlr8      | 3.026E-03 | 0.38 |
| Gm885     | 1.244E-02 | 0.59 |
| Adam22    | 2.693E-02 | 0.51 |
| Pitpnm3   | 2.457E-03 | 2.93 |
| Tex2      | 2.514E-06 | 0.62 |
| C3ar1     | 5.597E-03 | 0.41 |
| Gstm2     | 4.733E-04 | 0.45 |
| Apoc1     | 1.190E-02 | 0.43 |
| Mis12     | 4.388E-05 | 1.50 |
| Apobec1   | 3.829E-03 | 0.46 |
| Tmem51    | 2.758E-03 | 1.81 |
| Gemin8    | 2.904E-03 | 1.62 |
| Dok4      | 1.115E-03 | 2.22 |
| Cyp2b23   | 2.254E-02 | 0.04 |
| BC048355  | 1.267E-02 | 2.38 |
| Clcf1     | 5.415E-07 | 4.12 |
| Sh3bgr    | 2.593E-02 | 0.32 |
| Phc1      | 1.536E-02 | 1.59 |
| Mthfd1l   | 1.738E-04 | 3.89 |
| Apobec2   | 3.769E-04 | 0.12 |
| Cyp2s1    | 1.048E-02 | 4.60 |
| A93001600 | 3.465E-02 | 0.10 |
| St8sia4   | 8.579E-04 | 0.36 |
| Creg1     | 1.306E-04 | 0.25 |
| Klc3      | 3.516E-02 | 0.61 |
| Rcsd1     | 9.853E-06 | 0.43 |



|            |           |       |
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| Rnf167     | 9.338E-04 | 0.66  |
| Cd53       | 1.955E-02 | 0.51  |
| Siah1b     | 7.710E-04 | 2.66  |
| Lat2       | 1.009E-03 | 0.30  |
| Tex264     | 2.245E-05 | 0.33  |
| Hlcs       | 2.212E-03 | 0.62  |
| Snrpd2     | 9.408E-03 | 1.60  |
| 4930579G1  | 2.821E-03 | 1.67  |
| Six5       | 1.227E-03 | 1.62  |
| Reps2      | 5.972E-05 | 0.32  |
| Erf        | 3.201E-03 | 1.63  |
| Osbpl10    | 3.695E-02 | 2.43  |
| Wdr25      | 6.492E-03 | 1.51  |
| Ccr6       | 2.545E-04 | 0.34  |
| Atp1a3     | 1.728E-02 | 0.19  |
| Rcc2       | 1.280E-02 | 1.59  |
| Mgl2       | 2.624E-04 | 0.17  |
| Gm11992    | 6.995E-03 | 0.35  |
| Mill2      | 3.259E-04 | 0.27  |
| Cmtm8      | 9.924E-03 | 0.35  |
| Iffo2      | 1.451E-03 | 0.57  |
| Ramp3      | 1.211E-04 | 4.03  |
| Wwp1       | 1.268E-03 | 0.67  |
| Pif1       | 3.169E-04 | 3.13  |
| Fzd7       | 1.732E-02 | 0.62  |
| Elmo1      | 4.937E-06 | 0.38  |
| Iqsec2     | 5.005E-04 | 0.55  |
| Ripk2      | 4.413E-04 | 0.56  |
| Brca2      | 1.457E-04 | 2.27  |
| Prkd2      | 3.931E-03 | 1.53  |
| Pla2g5     | 3.786E-03 | 0.13  |
| Rpusd1     | 2.892E-05 | 1.67  |
| Pla2g2d    | 4.192E-04 | 0.21  |
| Arhgap11a  | 2.909E-05 | 1.90  |
| Elov6      | 3.883E-03 | 0.12  |
| Uspl1      | 7.647E-04 | 1.69  |
| Sox15      | 6.567E-04 | 7.01  |
| Slc7a1     | 7.825E-03 | 3.52  |
| Ankrd42    | 1.467E-03 | 1.66  |
| Wrap53     | 6.925E-03 | 1.86  |
| Rap1gap    | 9.662E-03 | 2.25  |
| D19Bwg13!  | 1.101E-02 | 1.68  |
| B4galnt3   | 1.059E-02 | 2.49  |
| Mdfic      | 4.370E-03 | 0.57  |
| Mettl18    | 4.404E-02 | 1.50  |
| BC055324   | 9.980E-03 | 2.21  |
| Pik3r1     | 5.695E-06 | 0.51  |
| Ccnb1      | 5.391E-05 | 3.05  |
| Cirh1a     | 3.297E-04 | 2.83  |
| Mfsd6      | 3.466E-03 | 0.55  |
| Gk5        | 2.649E-02 | 0.51  |
| Smpx       | 1.705E-03 | 0.28  |
| Syt15      | 2.536E-03 | 0.63  |
| Fam38b     | 3.749E-03 | 2.37  |
| Zfp281     | 2.876E-04 | 1.68  |
| Cep78      | 3.020E-03 | 1.67  |
| Kif14      | 5.936E-04 | 2.92  |
| Rrp9       | 5.357E-03 | 2.09  |
| H2-Ob      | 1.604E-03 | 0.38  |
| Hspb8      | 5.237E-04 | 0.59  |
| Ptchd1     | 3.965E-03 | 0.21  |
| Serpina12  | 1.218E-02 | 0.29  |
| Camsap2    | 8.438E-03 | 2.26  |
| Prelp      | 7.643E-04 | 0.33  |
| Tmtc4      | 8.953E-04 | 2.04  |
| 5730559C1  | 1.730E-02 | 1.81  |
| Ccdc64     | 2.085E-03 | 0.49  |
| Mmp1b      | 1.326E-03 | 12.34 |
| Kctd12b    | 6.691E-04 | 0.49  |
| Pnpla3     | 6.592E-05 | 0.15  |
| Slc39a11   | 7.534E-04 | 0.48  |
| Bbox1      | 1.043E-04 | 0.05  |
| Amot       | 1.446E-03 | 0.53  |
| Kcnj2      | 1.118E-04 | 0.46  |
| AK010878   | 3.036E-03 | 2.62  |
| Alg13      | 2.311E-02 | 1.55  |
| Pi4ka      | 1.343E-04 | 0.58  |
| Coro2b     | 1.201E-02 | 0.49  |
| Pgm5       | 2.088E-04 | 0.34  |
| Gm13178    | 4.568E-03 | 0.06  |
| Utp15      | 1.315E-03 | 1.69  |
| Plekha6    | 6.789E-03 | 0.47  |
| Gpr155     | 1.655E-05 | 0.45  |
| Ydjc       | 4.807E-02 | 2.08  |
| Lad1       | 4.256E-02 | 1.68  |
| Abca9      | 5.948E-05 | 0.23  |
| Phlda3     | 2.995E-02 | 1.54  |
| Abca8a     | 4.100E-06 | 0.16  |
| Syt13      | 1.858E-02 | 0.61  |
| Haus1      | 7.138E-03 | 1.64  |
| Mcm3       | 6.030E-03 | 2.26  |
| Wip1       | 6.713E-04 | 2.18  |
| Tmco7      | 6.904E-05 | 2.18  |
| Tnfrsf18   | 1.047E-03 | 0.54  |
| Elmod1     | 9.959E-04 | 0.32  |
| Hrrn       | 8.207E-03 | 0.18  |
| Rapgef5    | 3.286E-02 | 1.69  |
| Acacb      | 2.896E-06 | 0.14  |
| Ncapp2     | 7.219E-06 | 2.10  |
| Lce3b      | 1.424E-03 | 10.33 |
| Igsf3      | 1.312E-02 | 1.69  |
| Abhd14b    | 2.661E-03 | 0.61  |
| Arsb       | 2.779E-03 | 0.51  |
| Lce1c      | 3.955E-04 | 0.14  |
| 6230427J0: | 2.901E-03 | 1.51  |
| Vwa1       | 5.683E-05 | 3.08  |
| Lce1f      | 1.886E-04 | 0.30  |
| Rassf4     | 1.855E-04 | 0.22  |



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|-----------|-----------|-------|
| Cox10     | 1.015E-02 | 1.62  |
| Sprr2i    | 5.916E-04 | 16.75 |
| Sprr2d    | 9.060E-03 | 8.81  |
| Zfand4    | 1.030E-02 | 1.75  |
| Bag2      | 4.210E-03 | 4.51  |
| Tmc7      | 2.389E-03 | 5.07  |
| Adrbk2    | 1.263E-03 | 0.49  |
| Pelo      | 4.057E-04 | 1.79  |
| Itga1     | 1.726E-02 | 2.27  |
| Hsd3b7    | 7.228E-03 | 0.48  |
| S100a13   | 1.839E-02 | 0.65  |
| Prox2     | 4.987E-02 | 1.52  |
| Grap2     | 6.180E-03 | 0.51  |
| Gnl3      | 4.614E-04 | 1.83  |
| Gjb5      | 9.370E-04 | 0.25  |
| Gjb3      | 1.696E-05 | 0.17  |
| Esm1      | 2.950E-03 | 9.86  |
| Dennd4b   | 4.537E-05 | 0.54  |
| Agps      | 1.378E-04 | 1.58  |
| Reln      | 2.762E-03 | 0.46  |
| Dctpp1    | 1.595E-02 | 2.16  |
| Hoxd4     | 4.985E-03 | 0.64  |
| Faim3     | 1.871E-02 | 4.06  |
| Abcb4     | 3.300E-05 | 0.36  |
| Leo1      | 7.268E-03 | 1.69  |
| Clspn     | 2.228E-03 | 2.29  |
| Elf2c4    | 4.271E-03 | 0.57  |
| AA986860  | 2.658E-03 | 0.52  |
| Sun2      | 3.633E-05 | 0.57  |
| Acot5     | 7.610E-03 | 0.09  |
| Fam199x   | 7.392E-03 | 1.60  |
| Hrip3     | 3.010E-03 | 1.99  |
| Pbxip1    | 2.255E-02 | 0.63  |
| Maff      | 1.274E-02 | 1.74  |
| Npl       | 4.571E-04 | 0.42  |
| Jph1      | 8.987E-04 | 0.42  |
| Mapk6     | 3.870E-03 | 2.70  |
| Obfc1     | 1.406E-04 | 1.66  |
| Ppp1r3a   | 1.539E-06 | 0.12  |
| Ttc9      | 2.535E-05 | 4.37  |
| Exog      | 1.335E-04 | 1.87  |
| Mcts2     | 5.926E-03 | 1.54  |
| Flt3      | 1.916E-05 | 0.41  |
| Snai1     | 6.085E-03 | 2.35  |
| Trim72    | 2.948E-02 | 0.63  |
| Gng2      | 3.406E-02 | 0.66  |
| Tmem194b  | 7.345E-03 | 1.56  |
| Ptgir     | 3.547E-02 | 0.40  |
| Fam89a    | 3.454E-03 | 0.50  |
| Synpo     | 6.394E-03 | 1.71  |
| Arl11     | 2.329E-03 | 0.35  |
| Lor       | 4.862E-03 | 0.26  |
| 4732471D1 | 1.235E-04 | 1.75  |
| Tmem64    | 3.836E-02 | 0.51  |
| Gm5531    | 4.238E-02 | 1.65  |
| Pcdhb19   | 1.214E-02 | 2.22  |
| A030009HC | 5.536E-05 | 0.14  |
| Psap1     | 1.953E-04 | 0.12  |
| E130012A1 | 6.168E-03 | 7.68  |
| Gm9782    | 1.712E-02 | 4.85  |
| Pars2     | 8.759E-03 | 1.68  |
| Acpl2     | 3.658E-03 | 3.19  |
| Ecm2      | 5.985E-03 | 0.50  |
| Fam25c    | 5.343E-03 | 0.27  |
| Col6a6    | 2.661E-04 | 0.12  |
| B430306NC | 9.440E-03 | 0.33  |
| Ccdc64b   | 2.977E-02 | 0.58  |
| Gm14492   | 3.871E-03 | 0.50  |
| Clec4a3   | 7.957E-04 | 0.38  |
| Zmym1     | 7.858E-03 | 1.55  |
| Wdfy3     | 1.365E-03 | 0.65  |
| Ccri2     | 1.270E-02 | 0.41  |
| Orai3     | 6.339E-03 | 0.61  |
| Cep164    | 1.724E-06 | 1.75  |
| Gls2      | 1.764E-03 | 5.43  |
| Gpr133    | 7.736E-03 | 0.42  |
| Mrpl50    | 1.838E-02 | 1.51  |
| Pcdhb21   | 8.422E-03 | 2.90  |
| Ccdc141   | 8.662E-03 | 0.52  |
| Als2cl    | 2.360E-02 | 1.51  |
| Fmn1      | 1.215E-03 | 0.59  |
| S100a1    | 1.870E-04 | 0.22  |
| Lmod3     | 9.319E-04 | 0.32  |
| C130050O1 | 2.688E-02 | 2.01  |
| Ccdc166   | 8.537E-03 | 2.39  |
| Proca1    | 8.966E-04 | 0.53  |
| Nkrf      | 2.864E-05 | 1.88  |
| Naa38     | 1.955E-03 | 1.54  |
| Gpr146    | 6.176E-04 | 0.53  |
| Cdc25c    | 3.967E-05 | 3.01  |
| Vsig4     | 5.947E-03 | 0.31  |
| Nhlrc1    | 2.389E-02 | 1.69  |
| Il20rb    | 1.984E-03 | 0.43  |
| Osbpl1a   | 1.942E-04 | 0.30  |
| Pcsk9     | 5.728E-03 | 4.25  |
| Mab2113   | 1.239E-02 | 2.27  |
| 1700001O2 | 3.157E-02 | 2.32  |
| Cxcr7     | 9.388E-03 | 1.94  |
| Aplnr     | 3.206E-03 | 1.89  |
| Alkbh2    | 6.739E-05 | 2.07  |
| P2ry4     | 2.082E-04 | 0.06  |
| Adig      | 5.498E-03 | 0.05  |
| Sptsa     | 6.538E-03 | 0.57  |
| Camsap3   | 1.317E-02 | 0.44  |
| Shisa2    | 6.120E-05 | 0.31  |
| AB041803  | 2.703E-04 | 0.51  |
| 9930012K1 | 4.847E-04 | 0.21  |
| Tlr7      | 1.580E-04 | 0.31  |



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|-----------|-----------|-------|
| Liph      | 2.160E-02 | 0.35  |
| Cnrip1    | 6.989E-03 | 0.46  |
| Pard6b    | 9.193E-03 | 1.61  |
| Tmem201   | 2.038E-02 | 1.69  |
| Palb2     | 1.834E-04 | 2.45  |
| Abca6     | 1.027E-05 | 0.17  |
| AF251705  | 3.883E-02 | 0.54  |
| Lsm11     | 1.352E-03 | 2.19  |
| Ankrd50   | 7.982E-04 | 2.14  |
| Sy116     | 1.632E-03 | 19.76 |
| Rassf9    | 2.010E-03 | 0.18  |
| Klhl31    | 7.582E-05 | 0.17  |
| Mylik4    | 7.394E-03 | 0.07  |
| Fbxo48    | 8.826E-03 | 2.49  |
| Napepld   | 1.449E-02 | 0.54  |
| E13030410 | 7.017E-03 | 2.28  |
| Acer1     | 3.514E-03 | 0.29  |
| Lrln4     | 4.220E-04 | 2.10  |
| E130308A1 | 2.644E-02 | 1.60  |
| Arhgef37  | 6.218E-04 | 0.34  |
| Dmd       | 7.644E-03 | 0.59  |
| Pigw      | 1.473E-05 | 1.94  |
| AI467606  | 8.261E-03 | 0.43  |
| Shroom2   | 1.143E-03 | 2.30  |
| Hs6st1    | 1.724E-04 | 1.71  |
| Med26     | 9.102E-04 | 1.55  |
| Cenph     | 1.641E-03 | 3.05  |
| Lhfp12    | 3.069E-03 | 0.28  |
| 5430407P1 | 5.364E-03 | 2.14  |
| Cenpe     | 2.802E-04 | 2.98  |
| Zfp423    | 1.783E-02 | 0.63  |
| Sh2d5     | 2.066E-04 | 21.29 |
| Epcam     | 2.571E-03 | 0.35  |
| 2410002F2 | 3.061E-05 | 1.70  |
| Gprin3    | 2.209E-04 | 0.22  |
| Lce3c     | 1.426E-02 | 6.70  |
| A930002H2 | 1.843E-02 | 2.63  |
| Sprr4     | 1.894E-02 | 0.05  |
| Zfp553    | 1.418E-02 | 1.53  |
| Esf1      | 1.008E-03 | 1.52  |
| Mtus1     | 8.067E-06 | 0.36  |
| Pid1      | 1.449E-03 | 0.38  |
| Spred2    | 1.581E-04 | 2.09  |
| Col27a1   | 2.601E-02 | 2.53  |
| Adrb2     | 5.329E-03 | 0.50  |
| Mms22l    | 7.823E-04 | 2.20  |
| Ifitm10   | 1.581E-02 | 2.37  |
| Ptprcap   | 4.821E-03 | 0.58  |
| A43010511 | 2.115E-03 | 2.28  |
| Adra1a    | 1.198E-04 | 0.09  |
| 6330416G1 | 2.704E-02 | 0.57  |
| Sdpr      | 1.453E-04 | 0.32  |
| C2cd2     | 5.120E-04 | 0.41  |
| Stard5    | 2.830E-04 | 0.37  |
| Sbsn      | 4.809E-03 | 0.42  |
| Eid2      | 1.400E-02 | 1.65  |
| Tmem229b  | 5.821E-04 | 0.43  |
| Kcnrg     | 2.552E-02 | 1.59  |
| Adamts6   | 1.783E-02 | 2.42  |
| E2f8      | 6.671E-05 | 3.46  |
| Pcdhb20   | 1.135E-02 | 2.71  |
| Sprr2g    | 1.891E-02 | 9.35  |
| Pik3r6    | 1.397E-03 | 0.48  |
| Sprr2h    | 6.956E-04 | 5.12  |
| Tusc5     | 1.034E-03 | 0.35  |
| Ankle1    | 9.122E-04 | 2.67  |
| AI464131  | 6.018E-05 | 0.53  |
| Stxbp6    | 1.932E-02 | 0.37  |
| Ermp1     | 2.684E-03 | 0.61  |
| Slc25a23  | 2.207E-02 | 0.54  |
| Fam178b   | 2.565E-02 | 2.73  |
| Gjb2      | 1.115E-02 | 7.61  |
| Defb14    | 8.028E-03 | 2.31  |
| Jrk       | 9.119E-04 | 1.78  |
| Pcdhb17   | 3.583E-02 | 1.70  |
| Rbp1      | 4.700E-03 | 2.02  |
| Yod1      | 3.648E-02 | 0.48  |
| Ngfrap1   | 1.611E-02 | 2.21  |
| Ftsjd1    | 6.786E-04 | 2.00  |
| Sox18     | 8.047E-03 | 1.55  |
| Scn4b     | 2.379E-07 | 0.19  |
| Kctd4     | 1.802E-03 | 0.33  |
| Ar        | 4.388E-05 | 0.16  |
| Zfp526    | 1.565E-04 | 1.55  |
| Unc119b   | 2.889E-03 | 1.54  |
| Zfp518b   | 4.531E-02 | 1.55  |
| Ticrr     | 1.724E-04 | 3.37  |
| Gjb4      | 6.626E-05 | 0.17  |
| Lce1l     | 1.906E-04 | 0.15  |
| Tifa      | 8.956E-03 | 0.66  |
| Csnk2a2   | 4.045E-03 | 0.58  |
| Gprc5a    | 3.170E-03 | 6.62  |
| Fam83h    | 6.147E-03 | 1.59  |
| 2410016OC | 4.317E-03 | 1.68  |
| Ppp1r3b   | 1.686E-02 | 2.16  |
| Mpeg1     | 5.362E-03 | 0.31  |
| 3110062Ml | 1.621E-02 | 1.50  |
| Ddit4l    | 1.713E-02 | 0.20  |
| Fam187b   | 7.620E-03 | 1.74  |
| Ckap4     | 9.110E-04 | 1.75  |
| Fbl       | 1.568E-04 | 1.63  |
| Ltb4r1    | 3.033E-04 | 3.12  |
| Mars2     | 3.934E-04 | 1.95  |
| Spsb4     | 1.666E-02 | 0.35  |
| Mipol1    | 1.032E-03 | 2.10  |
| D030056L2 | 8.667E-04 | 1.63  |
| Tmem164   | 7.653E-04 | 0.59  |
| Tigd5     | 2.002E-03 | 1.84  |



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| Dusp18     | 1.550E-03 | 0.26  |
| Fam185a    | 4.288E-03 | 1.63  |
| Gm527      | 1.596E-02 | 1.72  |
| Hist1h2be  | 8.997E-05 | 2.02  |
| Sfn        | 2.888E-02 | 1.57  |
| B3gnt1     | 3.940E-04 | 1.60  |
| Tgif1      | 2.269E-02 | 1.90  |
| Gpr68      | 4.556E-03 | 0.58  |
| Cmya5      | 5.735E-08 | 0.15  |
| Fam180a    | 2.672E-02 | 0.24  |
| Fam132b    | 5.424E-04 | 2.23  |
| Ar4a       | 3.685E-03 | 0.51  |
| A530099J1' | 3.808E-06 | 0.11  |
| Adamts12   | 2.889E-02 | 2.36  |
| Mis18bp1   | 2.786E-04 | 2.54  |
| Mmp10      | 2.688E-02 | 4.77  |
| Nxpe5      | 4.494E-03 | 0.36  |
| BC029214   | 3.113E-03 | 0.64  |
| Fcgbp      | 5.654E-03 | 0.21  |
| Fbxo40     | 9.412E-04 | 0.37  |
| Rnf150     | 2.825E-02 | 0.54  |
| Fancb      | 3.269E-02 | 1.53  |
| Sned1      | 4.408E-06 | 0.23  |
| Trim16     | 7.726E-05 | 1.85  |
| Cdca4      | 5.922E-04 | 1.76  |
| Stx19      | 3.277E-02 | 0.61  |
| Gpr157     | 1.405E-02 | 0.64  |
| Serpinb6d  | 3.629E-02 | 0.07  |
| Pcdhb16    | 4.732E-02 | 1.82  |
| Timm8a1    | 1.651E-04 | 1.91  |
| Arxes2     | 2.417E-02 | 2.93  |
| Lmod1      | 3.129E-02 | 0.57  |
| Entpd1     | 6.234E-03 | 0.53  |
| Nat8l      | 4.022E-02 | 5.63  |
| Selpg      | 7.641E-03 | 0.50  |
| Efcab4a    | 2.145E-04 | 0.44  |
| A930001NC  | 3.003E-05 | 0.58  |
| Ckap2l     | 2.786E-07 | 3.07  |
| Pcdhb18    | 2.010E-02 | 2.38  |
| Selrc1     | 1.206E-02 | 1.81  |
| Pdp2       | 5.643E-03 | 1.78  |
| Fgfbp1     | 3.309E-03 | 3.05  |
| Osr1       | 5.512E-03 | 0.39  |
| Tprg       | 7.995E-05 | 0.31  |
| Gli2       | 4.432E-02 | 1.71  |
| Mif1       | 2.135E-03 | 0.25  |
| 2210020Ml  | 3.446E-04 | 0.59  |
| Ccdc57     | 3.371E-03 | 1.77  |
| Sprr1b     | 2.970E-04 | 3.15  |
| Cxcr1      | 8.202E-03 | 0.18  |
| Mypop      | 7.555E-03 | 1.61  |
| Fitm2      | 1.461E-03 | 0.55  |
| Nrip1      | 1.334E-06 | 1.60  |
| Cxcr6      | 2.924E-02 | 0.64  |
| Gm9828     | 8.871E-03 | 1.67  |
| Mex3d      | 3.726E-03 | 2.21  |
| Tbc1d12    | 2.483E-03 | 1.55  |
| Fndc9      | 5.349E-05 | 0.17  |
| Tmprss11f  | 1.020E-03 | 0.35  |
| Skint10    | 5.857E-05 | 0.08  |
| Serpinb13  | 3.764E-05 | 0.07  |
| Pthlh      | 5.591E-03 | 37.88 |
| Slc35e4    | 5.055E-04 | 0.58  |
| Arhgap30   | 1.615E-03 | 0.44  |
| Rnf24      | 4.232E-03 | 1.78  |
| Efna5      | 4.067E-02 | 1.55  |
| Zfp689     | 5.767E-04 | 1.61  |
| Cdca2      | 4.952E-06 | 2.71  |
| Atp13a5    | 2.062E-02 | 0.41  |
| Atxn7l2    | 2.159E-02 | 1.55  |
| Ndnf       | 5.657E-03 | 0.37  |
| Clec4a1    | 1.537E-02 | 0.59  |
| Ccr2       | 3.057E-03 | 0.43  |
| Agtr1a     | 7.348E-05 | 0.26  |
| C5ar1      | 4.577E-02 | 0.51  |
| Flg2       | 6.700E-04 | 0.04  |
| Nrap       | 2.896E-04 | 0.36  |
| Rgag4      | 2.503E-02 | 0.51  |
| Mblac1     | 1.838E-03 | 1.71  |
| Prmt6      | 2.944E-05 | 1.87  |
| Setd8      | 3.822E-03 | 1.65  |
| Rarres1    | 3.359E-04 | 0.12  |
| Chchd10    | 8.612E-06 | 0.33  |
| Fam58b     | 5.359E-04 | 1.52  |
| Htr1b      | 2.343E-02 | 3.47  |
| Cdc42ep1   | 1.042E-02 | 2.55  |
| Adamts16   | 1.317E-02 | 12.89 |
| Hist1h1a   | 1.207E-02 | 1.77  |
| Clip1      | 4.359E-04 | 0.58  |
| Aknad1     | 1.603E-02 | 2.89  |
| Tsku       | 8.176E-03 | 1.81  |
| Ccdc69     | 1.107E-04 | 0.45  |
| Lce1h      | 1.804E-04 | 0.20  |
| Omg        | 3.302E-03 | 1.56  |
| Catsperg1  | 1.166E-02 | 0.60  |
| Cyp2g1     | 1.002E-02 | 0.05  |
| Ucn2       | 9.605E-04 | 4.42  |
| Nlrp10     | 3.935E-03 | 0.48  |
| Lig4       | 5.367E-04 | 1.86  |
| Prss46     | 3.622E-03 | 0.15  |
| Mmp12      | 1.233E-02 | 0.29  |
| Arhgap15   | 1.367E-03 | 0.45  |
| Zfp280b    | 9.251E-04 | 1.57  |
| Fzd4       | 5.463E-06 | 0.40  |
| Armxc4     | 2.500E-03 | 1.63  |
| Zbtb12     | 1.284E-03 | 1.83  |
| Ceacam19   | 4.388E-04 | 0.37  |
| Fam26e     | 1.348E-02 | 0.11  |



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| Mettl21d   | 2.879E-02 | 1.62  |
| H2afx      | 1.099E-02 | 2.88  |
| Pgrmc2     | 3.855E-03 | 0.62  |
| Rpp38      | 6.155E-03 | 1.70  |
| Ccdc137    | 1.582E-02 | 1.79  |
| Glt1d1     | 1.761E-03 | 3.25  |
| Skint9     | 2.714E-04 | 0.05  |
| Ankrd55    | 6.736E-03 | 0.42  |
| Pitpnb     | 9.733E-06 | 1.56  |
| Amz1       | 4.339E-03 | 0.39  |
| Klk6       | 1.945E-02 | 0.52  |
| Bex1       | 1.417E-02 | 0.23  |
| Agmo       | 1.091E-05 | 0.25  |
| Gsg2       | 6.406E-03 | 1.60  |
| Bpifc      | 8.569E-04 | 0.49  |
| Lgr4       | 5.223E-03 | 0.62  |
| Cxcr3      | 7.536E-03 | 0.52  |
| Heatr1     | 4.105E-04 | 1.72  |
| D8Erttd82e | 9.086E-03 | 3.76  |
| Fzd2       | 2.511E-03 | 1.65  |
| Foxc1      | 3.939E-02 | 0.43  |
| Abca12     | 4.757E-02 | 0.65  |
| Synpo2     | 3.724E-05 | 0.34  |
| Lgals3     | 1.451E-03 | 0.36  |
| Sprr1a     | 1.182E-02 | 1.80  |
| Tcf19      | 3.176E-03 | 1.66  |
| Mrgprb2    | 1.075E-06 | 0.16  |
| Lypd6      | 4.532E-02 | 3.56  |
| Fam167b    | 1.104E-02 | 1.87  |
| Hyls1      | 3.778E-04 | 2.05  |
| Prokr2     | 5.033E-03 | 8.50  |
| Mmp13      | 9.458E-03 | 11.20 |
| Fam78a     | 3.052E-02 | 0.63  |
| 1700019N1  | 1.355E-02 | 3.75  |
| Sprr2f     | 3.660E-02 | 36.76 |
| Tmem150c   | 3.006E-02 | 3.09  |
| Ftl1       | 1.432E-03 | 0.33  |
| 4932442E0  | 1.625E-03 | 1.72  |
| Zbtb26     | 1.512E-03 | 1.65  |
| Plekho2    | 1.012E-02 | 0.46  |
| Ptges      | 2.213E-03 | 1.95  |
| Defb6      | 6.263E-03 | 0.06  |
| Prss27     | 1.860E-02 | 0.52  |
| Ccdc126    | 6.613E-05 | 1.51  |
| B3galt6    | 2.735E-02 | 1.70  |
| Hist1h2ba  | 3.079E-02 | 2.92  |
| Muc15      | 1.888E-02 | 0.40  |
| Tmem125    | 2.896E-02 | 2.23  |
| Phospho1   | 2.003E-02 | 0.51  |
| Cdr2l      | 1.009E-02 | 2.17  |
| Ankrd37    | 1.489E-02 | 2.08  |
| P2ry10     | 1.416E-03 | 0.57  |
| 4933403G1  | 2.147E-03 | 2.34  |
| Hist2h2bb  | 1.857E-03 | 1.73  |
| Gja1       | 4.641E-03 | 4.14  |
| D330012F2  | 3.105E-05 | 1.77  |
| Hs3st1     | 2.054E-02 | 8.54  |
| Olfml1     | 4.247E-05 | 0.25  |
| Gprc5c     | 1.202E-03 | 0.40  |
| P4ha3      | 3.726E-02 | 1.77  |
| 4930579K1  | 3.435E-02 | 1.61  |
| Gm4847     | 3.042E-02 | 0.19  |
| Adnp       | 1.687E-02 | 1.60  |
| Eml5       | 1.755E-02 | 1.62  |
| Rpusd3     | 1.823E-02 | 1.58  |
| Gpr183     | 2.740E-03 | 0.61  |
| Ercc6l     | 1.471E-03 | 3.11  |
| Fam83a     | 2.790E-02 | 2.05  |
| Gen1       | 2.203E-06 | 3.39  |
| Msrb3      | 1.948E-02 | 0.54  |
| 4930422G0  | 1.059E-05 | 2.09  |
| Nup160     | 4.706E-04 | 1.70  |
| Cacna1c    | 1.093E-02 | 2.41  |
| Zfp52      | 3.041E-03 | 2.08  |
| Plekhn3    | 5.263E-06 | 0.46  |
| Ncald      | 1.263E-05 | 0.23  |
| Pcdh1      | 4.754E-03 | 0.61  |
| Kif18b     | 2.941E-04 | 3.71  |
| Flrt3      | 3.369E-02 | 1.59  |
| Bbs12      | 1.272E-04 | 1.86  |
| Spn        | 6.921E-03 | 0.51  |
| Ufsp1      | 2.126E-02 | 1.56  |
| Wdfy4      | 8.229E-04 | 0.32  |
| Arhgef39   | 3.985E-05 | 2.47  |
| Rinl       | 3.212E-03 | 0.53  |
| Ttn        | 6.435E-06 | 0.23  |
| 1100001G2  | 4.844E-04 | 0.09  |
| Mest       | 4.950E-05 | 5.35  |
| Cd209f     | 1.729E-04 | 0.15  |
| Spats2     | 3.985E-04 | 2.17  |
| Lax1       | 4.518E-02 | 0.65  |
| Btla       | 5.725E-07 | 0.26  |
| Slc6a7     | 7.917E-04 | 0.22  |
| Pfdn4      | 1.086E-02 | 1.80  |
| Pard3b     | 1.410E-05 | 0.29  |
| Dock8      | 1.705E-07 | 0.39  |
| Rgs14      | 6.783E-03 | 0.59  |
| Rasa13     | 4.682E-02 | 0.53  |
| Gm9869     | 1.696E-03 | 3.25  |
| Pld4       | 9.970E-03 | 0.50  |
| Gm13476    | 7.610E-03 | 0.52  |
| 5330438D1  | 3.049E-02 | 1.73  |
| Taf9       | 5.135E-04 | 1.50  |
| Doc2a      | 1.744E-02 | 1.97  |
| Lrrc15     | 3.455E-02 | 3.45  |
| Ankrd44    | 3.332E-04 | 0.46  |
| 9930013L2  | 5.032E-04 | 3.44  |
| Actn2      | 2.768E-02 | 0.45  |



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|-----------|-----------|-------|
| Lrrc33    | 1.247E-03 | 0.47  |
| B4galt3   | 9.679E-03 | 1.61  |
| Prmt1     | 9.042E-03 | 2.02  |
| Bmpr1b    | 4.863E-04 | 5.54  |
| Zfp961    | 8.506E-04 | 1.70  |
| Atp6v1a   | 9.007E-04 | 0.54  |
| C13002612 | 2.382E-02 | 0.53  |
| Cherp     | 2.724E-04 | 1.65  |
| Epha3     | 4.248E-02 | 3.20  |
| Robo2     | 4.825E-03 | 1.67  |
| Magi3     | 5.254E-04 | 2.86  |
| Gan       | 3.610E-03 | 0.44  |
| Hist1h1d  | 1.126E-03 | 2.24  |
| Dlg2      | 1.123E-02 | 0.39  |
| Asap2     | 1.879E-05 | 2.17  |
| Rnf103    | 6.064E-05 | 0.65  |
| 5430435G2 | 6.111E-04 | 0.26  |
| Repin1    | 2.944E-04 | 0.40  |
| Nup107    | 7.352E-04 | 2.08  |
| Junb      | 2.326E-05 | 1.72  |
| Reep1     | 1.526E-02 | 2.92  |
| Prkcb     | 3.868E-05 | 0.27  |
| Ubxn8     | 6.303E-05 | 1.72  |
| Lamb2     | 8.667E-03 | 0.63  |
| Arhgef15  | 2.686E-04 | 1.99  |
| Glis3     | 2.757E-02 | 2.12  |
| Gas1      | 1.714E-02 | 1.84  |
| Cyp2f2    | 2.118E-06 | 0.05  |
| Uba2      | 5.892E-04 | 1.74  |
| Aph1c     | 6.359E-04 | 0.33  |
| Adh6a     | 4.856E-02 | 0.03  |
| Jam2      | 3.464E-05 | 0.43  |
| Clec12a   | 1.072E-05 | 0.31  |
| 270008101 | 5.557E-04 | 1.64  |
| Lins      | 1.222E-02 | 1.70  |
| Gpr141    | 3.106E-03 | 0.49  |
| Socs3     | 2.028E-02 | 2.01  |
| Rnf26     | 1.783E-04 | 1.59  |
| Fes       | 1.195E-02 | 0.62  |
| Bcl3      | 7.275E-03 | 1.64  |
| Aldh1a1   | 1.100E-04 | 0.17  |
| Ddx10     | 5.742E-03 | 1.70  |
| Pom121    | 4.226E-04 | 2.22  |
| Slamf8    | 2.485E-02 | 0.39  |
| Cbx7      | 2.909E-05 | 0.40  |
| Nrd1      | 4.518E-03 | 0.55  |
| 311008211 | 3.141E-02 | 1.95  |
| Ier2      | 4.022E-03 | 1.55  |
| Plxnb1    | 8.233E-04 | 2.02  |
| 2700023E2 | 6.228E-03 | 1.67  |
| Tgm5      | 1.530E-02 | 0.51  |
| Dpep2     | 8.056E-03 | 0.38  |
| Nebi      | 2.873E-03 | 0.30  |
| Dusp7     | 2.352E-06 | 2.32  |
| Oas1f     | 2.587E-05 | 0.08  |
| Exoc6     | 1.219E-03 | 0.60  |
| Grwd1     | 9.677E-03 | 2.09  |
| H2-T24    | 2.941E-02 | 0.41  |
| Ech1      | 3.133E-04 | 0.63  |
| Nanp      | 5.190E-04 | 1.77  |
| Lgals4    | 1.619E-03 | 0.58  |
| Pde5a     | 8.315E-03 | 2.22  |
| Mill1     | 2.345E-02 | 0.45  |
| Klk13     | 2.183E-02 | 3.75  |
| Rdh19     | 4.212E-02 | 0.11  |
| Utp18     | 6.488E-03 | 1.61  |
| Adm2      | 1.054E-02 | 7.61  |
| 483142611 | 2.091E-04 | 0.45  |
| O3far1    | 8.545E-03 | 0.14  |
| Ifi205    | 9.171E-05 | 0.22  |
| Sprr2k    | 3.514E-03 | 31.01 |
| Lifr      | 1.379E-07 | 0.35  |
| A630033H2 | 1.832E-02 | 0.42  |
| Taf4b     | 2.543E-03 | 3.25  |
| Lce3a     | 1.109E-02 | 8.97  |
| Sifn5     | 6.321E-04 | 0.41  |
| Tmem74    | 3.174E-02 | 20.58 |
| Gimap4    | 1.467E-02 | 1.55  |
| Syt15     | 3.375E-02 | 3.35  |
| Vsnl1     | 7.210E-04 | 4.62  |
| Tmem62    | 1.032E-03 | 0.42  |
| Gm14461   | 5.180E-05 | 0.12  |
| 2610204G2 | 2.214E-02 | 1.97  |
| Tmprss11e | 8.554E-03 | 3.18  |
| Adam12    | 6.358E-03 | 4.49  |
| Mettl7a1  | 6.379E-03 | 0.55  |
| Xlr       | 3.206E-04 | 0.33  |
| Mmrn1     | 7.579E-04 | 0.38  |
| Ano9      | 2.783E-05 | 0.15  |
| Emcn      | 2.318E-04 | 2.44  |
| Hmgb2     | 3.360E-03 | 1.99  |
| MsrA      | 7.366E-04 | 0.52  |
| Set       | 2.604E-03 | 1.85  |
| Cadm4     | 4.431E-04 | 4.75  |
| Elp6      | 1.559E-03 | 1.75  |
| Tmem158   | 2.881E-04 | 2.92  |
| Zfp667    | 2.568E-03 | 0.42  |
| Kcnmb4    | 1.961E-02 | 3.87  |
| Gm9958    | 1.019E-02 | 1.78  |
| 9130008F2 | 1.984E-04 | 2.82  |
| Cntn1     | 4.175E-03 | 4.28  |
| Smyd1     | 3.155E-04 | 0.28  |
| Pdlim1    | 3.973E-06 | 1.70  |
| Clra      | 1.574E-03 | 0.49  |
| Ntrk2     | 2.609E-06 | 0.27  |
| Zfp93     | 8.432E-03 | 1.81  |
| Pgbd1     | 5.868E-03 | 3.98  |
| Tns1      | 1.988E-04 | 0.35  |



|           |           |       |
|-----------|-----------|-------|
| Fat2      | 1.989E-02 | 1.78  |
| Snupn     | 5.470E-04 | 1.58  |
| Slc6a2    | 3.709E-02 | 0.21  |
| Gm9968    | 3.170E-03 | 0.63  |
| H2-Q5     | 3.783E-02 | 0.61  |
| Atp10b    | 1.118E-04 | 0.13  |
| Epm2a     | 3.596E-04 | 0.54  |
| Cdca7     | 2.398E-02 | 1.65  |
| B4galnt4  | 2.584E-02 | 2.36  |
| Hmcn2     | 9.927E-05 | 0.14  |
| Rras2     | 1.913E-03 | 2.46  |
| Ghr       | 7.960E-06 | 0.45  |
| Gemin6    | 1.759E-04 | 2.52  |
| Abcd2     | 8.583E-06 | 0.15  |
| Fmnl1     | 4.808E-02 | 0.64  |
| 1700034H1 | 1.034E-03 | 0.49  |
| Zfp1      | 5.577E-04 | 1.57  |
| Fancm     | 1.464E-03 | 1.56  |
| Skint1    | 1.354E-03 | 0.24  |
| Cldn23    | 9.095E-03 | 0.29  |
| Fut2      | 3.117E-02 | 0.49  |
| Nod2      | 3.656E-02 | 1.64  |
| Clca1     | 4.347E-03 | 0.20  |
| Lipm      | 3.260E-03 | 0.43  |
| St3gal5   | 3.103E-03 | 0.62  |
| H2-T22    | 4.725E-02 | 0.60  |
| B4gal6    | 3.883E-03 | 0.54  |
| Ticam2    | 4.002E-04 | 0.30  |
| Gm9992    | 8.645E-03 | 0.24  |
| Rdh9      | 5.576E-04 | 0.10  |
| Snx32     | 2.188E-03 | 0.51  |
| Npm3      | 1.504E-02 | 1.78  |
| Dennd1b   | 1.881E-03 | 0.59  |
| Usp39     | 4.286E-03 | 1.56  |
| 1810011O1 | 1.790E-03 | 2.02  |
| Myh1      | 2.575E-02 | 0.23  |
| Lig1      | 2.579E-04 | 2.27  |
| Pr12c3    | 2.702E-02 | 5.58  |
| Ptafr     | 9.941E-04 | 0.33  |
| Ccdc18    | 6.409E-03 | 2.80  |
| Mpz       | 1.631E-02 | 0.17  |
| Fry       | 6.399E-06 | 0.47  |
| Dsg3      | 2.196E-03 | 2.69  |
| Preld2    | 2.486E-04 | 4.60  |
| Nbeal2    | 3.777E-03 | 1.58  |
| Hmg2a     | 3.403E-02 | 6.19  |
| Gulp1     | 2.962E-02 | 0.56  |
| Gadl1     | 1.538E-03 | 0.19  |
| Glpr1     | 1.480E-02 | 0.49  |
| Usp13     | 4.825E-03 | 0.51  |
| Jmjd6     | 1.326E-03 | 1.84  |
| Ces1d     | 2.516E-05 | 0.03  |
| Ide       | 2.854E-02 | 0.47  |
| Myh4      | 1.295E-02 | 0.06  |
| Skap1     | 4.305E-03 | 0.50  |
| Ero1b     | 5.758E-03 | 0.63  |
| Ebf1      | 5.076E-03 | 0.59  |
| Npm1      | 8.786E-04 | 1.85  |
| Gja5      | 4.365E-04 | 2.75  |
| Atpbd4    | 7.393E-03 | 1.61  |
| Snrpg     | 9.277E-04 | 1.55  |
| Arhgap24  | 1.051E-03 | 0.50  |
| Whsc1     | 6.891E-03 | 1.58  |
| Lypd3     | 1.178E-02 | 1.79  |
| Fam136a   | 3.421E-02 | 1.73  |
| Ece1      | 4.411E-02 | 0.62  |
| Pus7      | 8.197E-03 | 1.54  |
| Lmcd1     | 6.621E-03 | 0.47  |
| Lce1a1    | 4.868E-04 | 0.17  |
| Pkn1      | 5.230E-03 | 0.52  |
| Vmn1r53   | 1.743E-02 | 16.54 |
| Sh3rf2    | 2.264E-03 | 0.34  |
| Lepr      | 2.330E-03 | 0.58  |
| Camk2b    | 4.365E-02 | 0.63  |
| Gpr111    | 5.395E-04 | 0.45  |
| Gm17136   | 4.025E-02 | 2.39  |
| Unc13d    | 3.003E-04 | 0.55  |
| Skint11   | 8.120E-06 | 0.15  |
| Adtrp     | 1.662E-02 | 0.40  |
| Nfam1     | 7.987E-03 | 0.47  |
| Gstm1     | 1.972E-04 | 0.17  |
| Chsy3     | 2.490E-02 | 2.79  |
| Gm5431    | 8.788E-03 | 0.47  |
| Espl1     | 1.157E-02 | 1.90  |
| Krt6a     | 4.536E-02 | 2.43  |
| Abce1     | 3.610E-04 | 1.84  |
| Hist1h2bg | 1.411E-02 | 1.61  |
| Rrp1b     | 6.494E-05 | 1.60  |
| Zfp82     | 2.663E-02 | 2.04  |
| Dhcr7     | 5.312E-03 | 0.46  |
| Wdr91     | 2.229E-03 | 0.58  |
| Rnf207    | 2.944E-02 | 2.80  |
| Gm5801    | 4.860E-02 | 2.01  |
| Tmod3     | 2.734E-04 | 1.56  |
| Samd12    | 4.541E-04 | 5.67  |
| Gcap14    | 2.070E-03 | 0.65  |
| Fcer1g    | 1.518E-02 | 0.49  |
| Lin9      | 1.685E-02 | 1.68  |
| Hist1h1b  | 8.375E-03 | 2.12  |
| Nap1l1    | 5.692E-05 | 1.75  |
| Col13a1   | 9.374E-04 | 5.86  |
| Lilrb3    | 1.860E-03 | 0.31  |
| Fam57b    | 2.674E-04 | 0.10  |
| Vwa8      | 5.804E-04 | 0.62  |
| Hnrnpa3   | 1.796E-04 | 1.82  |
| Gm5506    | 7.638E-04 | 1.70  |
| Rad51l1   | 4.618E-03 | 1.90  |
| Pde1a     | 1.846E-02 | 0.59  |



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| Lep        | 7.628E-04 | 0.08  |
| Olfr494    | 2.607E-02 | 0.04  |
| Gzmd       | 3.414E-02 | 37.68 |
| R74862     | 5.149E-03 | 1.66  |
| Hist1h3f   | 2.038E-03 | 2.44  |
| Slc27a4    | 4.054E-03 | 0.52  |
| Tonsl      | 1.963E-03 | 2.18  |
| Csf2ra     | 4.549E-02 | 0.50  |
| Fxyd2      | 5.447E-03 | 0.14  |
| Actg2      | 6.141E-04 | 4.36  |
| Trps3      | 1.357E-03 | 1.51  |
| Ear5       | 2.364E-02 | 0.27  |
| Nrm        | 6.477E-03 | 1.58  |
| Dbp        | 3.911E-02 | 0.56  |
| Kprp       | 1.641E-03 | 0.38  |
| Zfp930     | 2.664E-04 | 1.80  |
| Tmem40     | 1.151E-02 | 0.67  |
| Mug1       | 1.215E-04 | 0.06  |
| 9430015G1  | 3.757E-02 | 1.67  |
| Hspa2      | 4.887E-02 | 1.57  |
| Chpt1      | 8.545E-07 | 0.41  |
| Kif13b     | 4.037E-07 | 0.56  |
| Tmem26     | 1.947E-02 | 2.26  |
| Alox5ap    | 1.119E-02 | 0.45  |
| Hist1h4a   | 3.185E-02 | 1.98  |
| Sip1       | 2.172E-03 | 1.78  |
| Atp8b4     | 3.344E-04 | 0.41  |
| Zfp462     | 3.172E-02 | 1.57  |
| Alyref2    | 7.507E-03 | 1.73  |
| Ppih       | 1.087E-02 | 1.75  |
| Zfp941     | 8.498E-03 | 2.64  |
| Calm5      | 7.782E-04 | 0.22  |
| C030014I2: | 3.449E-03 | 1.68  |
| Sntb1      | 9.866E-04 | 0.13  |
| Tor3a      | 2.765E-03 | 0.54  |
| Ces4a      | 5.439E-04 | 0.05  |
| Fam78b     | 4.310E-02 | 2.16  |
| H2-Eb1     | 6.634E-03 | 0.44  |
| Layn       | 1.442E-02 | 0.42  |
| Eno3       | 1.104E-05 | 0.14  |
| Pla2g16    | 1.380E-02 | 0.58  |
| Hist1h4c   | 2.336E-03 | 2.02  |
| Cd302      | 1.665E-02 | 0.54  |
| Plekhh1    | 1.241E-03 | 2.07  |
| Ipmk       | 2.497E-03 | 0.63  |
| Gmfg       | 2.229E-02 | 0.57  |
| B2m        | 1.409E-02 | 0.50  |
| Ube2s      | 1.333E-03 | 1.98  |
| Acyp2      | 9.952E-04 | 0.47  |
| Csmc1      | 1.415E-02 | 0.31  |
| AI597468   | 3.100E-02 | 1.51  |
| Slc4a4     | 2.768E-05 | 0.27  |
| Irx1       | 2.672E-03 | 0.42  |
| Hist1h4h   | 7.987E-03 | 1.85  |
| Rrs1       | 7.682E-04 | 2.00  |
| Clasrp     | 1.378E-02 | 1.53  |
| Cdh3       | 1.414E-05 | 3.27  |
| Mcpt4      | 2.066E-05 | 0.26  |
| Myl4       | 3.583E-02 | 10.09 |
| Prcp       | 2.032E-04 | 0.53  |
| Blnk       | 3.809E-03 | 0.54  |
| Fnip2      | 5.335E-03 | 0.54  |
| H2-K1      | 1.260E-02 | 0.58  |
| Exosc5     | 1.230E-02 | 1.59  |
| Taok3      | 2.087E-03 | 0.55  |
| Cxcl12     | 3.642E-06 | 0.22  |
| Phf5a      | 1.763E-02 | 1.57  |
| Krt79      | 7.122E-04 | 0.04  |
| Efcab4b    | 3.400E-02 | 0.64  |
| Hipk2      | 3.382E-03 | 0.60  |
| Obscn      | 1.316E-03 | 0.28  |
| Snrpa      | 1.135E-04 | 1.54  |
| Hist1h4d   | 1.043E-03 | 1.89  |
| C1qtnf7    | 1.850E-04 | 0.21  |
| Orm2       | 3.457E-02 | 0.13  |
| UZaf1      | 2.569E-05 | 1.51  |
| Tnnt3      | 2.992E-04 | 0.14  |
| Ext1       | 1.494E-04 | 1.63  |
| Mospd2     | 1.305E-03 | 0.61  |
| Cfd        | 8.770E-05 | 0.05  |
| Myl1       | 6.598E-04 | 0.20  |
| Sphk1      | 4.607E-06 | 0.45  |
| Ccdc62     | 2.074E-02 | 1.62  |
| Iah1       | 9.994E-04 | 0.64  |
| Pgk1       | 2.044E-06 | 2.05  |
| Lmnb2      | 7.456E-03 | 1.61  |
| Trim54     | 4.154E-04 | 0.37  |
| Tgif2      | 3.037E-05 | 2.00  |
| 27000970C  | 7.822E-04 | 1.68  |
| Cks2       | 3.410E-05 | 2.72  |
| Opcml      | 2.253E-04 | 0.22  |
| Rpp25      | 2.219E-02 | 4.79  |
| Gm10115    | 8.275E-05 | 0.22  |
| Cyt11      | 4.320E-06 | 0.08  |
| Tmem65     | 1.647E-03 | 0.66  |
| Hist1h3g   | 5.165E-03 | 2.04  |
| Gm9705     | 6.342E-04 | 0.33  |
| Cys1       | 2.589E-02 | 0.44  |
| Cnr2       | 2.533E-03 | 0.47  |
| Lilrb4     | 1.545E-02 | 0.46  |
| Kcnj15     | 6.161E-05 | 2.00  |
| Hist1h2bk  | 9.781E-03 | 1.84  |
| Zfp599     | 1.829E-04 | 3.00  |
| I7Rn6      | 3.386E-03 | 1.52  |
| Hist1h3d   | 1.940E-03 | 2.28  |
| Ces2f      | 1.807E-02 | 2.29  |
| Phactr2    | 8.838E-03 | 0.64  |
| Impdh2     | 2.215E-03 | 1.61  |



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|------------|-----------|----------|
| Acadm      | 2.181E-05 | 0.52     |
| A43010701  | 2.223E-02 | 0.60     |
| Nrg1       | 7.384E-04 | 9.86     |
| Msln       | 3.124E-02 | 7.46     |
| 2010204K1  | 6.301E-03 | 8.03     |
| Hist1h2ak  | 1.285E-03 | 2.13     |
| Ing2       | 1.902E-04 | 1.66     |
| Lrrc40     | 2.759E-04 | 1.72     |
| Kif1b      | 2.780E-06 | 0.57     |
| Cd300lb    | 5.299E-03 | 0.28     |
| Ldha       | 9.726E-04 | 1.70     |
| Scoc       | 1.204E-02 | 1.54     |
| Ptpla      | 3.017E-03 | 2.52     |
| Tmem117    | 2.242E-02 | 3.24     |
| 1190007101 | 1.172E-02 | 1.92     |
| Krr1       | 9.517E-04 | 1.66     |
| Eno1       | 1.015E-03 | 1.74     |
| Sema3e     | 1.415E-02 | 0.49     |
| Aox1       | 2.340E-02 | 0.64     |
| Col23a1    | 1.235E-02 | 1.90     |
| Cnfn       | 3.734E-02 | 2.40     |
| Krt73      | 4.311E-02 | 0.13     |
| Hist2h2ab  | 7.076E-05 | 2.04     |
| S100a7a    | 3.191E-03 | 12.43    |
| Prpf38a    | 9.920E-03 | 1.55     |
| Hsrbp1     | 1.245E-02 | 1.57     |
| Alms1      | 7.313E-03 | 1.51     |
| Pepd       | 1.795E-06 | 0.52     |
| Nr6a1      | 3.237E-02 | 1.60     |
| Wlbg       | 9.213E-04 | 1.84     |
| Gpn1       | 7.464E-03 | 1.72     |
| Ipcef1     | 1.425E-02 | 0.57     |
| Cnnm2      | 4.536E-02 | 2.05     |
| Hcst       | 1.085E-02 | 0.43     |
| Cadm2      | 2.672E-02 | 0.30     |
| Zfp69      | 2.084E-02 | 1.76     |
| Hist1h2bh  | 3.703E-03 | 2.04     |
| Ifi271l    | 6.402E-05 | 0.54     |
| Gsdma3     | 1.169E-02 | 0.04     |
| Chi3l1     | 2.519E-02 | 0.44     |
| Zfp428     | 2.407E-02 | 2.85     |
| Hvcn1      | 2.111E-02 | 0.38     |
| Aox3       | 4.282E-04 | 0.20     |
| Sepp1      | 9.077E-06 | 0.18     |
| Snora41    | 2.705E-02 | 2.87     |
| SNORA2     | 2.045E-02 | 2.99     |
| Telomerase | 1.149E-02 | 3.57     |
| Snora43    | 1.375E-02 | 2.67     |
| Snord118   | 4.237E-02 | 2.88     |
| U1         | 6.208E-03 | 10.77    |
| SNORA4     | 3.109E-02 | 2.28     |
| SNORA32    | 2.442E-02 | 3.25     |
| SNORA25    | 2.307E-02 | 2.65     |
| Mir7-1     | 4.482E-02 | 63311.70 |
| U3         | 5.584E-03 | 3.78     |
| SNORA24    | 3.652E-02 | 0.10     |
| SNORA25    | 8.902E-05 | 2.83     |
| U1         | 7.965E-03 | 10.37    |
| U3         | 4.506E-02 | 1.71     |
| U1         | 4.940E-03 | 15.63    |
| Tacc1      | 4.356E-03 | 0.53     |
| Cd209b     | 1.532E-05 | 0.11     |
| Dhrs3      | 3.971E-05 | 0.27     |
| Gm1976     | 1.044E-02 | 2.14     |
| Adamts1    | 1.435E-03 | 0.38     |
| Prpf4      | 6.300E-03 | 1.63     |
| Slc31a2    | 1.312E-05 | 0.48     |
| AY512931   | 4.176E-04 | 0.56     |
| Vps37b     | 7.306E-04 | 2.33     |
| Serpina3c  | 3.672E-05 | 0.13     |
| Serpina3b  | 8.675E-03 | 0.06     |
| Akap13     | 2.121E-04 | 0.50     |
| Rdh11      | 7.246E-03 | 0.43     |
| Ttc32      | 6.981E-03 | 1.65     |
| Zbtb16     | 7.960E-03 | 0.20     |
| Cyp2b19    | 5.863E-06 | 0.13     |
| Rnasel     | 3.318E-03 | 0.58     |
| Hmcn1      | 1.484E-02 | 0.53     |
| Bub3       | 9.969E-05 | 1.50     |
| Serpinb7   | 2.657E-03 | 0.06     |
| Unc93a     | 4.040E-03 | 0.27     |
| Igj        | 4.915E-03 | 0.18     |
| Mrgpra4    | 4.862E-05 | 0.22     |
| H2-T23     | 1.009E-02 | 0.50     |
| Lgi1       | 1.268E-03 | 5.61     |
| Ppp1r3c    | 3.519E-05 | 0.16     |
| Lyar       | 1.024E-02 | 2.58     |
| Tspan6     | 3.153E-02 | 1.77     |
| Hist1h4j   | 5.923E-03 | 2.04     |
| Klra3      | 1.352E-03 | 0.15     |
| Dgat2l6    | 2.161E-03 | 0.04     |
| Lpar5      | 9.280E-04 | 1.77     |
| Xlr4b      | 3.411E-02 | 0.57     |
| Pl15       | 5.228E-03 | 7.32     |
| Snb3       | 5.025E-03 | 0.50     |
| Zfp948     | 1.911E-03 | 1.52     |
| 251004911  | 4.891E-02 | 0.14     |
| Mllt4      | 5.690E-03 | 0.54     |
| Cenpm      | 1.853E-03 | 2.79     |
| Col8a1     | 5.002E-03 | 3.36     |
| Pdpx       | 2.977E-02 | 1.92     |
| Ccdc48     | 2.497E-03 | 0.18     |
| Shroom4    | 1.305E-02 | 1.57     |
| Cep152     | 7.871E-05 | 1.79     |
| Rpl34-ps1  | 3.032E-02 | 2.33     |
| Actc1      | 2.657E-02 | 8.29     |
| Myoz1      | 3.825E-05 | 0.10     |
| Trp53l1    | 7.078E-05 | 2.44     |



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|------------|-----------|-------|
| Psrc1      | 4.627E-03 | 0.51  |
| Sort1      | 4.283E-08 | 0.29  |
| Ptprz1     | 1.705E-04 | 14.48 |
| Sf3b4      | 3.713E-04 | 1.53  |
| Cgn        | 4.393E-02 | 0.55  |
| Lce3f      | 9.890E-03 | 6.10  |
| Lce1j      | 1.779E-04 | 0.17  |
| Lce1i      | 4.788E-04 | 0.15  |
| Lce1e      | 7.241E-04 | 0.22  |
| Lce1a2     | 9.927E-03 | 0.14  |
| Pde7a      | 1.467E-02 | 1.69  |
| Zfp72      | 1.913E-03 | 1.84  |
| Serpinb6e  | 3.380E-02 | 0.05  |
| Hist1h3a   | 2.181E-02 | 2.26  |
| Hist1h3b   | 8.615E-03 | 2.02  |
| Hist1h2bf  | 3.492E-02 | 2.14  |
| Hist1h2ac  | 3.881E-03 | 2.72  |
| Hist1h2ae  | 1.269E-03 | 2.36  |
| Hist1h3e   | 1.512E-03 | 2.27  |
| Hist1h4f   | 2.384E-03 | 2.41  |
| Hist1h2bj  | 2.627E-03 | 1.95  |
| Hist1h2ag  | 1.557E-02 | 2.06  |
| Hist1h2ah  | 3.333E-02 | 2.09  |
| Hist1h2br  | 7.471E-03 | 2.10  |
| Hist1h4n   | 2.037E-02 | 2.11  |
| Hist1h4m   | 7.278E-03 | 1.99  |
| Hist1h2bp  | 1.170E-02 | 1.73  |
| Hist1h3c   | 3.163E-02 | 2.45  |
| Hist1h3h   | 3.270E-02 | 2.39  |
| Ctxn3      | 7.047E-04 | 0.22  |
| Dsg1a      | 1.573E-02 | 0.41  |
| Ly21       | 9.805E-03 | 0.37  |
| Ly22       | 8.721E-03 | 0.33  |
| Tmem19     | 9.348E-04 | 0.62  |
| Cd300lh    | 7.987E-03 | 0.36  |
| Gm11710    | 4.783E-03 | 0.38  |
| Pex11c     | 2.190E-02 | 0.65  |
| Sifn9      | 2.870E-03 | 2.34  |
| Fbp1       | 3.383E-03 | 0.34  |
| Ahnak      | 8.150E-03 | 0.60  |
| 4930438A0  | 2.874E-03 | 0.25  |
| 9930111J2: | 9.831E-03 | 0.50  |
| 9930111J2: | 7.163E-03 | 0.49  |
| Ccdc99     | 2.682E-04 | 2.90  |
| Fam196b    | 2.070E-04 | 0.38  |
| Fcho1      | 9.103E-05 | 0.35  |
| Sp140      | 1.597E-02 | 0.66  |
| Fat1       | 1.041E-02 | 1.77  |
| Snora33    | 2.219E-02 | 1.95  |
| 4930581F2  | 5.000E-04 | 1.69  |
| Mmp27      | 4.871E-03 | 0.31  |
| Ccnd1      | 9.576E-05 | 2.61  |
| Ampd1      | 3.057E-02 | 0.30  |
| Nlrp1b     | 2.550E-02 | 0.62  |
| Cyp3a57    | 1.997E-03 | 0.04  |
| Adamts13   | 6.419E-04 | 0.30  |
| Ndn12      | 8.884E-04 | 1.54  |
| Mrgprb1    | 1.672E-06 | 0.16  |
| Gm13177    | 1.762E-03 | 0.04  |
| Btdb8      | 1.270E-02 | 2.19  |
| Utp3       | 6.443E-04 | 1.51  |
| Sars2      | 1.901E-02 | 1.63  |
| Pla2g4d    | 1.012E-02 | 8.54  |
| Tmem200b   | 4.251E-02 | 1.52  |
| Gm12942    | 3.327E-02 | 0.67  |
| Rbm47      | 8.266E-03 | 0.61  |
| Gm1673     | 6.255E-03 | 2.54  |
| Zfp804a    | 2.062E-03 | 20.95 |
| Skint3     | 4.309E-04 | 0.20  |
| Rabepk     | 7.627E-03 | 1.75  |
| Ccl19      | 2.648E-04 | 0.10  |
| Sdr16c6    | 1.044E-03 | 0.11  |
| Zfp827     | 5.771E-03 | 2.57  |
| Ptges3     | 2.037E-04 | 1.58  |
| Gm10311    | 1.256E-02 | 1.51  |
| 2810008M:  | 2.909E-04 | 1.58  |
| Naip5      | 2.274E-02 | 0.64  |
| C1qtnf9    | 7.402E-05 | 0.46  |
| Zfp777     | 6.087E-04 | 1.56  |
| Hist1h2ai  | 1.042E-02 | 2.75  |
| Gprin2     | 2.391E-04 | 0.08  |
| Klrg2      | 2.008E-02 | 1.72  |
| 3425401B1  | 9.383E-04 | 0.33  |
| Nt5dc2     | 1.095E-02 | 2.82  |
| Lrrn4cl    | 2.345E-02 | 0.56  |
| Bsc12      | 1.048E-03 | 0.57  |
| Snx29      | 5.188E-06 | 0.43  |
| Csf2rb     | 3.551E-02 | 0.54  |
| Csf2rb2    | 3.690E-02 | 0.60  |
| Ncf4       | 2.865E-02 | 0.53  |
| Spin4      | 1.525E-03 | 2.62  |
| Zhx2       | 3.275E-02 | 1.62  |
| Apcdd1     | 3.694E-02 | 0.59  |
| 6720489N1  | 6.446E-03 | 1.74  |
| Ccnf       | 3.761E-07 | 2.78  |
| Ang        | 7.857E-03 | 0.61  |
| Trim6      | 3.012E-02 | 2.26  |
| Klf12      | 4.660E-02 | 2.06  |
| Dppa2      | 1.378E-03 | 0.18  |
| Fam84b     | 3.834E-06 | 2.27  |
| Slc39a2    | 5.969E-04 | 0.11  |
| Ear2       | 3.840E-02 | 0.39  |
| Ear1       | 2.618E-02 | 0.32  |
| 1810012P1  | 1.264E-02 | 1.62  |
| Gm10393    | 9.549E-04 | 0.27  |
| 1500011B0  | 1.656E-02 | 1.56  |
| Myo18b     | 3.877E-04 | 0.43  |
| Ahnak2     | 1.081E-04 | 0.32  |



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| Acot1      | 3.651E-04 | 0.11  |
| Oip5       | 9.268E-04 | 3.47  |
| Lrrc61     | 6.603E-03 | 0.53  |
| Gm10485    | 9.127E-03 | 0.34  |
| H2-Q6      | 3.658E-02 | 0.55  |
| H2-D1      | 6.897E-03 | 0.60  |
| C4b        | 2.405E-05 | 0.14  |
| H2-Ab1     | 2.010E-02 | 0.51  |
| H2-Ke6     | 1.962E-04 | 0.63  |
| Arhgdig    | 6.904E-03 | 2.93  |
| Wdr90      | 1.136E-02 | 1.55  |
| D330041Hc  | 1.607E-03 | 0.63  |
| Al607873   | 1.235E-02 | 0.46  |
| Gm10521    | 1.436E-02 | 0.35  |
| Cep76      | 8.451E-03 | 1.55  |
| Pcdhb22    | 2.142E-02 | 2.78  |
| Gm1614     | 2.824E-02 | 0.61  |
| Gm10564    | 2.066E-02 | 1.81  |
| Apitd1     | 1.790E-02 | 2.24  |
| Gm10565    | 2.478E-02 | 2.37  |
| 5730409E0  | 1.806E-02 | 0.64  |
| Sh3d21     | 2.383E-02 | 0.52  |
| Kti12      | 2.301E-02 | 1.60  |
| 8030451A0  | 1.557E-02 | 4.15  |
| Mup11      | 6.861E-03 | 0.04  |
| Mup7       | 4.461E-02 | 0.05  |
| Gm13305    | 5.253E-04 | 0.33  |
| Gm13306    | 3.367E-04 | 0.12  |
| Gm13304    | 1.323E-03 | 0.33  |
| Ccl27a     | 3.667E-02 | 0.11  |
| Il11ra1    | 3.253E-04 | 0.36  |
| Ggh        | 9.587E-04 | 0.40  |
| 49305200C  | 3.639E-03 | 1.67  |
| Mlycd      | 1.311E-03 | 0.62  |
| Snrnp40    | 1.230E-02 | 1.65  |
| Ntf5       | 4.334E-03 | 2.37  |
| Klk5       | 1.779E-02 | 0.37  |
| Znhit6     | 7.707E-05 | 1.80  |
| Zfp791     | 4.732E-02 | 1.63  |
| Adh1       | 3.497E-05 | 0.14  |
| Dnajb14    | 9.228E-04 | 0.61  |
| Cox7a1     | 3.976E-05 | 0.18  |
| Zfp568     | 2.994E-04 | 1.54  |
| Gramd2     | 6.946E-03 | 2.62  |
| Amy1       | 2.997E-07 | 0.18  |
| Ovgp1      | 2.990E-02 | 1.99  |
| Tnfaip8l3  | 3.054E-06 | 0.32  |
| AA386476   | 1.794E-03 | 1.68  |
| Hist2h3b   | 4.426E-02 | 2.08  |
| 2610203C2  | 2.497E-02 | 2.30  |
| Gm14548    | 1.870E-03 | 0.29  |
| 2310001H1  | 6.426E-03 | 4.70  |
| Gm15417    | 1.924E-02 | 0.65  |
| Mex3a      | 1.074E-03 | 2.46  |
| Mocs3      | 9.232E-03 | 1.96  |
| Fam65c     | 9.431E-04 | 0.54  |
| 1500012F0  | 2.614E-03 | 1.57  |
| Lekr1      | 4.653E-03 | 1.72  |
| 4930449A1  | 2.906E-03 | 0.06  |
| Zfp850     | 1.616E-02 | 2.42  |
| Gm826      | 3.890E-02 | 3.79  |
| Arhgap40   | 1.768E-04 | 0.29  |
| Cpne1      | 2.061E-06 | 1.81  |
| Elf2s2     | 2.239E-05 | 1.60  |
| Gm10737    | 6.316E-03 | 1.65  |
| Zcchc3     | 3.322E-04 | 3.12  |
| Thbd       | 4.352E-02 | 2.53  |
| lsm1       | 1.189E-03 | 0.18  |
| Plknc1     | 1.860E-04 | 0.45  |
| Slc4a11    | 4.733E-02 | 3.13  |
| Zfp934     | 2.791E-03 | 1.60  |
| Lcmt2      | 1.076E-02 | 1.58  |
| B3galt5    | 4.789E-02 | 2.65  |
| 5430417L2  | 4.534E-05 | 1.66  |
| Pak6       | 7.788E-04 | 2.42  |
| Grem1      | 9.245E-04 | 5.79  |
| Fjx1       | 5.754E-03 | 4.01  |
| 4631405J1! | 4.855E-02 | 9.10  |
| Prdm11     | 2.135E-03 | 2.60  |
| Hist1h2bb  | 6.402E-03 | 1.82  |
| Ccdc58     | 1.331E-02 | 1.87  |
| Cenpw      | 9.585E-04 | 3.67  |
| Ttc30a1    | 1.914E-02 | 1.63  |
| Aldh3b2    | 2.934E-03 | 0.50  |
| Kbtbd10    | 1.239E-04 | 0.38  |
| Hoxc4      | 4.693E-03 | 1.89  |
| 4930594M:  | 1.166E-02 | 2.08  |
| Gm12359    | 2.805E-03 | 1.59  |
| B130006Dc  | 4.072E-03 | 1.57  |
| 2300005B0  | 2.491E-03 | 0.02  |
| Gpx4       | 1.448E-02 | 0.63  |
| Dio3       | 4.138E-02 | 3.95  |
| Sox4       | 1.876E-03 | 1.79  |
| BC100451   | 1.390E-03 | 0.54  |
| 2700094K1  | 1.392E-05 | 2.69  |
| Ass1       | 1.215E-02 | 2.03  |
| Igkv2-137  | 2.133E-02 | 0.20  |
| Igkv4-79   | 2.222E-02 | 0.28  |
| Igkv4-56   | 2.122E-02 | 0.21  |
| Igkc       | 2.719E-02 | 0.27  |
| Tcrg-C2    | 3.579E-02 | 0.48  |
| SNORA66    | 1.285E-02 | 2.62  |
| n-RSs158   | 1.664E-02 | 0.04  |
| SNORA42    | 4.675E-02 | 90.11 |
| SNORA27    | 1.717E-02 | 2.79  |
| SNORA3     | 3.175E-02 | 2.31  |
| SNORA40    | 1.824E-02 | 60.50 |
| Snord17    | 4.926E-04 | 0.60  |



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|------------|-----------|------|
| F63002801  | 3.649E-02 | 0.62 |
| Capns2     | 3.699E-04 | 0.30 |
| AW011738   | 2.826E-02 | 1.61 |
| 3110003A1  | 8.406E-07 | 1.51 |
| 2310042D1  | 3.409E-03 | 0.63 |
| A930039A1  | 4.450E-03 | 0.49 |
| Gm13212    | 5.799E-03 | 0.60 |
| Gm438      | 2.582E-03 | 0.07 |
| Gm436      | 1.341E-03 | 0.04 |
| Gm13124    | 1.329E-03 | 0.05 |
| Aadac13    | 6.442E-04 | 0.06 |
| Ddi2       | 2.082E-04 | 0.61 |
| Aunlp      | 4.154E-03 | 4.81 |
| Bnlp3      | 1.617E-03 | 2.51 |
| Skint8     | 4.482E-03 | 0.27 |
| Aoc2       | 1.079E-02 | 1.60 |
| Psme3      | 7.993E-04 | 1.54 |
| Crnn       | 2.313E-02 | 8.10 |
| Lce1d      | 9.822E-04 | 0.22 |
| Fam174b    | 1.353E-03 | 0.56 |
| Mup19      | 4.810E-02 | 0.05 |
| Mup18      | 8.060E-03 | 0.04 |
| Mup10      | 9.366E-03 | 0.04 |
| Mup2       | 4.390E-02 | 0.04 |
| Gm2002     | 9.827E-03 | 0.41 |
| Haus5      | 6.875E-04 | 1.96 |
| Zfp566     | 1.688E-02 | 1.85 |
| Evi2a      | 5.410E-04 | 0.45 |
| Rad54b     | 5.116E-04 | 2.46 |
| Cpt1b      | 3.144E-05 | 0.27 |
| Naip6      | 2.758E-02 | 0.50 |
| Naip2      | 4.968E-02 | 0.65 |
| Hsbp1l1    | 4.495E-04 | 0.27 |
| Gm12033    | 2.442E-02 | 2.59 |
| Wdr92      | 2.406E-03 | 1.77 |
| Samd1      | 9.869E-04 | 1.57 |
| Serpina3j  | 2.597E-03 | 0.04 |
| Slc45a4    | 5.936E-03 | 0.63 |
| Prnp       | 7.148E-03 | 0.63 |
| Cyp4v3     | 2.941E-03 | 0.39 |
| Jrkl       | 1.965E-03 | 1.55 |
| Pr12c2     | 2.279E-02 | 3.52 |
| Pms2       | 2.687E-04 | 1.62 |
| Capn3      | 8.767E-04 | 0.46 |
| Kdelr2     | 1.524E-03 | 1.50 |
| Gm4204     | 6.948E-03 | 2.81 |
| A13001011  | 3.996E-03 | 1.62 |
| Tlr5       | 3.302E-02 | 0.65 |
| Cd209g     | 5.474E-04 | 0.15 |
| Slco1a6    | 2.282E-02 | 3.57 |
| Tmem233    | 1.621E-03 | 0.11 |
| Ccr1l      | 4.152E-03 | 0.35 |
| Gm3558     | 3.652E-02 | 1.74 |
| Gm5796     | 2.071E-02 | 2.13 |
| Gm2897     | 3.540E-02 | 1.88 |
| Gm11110    | 5.019E-03 | 2.82 |
| Gm2382     | 7.784E-03 | 0.66 |
| Tmprss11g  | 1.721E-03 | 6.76 |
| Gm7609     | 2.100E-02 | 0.43 |
| Utp14b     | 1.821E-03 | 1.96 |
| Sssca1     | 1.687E-02 | 1.97 |
| Phyhd1     | 4.532E-02 | 0.64 |
| Tmsb10     | 4.022E-02 | 1.64 |
| H2-DMb1    | 3.835E-02 | 0.59 |
| Kifc1      | 2.580E-08 | 2.50 |
| Haus3      | 2.700E-05 | 2.00 |
| Tmem182    | 8.979E-04 | 0.39 |
| Ankrd39    | 4.935E-03 | 1.70 |
| Tm4sf19    | 2.543E-03 | 0.10 |
| Rab26      | 3.953E-02 | 1.88 |
| Ulbp1      | 2.274E-02 | 2.57 |
| SNORA50    | 1.318E-02 | 4.50 |
| Hist3h2bb  | 3.093E-02 | 2.59 |
| Gm12564    | 1.647E-02 | 2.68 |
| Gm15613    | 1.420E-02 | 1.77 |
| Gm11442    | 4.386E-02 | 1.80 |
| Gm15739    | 3.332E-03 | 1.75 |
| Hist2h3c2  | 4.230E-02 | 2.31 |
| Rps12-ps2f | 2.177E-03 | 2.99 |
| BC022960   | 6.190E-03 | 2.99 |
| Gm12551    | 2.470E-03 | 0.08 |
| Cyp2j12    | 1.155E-02 | 0.06 |
| Gm11653    | 1.288E-02 | 1.91 |
| Gm15368    | 3.152E-02 | 1.54 |
| Slc48a1    | 7.598E-03 | 0.61 |
| Gm13717    | 1.060E-02 | 2.56 |
| Rplp0-ps1  | 3.358E-02 | 0.24 |
| Gm15922    | 3.850E-02 | 0.30 |
| Gm15931    | 1.821E-02 | 0.27 |
| Gm14441    | 3.960E-03 | 0.48 |
| Flg        | 3.175E-02 | 0.21 |
| Gm14276    | 5.828E-04 | 1.92 |
| Gm14382    | 2.461E-02 | 1.74 |
| Gm16074    | 2.430E-02 | 3.30 |
| Pisd-ps1   | 3.185E-02 | 0.60 |
| Btc        | 2.485E-02 | 0.28 |
| Gm11955    | 3.593E-02 | 2.30 |
| Gm13591    | 4.348E-02 | 1.66 |
| Gm15580    | 4.048E-02 | 2.21 |
| Gm12566    | 2.260E-03 | 0.25 |
| Gm15897    | 3.787E-03 | 0.56 |
| Gm12774    | 9.390E-03 | 1.77 |
| Gm15652    | 3.820E-02 | 1.82 |
| Rpl31-ps5  | 1.687E-02 | 2.57 |
| Gm9308     | 3.564E-02 | 0.28 |
| Gm13193    | 9.846E-04 | 2.40 |
| Gm15741    | 3.645E-04 | 0.12 |
| Cyp2j8     | 4.139E-03 | 0.07 |



|            |           |        |
|------------|-----------|--------|
| Gm15531    | 2.273E-04 | 0.21   |
| Gm12917    | 3.227E-02 | 1.80   |
| Gm14780    | 5.485E-05 | 2.02   |
| Ctsf       | 2.750E-03 | 0.49   |
| Gm12839    | 2.167E-02 | 0.37   |
| Gm12035    | 1.370E-02 | 1.97   |
| Gm15916    | 3.300E-02 | 0.66   |
| Gm11699    | 1.803E-02 | 0.36   |
| Gm2986     | 3.614E-02 | 1.77   |
| Gm13033    | 2.627E-02 | 2.91   |
| Gm15712    | 1.431E-04 | 0.55   |
| Gm15696    | 4.556E-02 | 1.55   |
| Gm8145     | 5.740E-03 | 0.60   |
| Gm6654     | 3.774E-02 | 1.62   |
| 2610024D1  | 6.951E-05 | 0.47   |
| Gm11576    | 3.593E-02 | 2.80   |
| U4         | 2.230E-02 | 0.15   |
| SNORA33    | 1.041E-02 | 0.32   |
| Y_RNA      | 1.154E-02 | 236.16 |
| 7SK        | 3.671E-02 | 0.39   |
| 4930564G2  | 3.641E-03 | 3.29   |
| Ccdc85c    | 6.271E-03 | 3.41   |
| Gm15230    | 1.252E-02 | 2.31   |
| B430010I2: | 1.793E-03 | 0.52   |
| Gm12977    | 3.515E-02 | 2.09   |
| Gm5860     | 2.712E-03 | 2.02   |
| Gm15834    | 1.239E-02 | 2.56   |
| Gm15635    | 5.833E-03 | 0.17   |
| Gm16070    | 2.318E-02 | 7.69   |
| Gm12609    | 2.754E-02 | 2.51   |
| Gm11974    | 8.245E-03 | 1.71   |
| Al838599   | 2.007E-03 | 0.22   |
| Gm12603    | 1.253E-02 | 8.25   |
| Gm13507    | 1.789E-02 | 2.13   |
| B430219N1  | 1.481E-02 | 0.48   |
| Gm15614    | 2.474E-03 | 2.50   |
| 4930430E1  | 8.806E-03 | 0.34   |
| Gm13684    | 8.140E-04 | 1.56   |
| 3010003L2  | 4.662E-03 | 2.48   |
| Gm16305    | 2.480E-03 | 0.56   |
| Gm14508    | 2.691E-02 | 1.73   |
| 9430008C0  | 4.026E-03 | 1.77   |
| 4930483C1  | 6.879E-03 | 3.26   |
| Gm16001    | 2.057E-02 | 2.41   |
| Gm16320    | 2.123E-03 | 4.36   |
| Gm14023    | 1.468E-02 | 1.72   |
| Gm12868    | 1.835E-03 | 4.74   |
| 4930412C1  | 6.618E-03 | 0.19   |
| A730017L2  | 1.859E-02 | 1.92   |
| Gm15868    | 3.078E-02 | 1.80   |
| Gm9855     | 1.810E-02 | 1.84   |
| 2700086A0  | 3.975E-02 | 1.64   |
| Gm11641    | 2.402E-02 | 1.77   |
| 5430405HC  | 3.260E-05 | 1.82   |
| Gm13536    | 2.004E-02 | 0.20   |
| 4930443B2  | 3.302E-03 | 1.89   |
| Gm13563    | 1.175E-02 | 1.64   |
| 2310050B0  | 9.538E-06 | 0.16   |
| Gm15987    | 3.651E-02 | 0.60   |
| Gm6963     | 2.840E-02 | 0.60   |
| Gm4285     | 2.543E-02 | 1.58   |
| 2010012P1  | 4.840E-02 | 0.54   |
| Gm15601    | 1.501E-03 | 0.49   |
| 4833417C1  | 1.362E-02 | 1.58   |
| Gm15797    | 5.887E-03 | 1.60   |
| Gm13391    | 4.279E-04 | 0.31   |
| Gm15513    | 7.954E-05 | 0.31   |
| Gm13705    | 9.821E-03 | 1.85   |
| Gm15645    | 3.531E-03 | 1.73   |
| 933016201  | 3.745E-02 | 0.57   |
| Gm12264    | 3.770E-04 | 1.79   |
| Gm12002    | 2.197E-03 | 0.22   |
| 4930562D2  | 2.451E-04 | 3.42   |
| Gm12867    | 3.919E-03 | 4.26   |
| E130102H2  | 2.939E-03 | 0.61   |
| Gm15675    | 3.149E-03 | 0.42   |
| Lce6a      | 2.280E-04 | 0.09   |
| Gm16365    | 3.203E-02 | 1.64   |
| Gm12248    | 8.121E-03 | 0.12   |
| Gm16314    | 2.005E-02 | 1.92   |
| 4933431E2  | 5.010E-04 | 0.30   |
| A230103J1  | 3.255E-03 | 1.63   |
| 2810442I2: | 3.691E-02 | 2.16   |
| Nctc1      | 2.183E-07 | 0.16   |
| Al662270   | 1.765E-03 | 0.42   |
| Gm11714    | 3.345E-03 | 2.91   |
| Gm16096    | 1.540E-02 | 2.05   |
| Plcd2      | 5.436E-03 | 0.44   |
| Skint6     | 6.488E-03 | 0.03   |
| Gm15261    | 5.186E-04 | 0.26   |
| 2810408I1: | 2.049E-03 | 4.08   |
| 2610035D1  | 5.190E-04 | 2.27   |
| Gm12349    | 2.140E-02 | 17.63  |
| Gm11946    | 3.629E-02 | 1.60   |
| Gm15884    | 1.031E-02 | 1.97   |
| BC042782   | 1.347E-02 | 1.74   |
| BC065397   | 9.290E-03 | 2.01   |
| Tmem170b   | 7.856E-06 | 0.57   |
| Gm16323    | 1.703E-02 | 0.35   |
| Gm16141    | 3.068E-02 | 2.64   |
| Gm14389    | 1.018E-03 | 0.21   |
| Gm12319    | 1.620E-02 | 0.57   |
| 9830144P2  | 4.036E-04 | 2.62   |
| C030037DC  | 7.977E-03 | 2.53   |
| Zfp111     | 1.577E-04 | 1.60   |
| Gm15050    | 2.077E-02 | 2.73   |
| Gm15051    | 7.451E-04 | 2.61   |
| Gm15845    | 3.582E-02 | 3.92   |



|            |           |       |
|------------|-----------|-------|
| Gm15674    | 7.295E-03 | 0.46  |
| Gm15283    | 2.688E-03 | 3.44  |
| 7SK        | 3.831E-02 | 0.58  |
| SNORA74    | 9.913E-03 | 2.01  |
| 7SK        | 1.461E-02 | 2.20  |
| SNORA61    | 8.326E-03 | 8.94  |
| U6         | 3.000E-02 | 0.29  |
| SNORA48    | 3.712E-02 | 2.39  |
| snoU109    | 3.777E-02 | 2.10  |
| 7SK        | 6.304E-04 | 1.74  |
| SNORA48    | 1.902E-02 | 2.69  |
| Scarna3a   | 1.038E-02 | 0.45  |
| Gm16326    | 2.242E-02 | 2.37  |
| 1700058P1  | 1.037E-02 | 1.78  |
| Fcor       | 7.773E-04 | 0.35  |
| Tnfsf13    | 7.781E-04 | 0.34  |
| Gp49a      | 8.541E-03 | 0.45  |
| Gm11711    | 2.197E-03 | 0.37  |
| Mir17hg    | 4.767E-03 | 3.22  |
| Clec2f-ps  | 1.279E-05 | 5.17  |
| Ier5l      | 6.046E-03 | 3.12  |
| Skint1     | 1.318E-04 | 0.27  |
| Rdh1       | 6.315E-04 | 0.16  |
| 1700028K0  | 2.782E-02 | 1.78  |
| A530032D1  | 4.419E-02 | 0.57  |
| Gm15853    | 4.632E-02 | 1.75  |
| Pira2      | 1.934E-03 | 0.29  |
| Gm16137    | 1.253E-02 | 2.16  |
| Ugt11a1    | 4.472E-05 | 0.11  |
| Ft3l       | 1.654E-03 | 0.60  |
| Abhd12b    | 5.039E-03 | 0.13  |
| Ugt1a7c    | 7.133E-04 | 0.52  |
| 9230105E0  | 4.154E-02 | 7.28  |
| Tmem189    | 7.762E-04 | 0.59  |
| Cfb        | 1.069E-03 | 0.39  |
| Gm17296    | 1.613E-04 | 1.80  |
| Gm17034    | 4.558E-02 | 2.13  |
| 2310050C0  | 1.708E-04 | 0.10  |
| 2810055G2  | 2.484E-04 | 0.46  |
| 4930523C0  | 3.370E-02 | 0.65  |
| Efna5      | 4.513E-02 | 1.63  |
| Gypc       | 4.741E-02 | 0.65  |
| Gm5538     | 1.906E-03 | 0.04  |
| Apold1     | 2.207E-04 | 1.93  |
| Klhl33     | 2.281E-03 | 0.33  |
| Gm17147    | 3.253E-02 | 0.57  |
| Ccdc71l    | 1.703E-02 | 1.78  |
| Gm17300    | 6.261E-03 | 1.92  |
| 9330020H0  | 1.513E-02 | 1.99  |
| Gm20390    | 5.174E-04 | 1.62  |
| Vgll3      | 2.617E-03 | 0.47  |
| Gm17430    | 7.206E-03 | 0.27  |
| Fth-ps2    | 3.952E-03 | 1.68  |
| Flg        | 1.063E-02 | 0.25  |
| Col6a5     | 2.485E-03 | 0.08  |
| Aadacl2    | 3.601E-02 | 0.53  |
| Hist2h4    | 3.380E-03 | 1.55  |
| 2610021A0  | 2.525E-03 | 1.56  |
| Gm17167    | 7.453E-03 | 0.39  |
| Cyp4f17    | 1.812E-03 | 1.93  |
| Gm17092    | 8.605E-03 | 2.26  |
| Lsm5       | 2.164E-03 | 1.95  |
| Yy2        | 1.853E-03 | 1.61  |
| D17H6556f  | 1.212E-02 | 1.79  |
| Tnnc1      | 3.406E-02 | 36.45 |
| 1700099I0  | 1.872E-02 | 1.65  |
| E130317F2  | 6.734E-03 | 1.70  |
| Bend4      | 2.023E-02 | 1.93  |
| Fancf      | 3.948E-04 | 2.11  |
| Gm3696     | 1.797E-02 | 2.08  |
| 1110038B1  | 4.075E-08 | 2.12  |
| Gm17907    | 2.607E-02 | 1.55  |
| Ly6g6c     | 5.715E-04 | 0.38  |
| Gm20442    | 6.530E-03 | 7.63  |
| 9130230NC  | 2.082E-02 | 2.60  |
| Snord8     | 3.628E-02 | 0.43  |
| SCARNA15   | 1.659E-02 | 0.24  |
| AA465934   | 2.074E-02 | 1.61  |
| 2610019E1  | 1.523E-03 | 1.54  |
| Gm20554    | 1.839E-02 | 0.54  |
| Gm19357    | 4.840E-02 | 1.70  |
| Hist2h3c1  | 2.204E-02 | 2.76  |
| U6         | 2.449E-02 | 0.29  |
| U1         | 9.118E-03 | 22.06 |
| SNORA25    | 1.199E-02 | 2.64  |
| Gm10598    | 2.257E-02 | 0.37  |
| Hmgcs1     | 2.854E-02 | 0.61  |
| SNORA17    | 4.169E-02 | 0.27  |
| EVI2B      | 2.365E-03 | 0.57  |
| AC073565.. | 4.373E-02 | 0.32  |
| AC158361.. | 4.149E-02 | 0.21  |
| S100a2     | 4.789E-02 | 15.15 |
| Ccl21b     | 1.395E-03 | 0.33  |
| Gm4767     | 9.345E-03 | 1.60  |
| RPP14      | 1.854E-02 | 1.71  |
| Hist1h2ao  | 7.810E-03 | 2.35  |
| AC158361.. | 7.897E-03 | 0.24  |
| AC174742.. | 6.386E-03 | 1.77  |
| Gm20382    | 4.044E-02 | 1.93  |
| Ccl21a     | 1.885E-04 | 0.31  |
| AC122322.. | 4.477E-02 | 0.41  |
| Hist1h2ap  | 9.612E-03 | 2.14  |
| PLAC9      | 1.012E-03 | 0.27  |
| U1         | 4.828E-04 | 7.12  |
| ZFP936     | 1.127E-03 | 1.80  |
| AC155333.. | 3.228E-02 | 0.27  |
| AC158361.. | 8.615E-03 | 0.22  |
| AC160982.. | 2.507E-02 | 0.22  |



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|------------|-----------|-------|
| AC079181.. | 3.206E-02 | 0.25  |
| AC073939.. | 1.599E-02 | 0.21  |
| AW146154   | 1.432E-03 | 1.71  |
| Gm9944     | 2.989E-03 | 0.07  |
| F930015N0  | 7.160E-03 | 9.00  |
| U1         | 9.645E-03 | 9.66  |
| AC116573.. | 2.316E-02 | 2.29  |
| Gm12407    | 5.993E-03 | 0.12  |
| Plac9      | 2.280E-03 | 0.30  |
| AC169518.. | 1.302E-04 | 0.40  |
| U6         | 3.913E-02 | 8.11  |
| Gm3892     | 6.966E-03 | 0.36  |
| U6         | 2.449E-02 | 0.29  |
| U1         | 8.473E-03 | 10.91 |
| Noc2l      | 2.038E-02 | 1.81  |
| U1         | 3.877E-03 | 10.13 |
| Ccl21c     | 6.060E-03 | 0.38  |
| U1         | 7.942E-03 | 10.48 |
| AC158361.. | 2.894E-02 | 0.27  |
| Lce1k      | 3.519E-02 | 0.15  |
| Gm10592    | 1.866E-02 | 0.41  |
| Hist4h4    | 1.893E-02 | 1.59  |
| SYNE1      | 3.332E-02 | 0.50  |
| Cmtm4      | 2.246E-03 | 1.58  |
| Gm10592    | 4.447E-02 | 0.41  |
| Samd11     | 1.024E-02 | 2.11  |
| MOAP1      | 2.458E-02 | 1.71  |
| AC160990.. | 4.434E-02 | 0.26  |
| Cdkn2d     | 1.137E-02 | 1.61  |
| Gm10591    | 1.426E-02 | 0.40  |
| GM5849     | 3.219E-03 | 0.01  |
| Mup15      | 2.612E-02 | 0.04  |
| Zfp781     | 3.592E-03 | 1.79  |
| Hist1h2bm  | 2.453E-02 | 2.27  |
| Ccl27b     | 1.016E-05 | 0.10  |
| U1         | 2.300E-04 | 9.96  |
| Gm4767     | 9.219E-03 | 1.62  |
| AC158361.. | 4.956E-03 | 0.26  |
| mmu-mir-2  | 8.024E-03 | 0.61  |
| RP23-2516  | 4.073E-03 | 0.37  |
| AL627077.. | 3.434E-02 | 0.56  |
| AC153516.. | 7.093E-03 | 1.63  |
| AC163357.. | 3.991E-04 | 4.45  |
| CT025649.. | 2.050E-03 | 3.06  |
| AC124998.. | 7.544E-04 | 1.62  |
| AC122371.. | 1.023E-02 | 1.82  |
| AC140326.. | 7.866E-06 | 1.62  |
| AL732311.. | 1.194E-02 | 1.63  |
| AL589650.. | 1.190E-03 | 1.88  |
| AL663030.. | 1.617E-02 | 1.73  |
| AC133646.. | 2.469E-02 | 1.69  |
| AL672219.. | 2.312E-03 | 1.90  |
| AC132304.. | 2.401E-02 | 5.03  |
| AC125483.. | 1.957E-02 | 5.76  |
| RP23-302C  | 8.870E-03 | 2.51  |
| AC117663.. | 5.930E-03 | 1.93  |
| RP23-399J8 | 1.799E-02 | 2.50  |
| AC025794.. | 7.457E-03 | 1.85  |
| CT025673.. | 6.786E-04 | 1.53  |
| AARSD1     | 1.072E-02 | 2.31  |
| AC121121.. | 2.436E-02 | 1.56  |
| mmu-mir-1  | 7.230E-05 | 0.56  |
| AC124550.. | 2.749E-02 | 1.69  |
| Tnfrsf12   | 2.952E-03 | 0.28  |
| AC020971.. | 1.097E-02 | 2.23  |
| AL591113.. | 1.886E-03 | 1.88  |
| AC154200.. | 1.603E-02 | 1.75  |
| mmu-mir-4  | 4.423E-02 | 2.23  |
| AC124550.. | 6.370E-03 | 2.79  |
| AC163637.. | 1.032E-02 | 2.09  |
| AC136008.. | 4.199E-02 | 0.59  |
| AC158898.. | 1.647E-02 | 1.50  |
| AC119214.. | 1.367E-03 | 2.43  |
| RP23-73F2  | 5.243E-04 | 1.88  |
| AC102249.. | 4.583E-02 | 4.70  |
| AC123702.. | 5.236E-05 | 1.82  |
| BX537302.. | 5.737E-04 | 2.14  |
| AC161602.. | 1.704E-04 | 0.15  |
| CT030166.. | 5.003E-03 | 0.50  |
| AC164612.. | 1.064E-02 | 3.49  |
| AC123834.. | 4.541E-02 | 2.02  |
| AC107744.. | 5.791E-04 | 1.97  |
| AL607108.. | 1.299E-02 | 3.44  |
| AC125169.. | 1.754E-03 | 2.34  |
| mmu-mir-2  | 1.800E-02 | 2.10  |
| AL844859.. | 1.561E-03 | 1.58  |
| AC161534.. | 3.853E-02 | 0.46  |
| AC147987.. | 3.516E-03 | 2.31  |
| AC102862.. | 4.244E-02 | 2.05  |
| AC136147.. | 3.667E-03 | 10.95 |



gene signature PAP-SCC

| Gene     | p-value   | fold<br>change<br>SCC/PAP |
|----------|-----------|---------------------------|
| Wnt3     | 3.840E-02 | 0.34                      |
| Scnn1g   | 4.229E-02 | 0.48                      |
| Clec2g   | 2.900E-02 | 0.61                      |
| Trim25   | 2.907E-02 | 0.61                      |
| Ckmt1    | 5.473E-03 | 0.59                      |
| Fap      | 3.444E-02 | 2.39                      |
| Loxl3    | 2.523E-02 | 4.60                      |
| Serpinf1 | 1.436E-02 | 3.79                      |
| Gnb1l    | 3.161E-02 | 0.66                      |
| Mmp14    | 1.515E-02 | 2.38                      |
| Slc7a7   | 2.077E-02 | 2.17                      |
| S100a4   | 9.484E-03 | 3.16                      |
| Col6a1   | 3.414E-02 | 3.63                      |
| Ramp2    | 6.229E-04 | 1.79                      |
| Efnb2    | 5.632E-03 | 0.59                      |
| Cnn1     | 3.227E-02 | 1.76                      |
| Meox1    | 1.091E-02 | 2.49                      |
| Irx2     | 3.902E-02 | 0.47                      |
| Sgca     | 4.344E-03 | 8.81                      |
| Fkbp10   | 1.507E-02 | 2.33                      |
| Gstt1    | 2.620E-02 | 3.85                      |
| Il16     | 3.449E-02 | 1.81                      |
| Lrp3     | 2.765E-03 | 3.50                      |
| Cpa3     | 2.159E-02 | 2.29                      |
| Ltbp2    | 1.968E-02 | 5.13                      |
| Celf2    | 3.135E-02 | 2.53                      |
| Nr1h3    | 1.138E-02 | 1.79                      |
| Rhoc     | 5.473E-03 | 2.87                      |
| Rpl3l    | 1.954E-02 | 3.17                      |
| Axl      | 4.854E-02 | 1.86                      |
| Fkbp7    | 1.419E-02 | 2.54                      |
| Pla1a    | 1.223E-02 | 3.09                      |
| Cd97     | 1.842E-02 | 1.96                      |
| Lamb1    | 2.223E-02 | 1.97                      |
| Cd36     | 2.840E-02 | 7.83                      |
| Apoc2    | 2.839E-02 | 3.64                      |
| Fcgrt    | 3.645E-02 | 3.86                      |
| Phyhip   | 7.015E-03 | 0.49                      |
| Psg18    | 6.876E-03 | 0.36                      |
| Dusp3    | 3.347E-02 | 1.72                      |
| Fosb     | 9.366E-03 | 0.33                      |
| As3mt    | 3.651E-02 | 2.32                      |
| Cp       | 1.034E-02 | 6.21                      |
| Lin7b    | 3.099E-02 | 0.58                      |
| Col5a3   | 1.434E-02 | 3.89                      |



|           |           |       |
|-----------|-----------|-------|
| Angptl2   | 1.353E-02 | 2.88  |
| Etv1      | 4.930E-03 | 3.82  |
| Ptpn6     | 4.594E-02 | 1.58  |
| Clec11a   | 3.114E-02 | 1.75  |
| Arhgef40  | 2.552E-02 | 2.03  |
| Sgce      | 1.077E-02 | 2.49  |
| Aqp1      | 2.657E-03 | 2.01  |
| Ly9       | 2.790E-02 | 2.16  |
| Emr1      | 2.781E-02 | 2.92  |
| Pgf       | 1.458E-02 | 0.31  |
| Nes       | 1.678E-02 | 2.38  |
| Slc25a18  | 1.819E-02 | 0.57  |
| Rasa4     | 4.799E-02 | 1.79  |
| Prkacb    | 1.243E-02 | 1.60  |
| Wisp1     | 1.162E-02 | 2.87  |
| Ndr1      | 2.436E-02 | 0.54  |
| Ripk4     | 3.420E-03 | 0.65  |
| Prlr      | 4.836E-02 | 0.44  |
| Nid1      | 1.228E-02 | 2.53  |
| Adcy9     | 4.168E-03 | 0.65  |
| Mef2c     | 3.784E-03 | 4.08  |
| Prg4      | 9.747E-03 | 3.30  |
| Hspb7     | 1.167E-02 | 16.32 |
| Crip1     | 3.303E-02 | 2.16  |
| Tek       | 2.209E-02 | 1.72  |
| Adamts4   | 3.492E-02 | 2.05  |
| Actn3     | 1.015E-02 | 11.53 |
| Abhd1     | 3.094E-02 | 0.60  |
| Hspa1l    | 5.164E-03 | 0.66  |
| Ddah2     | 2.284E-02 | 1.58  |
| Atp1a2    | 2.484E-03 | 12.16 |
| Casq1     | 1.953E-02 | 9.65  |
| Twist2    | 6.973E-03 | 2.74  |
| Tcap      | 9.081E-03 | 11.10 |
| Gprc5b    | 1.375E-02 | 1.94  |
| Bcl2l13   | 3.093E-03 | 0.67  |
| Ascl2     | 3.031E-02 | 0.50  |
| Sardh     | 3.258E-02 | 2.17  |
| Tnfrsf13b | 1.142E-02 | 2.26  |
| Psen2     | 2.413E-02 | 1.77  |
| Fads1     | 4.513E-02 | 1.94  |
| Kdelr3    | 8.209E-03 | 2.03  |
| Adssl1    | 4.039E-03 | 4.58  |
| Adam19    | 2.440E-02 | 2.21  |
| Scarf2    | 4.423E-02 | 2.20  |
| Steap4    | 2.820E-02 | 1.99  |
| Podn1     | 3.530E-02 | 2.24  |
| Zfp651    | 3.287E-02 | 1.69  |
| Pea15a    | 1.804E-02 | 1.59  |



|          |           |       |
|----------|-----------|-------|
| Clip3    | 1.889E-02 | 2.74  |
| Bicc1    | 1.388E-02 | 3.07  |
| Mertk    | 4.538E-02 | 3.34  |
| Slamf6   | 4.476E-02 | 2.51  |
| Cybb     | 4.200E-02 | 3.75  |
| Cd48     | 4.608E-02 | 2.12  |
| Lpl      | 3.106E-02 | 4.94  |
| Gata3    | 2.898E-02 | 0.46  |
| Lass2    | 3.110E-02 | 1.71  |
| Eps8     | 4.049E-02 | 2.41  |
| Fcgr1    | 3.905E-02 | 2.30  |
| Chdh     | 2.643E-02 | 0.51  |
| Fli1     | 2.984E-03 | 2.16  |
| Ctsz     | 4.609E-02 | 3.28  |
| Eef1a2   | 8.276E-03 | 17.81 |
| Sulf1    | 1.393E-02 | 5.79  |
| Tnnc2    | 5.947E-03 | 13.52 |
| Aldoc    | 1.379E-02 | 0.65  |
| Stac2    | 4.820E-02 | 2.10  |
| C1qtnf1  | 1.089E-02 | 2.73  |
| Timp2    | 2.958E-02 | 3.31  |
| Igfbp4   | 1.594E-02 | 4.19  |
| Tns4     | 1.510E-02 | 0.62  |
| Rhbdl3   | 1.936E-02 | 0.58  |
| Pltp     | 4.048E-02 | 2.41  |
| Jph2     | 8.558E-03 | 2.74  |
| Cyth4    | 3.521E-02 | 2.92  |
| Erbb3    | 6.884E-03 | 0.60  |
| Pmp22    | 3.446E-02 | 2.46  |
| Gpx3     | 2.023E-02 | 3.74  |
| Anxa6    | 1.168E-02 | 2.31  |
| Trpv2    | 3.717E-02 | 1.96  |
| Sparc    | 2.547E-02 | 3.45  |
| Copz2    | 4.899E-02 | 1.81  |
| Slc25a35 | 1.167E-02 | 0.54  |
| BC096441 | 1.025E-02 | 4.11  |
| Lsp1     | 9.632E-03 | 3.42  |
| Myh11    | 6.370E-03 | 2.64  |
| Unc45b   | 2.096E-02 | 4.36  |
| Mb       | 2.238E-02 | 7.71  |
| Scn1b    | 1.520E-02 | 2.17  |
| Mtap1s   | 4.754E-02 | 2.02  |
| Aoc3     | 8.686E-03 | 2.78  |
| Ptger1   | 3.151E-02 | 1.75  |
| Gyg      | 1.725E-02 | 2.52  |
| Rcn3     | 1.430E-02 | 3.50  |
| Akt3     | 4.993E-02 | 1.70  |
| Syne1    | 4.269E-02 | 1.59  |
| Trdn     | 6.625E-03 | 11.52 |



|           |           |       |
|-----------|-----------|-------|
| Rab32     | 4.485E-02 | 1.76  |
| Tube1     | 1.261E-02 | 0.64  |
| Lama4     | 2.095E-02 | 2.01  |
| Lama2     | 1.813E-02 | 3.55  |
| Dcn       | 1.589E-02 | 7.87  |
| Ikbip     | 2.672E-02 | 1.86  |
| Pde7b     | 4.102E-03 | 2.83  |
| Ctgf      | 3.945E-02 | 2.86  |
| Nudt4     | 9.432E-03 | 1.54  |
| Timp3     | 4.815E-02 | 1.79  |
| Dram1     | 3.984E-02 | 1.73  |
| Mybpc1    | 6.742E-03 | 20.05 |
| 2010107G2 | 8.019E-03 | 0.57  |
| 4632428N0 | 1.651E-02 | 3.55  |
| Avpr1a    | 2.663E-02 | 5.15  |
| Grb10     | 2.063E-02 | 2.02  |
| Jsrp1     | 5.925E-03 | 11.82 |
| Col6a2    | 3.638E-02 | 3.19  |
| Glyctk    | 4.220E-02 | 0.66  |
| Shc2      | 1.468E-02 | 3.73  |
| Sgcd      | 3.562E-03 | 4.35  |
| Pdlim4    | 2.423E-02 | 3.55  |
| Igfbp3    | 1.974E-03 | 2.83  |
| Tcn2      | 8.003E-03 | 1.95  |
| Osbp2     | 7.371E-03 | 0.58  |
| Patz1     | 4.540E-02 | 1.52  |
| Aebp1     | 1.452E-02 | 4.06  |
| Pgam2     | 1.393E-02 | 2.92  |
| 4-Sep     | 2.566E-03 | 2.01  |
| Pik3cg    | 3.823E-02 | 1.76  |
| Rnf144a   | 5.404E-03 | 3.17  |
| Pxdn      | 3.907E-02 | 2.24  |
| Ace       | 1.810E-02 | 5.30  |
| Itgb3     | 2.249E-02 | 1.56  |
| Adap2     | 3.602E-02 | 2.24  |
| Pecam1    | 2.935E-03 | 1.82  |
| Cacng1    | 1.524E-03 | 11.49 |
| Cygb      | 1.568E-02 | 4.52  |
| Mxra7     | 1.265E-02 | 2.56  |
| Cacna1g   | 4.228E-02 | 2.63  |
| Cacnb1    | 1.213E-02 | 2.24  |
| Dlg4      | 2.550E-02 | 2.35  |
| Ntn1      | 2.186E-02 | 2.78  |
| Myh3      | 2.882E-02 | 93.74 |
| Nin       | 2.623E-02 | 1.56  |
| Serpina3n | 3.826E-02 | 4.14  |
| Galnt1    | 3.014E-02 | 3.57  |
| Fbln5     | 4.782E-02 | 1.91  |
| Akr1c13   | 3.400E-02 | 1.87  |



|          |           |      |
|----------|-----------|------|
| Fos      | 2.803E-02 | 0.46 |
| Tgfb3    | 3.360E-02 | 2.00 |
| Angel1   | 5.218E-03 | 0.56 |
| Hhip1    | 2.129E-02 | 2.18 |
| Exoc3l4  | 4.061E-02 | 2.28 |
| Gpr137b  | 4.826E-02 | 2.11 |
| Aoah     | 2.080E-02 | 2.18 |
| Tfap2a   | 2.889E-03 | 0.57 |
| Cap2     | 2.807E-03 | 8.68 |
| Ly86     | 1.159E-02 | 2.66 |
| Cxcl14   | 2.753E-02 | 2.88 |
| Slc25a48 | 2.953E-02 | 0.59 |
| Adcy2    | 3.503E-02 | 2.31 |
| Nkd2     | 2.871E-02 | 1.75 |
| Srd5a1   | 2.682E-02 | 0.66 |
| Mctp1    | 3.680E-02 | 2.39 |
| Vcan     | 4.201E-02 | 2.35 |
| Ckmt2    | 1.812E-02 | 9.08 |
| Rgs7bp   | 4.195E-02 | 0.44 |
| Slc4a7   | 2.367E-02 | 1.57 |
| Gpx8     | 4.683E-02 | 2.22 |
| Ldb3     | 9.529E-03 | 7.87 |
| Txndc16  | 2.896E-02 | 1.68 |
| Samd4    | 1.540E-02 | 2.27 |
| Gpr65    | 1.072E-02 | 2.55 |
| Tsc22d1  | 1.569E-02 | 1.59 |
| Epsti1   | 3.833E-02 | 2.13 |
| Tnfsf11  | 2.098E-02 | 5.20 |
| Trim35   | 1.571E-03 | 2.24 |
| Dpysl2   | 2.439E-02 | 2.00 |
| Sorbs3   | 6.821E-03 | 2.30 |
| Bmp1     | 1.487E-02 | 2.22 |
| Rcbtb2   | 1.732E-02 | 1.63 |
| Ednrb    | 3.864E-02 | 1.80 |
| Fyb      | 8.499E-03 | 2.17 |
| Dab2     | 2.900E-02 | 3.03 |
| C6       | 1.794E-02 | 9.38 |
| Amacr    | 2.996E-02 | 0.60 |
| Angpt1   | 6.227E-03 | 3.54 |
| Khdrbs3  | 8.221E-03 | 2.94 |
| Sla      | 3.720E-02 | 2.16 |
| Wnt7b    | 8.799E-03 | 0.46 |
| Enpp2    | 2.360E-02 | 3.42 |
| C1qtnf6  | 1.355E-02 | 2.84 |
| Apod     | 1.904E-02 | 6.20 |
| Oplah    | 4.516E-02 | 0.60 |
| Gsdmd    | 4.668E-02 | 2.34 |
| Gpihbp1  | 4.582E-04 | 2.76 |
| Ccdc80   | 1.375E-02 | 2.80 |



|           |           |       |
|-----------|-----------|-------|
| Cd200r1   | 3.660E-02 | 3.08  |
| Zbtb20    | 1.633E-02 | 1.74  |
| Klhl22    | 2.416E-02 | 2.16  |
| Arhgap31  | 3.080E-02 | 1.64  |
| Fstl1     | 9.564E-03 | 4.38  |
| Hcls1     | 4.818E-02 | 2.14  |
| Ets2      | 8.579E-03 | 0.66  |
| Cbr3      | 4.110E-02 | 0.66  |
| Setd4     | 6.359E-03 | 0.66  |
| Amhr2     | 7.095E-03 | 0.38  |
| Npff      | 3.072E-02 | 0.65  |
| Cxcl13    | 2.396E-02 | 6.55  |
| Fhl1      | 5.133E-03 | 8.08  |
| Serping1  | 1.155E-02 | 6.15  |
| Guca2a    | 2.899E-02 | 0.30  |
| Parp3     | 4.949E-02 | 1.56  |
| Clec4n    | 3.291E-02 | 4.19  |
| Nfatc4    | 1.546E-02 | 2.64  |
| Agpat4    | 3.656E-02 | 1.53  |
| Pde10a    | 4.216E-03 | 3.22  |
| Thbs2     | 1.716E-02 | 3.12  |
| Pla2g7    | 2.854E-02 | 3.10  |
| Vegfa     | 5.217E-03 | 0.49  |
| Clic5     | 3.860E-03 | 4.75  |
| Cyp39a1   | 1.497E-02 | 0.52  |
| Trem2     | 4.094E-02 | 5.17  |
| Pi16      | 4.785E-02 | 10.79 |
| Fgd2      | 1.385E-02 | 2.18  |
| Myom1     | 3.398E-03 | 7.39  |
| Emilin2   | 4.654E-02 | 2.57  |
| Lbh       | 1.467E-02 | 2.19  |
| Cyp1b1    | 1.368E-02 | 5.11  |
| Tmem204   | 3.437E-02 | 1.61  |
| Zeb1      | 8.993E-03 | 2.36  |
| Tmem173   | 2.936E-02 | 2.31  |
| 2010001M( | 4.182E-02 | 4.37  |
| Epb4.1l4a | 5.294E-03 | 0.64  |
| Bin1      | 2.019E-02 | 2.48  |
| Aif1      | 2.038E-02 | 2.43  |
| Zfp521    | 5.802E-03 | 2.05  |
| Myot      | 4.543E-03 | 14.30 |
| Dpysl3    | 2.745E-02 | 2.88  |
| Lox       | 1.220E-02 | 7.57  |
| Ppic      | 4.133E-02 | 1.67  |
| Slc27a6   | 4.419E-02 | 0.60  |
| Cd74      | 4.860E-02 | 2.12  |
| Pdgfrb    | 8.759E-03 | 3.67  |
| Rab3il1   | 2.162E-02 | 3.51  |
| Fads2     | 4.168E-02 | 2.28  |



|            |           |       |
|------------|-----------|-------|
| Ms4a7      | 1.943E-02 | 3.29  |
| Ms4a6b     | 1.897E-02 | 2.84  |
| Ms4a4d     | 3.564E-03 | 3.74  |
| Ms4a6d     | 4.539E-02 | 3.69  |
| Lpxn       | 3.619E-02 | 2.24  |
| Pcsk5      | 1.936E-02 | 5.25  |
| Slc15a3    | 4.742E-02 | 3.11  |
| Lipa       | 2.795E-02 | 2.54  |
| Ankrd1     | 3.295E-03 | 58.42 |
| Aldh3b1    | 2.318E-02 | 3.17  |
| Efemp2     | 2.412E-02 | 2.29  |
| Fosl1      | 4.312E-02 | 0.53  |
| Ehbp1l1    | 2.654E-02 | 1.54  |
| Fermt3     | 2.953E-02 | 2.43  |
| Msr1       | 2.298E-02 | 4.09  |
| Gfra1      | 1.774E-02 | 4.21  |
| Maged1     | 3.065E-02 | 1.85  |
| Ankrd2     | 2.980E-02 | 40.60 |
| Hexa       | 2.096E-02 | 2.85  |
| Fam120c    | 1.192E-02 | 0.65  |
| Maged2     | 2.536E-02 | 2.11  |
| Itgb8      | 3.700E-02 | 0.53  |
| Cd63       | 3.291E-02 | 1.97  |
| Gdf11      | 6.526E-03 | 2.00  |
| Cox8b      | 1.880E-03 | 9.52  |
| Ifitm5     | 1.865E-03 | 0.67  |
| 1600016N2  | 4.664E-03 | 0.50  |
| Tspan4     | 1.588E-02 | 2.28  |
| Zfp711     | 4.812E-02 | 0.62  |
| Nptx1      | 4.373E-03 | 0.26  |
| Cpeb1      | 1.376E-02 | 2.88  |
| Rps6ka6    | 1.607E-02 | 0.48  |
| Tmem47     | 4.347E-03 | 2.26  |
| Il6        | 4.269E-02 | 2.19  |
| D3Ertd751e | 4.986E-02 | 0.66  |
| Nrp1       | 1.344E-02 | 2.22  |
| Hk3        | 4.359E-02 | 3.59  |
| Smad7      | 6.651E-03 | 0.63  |
| Adam23     | 3.495E-02 | 1.74  |
| Col5a2     | 1.449E-02 | 4.09  |
| 1500015O1  | 5.061E-03 | 13.95 |
| Il1rl1     | 1.577E-03 | 3.08  |
| Il1r1      | 1.952E-02 | 2.40  |
| Ptpn18     | 3.942E-02 | 1.88  |
| Igfbp5     | 3.766E-02 | 6.70  |
| Des        | 2.532E-03 | 18.02 |
| Slc16a14   | 3.421E-02 | 0.32  |
| Itm2c      | 1.100E-02 | 1.64  |
| Epha4      | 7.121E-03 | 0.61  |



|           |           |          |
|-----------|-----------|----------|
| Serpine2  | 4.710E-02 | 2.35     |
| Inpp5d    | 3.255E-02 | 1.83     |
| Cfh       | 3.792E-02 | 9.03     |
| Steap3    | 7.939E-03 | 2.41     |
| Ptpcr     | 3.209E-02 | 2.48     |
| Cacna1s   | 4.191E-03 | 9.16     |
| Fcamr     | 3.821E-02 | 0.57     |
| Myog      | 4.052E-02 | 14002.82 |
| Glul      | 1.068E-02 | 2.53     |
| Adck3     | 2.899E-02 | 1.95     |
| F5        | 4.281E-02 | 2.11     |
| Prrx1     | 1.072E-02 | 3.35     |
| Sec16b    | 2.242E-02 | 2.47     |
| Soat1     | 1.877E-02 | 2.42     |
| Rgs5      | 2.578E-02 | 2.05     |
| Vim       | 1.652E-02 | 3.01     |
| Nek6      | 1.525E-02 | 1.53     |
| Apbb1ip   | 4.173E-02 | 1.86     |
| Stxbp1    | 1.405E-02 | 1.51     |
| Dnm1      | 2.834E-02 | 2.55     |
| Gbgt1     | 3.563E-02 | 2.82     |
| Col5a1    | 2.559E-02 | 3.07     |
| Zeb2      | 1.645E-02 | 3.51     |
| Neb       | 3.151E-03 | 13.50    |
| 2010317E2 | 1.049E-02 | 0.62     |
| Itga4     | 2.472E-02 | 1.97     |
| Xirp2     | 1.890E-02 | 29.09    |
| Slc43a3   | 2.479E-03 | 2.68     |
| Tfpi      | 2.759E-02 | 1.69     |
| Hoxd8     | 1.169E-02 | 1.88     |
| Myef2     | 4.597E-03 | 2.03     |
| Fbn1      | 1.430E-02 | 4.93     |
| Fgf7      | 8.731E-03 | 8.79     |
| Slc28a2   | 2.667E-02 | 1.81     |
| Mdk       | 6.898E-03 | 2.99     |
| Lrp4      | 4.245E-02 | 0.59     |
| Siglec1   | 2.217E-02 | 3.93     |
| Rassf2    | 3.291E-02 | 2.69     |
| Cpxm1     | 2.958E-02 | 5.59     |
| Acss1     | 2.802E-02 | 1.79     |
| Mylk2     | 5.970E-03 | 9.51     |
| Pkia      | 3.535E-02 | 2.42     |
| Car3      | 1.493E-02 | 20.25    |
| Procr     | 3.353E-02 | 0.60     |
| Wisp2     | 1.351E-02 | 7.29     |
| Gnb4      | 1.967E-02 | 1.80     |
| Slc7a11   | 3.427E-02 | 2.16     |
| Aadac     | 1.036E-02 | 0.46     |
| Dclk1     | 1.316E-02 | 3.50     |



|          |           |       |
|----------|-----------|-------|
| Olfml3   | 1.733E-02 | 3.33  |
| Tbx15    | 9.832E-03 | 4.02  |
| Npr1     | 3.246E-02 | 1.86  |
| Vcam1    | 3.218E-02 | 2.21  |
| Col11a1  | 4.966E-03 | 2.72  |
| Sfrp2    | 1.453E-02 | 3.54  |
| Thbs3    | 1.483E-02 | 3.16  |
| Pear1    | 2.267E-03 | 2.11  |
| Fmo5     | 7.569E-03 | 0.61  |
| Nudt17   | 3.546E-02 | 0.59  |
| Ctsk     | 1.723E-02 | 3.67  |
| Myoz2    | 6.507E-03 | 25.40 |
| F3       | 2.107E-02 | 0.49  |
| Ddah1    | 7.263E-03 | 3.56  |
| Col15a1  | 1.992E-02 | 1.99  |
| Nr4a3    | 7.315E-03 | 0.45  |
| Murc     | 8.316E-03 | 11.14 |
| Dbc1     | 1.233E-02 | 3.21  |
| Tnc      | 3.149E-02 | 2.85  |
| Svep1    | 3.287E-02 | 2.61  |
| Pappa    | 2.184E-02 | 2.36  |
| Ptprd    | 2.749E-02 | 2.61  |
| Aqp7     | 3.250E-02 | 0.50  |
| Aqp3     | 3.482E-02 | 0.62  |
| Car9     | 5.578E-03 | 0.46  |
| Npr2     | 3.549E-03 | 2.59  |
| Glipr2   | 1.587E-02 | 3.43  |
| Ak4      | 3.367E-02 | 0.59  |
| B4galt2  | 1.940E-02 | 1.63  |
| Ttc39a   | 4.473E-02 | 0.60  |
| Pdpn     | 2.350E-02 | 3.54  |
| Gpx7     | 1.585E-02 | 2.77  |
| Podn     | 9.366E-03 | 4.36  |
| Ptch2    | 2.666E-02 | 0.56  |
| Hspg2    | 1.353E-02 | 1.84  |
| Fabp3    | 1.278E-03 | 5.05  |
| Adc      | 2.210E-02 | 1.70  |
| Trim63   | 9.768E-04 | 17.04 |
| Hgf      | 1.302E-03 | 3.54  |
| Cdk14    | 1.333E-02 | 2.43  |
| Slc2a5   | 2.001E-02 | 0.46  |
| Mmp23    | 2.715E-02 | 2.61  |
| Mxra8    | 4.167E-03 | 4.35  |
| Cd38     | 2.414E-02 | 2.21  |
| Htra3    | 3.625E-02 | 3.43  |
| Ppp2r2c  | 2.925E-02 | 0.13  |
| Emilin1  | 1.260E-02 | 3.65  |
| Mapre3   | 1.044E-02 | 0.54  |
| Fam114a1 | 2.100E-02 | 1.80  |



|            |           |       |
|------------|-----------|-------|
| Pdgfra     | 7.547E-03 | 5.61  |
| Stap1      | 3.445E-02 | 1.81  |
| Fam69a     | 3.435E-02 | 0.58  |
| Gbp9       | 3.247E-02 | 2.42  |
| Abcg3      | 4.983E-03 | 2.38  |
| Sparcl1    | 3.321E-03 | 2.30  |
| Hsd17b11   | 2.249E-02 | 2.60  |
| Pf4        | 3.925E-02 | 4.62  |
| P2rx4      | 1.974E-02 | 2.02  |
| Lfng       | 3.080E-02 | 1.53  |
| Oas1b      | 3.673E-02 | 0.61  |
| 6330406115 | 2.290E-02 | 2.62  |
| Tfpi2      | 1.136E-02 | 3.49  |
| Eln        | 1.034E-02 | 6.63  |
| Lmod2      | 3.751E-03 | 9.32  |
| Pcolce     | 8.552E-03 | 3.33  |
| Herc3      | 7.344E-03 | 0.65  |
| Gpnmb      | 4.607E-02 | 5.83  |
| Hoxa1      | 4.266E-02 | 0.62  |
| Ephb6      | 1.457E-02 | 0.55  |
| Prdm5      | 9.215E-03 | 2.55  |
| Clec5a     | 4.161E-02 | 2.78  |
| Wdr54      | 6.544E-03 | 0.60  |
| Gm20696    | 3.801E-02 | 0.59  |
| Gxylt2     | 4.632E-02 | 2.35  |
| Slc41a3    | 2.215E-02 | 1.69  |
| Itpr1      | 3.719E-02 | 1.55  |
| A2m        | 3.121E-02 | 50.85 |
| Mfap5      | 3.822E-02 | 9.87  |
| Zfp248     | 4.340E-02 | 0.65  |
| Clec4a2    | 2.842E-03 | 3.25  |
| Klra2      | 4.944E-02 | 2.28  |
| Art4       | 3.962E-02 | 0.52  |
| Mgp        | 8.881E-03 | 5.51  |
| Ptpro      | 3.860E-02 | 2.26  |
| Kcnj8      | 1.066E-02 | 2.47  |
| Abcc9      | 9.933E-03 | 2.27  |
| Sspn       | 2.935E-02 | 2.58  |
| Lrmp       | 2.734E-02 | 2.34  |
| Camk1      | 4.637E-02 | 1.96  |
| Caprin2    | 6.755E-03 | 0.58  |
| Tspan11    | 3.560E-03 | 3.27  |
| Ckm        | 2.440E-02 | 8.31  |
| Rtn2       | 8.820E-03 | 2.26  |
| Dmpk       | 6.528E-03 | 2.11  |
| Lilra6     | 2.495E-02 | 3.42  |
| Csrp3      | 7.386E-03 | 49.70 |
| Tarsl2     | 1.038E-02 | 0.59  |
| Nr2f2      | 9.493E-03 | 1.99  |



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|-----------|-----------|-------|
| Rab38     | 3.303E-02 | 0.64  |
| Tyrobp    | 4.200E-02 | 3.16  |
| Ryr1      | 3.368E-03 | 11.61 |
| Pde3b     | 3.827E-02 | 2.46  |
| Mylpf     | 1.284E-02 | 10.28 |
| Coro1a    | 4.291E-02 | 2.17  |
| Atp2a1    | 2.459E-02 | 10.48 |
| Slco2b1   | 1.322E-02 | 2.22  |
| Myo7a     | 1.685E-02 | 2.69  |
| Dkk3      | 9.093E-03 | 2.13  |
| Tgfb1i1   | 3.511E-02 | 1.87  |
| Cox6a2    | 4.983E-03 | 11.37 |
| Rgs10     | 3.689E-02 | 1.94  |
| 2010110P0 | 4.157E-02 | 4.71  |
| Art1      | 3.703E-03 | 9.51  |
| Usp11     | 1.456E-02 | 1.92  |
| Mrgprf    | 3.505E-02 | 2.35  |
| Ano1      | 1.582E-02 | 0.55  |
| Tnni2     | 5.894E-03 | 6.91  |
| Sash3     | 4.247E-02 | 2.10  |
| Arhgef6   | 3.783E-02 | 2.23  |
| Ccdc120   | 3.784E-02 | 0.66  |
| Stard8    | 3.379E-02 | 2.65  |
| Sh3bgrl   | 1.083E-02 | 2.18  |
| Srpx2     | 1.394E-02 | 2.93  |
| Btk       | 1.983E-02 | 2.15  |
| Itgb1bp2  | 2.428E-02 | 1.85  |
| Gpm6b     | 9.357E-03 | 3.14  |
| Bgn       | 9.851E-03 | 5.43  |
| Abcd1     | 2.774E-02 | 1.77  |
| Renbp     | 1.288E-02 | 3.14  |
| Adprhl1   | 8.307E-03 | 12.32 |
| Rasa3     | 3.860E-02 | 1.55  |
| Myom2     | 4.070E-03 | 21.36 |
| Gpr124    | 3.017E-02 | 2.11  |
| Asb5      | 3.695E-03 | 30.98 |
| Dlc1      | 2.336E-02 | 1.71  |
| Plat      | 4.706E-02 | 1.94  |
| Slit2     | 5.406E-03 | 5.30  |
| Fgfr1     | 1.393E-02 | 2.13  |
| Pdgfrl    | 6.124E-03 | 4.01  |
| Hpgd      | 3.143E-02 | 0.39  |
| Sorbs2    | 4.936E-04 | 2.18  |
| MIlf1ip   | 1.963E-02 | 0.59  |
| Pdlim3    | 3.410E-03 | 25.41 |
| Adcy7     | 1.858E-02 | 2.46  |
| Cdh11     | 2.336E-02 | 2.81  |
| Hp        | 1.502E-02 | 5.66  |
| Mmp2      | 8.554E-03 | 4.60  |



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|----------|-----------|-------|
| Tmem38a  | 2.419E-02 | 2.07  |
| Lpar2    | 6.111E-03 | 0.48  |
| Cmtm3    | 2.081E-02 | 2.26  |
| Pla2g15  | 3.173E-02 | 2.04  |
| Vstm5    | 8.447E-04 | 0.41  |
| Bmper    | 2.087E-02 | 5.85  |
| Jam3     | 9.766E-03 | 1.94  |
| Pdgfd    | 9.372E-03 | 2.03  |
| Oaf      | 2.561E-02 | 2.00  |
| Clmp     | 3.711E-02 | 3.06  |
| Pou2af1  | 1.933E-02 | 4.46  |
| Cryab    | 1.512E-02 | 4.08  |
| Cadm1    | 4.104E-02 | 0.60  |
| Tagln    | 5.007E-03 | 3.75  |
| Bace1    | 4.496E-02 | 1.66  |
| Mcam     | 4.607E-03 | 1.68  |
| Olfm2    | 6.901E-03 | 0.36  |
| Kank2    | 2.925E-02 | 1.82  |
| Nnmt     | 1.565E-02 | 2.28  |
| Al118078 | 3.936E-03 | 0.40  |
| Pstpip1  | 3.307E-02 | 1.74  |
| Stra6    | 1.295E-02 | 3.56  |
| Col12a1  | 2.966E-02 | 2.48  |
| Loxl1    | 1.301E-02 | 4.34  |
| Lrrc1    | 1.079E-02 | 0.57  |
| Adamts7  | 8.189E-03 | 2.88  |
| Zic1     | 7.101E-03 | 4.23  |
| Car12    | 4.587E-02 | 0.67  |
| Tgfbr2   | 4.908E-02 | 1.61  |
| Clstn2   | 1.368E-02 | 2.76  |
| Pth1r    | 2.291E-02 | 2.94  |
| Nudt16   | 4.280E-02 | 2.72  |
| Pygm     | 2.981E-02 | 5.43  |
| Lmo2     | 2.155E-02 | 1.70  |
| Trib3    | 2.336E-02 | 0.62  |
| Gng11    | 1.172E-02 | 2.22  |
| Arap1    | 2.732E-02 | 2.04  |
| Pfkm     | 1.779E-02 | 2.14  |
| Rnf125   | 1.873E-02 | 1.97  |
| Podxl2   | 3.219E-02 | 1.87  |
| Myh2     | 2.694E-02 | 27.04 |
| Rac2     | 3.077E-02 | 2.36  |
| Ptprm    | 1.072E-02 | 1.65  |
| Gstt2    | 1.240E-02 | 2.04  |
| Palmd    | 2.281E-02 | 0.62  |
| Armxcx2  | 1.774E-02 | 1.65  |
| BC026585 | 2.895E-03 | 3.06  |
| Angptl1  | 2.515E-02 | 2.49  |
| Apol6    | 2.769E-02 | 2.64  |



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|------------|-----------|-------|
| Ndn        | 9.263E-03 | 4.22  |
| Stard9     | 1.838E-02 | 1.88  |
| Adra2a     | 4.371E-02 | 2.58  |
| Tlr13      | 2.336E-02 | 3.08  |
| Tpsb2      | 2.132E-02 | 2.22  |
| Ppargc1b   | 8.104E-03 | 0.57  |
| Fgd5       | 2.412E-02 | 2.03  |
| Wbscr17    | 1.649E-02 | 3.85  |
| Lyl1       | 4.538E-02 | 2.52  |
| Phka1      | 3.188E-02 | 1.79  |
| Tpst1      | 3.941E-02 | 1.64  |
| Loxl2      | 7.410E-03 | 3.05  |
| Batf       | 3.747E-02 | 1.85  |
| Pkd2       | 1.937E-02 | 1.70  |
| Scara3     | 3.239E-02 | 4.93  |
| Zfp418     | 4.715E-02 | 0.62  |
| Exph5      | 9.086E-03 | 0.59  |
| Chst11     | 4.723E-02 | 2.28  |
| Cd300ld    | 3.746E-02 | 2.30  |
| Dbn1       | 1.200E-02 | 2.09  |
| Ttyh2      | 2.624E-02 | 1.85  |
| Dgkh       | 1.508E-02 | 2.05  |
| Scn7a      | 2.898E-02 | 6.51  |
| Plvap      | 2.579E-03 | 1.96  |
| Filip1     | 7.203E-03 | 2.26  |
| Ccl5       | 2.257E-02 | 3.24  |
| Eef2k      | 1.537E-02 | 0.62  |
| Egln3      | 1.829E-02 | 0.55  |
| Fam5c      | 3.660E-02 | 72.41 |
| Abi3bp     | 7.367E-03 | 5.11  |
| Pkig       | 5.024E-03 | 1.64  |
| Ssc5d      | 1.229E-02 | 3.71  |
| Pdzrn3     | 4.600E-03 | 3.46  |
| 4930524J08 | 2.812E-02 | 0.39  |
| Dok3       | 4.878E-02 | 1.68  |
| Usp35      | 8.555E-04 | 1.63  |
| Acta2      | 7.783E-03 | 2.68  |
| Zfp57      | 1.458E-03 | 1.73  |
| Adamtsl2   | 4.565E-02 | 0.51  |
| Colec12    | 1.272E-02 | 2.20  |
| Prickle1   | 8.548E-03 | 1.76  |
| Ska1       | 1.712E-02 | 0.59  |
| Igfbp7     | 6.791E-03 | 2.70  |
| P2ry12     | 1.918E-02 | 2.11  |
| Csgalnact1 | 2.236E-02 | 1.72  |
| Arsi       | 2.923E-02 | 2.92  |
| Phpt1      | 1.173E-02 | 0.66  |
| Adamts2    | 1.367E-02 | 2.91  |
| Fxyd1      | 1.170E-02 | 4.25  |



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|------------|-----------|-------|
| H2-Aa      | 3.862E-02 | 2.21  |
| Klhl13     | 7.719E-03 | 6.78  |
| Amdhd2     | 2.316E-02 | 1.60  |
| Lpar3      | 3.779E-02 | 0.36  |
| BC053749   | 3.726E-02 | 0.54  |
| C1qa       | 3.940E-02 | 3.53  |
| C1qc       | 2.787E-02 | 3.64  |
| C1qb       | 2.682E-02 | 3.70  |
| Unc93b1    | 1.330E-02 | 3.17  |
| Asap3      | 3.194E-02 | 1.55  |
| Xpnpep2    | 2.843E-02 | 0.36  |
| Lrg1       | 2.588E-02 | 2.74  |
| Islr       | 2.677E-02 | 4.19  |
| Fgf2       | 8.072E-04 | 3.83  |
| Ovol2      | 2.368E-02 | 0.44  |
| Traf3ip3   | 2.697E-02 | 1.99  |
| Enpp1      | 1.589E-02 | 4.54  |
| Tbc1d2b    | 3.669E-02 | 1.55  |
| Cdkn1c     | 3.256E-02 | 2.24  |
| Fermt2     | 8.687E-03 | 2.62  |
| Darc       | 3.009E-02 | 2.05  |
| Wnk2       | 2.602E-02 | 0.46  |
| Fkbp14     | 2.464E-02 | 2.11  |
| Hspb2      | 2.818E-04 | 4.02  |
| AW551984   | 2.187E-02 | 8.60  |
| 5033430115 | 7.761E-03 | 0.50  |
| Spon1      | 7.159E-03 | 4.01  |
| Leprel1    | 2.724E-03 | 0.49  |
| Pde4dip    | 2.672E-02 | 1.61  |
| Scarf1     | 7.294E-03 | 1.80  |
| Hrc        | 9.568E-03 | 5.07  |
| Bcl9       | 4.343E-03 | 0.65  |
| Atg9b      | 2.063E-02 | 1.51  |
| Hfe2       | 6.350E-03 | 9.75  |
| Egr1       | 1.916E-02 | 0.61  |
| Dennd2a    | 4.458E-02 | 2.37  |
| Olfml2b    | 1.009E-02 | 3.16  |
| Rgs4       | 2.401E-02 | 1.98  |
| BC028528   | 1.261E-02 | 1.78  |
| Tm6sf1     | 1.443E-02 | 1.85  |
| Lpar1      | 1.611E-02 | 4.78  |
| Mybpc2     | 3.217E-02 | 9.56  |
| Akap2      | 7.798E-03 | 1.82  |
| Alpk3      | 2.666E-03 | 13.11 |
| Gngt2      | 3.290E-02 | 2.32  |
| Plcl2      | 3.984E-02 | 1.91  |
| 1700019L01 | 3.159E-02 | 0.60  |
| Tlr4       | 3.355E-02 | 2.43  |
| Pgcp       | 4.167E-02 | 2.37  |



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|------------|-----------|-------|
| St6galnac5 | 2.588E-02 | 3.29  |
| F13a1      | 4.932E-02 | 5.47  |
| Itga9      | 1.026E-02 | 2.37  |
| Prune2     | 2.291E-02 | 2.50  |
| Daglb      | 4.100E-02 | 1.66  |
| Rpl39l     | 2.195E-02 | 2.75  |
| Isg20      | 3.783E-02 | 0.51  |
| Rftn1      | 1.941E-02 | 2.63  |
| Atp6v0e2   | 3.791E-02 | 2.57  |
| Synpo2l    | 7.675E-03 | 31.21 |
| Neil3      | 3.507E-02 | 0.65  |
| Prrx2      | 2.387E-02 | 2.02  |
| Ncam1      | 1.778E-02 | 3.29  |
| Cpeb3      | 7.923E-03 | 0.55  |
| Capsl      | 3.011E-03 | 0.36  |
| Ldb2       | 2.549E-04 | 2.19  |
| Dock3      | 3.467E-02 | 0.38  |
| Dnajc28    | 7.193E-03 | 0.65  |
| Lrrc17     | 2.195E-02 | 2.44  |
| Txlnb      | 9.331E-03 | 3.44  |
| Fgl2       | 1.062E-02 | 3.03  |
| Pik3cd     | 4.778E-02 | 2.17  |
| Dtx4       | 8.609E-03 | 2.98  |
| Cacna2d1   | 9.155E-03 | 3.40  |
| Gpr176     | 8.898E-03 | 3.19  |
| Ndufa4l2   | 4.215E-02 | 0.50  |
| Plekha4    | 1.184E-02 | 2.20  |
| Ppp1r15a   | 1.829E-02 | 0.65  |
| Tlr8       | 3.232E-02 | 4.23  |
| C3ar1      | 2.078E-02 | 3.27  |
| Rundc3b    | 2.151E-02 | 0.28  |
| Cd79b      | 3.679E-02 | 2.87  |
| Bace2      | 1.328E-02 | 0.55  |
| Apobec2    | 1.049E-02 | 5.04  |
| Limd2      | 4.813E-02 | 1.60  |
| St8sia4    | 1.284E-02 | 1.82  |
| Rcsd1      | 1.268E-02 | 2.05  |
| Eml2       | 2.299E-02 | 0.54  |
| Plekhh2    | 2.454E-02 | 1.89  |
| Cables1    | 2.257E-02 | 0.55  |
| Trim62     | 1.535E-02 | 0.53  |
| Pif1       | 1.523E-02 | 0.66  |
| Chrnbl     | 4.536E-02 | 1.90  |
| Cldn5      | 9.969E-03 | 1.57  |
| Smpx       | 6.328E-03 | 19.05 |
| Fmod       | 2.157E-02 | 4.14  |
| Prelp      | 4.628E-02 | 3.13  |
| Klf8       | 4.829E-02 | 0.57  |
| Pnpla3     | 2.682E-02 | 0.39  |



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|-----------|-----------|-------|
| Amot      | 9.487E-03 | 2.55  |
| Rasl12    | 9.774E-03 | 3.33  |
| 1810011H1 | 2.991E-02 | 2.81  |
| Abca9     | 2.236E-02 | 4.36  |
| Abca8a    | 4.635E-02 | 3.94  |
| Shisa4    | 1.556E-03 | 4.80  |
| Dlx1      | 3.111E-02 | 0.49  |
| Mfsd9     | 3.133E-02 | 0.63  |
| Sln       | 4.127E-03 | 41.11 |
| Uggt2     | 3.228E-02 | 1.80  |
| Rassf4    | 4.602E-02 | 2.22  |
| Cmklr1    | 3.900E-02 | 3.34  |
| Lyn       | 1.125E-02 | 2.59  |
| Tmc7      | 4.841E-02 | 0.65  |
| Cilp      | 1.185E-02 | 13.78 |
| Itga1     | 1.382E-02 | 2.37  |
| Ctf1      | 2.503E-02 | 0.49  |
| Gjb5      | 2.261E-02 | 0.47  |
| Gjb3      | 3.830E-02 | 0.48  |
| Esm1      | 4.134E-02 | 0.56  |
| Mfap4     | 4.691E-02 | 3.58  |
| Mybph     | 1.643E-02 | 5.29  |
| Mustn1    | 1.245E-03 | 8.65  |
| Hirip3    | 3.511E-02 | 0.63  |
| Pbxip1    | 2.052E-02 | 2.38  |
| 1700015E1 | 1.812E-02 | 0.48  |
| Gpr153    | 2.017E-02 | 2.31  |
| Hecw2     | 8.426E-05 | 0.61  |
| Gpr151    | 1.917E-02 | 0.53  |
| Snai1     | 1.496E-03 | 3.25  |
| Trim72    | 9.787E-03 | 3.13  |
| D0H4S114  | 4.467E-02 | 2.62  |
| Abra      | 3.525E-02 | 3.67  |
| Klhl6     | 7.779E-03 | 1.58  |
| Il17re    | 4.145E-02 | 0.56  |
| Hic1      | 1.352E-02 | 3.06  |
| C030030A0 | 4.676E-02 | 0.43  |
| B3galnt1  | 2.784E-02 | 4.64  |
| Pcdhb19   | 4.129E-03 | 0.52  |
| Gimap5    | 2.934E-02 | 1.96  |
| Kcns3     | 2.247E-02 | 0.53  |
| Gm14492   | 1.745E-02 | 2.79  |
| Clec4a3   | 8.212E-03 | 3.26  |
| S1pr2     | 4.259E-02 | 1.52  |
| Naalad2   | 9.993E-03 | 2.27  |
| Tmem20    | 4.633E-02 | 0.66  |
| Proca1    | 9.404E-03 | 0.65  |
| Gpr146    | 4.044E-02 | 1.65  |
| Nhlrc1    | 2.733E-02 | 0.62  |



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|-----------|-----------|-------|
| Il20rb    | 4.331E-02 | 0.57  |
| Ctla2a    | 2.356E-04 | 2.04  |
| Dsg2      | 1.259E-02 | 0.53  |
| Camsap3   | 2.754E-02 | 0.61  |
| Tlr7      | 3.930E-02 | 2.41  |
| Dnd1      | 9.022E-03 | 0.64  |
| Cnrip1    | 1.081E-02 | 3.15  |
| AF251705  | 4.180E-02 | 2.88  |
| Tlr1      | 8.002E-03 | 2.41  |
| Fbxo48    | 2.031E-03 | 0.53  |
| S1pr1     | 3.648E-03 | 1.79  |
| Lhfpl2    | 2.041E-02 | 3.70  |
| Niacr1    | 4.544E-03 | 0.56  |
| A930002H2 | 1.168E-02 | 0.50  |
| Col27a1   | 4.997E-02 | 2.34  |
| Adrb2     | 3.756E-03 | 0.40  |
| Zswim3    | 6.834E-03 | 0.67  |
| Serpinb9  | 3.416E-02 | 1.84  |
| Clec14a   | 1.136E-04 | 1.62  |
| Sdpr      | 4.452E-03 | 1.94  |
| C2cd2     | 2.163E-02 | 0.64  |
| Fam26f    | 3.358E-02 | 2.92  |
| Pcdhb20   | 1.625E-02 | 0.59  |
| Pilra     | 2.578E-02 | 2.57  |
| Ankle1    | 8.750E-03 | 0.59  |
| Al464131  | 5.329E-03 | 0.61  |
| Ccbe1     | 4.478E-03 | 3.80  |
| C1qtnf2   | 4.544E-02 | 2.39  |
| Fam43a    | 4.797E-02 | 0.66  |
| Cxxc5     | 1.040E-02 | 1.77  |
| Tifa      | 2.078E-02 | 1.81  |
| Gprc5a    | 3.291E-02 | 0.38  |
| Rhoj      | 8.429E-03 | 2.61  |
| Mpeg1     | 2.404E-02 | 4.12  |
| C230030NC | 4.773E-02 | 0.63  |
| Kcne4     | 5.693E-03 | 4.14  |
| Cmya5     | 5.504E-03 | 10.03 |
| Rnf152    | 2.083E-02 | 0.49  |
| Adamts12  | 4.250E-02 | 2.58  |
| Fbxo40    | 2.533E-02 | 3.54  |
| Rnf150    | 4.990E-02 | 2.30  |
| A4galt    | 1.097E-02 | 2.05  |
| 4933428G2 | 4.609E-02 | 0.66  |
| Prrg1     | 1.927E-02 | 2.00  |
| Zfp473    | 4.725E-02 | 0.63  |
| Entpd1    | 2.620E-02 | 1.93  |
| Col6a3    | 2.513E-02 | 4.10  |
| Rnf149    | 2.893E-02 | 1.64  |
| Bcl11b    | 3.191E-02 | 0.58  |



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|------------|-----------|-------|
| Sacs       | 2.330E-02 | 1.71  |
| Lhfp       | 1.755E-02 | 2.62  |
| Pcdhb18    | 3.433E-02 | 0.53  |
| F2r        | 2.394E-02 | 2.18  |
| Gli2       | 4.973E-02 | 0.63  |
| Amica1     | 2.438E-02 | 2.39  |
| Tmem252    | 3.147E-03 | 1.99  |
| Gm9828     | 3.979E-02 | 0.62  |
| Gm6377     | 4.106E-02 | 1.81  |
| Arhgap30   | 1.882E-02 | 2.13  |
| 2810453I06 | 1.865E-02 | 0.50  |
| Efna5      | 1.500E-02 | 0.51  |
| Clec4a1    | 8.407E-03 | 2.41  |
| Armxc3     | 9.547E-03 | 2.64  |
| Ccr2       | 1.281E-02 | 2.58  |
| C5ar1      | 3.236E-02 | 2.85  |
| Nrap       | 4.326E-03 | 23.48 |
| Rgag4      | 6.623E-03 | 2.97  |
| Iba57      | 1.106E-02 | 0.62  |
| Lix1l      | 7.861E-03 | 2.27  |
| Fut4       | 1.133E-02 | 2.49  |
| Tifab      | 4.485E-02 | 2.55  |
| Armxc4     | 3.988E-03 | 1.71  |
| Fam161a    | 4.930E-02 | 1.66  |
| Arl4c      | 3.521E-02 | 2.15  |
| Rasl11b    | 1.528E-02 | 2.07  |
| Lrrc4      | 1.143E-02 | 0.46  |
| Lrrc25     | 1.725E-02 | 2.83  |
| Grem2      | 9.064E-03 | 2.65  |
| Synpo2     | 8.573E-03 | 3.05  |
| Prokr2     | 2.960E-02 | 2.98  |
| Vstm4      | 3.416E-02 | 2.62  |
| Plekho2    | 4.065E-02 | 2.50  |
| Cdr2l      | 1.940E-02 | 1.88  |
| Olfml1     | 1.281E-02 | 5.01  |
| Gprc5c     | 1.725E-02 | 5.97  |
| Mb21d2     | 2.193E-02 | 0.65  |
| Cited1     | 8.408E-03 | 0.20  |
| Msrb3      | 5.783E-03 | 2.62  |
| Cacna1c    | 1.737E-02 | 2.33  |
| Flrt3      | 1.391E-02 | 0.54  |
| Siglech    | 4.545E-02 | 1.80  |
| Wdfy4      | 3.835E-02 | 2.85  |
| Senp8      | 2.475E-02 | 0.64  |
| Kctd14     | 3.578E-02 | 0.36  |
| Ttn        | 7.374E-03 | 19.48 |
| Pld4       | 8.772E-03 | 2.97  |
| Gm13476    | 7.370E-03 | 2.63  |
| Fpr2       | 2.790E-02 | 3.60  |



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|-----------|-----------|-------|
| Doc2a     | 1.985E-02 | 0.61  |
| Actn2     | 7.466E-03 | 19.04 |
| Lrrc33    | 2.340E-02 | 2.69  |
| Epha3     | 1.457E-02 | 7.99  |
| Zfp608    | 1.365E-02 | 2.31  |
| 4833418N1 | 2.751E-02 | 0.51  |
| 1700030K0 | 2.644E-02 | 0.61  |
| Prkg1     | 1.335E-02 | 2.59  |
| Clec12a   | 2.085E-03 | 2.91  |
| Fes       | 3.383E-02 | 1.88  |
| Tnfaip6   | 4.611E-02 | 2.84  |
| Cnn3      | 2.018E-02 | 2.22  |
| A930004D1 | 2.202E-03 | 0.54  |
| 4930517O1 | 1.161E-02 | 0.35  |
| Adam12    | 1.941E-02 | 2.91  |
| Gm9949    | 1.884E-03 | 0.45  |
| Mettl7a1  | 4.502E-02 | 0.54  |
| Slc8a1    | 2.454E-02 | 2.31  |
| Mmrn1     | 4.290E-02 | 2.92  |
| Ano9      | 4.206E-02 | 0.48  |
| Tmem119   | 2.270E-02 | 2.20  |
| Zfp174    | 5.321E-04 | 0.57  |
| 9130008F2 | 2.002E-02 | 0.64  |
| Smyd1     | 1.340E-03 | 6.81  |
| Tns1      | 4.228E-02 | 1.70  |
| Zcchc24   | 8.384E-03 | 2.42  |
| Lair1     | 1.506E-02 | 2.52  |
| Gpc3      | 3.431E-02 | 3.10  |
| Tmem191c  | 2.363E-03 | 0.65  |
| Myh8      | 4.344E-02 | 13.17 |
| Tmem150a  | 2.317E-02 | 1.53  |
| Skint4    | 4.901E-02 | 0.54  |
| Irs1      | 4.349E-02 | 1.96  |
| B4galt6   | 1.935E-02 | 1.99  |
| Col8a2    | 1.940E-02 | 3.81  |
| Snx32     | 3.754E-02 | 1.86  |
| Ms4a4b    | 2.283E-02 | 2.17  |
| Myh1      | 9.446E-03 | 22.85 |
| Slit3     | 1.812E-02 | 2.75  |
| Cd248     | 3.254E-02 | 2.34  |
| Gpr116    | 7.960E-03 | 1.57  |
| Apol8     | 1.380E-02 | 0.43  |
| Gulp1     | 3.897E-02 | 2.22  |
| Usp13     | 5.164E-03 | 3.57  |
| Ebf1      | 4.676E-03 | 3.47  |
| Gja5      | 9.263E-03 | 1.98  |
| AB124611  | 3.101E-02 | 2.74  |
| Mettl15   | 4.314E-02 | 0.65  |
| Cep170    | 2.202E-02 | 1.55  |



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| Lmcd1      | 2.020E-03 | 4.18  |
| Pkn1       | 1.914E-02 | 2.24  |
| Vmn1r53    | 2.797E-02 | 8.38  |
| Sh3rf2     | 3.243E-02 | 0.52  |
| Ankrd29    | 3.122E-02 | 0.57  |
| Camk2b     | 3.346E-03 | 4.76  |
| Cacnb2     | 4.798E-02 | 0.64  |
| Gpc6       | 1.863E-02 | 3.01  |
| Fcer1g     | 2.155E-02 | 3.48  |
| Lilrb3     | 2.918E-02 | 3.86  |
| C1qtnf3    | 9.543E-03 | 3.41  |
| Rad51l1    | 2.382E-02 | 0.59  |
| Fcgr4      | 1.972E-02 | 4.85  |
| Ifitm6     | 3.620E-02 | 2.37  |
| Pde1a      | 6.162E-03 | 4.74  |
| Gzmd       | 4.341E-02 | 12.37 |
| Actg2      | 3.440E-02 | 1.80  |
| Gm16218    | 8.410E-03 | 0.48  |
| Cdh24      | 1.943E-02 | 0.64  |
| Flot1      | 4.311E-02 | 1.51  |
| Zfp341     | 1.878E-02 | 0.64  |
| Dsc3       | 2.032E-02 | 0.61  |
| Alox5ap    | 2.979E-02 | 2.82  |
| Pyroxd2    | 4.759E-02 | 2.46  |
| Layn       | 3.982E-02 | 2.79  |
| Eno3       | 7.648E-03 | 5.20  |
| Pla2g16    | 8.174E-03 | 2.11  |
| Cd302      | 1.211E-02 | 2.91  |
| Gmfg       | 2.338E-02 | 3.09  |
| AI597468   | 2.960E-02 | 1.52  |
| Mcpt4      | 1.819E-02 | 2.44  |
| Myl4       | 3.376E-02 | 11.64 |
| Cxcl12     | 2.896E-02 | 5.50  |
| Obecn      | 3.902E-03 | 13.96 |
| C1qtnf7    | 7.397E-03 | 4.19  |
| Tnnt3      | 6.777E-03 | 12.76 |
| Myl1       | 3.801E-03 | 16.23 |
| Trim54     | 2.688E-03 | 19.72 |
| Hs6st2     | 3.620E-02 | 2.46  |
| Cav3       | 7.579E-03 | 26.49 |
| A430107O1  | 6.791E-03 | 3.80  |
| Msln       | 2.053E-02 | 19.26 |
| Kcnma1     | 9.113E-03 | 12.25 |
| Bcl9l      | 1.906E-02 | 0.66  |
| Ube2d2b    | 1.181E-02 | 0.59  |
| 1700112E0  | 8.944E-03 | 2.30  |
| 2010109I03 | 3.221E-02 | 0.44  |
| Jazf1      | 1.263E-02 | 0.64  |
| Ccdc102a   | 1.385E-02 | 2.39  |



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| Gm10134    | 3.550E-02 | 3.06  |
| Fbln2      | 2.230E-02 | 2.85  |
| Rhox8      | 9.245E-04 | 0.61  |
| Gimap8     | 1.779E-02 | 1.51  |
| mt-Rnr1    | 3.557E-02 | 0.49  |
| Sepp1      | 4.021E-02 | 3.63  |
| n-R5s40    | 4.401E-02 | 0.17  |
| SNORA2     | 3.001E-02 | 2.53  |
| U6         | 1.117E-02 | 0.00  |
| Tacc1      | 1.283E-02 | 2.05  |
| Pilrb2     | 1.826E-02 | 2.05  |
| Pilrb1     | 1.732E-02 | 2.26  |
| Fxyd6      | 1.090E-02 | 3.53  |
| Hmcn1      | 1.456E-02 | 2.67  |
| Serpinb7   | 4.843E-02 | 0.33  |
| Ppp1r3c    | 8.040E-04 | 10.27 |
| Ankrd23    | 2.056E-03 | 4.92  |
| Lpar5      | 6.011E-03 | 0.64  |
| Myl9       | 5.872E-03 | 2.74  |
| Pex26      | 1.944E-03 | 0.58  |
| Cst7       | 3.034E-02 | 1.68  |
| Col8a1     | 9.780E-03 | 3.19  |
| MacroD2    | 4.356E-02 | 0.58  |
| Lgals1     | 8.879E-03 | 3.58  |
| Dok1       | 3.075E-02 | 2.15  |
| Actc1      | 2.814E-02 | 7.62  |
| Myoz1      | 1.897E-02 | 7.13  |
| Flnc       | 3.878E-03 | 9.30  |
| Il3ra      | 3.011E-02 | 1.82  |
| Gm128      | 6.673E-03 | 0.60  |
| Cd300lh    | 9.519E-03 | 3.43  |
| Gm11710    | 2.760E-02 | 3.22  |
| Tmem100    | 1.127E-02 | 5.36  |
| B3gnt9-ps  | 3.166E-02 | 1.51  |
| Prss36     | 3.089E-02 | 0.65  |
| Gm9696     | 4.132E-02 | 0.47  |
| 1700029J07 | 1.463E-02 | 0.45  |
| Mboat4     | 1.934E-02 | 0.36  |
| Serpina1b  | 1.764E-03 | 3.02  |
| Fam189a2   | 4.409E-02 | 0.59  |
| Gspt2      | 3.968E-02 | 4.82  |
| Ccdc112    | 3.654E-02 | 0.61  |
| Fndc1      | 4.826E-02 | 3.42  |
| Klf12      | 2.880E-02 | 0.49  |
| Gm7489     | 1.681E-02 | 0.58  |
| Myo18b     | 2.911E-03 | 12.42 |
| Sod3       | 1.459E-02 | 11.26 |
| Vamp5      | 3.635E-03 | 2.26  |
| Nudt11     | 3.312E-02 | 0.41  |



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| Lst1      | 1.593E-02 | 2.13    |
| C4b       | 2.626E-02 | 8.02    |
| Ifi204    | 3.268E-02 | 2.34    |
| Sh3d21    | 3.928E-02 | 0.51    |
| Kbtbd5    | 2.321E-03 | 31.28   |
| 49305200C | 1.268E-03 | 0.63    |
| Ntf5      | 3.386E-02 | 0.63    |
| Cox7a1    | 1.890E-03 | 5.00    |
| Gramd2    | 1.913E-02 | 0.58    |
| Ceacam1   | 3.626E-02 | 2.05    |
| Gm14548   | 2.568E-02 | 3.56    |
| 6430550D2 | 2.359E-02 | 0.61    |
| Foxs1     | 1.967E-02 | 2.84    |
| Hspa12b   | 3.279E-03 | 1.53    |
| Gm14005   | 4.047E-02 | 1.93    |
| BC025920  | 4.926E-02 | 0.66    |
| Ctla2b    | 3.587E-03 | 3.05    |
| Grem1     | 4.060E-03 | 3.64    |
| Fibin     | 6.814E-03 | 13.16   |
| AW112010  | 4.632E-02 | 3.10    |
| Heg1      | 4.195E-02 | 2.00    |
| Gm10818   | 2.568E-02 | 0.61    |
| Wipf1     | 3.783E-02 | 2.34    |
| H60b      | 4.758E-02 | 2.90    |
| Kbtbd10   | 7.816E-03 | 2.93    |
| Gm17151   | 6.950E-03 | 0.46    |
| Gm11545   | 3.543E-02 | 0.43    |
| Selm      | 1.095E-02 | 2.69    |
| Dio3      | 1.980E-02 | 7.86    |
| BC100451  | 4.649E-02 | 1.73    |
| Igkv2-137 | 2.288E-02 | 8.53    |
| Igkv4-70  | 3.987E-02 | 146.48  |
| Igkv6-32  | 4.019E-02 | 10.24   |
| Igkv8-24  | 3.035E-02 | 9.82    |
| Igkv6-20  | 4.914E-02 | 64.12   |
| Igkv3-7   | 3.650E-02 | 4789.12 |
| U1        | 2.934E-02 | 0.00    |
| SNORA17   | 1.552E-02 | 0.00    |
| SNORA42   | 3.120E-02 | 0.37    |
| SNORA58   | 4.061E-02 | 0.08    |
| Snord83b  | 1.750E-02 | 0.09    |
| F630028Q1 | 1.470E-02 | 3.26    |
| Dnm3os    | 8.262E-03 | 3.23    |
| Gm17106   | 3.646E-02 | 0.51    |
| Gm13157   | 2.392E-02 | 2.59    |
| Gm13212   | 5.465E-03 | 2.70    |
| Gm17546   | 4.020E-03 | 0.57    |
| Evi2a     | 2.676E-02 | 2.14    |
| Dact3     | 4.442E-02 | 2.20    |



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| Gm6746    | 4.656E-02 | 0.63   |
| Naip2     | 4.423E-02 | 2.15   |
| Xirp1     | 4.418E-02 | 3.22   |
| Gbp4      | 3.816E-02 | 3.39   |
| Gm3558    | 2.018E-02 | 2.07   |
| Gm5796    | 8.719E-03 | 2.74   |
| Gm2897    | 1.355E-02 | 2.50   |
| Ms4a6c    | 1.531E-02 | 2.33   |
| Tceal7    | 3.288E-02 | 19.13  |
| Nhsl2     | 2.026E-02 | 2.54   |
| Phyhd1    | 3.232E-02 | 2.38   |
| Gm11131   | 4.431E-02 | 0.57   |
| Tmem182   | 3.864E-03 | 34.31  |
| C1qtnf5   | 1.757E-02 | 3.23   |
| Hspa14    | 1.319E-02 | 0.35   |
| Tm4sf19   | 4.151E-02 | 3.73   |
| Rab26     | 4.572E-02 | 0.66   |
| Gm17235   | 2.678E-02 | 0.57   |
| Rps2-ps9  | 3.368E-02 | 0.60   |
| Gm15661   | 2.589E-02 | 0.46   |
| BC022960  | 2.965E-02 | 0.59   |
| Gm11517   | 7.776E-03 | 0.65   |
| Gm12275   | 3.903E-02 | 0.61   |
| Gm16071   | 2.551E-02 | 0.64   |
| Gm15953   | 9.625E-03 | 0.51   |
| Gm16210   | 3.460E-02 | 0.55   |
| Gm14212   | 3.744E-02 | 0.67   |
| Gm12363   | 6.466E-03 | 0.57   |
| Gm12741   | 1.928E-02 | 0.61   |
| Gm14001   | 2.101E-02 | 0.37   |
| Gm12987   | 2.613E-02 | 0.62   |
| Gm13193   | 4.056E-02 | 0.57   |
| Gm15741   | 1.760E-02 | 0.24   |
| Gm12630   | 4.374E-02 | 0.62   |
| Gm12749   | 1.017E-02 | 0.64   |
| Gm15916   | 1.455E-02 | 0.64   |
| Gm11699   | 3.879E-02 | 4.92   |
| Gm13786   | 2.503E-02 | 0.60   |
| Rps10-ps4 | 1.150E-02 | 0.50   |
| Gm14000   | 1.935E-02 | 0.37   |
| SNORA35   | 3.672E-02 | 7.53   |
| U6        | 4.370E-02 | 0.00   |
| Y_RNA     | 1.177E-02 | 128.76 |
| U2        | 2.612E-02 | 0.34   |
| A430104N1 | 3.664E-02 | 2.63   |
| 2610204G0 | 4.219E-02 | 0.58   |
| Gm16278   | 5.446E-03 | 0.62   |
| Gm5724    | 1.062E-02 | 0.22   |
| A430071A1 | 1.890E-02 | 0.62   |



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| Gm15774    | 2.807E-02 | 0.51  |
| C130046K2  | 1.207E-02 | 0.58  |
| Gm10785    | 4.715E-02 | 0.66  |
| 1700064E0  | 2.012E-02 | 0.59  |
| Gm13185    | 2.287E-02 | 0.63  |
| BC046401   | 2.587E-02 | 0.63  |
| 4930430E1  | 2.808E-02 | 1.89  |
| Gm15964    | 2.208E-02 | 0.62  |
| 3010003L2  | 1.020E-02 | 0.60  |
| Gm13480    | 2.206E-02 | 0.65  |
| C530005A1  | 4.217E-02 | 0.67  |
| Gm15736    | 3.983E-02 | 4.67  |
| Gm12158    | 3.900E-02 | 3.19  |
| 1700003G1  | 2.445E-02 | 0.50  |
| Gm14540    | 3.957E-02 | 0.62  |
| Gm12750    | 2.833E-02 | 0.57  |
| Gm15342    | 3.028E-04 | 0.66  |
| Gm13421    | 1.143E-02 | 0.50  |
| Gm16159    | 2.834E-02 | 1.80  |
| 2700033N1  | 3.179E-02 | 0.54  |
| Gm13830    | 4.458E-04 | 0.50  |
| Gm16144    | 1.054E-02 | 0.63  |
| 933016201  | 1.815E-02 | 0.51  |
| Gm11206    | 4.777E-02 | 2.33  |
| Gm15247    | 4.337E-02 | 0.48  |
| B230206HC  | 1.651E-02 | 0.60  |
| Gm16314    | 1.360E-02 | 0.58  |
| Gm13889    | 5.692E-03 | 3.43  |
| 2810442I21 | 2.740E-02 | 0.53  |
| Gm12454    | 9.329E-03 | 0.43  |
| Gm15246    | 1.565E-02 | 0.64  |
| Skint6     | 2.998E-02 | 0.16  |
| Gm16062    | 1.498E-02 | 0.61  |
| Gm15317    | 3.360E-02 | 0.43  |
| Gm16235    | 3.699E-02 | 0.58  |
| Gm13999    | 4.496E-02 | 0.41  |
| Gm13062    | 3.203E-02 | 0.45  |
| Gm13427    | 2.949E-02 | 0.56  |
| C030037D0  | 3.718E-02 | 0.57  |
| Gm11712    | 1.988E-02 | 0.53  |
| 7SK        | 3.163E-02 | 5.38  |
| 7SK        | 5.152E-03 | 0.55  |
| 7SK        | 3.910E-02 | 0.57  |
| U6         | 4.359E-02 | 53.11 |
| 7SK        | 3.663E-03 | 0.40  |
| U6         | 4.048E-02 | 51.85 |
| U1         | 3.872E-02 | 0.35  |
| Cbx6       | 2.104E-02 | 2.41  |
| Gm11711    | 7.818E-03 | 3.20  |



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| Gm4117     | 3.417E-04 | 0.43    |
| Pira2      | 2.166E-02 | 3.87    |
| Gm16137    | 2.966E-03 | 0.58    |
| Gm6921     | 3.990E-02 | 0.54    |
| Gm16161    | 1.618E-02 | 0.46    |
| AU015336   | 5.159E-03 | 0.44    |
| Cfb        | 2.186E-02 | 3.74    |
| Gm4524     | 6.624E-03 | 0.48    |
| Eif4ebp3   | 2.316E-02 | 0.61    |
| Gm6189     | 3.668E-02 | 0.18    |
| F830016B0  | 3.186E-02 | 2.02    |
| Gm17251    | 3.215E-02 | 0.66    |
| 4921509A0  | 2.505E-02 | 0.24    |
| Gm2895     | 5.377E-03 | 0.38    |
| Sco2       | 2.533E-02 | 0.58    |
| Gm17022    | 3.631E-02 | 0.65    |
| E130317F20 | 4.103E-02 | 0.63    |
| BC049352   | 4.247E-02 | 0.52    |
| Gbp11      | 3.971E-02 | 2.47    |
| D030025P2  | 1.907E-02 | 4.24    |
| Gm3696     | 1.325E-02 | 2.46    |
| 4930515G0  | 1.653E-02 | 0.63    |
| Gm20471    | 1.287E-02 | 2.83    |
| Gm20540    | 3.865E-02 | 0.61    |
| Gm19684    | 3.772E-02 | 0.46    |
| 4930518C0  | 4.242E-02 | 3.29    |
| Mir3074-1  | 5.214E-03 | 0.11    |
| Metazoa_S  | 4.924E-02 | 0.16    |
| AC165250.1 | 4.793E-02 | 0.29    |
| Gm20702    | 5.839E-03 | 0.42    |
| Gm20695    | 4.916E-02 | 0.43    |
| Gm20554    | 1.785E-02 | 0.42    |
| Gm20683    | 8.879E-03 | 0.66    |
| EVI2B      | 1.097E-02 | 1.64    |
| Gm10406    | 4.524E-02 | 2.40    |
| AC155333.1 | 4.909E-02 | 19.34   |
| AC153855.1 | 1.164E-02 | 5885.35 |
| AC156953.1 | 1.716E-02 | 6251.60 |
| AC139157.1 | 3.377E-02 | 0.48    |
| AC073565.1 | 4.028E-02 | 9.78    |
| AC122322.1 | 4.175E-02 | 15.20   |
| AL607070.1 | 5.824E-03 | 0.65    |
| AC073561.1 | 2.579E-02 | 63.68   |
| AC160985.1 | 2.095E-02 | 25.45   |
| AC090887.1 | 2.142E-02 | 15.00   |
| AC169518.1 | 4.952E-02 | 2.10    |
| AC151712.1 | 2.615E-02 | 0.32    |
| AC153928.1 | 4.560E-02 | 5629.78 |
| AC073561.2 | 1.515E-02 | 15.23   |



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| AC073939.3 | 2.947E-02 | 5051.87 |
| AC090887.5 | 3.643E-02 | 12.95   |
| Sirpb1a    | 3.184E-02 | 2.54    |
| Ptrhd1     | 3.478E-03 | 0.65    |
| AC090887.7 | 3.758E-02 | 10.55   |
| AC090887.8 | 3.277E-02 | 32.29   |
| AC131065.3 | 4.948E-02 | 0.56    |
| AC160985.6 | 3.468E-02 | 8525.09 |
| AC153928.3 | 4.590E-02 | 39.78   |
| AC073563.9 | 4.575E-02 | 5109.70 |
| AC130841.3 | 4.378E-02 | 0.59    |
| AC156618.3 | 5.339E-03 | 0.64    |
| AC142103.3 | 9.014E-03 | 0.45    |
| AC133646.3 | 1.688E-02 | 0.66    |
| RP23-302C  | 1.871E-02 | 2.06    |
| AC092094.3 | 2.557E-02 | 0.64    |
| CT033751.2 | 2.747E-02 | 0.63    |
| AC148011.3 | 2.063E-02 | 2.47    |
| AC129082.3 | 2.059E-02 | 0.54    |
| AC131692.3 | 4.676E-02 | 0.54    |
| RP24-547D  | 2.804E-03 | 8.42    |
| RP23-111M  | 3.172E-02 | 0.47    |
| AC123834.3 | 4.984E-04 | 0.44    |
| AC108434.3 | 2.595E-02 | 0.59    |
| AL772401.1 | 1.709E-02 | 2.11    |



## Appendix 5.

### GSEA results in transcription factor (TRANSFAC) analysis



mRNA AK-over-NS up-regulated genes, -log10(p-value)  
 mRNA SCCover-AK up-regulated genes, -log10(p-value)  
 mRNA SCCover-NS up-regulated genes, -log10(p-value)  
 mRNA PAP-over-CHR up-regulated genes, -log10(p-value)  
 mRNA SCC-over-CHR up-regulated genes, -log10(p-value)  
 mRNA SCCover-PAP up-regulated genes, -log10(p-value)  
 mRNA AK-over-NS up-regulated genes, -log10(p-value)  
 mRNA SCC-over-NS up-regulated genes, -log10(p-value)

miRNA SCC-over-PAP up-regulated genes







|          |      |      |      |      |      |          |   |                        |  |
|----------|------|------|------|------|------|----------|---|------------------------|--|
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | ADNP, GNAO1, GAPDH, REXO1, KIF15, ERH, AB            |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | REXO1, KIF15, ERH, AB                                |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | M15B, BCL2L13, FZD8, DEAF1, ANAPC10, KLF7            |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | CTB502, MARK3, B3G                                   |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | ALTB, RIF1, ETT1, PAO2                               |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 1, TET2, PIGL, SMYD5, PI                             |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | GV, SART3, INP26, MAT                                |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | ADNP, UBE2J2, KIF15, ERH, KL                         |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | BL, THAP1, NASP, PRDM                                |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | F7, MARR3, B3GAT6, RIF1, EX                          |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 10, TET2, B3GAT6, HOXA2, 26, NATL, PRK3, THAP1, NAS  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | JER2, ZBTB40, HOXA2, 26, NATL, PRK3, THAP1, NAS      |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | SRBP, ABCF1, TOP3A, P, TTPA, C, CND1, ER2, ABCF1     |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | ACCN, MAFK, STX1A, PHF16, A                          |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | NRK013B, USP1, NGF5                                  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | LC23A3, KCOR2, ABNS                                  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | SMOX, GRN12, GRHL3, J, ALOX12, DDC1, SRSF7,          |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | TIMELESS, ZC3H10, DP                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | Y30, DSX3, CTFE1, S9A, GF, RCON2, ABNS, GREM1, OD    |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | T32, DDIT4, STRA6, DAB, C1, C1STN2, SRSF7, CHCHD4,   |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | ZIP, EHF, ENO1, TINKS18, TIMELESS, DP30, TGBR11, B   |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | P1, PHF7, BZBP1, PHL, AGAT12, SPAT12, DDIT4, STRA    |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | SOO3, STRA6, EFEMP2,                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | DB3, FOXN1, METTL8, 6, DAB2P, ENO1, DLL4, DSX3,      |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | RTN2, JPH2, GRG3, LIM                                |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 274, CHCHD4, IL11, LSM, FOXN1, E2F4, CNI1, GRHL2, J  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | D2, TGBR11, PRELP, B4                                |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 12, DLL4, LUN54, RNFI4, L11, LSM12, TGIF1, PHF7, ES  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 6, ALT2, CAV3, C1STN2, J                             |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 5, ESMT, M1, TGBR1P2,                                |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | POLIM4, ACTN3, STAC2                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | MAGEB2, HSPG2, ENP                                   |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | P2, ZIC1, DPVSL2, ANGP                               |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | TL,  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | TIME88, AGR15, IGF1, RVSNL, LINS, EPHA2,             |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | CNTN1, STPL, ANKRD3                                  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 9, KLF12, PRICKLE3, TFA                              |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | PPA, CNE1, HMA5, NB                                  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | TBDB, VARS2, RBN1, A, T                              |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | ESD1A, ACV2B, KPN, JHOK4, CNTN1, ANKRD39, K          |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | BL11BP1, ASCL2, BCL1, LF12, TPA2A, TGIF1, CNE1,      |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 1A, KOC04, NDNL2, JIR, CACNA1C, HAUS, KBTBD, V       |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | ETV1, MTH11, PMIP22,                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 2BR, LEH, HNLI, VEGF, ARS2, NDNL2, TES, CBH5, CIA    |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | MTH1, HSP22, MAGEB                                   |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | A, JARID2, E2F4, PTPN1, SRP, IGF1R, LINS, KCNO4, KPN |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 1, S5GCD, CRYAB, PIA, C                              |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 2, FRS3, BEL12, WNT4, B1, HMGA2, EPHA2, HNLI, VE     |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | ACNA1C, CTGF, AGPAT                                  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | DM6, HES1, PAK6, PTC4, GFA, E2F4, SEMA3F, PTPN12,    |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 4, TTN, MKR48, 50NB                                  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 1, RNFI22, BCL3, ELMO                                |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | FRG5, WNT4, COL12A1, CD6                             |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 3, NFATC4, ZEB1, CXCL                                |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 3, HES1, PAK6, BCL3,                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 4, COL12A1, NR1H3,                                   |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | N, TREF1, SLC6A9, JUN                                |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | BLARID2, BEND4, GEN                                  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 1, BMPRI1B, SCHIP1, SO                               |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | X6, SRSF7, RAVER1, CPN                               |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | E1, PVL1, NR2C2AP, S                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | AMD1, CNOT7, DLX1, J                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | CF7, CEFA, SIRT6, LTB                                |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 1, MRP56, INR43, PGM                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | JUNB, JARID2, GENT, BAPPI                            |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 1, MRP51B, SMITN, CA                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | B, SCIP1, SRSF7, ADAMTS6,                            |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | C, NOD3, WPCAN6                                      |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | NR6A1, CNE1, SPND1, BEN                              |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | SCN7A, STAC2, ANKRD                                  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | A1, CAVK1G, CND1, S                                  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | DA, CEH4, SIRT6, PGM1, LMR                           |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 2, SLC39A3, DPM13, C                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | RNM4, RPA3, PCDH7, Z                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | S18B, PAPA, WPCD, OSBP                               |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | FB, PIGER1, PAPP1, PT                                |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | BTB40, NANO51, HOXA                                  |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | 7, JARVER1, CND1, RPA3, PCD                          |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | PRC2, C1, HOXD8, ANG                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | H7, PTL1, RFXP1,                                     |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | PTG52, PCGF2, ETVA, GI                               |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | N53, GNAO1, SLC6A9, P                                |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | PM1, LARID2, RPA3, W                                 |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU, WDR77, WDR77, GTF2A1, UBR3, HSP | THAP1, TFAM4, HSP98, G | PTG52, LIF, PCGF2, ETVA, GINS                        |
| VSCT1_02 | 2.01 | 1.62 | 2.99 | 4.71 | 2.91 | VSCT1_02 | AT1AAU                                  |                        |  |



|          |      |      |      |      |      |          |   |
|----------|------|------|------|------|------|----------|---|
| VSUSE_01 | 1.90 | 1.54 | 4.39 | 4.87 | 3.65 | VSUSE_01 | GTFTAL, R376, CM2, PR376, OTRTD1, NUDCO1, ST MNI, PRH3, S, KDEL, P SWD11, PPRC1, JARH02, KATZA, POIR, IB, FEN1, GELL1, DDX1, ANKRD1 38, FTS1, PRP4, CDC6, IQGAP3, NFATC2IP, CC DC126, BUB1B, INO80E , SIKP2, CTFL1, BOD1, EXO 1, ZNW10, ZEP1, PAZG4, C MAS, CDC43, GRW0D1, RE2BP1, ESPL1, LUG1, LR RC29, TRC1D08, BNM, CTRTD1, NUDCO1, TMOD3, A UBRN8, SETMAR, KRT8, HCT1, KDEL, C1, PAPR, C1, NFA D8, TPAP4, CYP99A1, B TCIP, JARND2, KATYA, POLR1 R, QUA1, CTB5, G1D2, PRP4 B, FEN1, S1C29A2, BUB1B, K6 0, ATXN1, Z12, BUB3, JMRP T808, PRP4, CDC6, IQGAP3, L19, CDC25A, PRMT6, R CDC126, SAMD12, EXO1, ZF ANGA, P1, PASK, DCUN1 P1, SHMT2, PRIM1, CDC43, G DA, NTH1, WMAP53, S RWD1, ESPL1, LUG1, UBRN8, B UFU, SAMD12, ARV1, H RC41, TFAP4, NOS3, ATXN1, Z12, SFR3, SHMT2, SAMU, BUB3, CDC25A, PRMT6, PRM1 LRV0D1, RNASEH2C, CL T5, WMAP53, SUV1, ARV1, JN P1, PRMT5, DOCK4, PNI O80E, PA2G4, LRWD1, JARD5 M1, PRMT15, DOP1, TM A, CLP1, DCAD, MRP1, 50 PO EMM4, AKR8B, CDC45, P1, TMEM48, CDC45, AKR84 NCCCR, U R15, ZNCR2, WMAP53, CD10, CDC45, RNASEH2A, AKR84, HIRP3, TOP3A, AM168, TOP3A, SPDC2, PP2 , SPDC5, LUC92A, , H55, HIRP3, RASGPR3, FEN1, BPG M, TMEM151B, GNB1L, ITG6, 3P, LUNC2, SNAAR CQ5, SOK5, MAN1, 3, 50 X15, MEIS2, ATXN1, Z12, A NGP1, Z1, FBX1, B, ERBB3, LTRP1, GNB3, EHF, PLA G12, F1R13, CACNA2D3 , ARTX, ENDOU, EGFLN1, PCDH7, CRLS1, HES1, EC HCC2, PPCS, CELF4, RASSF6, CTNNA L1, JER3, ANKRD39, KLF 12, NR6A1, ZH2, CPNE 1, MAB21, 3, PVRL1, JN HBA, COL13A1, HAS2, A 1, JER3, ANKRD39, KLF12, NR6 RTN, BUB1, PRMT6, JMR A1, ZH2, C, GNE1, MAB21, 3, P 95188, HNTL, GPCC2, PO VRL1, H4S2, 4, ARTN, CMG1, OR XN1, TFAP4, FAM20, N C4, PRMT6, MRS158, HNTL, C1, GIPC, FOXN1, TFAP4, FAM2 12, PLAT4, ARHGAP20, GRN1, FLOT1, ANGR1L 1, ZEB2, ZEB1, XIRP1, AM |
| VSUSE_01 | 1.90 | 1.54 | 4.39 | 4.87 | 3.65 | VSUSE_01 | GTFTAL, R376, CM2, PR376, OTRTD1, NUDCO1, ST MNI, PRH3, S, KDEL, P SWD11, PPRC1, JARH02, KATZA, POIR, IB, FEN1, GELL1, DDX1, ANKRD1 38, FTS1, PRP4, CDC6, IQGAP3, NFATC2IP, CC DC126, BUB1B, INO80E , SIKP2, CTFL1, BOD1, EXO 1, ZNW10, ZEP1, PAZG4, C MAS, CDC43, GRW0D1, RE2BP1, ESPL1, LUG1, LR RC29, TRC1D08, BNM, CTRTD1, NUDCO1, TMOD3, A UBRN8, SETMAR, KRT8, HCT1, KDEL, C1, PAPR, C1, NFA D8, TPAP4, CYP99A1, B TCIP, JARND2, KATYA, POLR1 R, QUA1, CTB5, G1D2, PRP4 B, FEN1, S1C29A2, BUB1B, K6 0, ATXN1, Z12, BUB3, JMRP T808, PRP4, CDC6, IQGAP3, L19, CDC25A, PRMT6, R CDC126, SAMD12, EXO1, ZF ANGA, P1, PASK, DCUN1 P1, SHMT2, PRIM1, CDC43, G DA, NTH1, WMAP53, S RWD1, ESPL1, LUG1, UBRN8, B UFU, SAMD12, ARV1, H RC41, TFAP4, NOS3, ATXN1, Z12, SFR3, SHMT2, SAMU, BUB3, CDC25A, PRMT6, PRM1 LRV0D1, RNASEH2C, CL T5, WMAP53, SUV1, ARV1, JN P1, PRMT5, DOCK4, PNI O80E, PA2G4, LRWD1, JARD5 M1, PRMT15, DOP1, TM A, CLP1, DCAD, MRP1, 50 PO EMM4, AKR8B, CDC45, P1, TMEM48, CDC45, AKR84 NCCCR, U R15, ZNCR2, WMAP53, CD10, CDC45, RNASEH2A, AKR84, HIRP3, TOP3A, AM168, TOP3A, SPDC2, PP2 , SPDC5, LUC92A, , H55, HIRP3, RASGPR3, FEN1, BPG M, TMEM151B, GNB1L, ITG6, 3P, LUNC2, SNAAR CQ5, SOK5, MAN1, 3, 50 X15, MEIS2, ATXN1, Z12, A NGP1, Z1, FBX1, B, ERBB3, LTRP1, GNB3, EHF, PLA G12, F1R13, CACNA2D3 , ARTX, ENDOU, EGFLN1, PCDH7, CRLS1, HES1, EC HCC2, PPCS, CELF4, RASSF6, CTNNA L1, JER3, ANKRD39, KLF 12, NR6A1, ZH2, CPNE 1, MAB21, 3, PVRL1, JN HBA, COL13A1, HAS2, A 1, JER3, ANKRD39, KLF12, NR6 RTN, BUB1, PRMT6, JMR A1, ZH2, C, GNE1, MAB21, 3, P 95188, HNTL, GPCC2, PO VRL1, H4S2, 4, ARTN, CMG1, OR XN1, TFAP4, FAM20, N C4, PRMT6, MRS158, HNTL, C1, GIPC, FOXN1, TFAP4, FAM2 12, PLAT4, ARHGAP20, GRN1, FLOT1, ANGR1L 1, ZEB2, ZEB1, XIRP1, AM |
| VSUSE_01 | 1.90 | 1.54 | 4.39 | 4.87 | 3.65 | VSUSE_01 | GTFTAL, R376, CM2, PR376, OTRTD1, NUDCO1, ST MNI, PRH3, S, KDEL, P SWD11, PPRC1, JARH02, KATZA, POIR, IB, FEN1, GELL1, DDX1, ANKRD1 38, FTS1, PRP4, CDC6, IQGAP3, NFATC2IP, CC DC126, BUB1B, INO80E , SIKP2, CTFL1, BOD1, EXO 1, ZNW10, ZEP1, PAZG4, C MAS, CDC43, GRW0D1, RE2BP1, ESPL1, LUG1, LR RC29, TRC1D08, BNM, CTRTD1, NUDCO1, TMOD3, A UBRN8, SETMAR, KRT8, HCT1, KDEL, C1, PAPR, C1, NFA D8, TPAP4, CYP99A1, B TCIP, JARND2, KATYA, POLR1 R, QUA1, CTB5, G1D2, PRP4 B, FEN1, S1C29A2, BUB1B, K6 0, ATXN1, Z12, BUB3, JMRP T808, PRP4, CDC6, IQGAP3, L19, CDC25A, PRMT6, R CDC126, SAMD12, EXO1, ZF ANGA, P1, PASK, DCUN1 P1, SHMT2, PRIM1, CDC43, G DA, NTH1, WMAP53, S RWD1, ESPL1, LUG1, UBRN8, B UFU, SAMD12, ARV1, H RC41, TFAP4, NOS3, ATXN1, Z12, SFR3, SHMT2, SAMU, BUB3, CDC25A, PRMT6, PRM1 LRV0D1, RNASEH2C, CL T5, WMAP53, SUV1, ARV1, JN P1, PRMT5, DOCK4, PNI O80E, PA2G4, LRWD1, JARD5 M1, PRMT15, DOP1, TM A, CLP1, DCAD, MRP1, 50 PO EMM4, AKR8B, CDC45, P1, TMEM48, CDC45, AKR84 NCCCR, U R15, ZNCR2, WMAP53, CD10, CDC45, RNASEH2A, AKR84, HIRP3, TOP3A, AM168, TOP3A, SPDC2, PP2 , SPDC5, LUC92A, , H55, HIRP3, RASGPR3, FEN1, BPG M, TMEM151B, GNB1L, ITG6, 3P, LUNC2, SNAAR CQ5, SOK5, MAN1, 3, 50 X15, MEIS2, ATXN1, Z12, A NGP1, Z1, FBX1, B, ERBB3, LTRP1, GNB3, EHF, PLA G12, F1R13, CACNA2D3 , ARTX, ENDOU, EGFLN1, PCDH7, CRLS1, HES1, EC HCC2, PPCS, CELF4, RASSF6, CTNNA L1, JER3, ANKRD39, KLF 12, NR6A1, ZH2, CPNE 1, MAB21, 3, PVRL1, JN HBA, COL13A1, HAS2, A 1, JER3, ANKRD39, KLF12, NR6 RTN, BUB1, PRMT6, JMR A1, ZH2, C, GNE1, MAB21, 3, P 95188, HNTL, GPCC2, PO VRL1, H4S2, 4, ARTN, CMG1, OR XN1, TFAP4, FAM20, N C4, PRMT6, MRS158, HNTL, C1, GIPC, FOXN1, TFAP4, FAM2 12, PLAT4, ARHGAP20, GRN1, FLOT1, ANGR1L 1, ZEB2, ZEB1, XIRP1, AM |
| VSUSE_01 | 1.90 | 1.54 | 4.39 | 4.87 | 3.65 | VSUSE_01 | GTFTAL, R376, CM2, PR376, OTRTD1, NUDCO1, ST MNI, PRH3, S, KDEL, P SWD11, PPRC1, JARH02, KATZA, POIR, IB, FEN1, GELL1, DDX1, ANKRD1 38, FTS1, PRP4, CDC6, IQGAP3, NFATC2IP, CC DC126, BUB1B, INO80E , SIKP2, CTFL1, BOD1, EXO 1, ZNW10, ZEP1, PAZG4, C MAS, CDC43, GRW0D1, RE2BP1, ESPL1, LUG1, LR RC29, TRC1D08, BNM, CTRTD1, NUDCO1, TMOD3, A UBRN8, SETMAR, KRT8, HCT1, KDEL, C1, PAPR, C1, NFA D8, TPAP4, CYP99A1, B TCIP, JARND2, KATYA, POLR1 R, QUA1, CTB5, G1D2, PRP4 B, FEN1, S1C29A2, BUB1B, K6 0, ATXN1, Z12, BUB3, JMRP T808, PRP4, CDC6, IQGAP3, L19, CDC25A, PRMT6, R CDC126, SAMD12, EXO1, ZF ANGA, P1, PASK, DCUN1 P1, SHMT2, PRIM1, CDC43, G DA, NTH1, WMAP53, S RWD1, ESPL1, LUG1, UBRN8, B UFU, SAMD12, ARV1, H RC41, TFAP4, NOS3, ATXN1, Z12, SFR3, SHMT2, SAMU, BUB3, CDC  |























|          |      |      |       |       |       |  |   |  |  |
|----------|------|------|-------|-------|-------|--|---|--|--|
| VSEF1_Q4 | 4.01 | 1.61 | 5.90  | 16.65 | 17.88 | 4  | VSEF1_Q<br>AS56, CDC4<br>O, CDC2AP1,<br>PKNMT1,<br>1, OSBP17, CDC6,<br>HSBP1,<br>S1, SAS56,<br>CDC5, SAS56,   | EEF7, HMG<br>N2, MCM2,<br>CDC47, SAS<br>56, SMC6,<br>MCM4, MC<br>CDC45, FHO<br>M2, HISTH2BK, FHOD1,<br>M3, RRM2,<br>CDC45, AR<br>KMTT1, ADA<br>1, ARHGAP11A, RAD51.C,<br>DDC5, SAS56,  | GAPDH, PKNMT1, HISTH<br>2AH, KIAA0101, CDC6, AD<br>AMT52, SMC6, CDC47, RR<br>M2, RANBP1, TFAP4, SIC<br>38A1, MCM7, MCM4, MC<br>MCM6, ATAD5, RANBP<br>MCM6, ATAD5, RANBP1, SAS<br>DK1, MCM4, NCL, ARHG<br>AP11A, RAD51, CDC45,<br>PHF5A, DCK, RRM2,<br>DDC5, PHF5A, RRM2,<br>NUT72, POLA1, STMN1,<br>CLSPN, USP1, SMA, D6, G<br>APDH, PCSK4, PELP1, KI<br>F15, E2F1, EZH2, DCTP<br>1, FBXO5, MCM8, GNM<br>NATAD2, MXO3, CDC6,<br>USP37, PAN2, SRSF7, D<br>NAC9, RAVEN1, TPIN,<br>SRS, DNMT1, ANAPC1<br>0, GEN1, TMN6, POLD1, NUT72, POLA1, CLSPN, USP1,<br>J, F5, G, P83, CDC47, AR, PLK4, PCSK4, GEN1, INT3, DC<br>M2, PHC1, HISTH2BK, TPPL1, FBXO5, GNM, NATAD2,<br>HNRNP, DDC25A, IIRX, MDX3, CDC6, SIC, CNA5, SRSF7,<br>3, SRS3, TFAP4, TCF1, A, RAVEN1, TPIN, SRS, WEI5, C<br>BL, RCD1, NOLC1, IER, ACNA16, TMN6, POLD1, KLF<br>5, LORC1, LOR1, MCM2, 5, PHC1, CDC47, RRM2, MCM<br>, MCM7, PKNMT1, NFAT, 8, HNRNP, DDC25A, POLE2,<br>C21P, HIST1, H1D, TOPBP, TFAP4, RBL1, RCD1, NOLC1,<br>1, GABRB3, SHMT1, MA, IER5, LORC1, MCM7, MCM2,<br>M3, E2F7, GINS3, NAG, MCM3, PKNMT1, NFATC2IP,<br>P, RPS6K45, SRRBP1, M, HIST1, H1D, TOPBP1, GABRB3,<br>CM6, ATAD5, PRPF3A, SHMT1, HISTH2BK, E2F7, GI<br>SAS6, RRM2, POLE2, J, NS3, NASP, DNAC9, SRRBP1,<br>MPO, E2F8, COK1, PLK4, MCM6, ATAD5, PRPF3A, SAS<br>NCL, ARHGAP11A, TRI, S6, TMPO, E2F8, COK1, HIST1<br>BCE1, DCK, OVOL2, E1, OVOL2,<br>POLA2, STMN1, CLSPN,<br>SMA, D6, REC1, RIR, C1, M<br>ER3, EZH2, FBXO5, OT,<br>SYNP, CWS, RPA2, CB<br>X3, CDC6, DCK, E1A, SXP<br>2, WDR28, ERH, PPH13,<br>KNTC1, CSRP1, DBR1,<br>PVRL1, PELO, SRRBP2, P, POLA2, LIF, SLBP, SYNP, C1S<br>RIM1, BORA, A, DDB2, MY, PN, ITGA1, RF, C1, RIBC1, FBXO<br>C, EIF5A, HNRNP, D, TRI, 5, CIT, TRIM28, RPA2, CBX3, C<br>M27, INTS7, RRM2, SIC3, DCK6, DCK, E1A, ERH, KNTC1, P<br>8A2, HNRNP, A3, SP2, P8, VRIL, PELO, SRRBP2, PRIMI1,<br>MT1, CDC6, GPC2, MC, BORA, DIO3, DDB2, MYC, HNR<br>M4, PKNMT1, CHTF18, NP, TRIM27, INTS7, SIC3A<br>UNG, PRKDC, WEI1, AP, 2, HNRNP, A3, PNM1, GPC2,<br>5, KAS5, E2F7, NASP, ETV, MCM4, PKNMT1, CHTF18, UN<br>4, E2F1, RANBP1, KPNB, GOSBP7, E2F7, NASP, ETV, A<br>1, E2F8, MEK, APIN1, RANBP1, KPNB1, E2F8, MEK<br>APIN1, LYAR, POLE2, RAD51, C, DDC5, SAS56, |
| VSEF1_Q3 | 6.46 | 1.61 | 9.51  | 30.11 | 29.11 | 3  | VSEF1_Q<br>ARRHGAP11<br>DH, PKNMT1,<br>A,<br>ADAMT52,<br>1A, SAS56,   | EEF7, HMG<br>N2, MCM2,<br>USP1, SAS5<br>6, PLK4, OR<br>C1, MCM3,<br>MCM7, MCM2,<br>HISTH2<br>G6, CDC47,<br>FHOD1, GAP<br>BK, FHOD1, SRRBP1, TFA<br>NCL, ARHGAP11A, TRI, S6,<br>TMPO, E2F8, COK1, HIST1<br>BCE1, DCK, OVOL2, E1, OVOL2,<br>POLA2, STMN1, CLSPN,<br>SMA, D6, REC1, RIR, C1, M<br>ER3, EZH2, FBXO5, OT,<br>SYNP, CWS, RPA2, CB<br>X3, CDC6, DCK, E1A, SXP<br>2, WDR28, ERH, PPH13,<br>KNTC1, CSRP1, DBR1,<br>PVRL1, PELO, SRRBP2, P, POLA2, LIF, SLBP, SYNP, C1S<br>RIM1, BORA, A, DDB2, MY, PN, ITGA1, RF, C1, RIBC1, FBXO<br>C, EIF5A, HNRNP, D, TRI, 5, CIT, TRIM28, RPA2, CBX3, C<br>M27, INTS7, RRM2, SIC3, DCK6, DCK, E1A, ERH, KNTC1, P<br>8A2, HNRNP, A3, SP2, P8, VRIL, PELO, SRRBP2, PRIMI1,<br>MT1, CDC6, GPC2, MC, BORA, DIO3, DDB2, MYC, HNR<br>M4, PKNMT1, CHTF18, NP, TRIM27, INTS7, SIC3A<br>UNG, PRKDC, WEI1, AP, 2, HNRNP, A3, PNM1, GPC2,<br>5, KAS5, E2F7, NASP, ETV, MCM4, PKNMT1, CHTF18, UN<br>4, E2F1, RANBP1, KPNB, GOSBP7, E2F7, NASP, ETV, A<br>1, E2F8, MEK, APIN1, RANBP1, KPNB1, E2F8, MEK<br>APIN1, LYAR, POLE2, RAD51, C, DDC5, SAS56,  |  |
| VSEF1_Q6 | 5.81 | 2.39 | 12.43 | 31.05 | 30.50 | VSEF1_Q6<br>HGAP11A, MT52,<br>DDC5, SAS56, | EEF7, HMG<br>N2, MCM2,<br>CDC47, SAS<br>56, SMC6,<br>MCM4, MC<br>CDC45, FHO<br>M2, HISTH2BK, FHOD1,<br>M3, RRM2,<br>CDC45, AR<br>KMTT1, ADA<br>1, ARHGAP11A, RAD51.C,<br>DDC5, SAS56, | GAPDH, PKNMT1, HISTH<br>2AH, KIAA0101, CDC6, AD<br>AMT52, SMC6, CDC47, RR<br>M2, RANBP1, TFAP4, SIC<br>38A1, MCM7, MCM4, MC<br>MCM6, ATAD5, RANBP<br>MCM6, ATAD5, RANBP1, SAS<br>DK1, MCM4, NCL, ARHG<br>AP11A, RAD51, CDC45,<br>PHF5A, DCK, RRM2,<br>DDC5, PHF5A, RRM2,<br>NUT72, POLA1, STMN1,<br>CLSPN, USP1, SMA, D6, G<br>APDH, PCSK4, PELP1, KI<br>F15, E2F1, EZH2, DCTP<br>1, FBXO5, MCM8, GNM<br>NATAD2, MXO3, CDC6,<br>USP37, PAN2, SRSF7, D<br>NAC9, RAVEN1, TPIN,<br>SRS, DNMT1, ANAPC1<br>0, GEN1, TMN6, POLD1, NUT72, POLA1, CLSPN, USP1,<br>J, F5, G, P83, CDC47, AR, PLK4, PCSK4, GEN1, INT3, DC<br>M2, PHC1, HISTH2BK, TPPL1, FBXO5, GNM, NATAD2,<br>HNRNP, DDC25A, IIRX, MDX3, CDC6, SIC, CNA5, SRSF7,<br>3, SRS3, TFAP4, TCF1, A, RAVEN1, TPIN, SRS, WEI5, C<br>BL, RCD1, NOLC1, IER, ACNA16, TMN6, POLD1, KLF<br>5, LORC1, LOR1, MCM2, 5, PHC1, CDC47, RRM2, MCM<br>, MCM7, PKNMT1, NFAT, 8, HNRNP, DDC25A, POLE2,<br>C21P, HIST1, H1D, TOPBP, TFAP4, RBL1, RCD1, NOLC1,<br>1, GABRB3, SHMT1, MA, IER5, LORC1, MCM7, MCM2,<br>M3, E2F7, GINS3, NAG, MCM3, PKNMT1, NFATC2IP,<br>P, RPS6K45, SRRBP1, M, HIST1, H1D, TOPBP1, GABRB3,<br>CM6, ATAD5, PRPF3A, SHMT1, HISTH2BK, E2F7, GI<br>SAS6, RRM2, POLE2, J, NS3, NASP, DNAC9, SRRBP1,<br>MPO, E2F8, COK1, PLK4, MCM6, ATAD5, PRPF3A, SAS<br>NCL, ARHGAP11A, TRI, S6, TMPO, E2F8, COK1, HIST1<br>BCE1, DCK, OVOL2, E1, OVOL2,<br>POLA2, STMN1, CLSPN,<br>SMA, D6, REC1, RIR, C1, M<br>ER3, EZH2, FBXO5, OT,<br>SYNP, CWS, RPA2, CB<br>X3, CDC6, DCK, E1A, SXP<br>2, WDR28, ERH, PPH13,<br>KNTC1, CSRP1, DBR1,<br>PVRL1, PELO, SRRBP2, P, POLA2, LIF, SLBP, SYNP, C1S<br>RIM1, BORA, A, DDB2, MY, PN, ITGA1, RF, C1, RIBC1, FBXO<br>C, EIF5A, HNRNP, D, TRI, 5, CIT, TRIM28, RPA2, CBX3, C<br>M27, INTS7, RRM2, SIC3, DCK6, DCK, E1A, ERH, KNTC1, P<br>8A2, HNRNP, A3, SP2, P8, VRIL, PELO, SRRBP2, PRIMI1,<br>MT1, CDC6, GPC2, MC, BORA, DIO3, DDB2, MYC, HNR<br>M4, PKNMT1, CHTF18, NP, TRIM27, INTS7, SIC3A<br>UNG, PRKDC, WEI1, AP, 2, HNRNP, A3, PNM1, GPC2,<br>5, KAS5, E2F7, NASP, ETV, MCM4, PKNMT1, CHTF18, UN<br>4, E2F1, RANBP1, KPNB, GOSBP7, E2F7, NASP, ETV, A<br>1, E2F8, MEK, APIN1, RANBP1, KPNB1, E2F8, MEK<br>APIN1, LYAR, POLE2, RAD51, C, DDC5, SAS56, |  |







[illegible]







[illegible]















|            |      |      |       |       |                      |   |   |   |
|------------|------|------|-------|-------|----------------------|---|---|---|
| VSEF_Q2    | 1.37 | 1.95 | 3.02  | 5.50  | VSEF_Q2_2ORCL,       | USP1, GAPZ<br>A1, MGN   | RCC3, GAPZ, A1, MGN<br>P1, ORC1, PRKCEB, BAGA,<br>LTD, LCK,   | PHWHPL, LSTNN1, USP1<br>, TINA, G1, PABPC4, EF2<br>2B3, ANP32E, ATXN7L2<br>, MPZL1, TPAPE, COL1<br>3A1, MAG3, RNF207, K, B3, KIF17, ATXN7L2, MPZL1, P<br>ONQ4, SUV39H2, RCC3, PM11, MAG3, RNF207, BAGA<br>ORC1, PIG, SNRNP40, L72, CTRG1, KONO4, SUV39H<br>PPTF38A, LPR8, R1F, R1F, 2, SNRNP40, ORC1, SCMH1, R<br>17, WNT9A, SERBP1, ZB, CC2, PPTF38A, LPR8, COL13A<br>TBA8, 1, WNT9A, ZBTB48, DDNHL,   |
| VSEF_Q2_01 | 1.61 | 1.75 | 9.43  | 5.21  | VSEF_Q2_01, A1, 612, | CLCN3, POE<br>7A, CENPE, PITX2, PREU<br>VSCORE_Q, PLK4, GTF2, D1, CHPF5, EZ | TRIM39, PRK3, ADNP, H<br>DAG5, CTC1, EPHA2, SP<br>RED2, RUNDCA, PRPD<br>1A, ERF, PREUD1, TPMA<br>, CBX8, NOCAL, MAF, FL<br>T1, AREG, DDX51, WNT<br>10A, FAM167A, AFF4, V<br>PS37B, CNOT7, LDHA, P<br>FAS, SARNP, TRAF4, LTB<br>P1, DNTT1, I, CENPE, Y1<br>HDG2, IRF2BRL, PLK4, U<br>BAG6, THOC1, ITFG2, SYN<br>GRIP, PTPRU, SUIT4A1, AREG, WNT10A, DDX51, VP53<br>SRMNA, PPTF15A, PTT<br>PNC1, NPTX1, TGIF2, ES<br>M1, MRE, A6, ESM1, TGIF2, PTFNCL1,<br>POLA2, POLA1, SMC2, S<br>TNM1, PRF13, MCM2,<br>USP1, SMD6, PRCL1, R<br>FCL, GAPDH, RIBC1, ME<br>IS2, PRDC, E2F1, EZH2,<br>DCTP1, FBXO5, GWMN<br>, GBX5, E2F8, MXD3, CD<br>C6, DCRE1A, PAN2, PO<br>LE2, NATC2IP, DCK, TIP<br>IN, DNMT1, CSRNP1, GE<br>N1, PVRL1, KLF5, GNG3,<br>CDOA, DDB2, JMYC, MC<br>M8, HNRPD, WDR67, JEF,<br>STR35, INTS7, NUP155,<br>PCDH7, SUV39H1, TRIM<br>T6, CDD25A, KPNB1, JER<br>5L, MCM7, SETD8, MC<br>M4, MCM3, PIM1, TLU<br>NG, HISTH1D, PELP1, P155,<br>WEE1, HISTH2BK, E2F, 25A,<br>DCG, ADAMTS2, SMC6, C<br>MEIK, MCM<br>M4, MCM3<br>, ARHGAP1<br>1A, CDD5, CDD5, GAP<br>HISTH2BK, MAZ, CCK1,<br>ADAMTS2, C45, SAS56,<br>VQZ, | TRIM39, PRK3, ADNP, H<br>DAG5, CTC1, EPHA2, SP<br>RED2, RUNDCA, PRPD<br>1A, ERF, PREUD1, TPMA<br>, CBX8, NOCAL, MAF, FL<br>T1, AREG, DDX51, WNT<br>10A, FAM167A, AFF4, V<br>PS37B, CNOT7, LDHA, P<br>FAS, SARNP, TRAF4, LTB<br>P1, DNTT1, I, CENPE, Y1<br>HDG2, IRF2BRL, PLK4, U<br>BAG6, THOC1, ITFG2, SYN<br>GRIP, PTPRU, SUIT4A1, AREG, WNT10A, DDX51, VP53<br>SRMNA, PPTF15A, PTT<br>PNC1, NPTX1, TGIF2, ES<br>M1, MRE, A6, ESM1, TGIF2, PTFNCL1,<br>POLA2, POLA1, SMC2, S<br>TNM1, PRF13, MCM2,<br>USP1, SMD6, PRCL1, R<br>FCL, GAPDH, RIBC1, ME<br>IS2, PRDC, E2F1, EZH2,<br>DCTP1, FBXO5, GWMN<br>, GBX5, E2F8, MXD3, CD<br>C6, DCRE1A, PAN2, PO<br>LE2, NATC2IP, DCK, TIP<br>IN, DNMT1, CSRNP1, GE<br>N1, PVRL1, KLF5, GNG3,<br>CDOA, DDB2, JMYC, MC<br>M8, HNRPD, WDR67, JEF,<br>STR35, INTS7, NUP155,<br>PCDH7, SUV39H1, TRIM<br>T6, CDD25A, KPNB1, JER<br>5L, MCM7, SETD8, MC<br>M4, MCM3, PIM1, TLU<br>NG, HISTH1D, PELP1, P155,<br>WEE1, HISTH2BK, E2F, 25A,<br>DCG, ADAMTS2, SMC6, C<br>MEIK, MCM<br>M4, MCM3<br>, ARHGAP1<br>1A, CDD5, CDD5, GAP<br>HISTH2BK, MAZ, CCK1,<br>ADAMTS2, C45, SAS56,<br>VQZ, |
| VSEF_Q2_01 | 7.54 | 1.66 | 11.45 | 30.61 | 27.51                | VSEF_Q2_01, A1, 612,  | USP1, GAPZ<br>A1, MGN   | TRIM39, PRK3, ADNP, H<br>DAG5, CTC1, EPHA2, SP<br>RED2, RUNDCA, PRPD<br>1A, ERF, PREUD1, TPMA<br>, CBX8, NOCAL, MAF, FL<br>T1, AREG, DDX51, WNT<br>10A, FAM167A, AFF4, V<br>PS37B, CNOT7, LDHA, P<br>FAS, SARNP, TRAF4, LTB<br>P1, DNTT1, I, CENPE, Y1<br>HDG2, IRF2BRL, PLK4, U<br>BAG6, THOC1, ITFG2, SYN<br>GRIP, PTPRU, SUIT4A1, AREG, WNT10A, DDX51, VP53<br>SRMNA, PPTF15A, PTT<br>PNC1, NPTX1, TGIF2, ES<br>M1, MRE, A6, ESM1, TGIF2, PTFNCL1,<br>POLA2, POLA1, SMC2, S<br>TNM1, PRF13, MCM2,<br>USP1, SMD6, PRCL1, R<br>FCL, GAPDH, RIBC1, ME<br>IS2, PRDC, E2F1, EZH2,<br>DCTP1, FBXO5, GWMN<br>, GBX5, E2F8, MXD3, CD<br>C6, DCRE1A, PAN2, PO<br>LE2, NATC2IP, DCK, TIP<br>IN, DNMT1, CSRNP1, GE<br>N1, PVRL1, KLF5, GNG3,<br>CDOA, DDB2, JMYC, MC<br>M8, HNRPD, WDR67, JEF,<br>STR35, INTS7, NUP155,<br>PCDH7, SUV39H1, TRIM<br>T6, CDD25A, KPNB1, JER<br>5L, MCM7, SETD8, MC<br>M4, MCM3, PIM1, TLU<br>NG, HISTH1D, PELP1, P155,<br>WEE1, HISTH2BK, E2F, 25A,<br>DCG, ADAMTS2, SMC6, C<br>MEIK, MCM<br>M4, MCM3<br>, ARHGAP1<br>1A, CDD5, CDD5, GAP<br>HISTH2BK, MAZ, CCK1,<br>ADAMTS2, C45, SAS56,<br>VQZ, |



[illegible]441











|                  |      |      |      |       |      |       |   |   |
|------------------|------|------|------|-------|------|-------|---|---|
| TGACATY_UNKNOWN  | 3.29 | 1.97 | 4.00 | 2.02  | 4.59 | 14.78 | N | SELLCTS<br>C56P2,PUB<br>D1,CALMI,<br>SPAG5,D5<br>C2,ARRGE<br>F3,G8P5,A<br>RHHGA90,<br>TNRFSF21,<br>1,TIMM9,FH<br>C,TNRFSF21,PRH11,PTP<br>UNKNOW<br>SIK,SPH81<br>ALIN54,<br>ZICL,<br>RS,C,<br>CONO1A,SPRR1A,CD247<br>P,6GR2,ITPBP,MBX3<br>SC2,KCKMLJES1,CQCAI<br>TAG2,ISG220,LEMP2<br>D,IGSF3,FGF2,FGH8,<br>G,PIOD2,JHNNNP3A,HNRNP<br>1,NUD7A,MCCAM,SLN,<br>SYNCBP,PA6G,PAH16<br>D,POLE2,WIP1L,LSM5,ORCA,<br>MSRB3,TS9AN4,IMKR<br>14L,FHL3,CTSC,PIB01L15<br>2A,NOS1AP,CCDC138,<br>SPAG5,MCCAM,FLRT3,CHERP<br>A8,WBP1,RA5A3,CIN<br>OBFC1,C1QTNF4,CTN<br>VASP,IGSF3,FGH2,OSBP17,<br>1,CNN3,ARMCD4,ABI3<br>E1,TRIM8,PRH11,PTP<br>TAGLN,CY7B1,CNN1,FAM1<br>BP,ARHGAP30,CONO1<br>NCL,CD6,CRL51,PTHL<br>62A,ARMCD4,CCDC138,RPA<br>A,PTPNC,ANGPT12,MY<br>H,CSNRP1,UNG4,TFDP<br>2,PP2R58,PRH1,ESM1,CD<br>OZZ,COLEA3,MVO7A,<br>2,ESM1,ATXN1,<br>LSM12,PUS7L,PKMTT<br>K6,PAK6,JARID2,PTPNC1,<br>STEAP4,<br>1,PAH41,VSNL1,DDNM<br>T1,MAPRE3,TBCD1,A<br>RHGEF15,DY930,NR2C<br>1,PMS2,TDIP,USP37,K<br>CTD13,SNRPD2,PCGF6<br>,PTPN12,POPT,MIRP14<br>5,CTBP2,FAM122A,FA<br>M122B,MIRP22,BRYA<br>NK,FRS3,SRINC2,GTF<br>3CL,SPN2,NDRG1XR<br>CCLXKCC3,IFR9A,SN5<br>F7,CBX3,AF4,STT12P<br>NUCCD2,HMMNR,PP38,VS<br>PMEL1,TUBD1,FLWCH,NLJ,MNP122,PABPCL,AMP<br>2,HMMNR,FAM98A,PIG<br>2,POU1L1,KAT7A,CNG2,PAH<br>L,HERC4,ING2,ZC3H8,<br>A1,HDXA1,NDRG1,XRC2,M<br>TA5,RP56A5,TFAP4,<br>XD3,SNARCA5,CCDC7,SRF7,<br>PALB2,TTG37,RP17L1,<br>CBX3,XRCC5,LSM12,PRE7A<br>WNT5A,KDM3A,BTBD<br>ING2,CNS2,TUBDL,EIF52,FL<br>3,NUCCD2,RP38,ACP<br>YWCH2,AURKA,PUS7,ARH<br>1,EF2B5,CNCG2,ELD2<br>GEF15,ROCD1,RAO21,DPV3<br>B,CBX5,MXD3,POLC<br>0,ORCA,MRP518B,HOKC4,N<br>DCT,ISEN2,FANCL,BCL<br>R2CL,PKMTT1,SUFL,ANF24,<br>IF5A,RAB10,DIEU1,CDG<br>7A,ROCD1,CNS2,MRP5<br>PMS2,WNT5A,TDIP2,ZC3H8,<br>7,CENPO,FAM98A,HEAT<br>188,SRF,NRDOT11,KAT<br>TA5,NA48,SNRP2,TFAP<br>4,PCGF6,PTPN12,PALB2,CT<br>B3,ATAD3A,CNS2,CDH7<br>2A,RP2A,MTHFMT,YA<br>4,PCGF6,PTPN12,PALB2,CT<br>MTPN,RCG1,ZC3H8,TF<br>A38,WDR12,HOKX1,<br>FL,PCDH7,TUBG1,WDR12,EL<br>AP4,PCGF6,WNT5A,BTB<br>MARS,POU1A,MNP2,C<br>D2,MIRP45,PNN,CTBP2,IGI<br>D3,<br>CDO3,SNARCA5,IF2,FL,<br>AGEL3,MNP,AS2BLN<br>IBCL,POLC,SNRG3C<br>C7B,TSYL,DENR,H5PA<br>4,SKA3,TNEN209,NO<br>L11,TROAP,SUV39H1,<br>THAP1,AGB3,FUS,ASH2LP<br>LNUD72,IFT74,MMS22<br>LOD2,IFT74,SUV39H1,MMS<br>L,NOI9,CENPT,DBR1,7<br>22L,RIKCI,ADNP,TSRL,SKA3<br>HAP1,COX11,WDR73,<br>NOI9,TNEM209,WDR73,C<br>CNU1,<br>ENPT,NOL11,TROAP,<br>SCN7A,PDGFR,INFAT<br>CALPN,PCYD1,DES,C<br>DR2,MYOT,ADAMTS<br>12,LRNP2,TRIM54,SOR<br>B53,NR272,PRBP1,M<br>BLES1,HBS1L,HNRNP<br>HI,H,ORC1,ADAMTS12,SCH<br>EFPC,CDPR,ARRGFE6,<br>JRX3,POL2,ERBB3,SP<br>1P1,HAND1,SPRR1A,KRTB8<br>SULF1,COCA1G,RTT<br>AGS,ITBP1,LSM5,TEF<br>,MRC3D,IOGA9,JUB,MBP,<br>N1,PTPRD,TTN,ZIC1,T<br>2,JARID2,FLRT3,CHER<br>TRIM8,ZNF2,TTN,CNNE1D<br>AGLN,PIGK1,DO9P3,S<br>TGRB2,AOC2,RRAD,TT<br>F2,MES2,SIC25A35,<br>WIP1,OTOP2,SCHIP1,<br>HAND1,SPRR1A,P2RX<br>3,RP42,FAM83F,IOGA<br>P3,JUB,SEP2,TEPP,MB<br>IP,ZHX2,RTTN,BCL11A<br>,JBM14,DS2,C,KCNK1,<br>CATSPER2,KRTB8,HN<br>SAT1,TGRB2,AOC2,NFATC4,<br>12,LRNP2,TRIM54,SOR<br>RNP43,SKA2,NHL3,CA<br>RRAD,TTF2,SKA2,CORL,PT<br>B53,NR272,PRBP1,M<br>BLES1,HBS1L,HNRNP<br>HI,H,ORC1,ADAMTS12,SCH<br>EFPC,CDPR,ARRGFE6,<br>JRX3,POL2,ERBB3,SP<br>1P1,HAND1,SPRR1A,KRTB8<br>SULF1,COCA1G,RTT<br>AGS,ITBP1,LSM5,TEF<br>,MRC3D,IOGA9,JUB,MBP,<br>N1,PTPRD,TTN,ZIC1,T<br>2,JARID2,FLRT3,CHER<br>TRIM8,ZNF2,TTN,CNNE1D<br>AGLN,PIGK1,DO9P3,S |
| TGCGGAMR_UNKNOWN | 1.50 |      |      | 3.29  | 3.23 |       |   | TMTGGG MARK14.5<br>AMR_UNK KA3,ZNF78<br>NOVN 6A,PROX1,<br>TMTGGGAMR_UNKNOWN   |
| TGCGGANK_UNKNOWN | 4.17 |      | 4.09 | 16.45 | 8.84 |       |   | CENPO,H<br>MMR,WD<br>RS3,ATAD<br>65,CNS2,C<br>ABB9,PD7<br>A,TMX1,G<br>TEPA1,BA8<br>TGGGAN 10,LEU1,<br>K,UNKNOW<br>WNT5A,CD<br>WN<br>C7,<br>HMMNR,PP38,VSNL1,LA1<br>R3,ATAD3A,CNS2,CDH7<br>2A,RP2A,MTHFMT,YA<br>4,PCGF6,PTPN12,PALB2,CT<br>MTPN,RCG1,ZC3H8,TF<br>A38,WDR12,HOKX1,<br>FL,PCDH7,TUBG1,WDR12,EL<br>AP4,PCGF6,WNT5A,BTB<br>MARS,POU1A,MNP2,C<br>D2,MIRP45,PNN,CTBP2,IGI<br>D3,<br>CDO3,SNARCA5,IF2,FL,<br>AGEL3,MNP,AS2BLN<br>IBCL,POLC,SNRG3C<br>C7B,TSYL,DENR,H5PA<br>4,SKA3,TNEN209,NO<br>L11,TROAP,SUV39H1,<br>THAP1,AGB3,FUS,ASH2LP<br>LNUD72,IFT74,MMS22<br>LOD2,IFT74,SUV39H1,MMS<br>L,NOI9,CENPT,DBR1,7<br>22L,RIKCI,ADNP,TSRL,SKA3<br>HAP1,COX11,WDR73,<br>NOI9,TNEM209,WDR73,C<br>CNU1,<br>ENPT,NOL11,TROAP,<br>SCN7A,PDGFR,INFAT<br>CALPN,PCYD1,DES,C<br>DR2,MYOT,ADAMTS<br>12,LRNP2,TRIM54,SOR<br>B53,NR272,PRBP1,M<br>BLES1,HBS1L,HNRNP<br>HI,H,ORC1,ADAMTS12,SCH<br>EFPC,CDPR,ARRGFE6,<br>JRX3,POL2,ERBB3,SP<br>1P1,HAND1,SPRR1A,KRTB8<br>SULF1,COCA1G,RTT<br>AGS,ITBP1,LSM5,TEF<br>,MRC3D,IOGA9,JUB,MBP,<br>N1,PTPRD,TTN,ZIC1,T<br>2,JARID2,FLRT3,CHER<br>TRIM8,ZNF2,TTN,CNNE1D<br>AGLN,PIGK1,DO9P3,S   |















|                        |      |      |       |       |       |  |
|------------------------|------|------|-------|-------|-------|--|
| SGGSSAMA_V\$E2F1D92_01 | 2.78 | 1.40 | 9.10  | 25.24 | 26.60 | <p> MCM2,SM<br/> G6,MCM4,<br/> SGGSSAA,<br/> MCM3,RR<br/> FOD1,PKM<br/> RRM2,KIAA0101,RAABP<br/> P1,NR6A1,ATAD2,MC<br/> NR6A1,ATAD2,HIST12AH,<br/> M4,NCL,POLE2,TRIM3<br/> MCM4,NCL,POLE2,PHF5A,<br/> 9,PHF5A,DCX,MCM2,<br/> MCM2,<br/> PARS2,PLK4,SPRED2,<br/> PARS2,TGDS,PLK4,SPRED2,P<br/> MEIS2,PHF1D2,PHF1L1,<br/> H1D12,PHF1L1,POUR3D,NUDT<br/> RRC49,NUDT21,DOG1,<br/> 21,LOG61,LEFTUD2,TPX2,RIF<br/> ,DMTTP1,TPX2,KCTD1,<br/> 1,NPAT,GRWD1,ZFP64,B3G<br/> 3,EM12,RPF1,DMNT1,<br/> ALT6,SETD8,CHEBP,FBXK8,N<br/> NPAT,GRWD1,EFSEC,<br/> ME7,FTSID1,ER2,KT112,ERN<br/> ZFP64,MAPRE1,IRX3,Z<br/> 1,ELK3,ZSCAN12,EMEL,HIRI<br/> SCAN20,B3GALT4,SM<br/> P3,ADNP,PABPC1,PABPC4,K<br/> UG1,B3GALT6,TCOF1,<br/> RRL,EXOSC3,EXOSC5,HCCS,<br/> CICN2,RHESD,CB83,SE<br/> SR59,CCT7,MEIS1,RCDN3<br/> TDB,CHEBP,PROSER1,<br/> D,PO1,R3H,CTNNB1,POE5A<br/> DOX49,FBXK8,WDR55,<br/> GAR1,RLH35,SIRT6,BLM,U<br/> NMET7,TTB,FTSID1,ERN<br/> BA2,MN67P,ANPC2,POUR<br/> LA0103,CBP3,EF59A,TP<br/> 2,KT1D2,IRH1,ELK3,NT<br/> 2H5,CE9A6,WASP,MAT1PA<br/> K2,NR6A2,SP92,UBRCP4,<br/> HLL,ZSCAN12,EMEL,1H<br/> LB2,SHQ1,NUPT15,PHF5A,C<br/> ,DDX39A,NEDD1,INVS,C<br/> HBP3,TRIM39,ADNP,D<br/> NTROB,RRP15,NUIT2,RFCA,<br/> CAND,PABPC4,GAPOH<br/> RFCA,CIOBP,PANCD2,DNA<br/> AP1,SC36A1,SMC6,CD<br/> 2,SRP2,SLC,<br/> POLR2H,CBP<br/> CA3,OVC42,RPE,LSM1L,<br/> ,GT3C1,POUR1,C,KRR<br/> F2,POH,CEP164,MCC3,NE<br/> 36A1,SMC,<br/> F,H5H1,RRS<br/> IMD2,DXK37,CENPO,TY<br/> 1,EXOSC3,RRM19,DHX<br/> DD1,NOCL,MASTL,CXSB1,T<br/> 6,PSM2,<br/> 1,PRDS,GA<br/> MP,RRS1,LRPC2,C17orf<br/> 37,HCCS,WDR46,SRF,<br/> RADO,TMNT6,FANCF,F1IR,<br/> MFSO9,AT<br/> POHSHANK<br/> 80,CEP41,MT6,PIK4M<br/> 37,HCCS,WDR46,SRF,<br/> RADO,TMNT6,FANCF,F1IR,<br/> M,NUP107,<br/> 2,ACYP1,CD<br/> CM7,MTNP,UNC130,IFI<br/> FTUD2,PMVE1,POR3<br/> ASRP,PUS1,NUP107,RRS1E<br/> ,SUPT16H,<br/> CA3,TYMP,PI<br/> 30,ZNF73,POLR2H,PCGF<br/> H1BP1L,PDE5A,GAR1,<br/> FNAS,DAB2P,DPH2,FAM96<br/> C17orf80,T,TX2,PREDU1,<br/> 1,JAG1,RRM45,HIRA,PT<br/> ED30,NUPT5,SIRT6M<br/> B,INQ2,CHRNA1,EBNA1BP2,<br/> MX1,RRM,<br/> WRAP53,CD<br/> HLH,MEITIS,NUPT7,UB<br/> E3D,NUPT5,BLM,UB<br/> SEMA3F,PPAN,DCAD,ANK4,<br/> 45,GPR155,C45,PTTH1,C<br/> EF2,PTM2C,BANF1,SLC3<br/> A2,HIFC4,CCP110,NK<br/> SF3B4,BANF1,CCG45,NV16<br/> SGGGAAG,FTSID1,CD<br/> UIZ,CXK6A1,<br/> SBR,PRKACB,CDC45,TM<br/> 1671P,PTNP2,GARTAP<br/> B,POA1,UTP9,FRCC1,CEP5<br/> _V\$E2F1,OC45,FBXO3,<br/> JAG1,DH3<br/> EMT297,AT5L,ILTRAG<br/> TX,POLR2H,SLC39A6,T<br/> 5,GEN1,PREDU1,NUPT7,EF<br/> _N\$E2F1,OC45,FBXO3,<br/> JAG1,DH3<br/> EMT297,AT5L,ILTRAG<br/> NK2,INSP,POLIM1,WF<br/> 251,UBOX5,PTNR23,BAVER </p>  |
| SGGGAAG_V\$E2F1D2_02   | 6.38 | 5.64 | 14.27 | 27.52 | 17.07 | <p> HIST1H4A,CDCC25A,CL<br/> SPNE2F1,SMAD6,UN<br/> G,POA1,PKMYT1,PRK<br/> DC,DCTP1,FBXO5,G<br/> MNN,EZF8,MXD3,CDC<br/> 6,RM12,PAN2,SRF7,R<br/> AVR1,DMNT1,GEN1,<br/> HIST1H4A,CDCC25A,CLSPN,U<br/> POLO1,PHC1,CDCA7,R<br/> NG,POA1,PRMYT1,GEN1,D<br/> RM2,MVC,USP97,HNK<br/> CTPPL,FBXO5,GANN1218,<br/> NPD,NOTC1,STK35,TF<br/> MDX1,CDC6,SLC6A5,SRF7<br/> AP4,ROCD1,GEN3,SU<br/> BAVER1,POLO1,PHC1,CDCA<br/> VBP1,EFNAS,IERG,<br/> 7,RRM2,MVC,HNRP1,NOL<br/> MRB3,MCP7,MCM6,<br/> CL,TPP44,NOCD1,SUV39H1,<br/> HIST1H4A,MCM3,AB<br/> EFNAS,IERG,MCM7,MCM6,<br/> CL,INAPC2,P,TOBP1,<br/> HIST1H4A,MCM3,AB,CL,IN<br/> APC2,P,TOBP1,GAAR3,HI<br/> GAAR3,HIST1H2B,K5<br/> ATCIP,TOBP1,GAAR3,HI<br/> VNCBP,NASP,DNAJC9,<br/> STH2BK,GEN3,NASP,DNA<br/> J,SNRPD1,ATAD5,IRANB<br/> C9,SNRPD1,ATAD5,IRANB,P1,<br/> P1,NR6A1,ATAD2,MC<br/> NR6A1,ATAD2,HIST12AH,<br/> M4,NCL,POLE2,TRIM3<br/> MCM4,NCL,POLE2,PHF5A,<br/> 9,PHF5A,DCX,MCM2,<br/> MCM2,<br/> PARS2,PLK4,SPRED2,<br/> PARS2,TGDS,PLK4,SPRED2,P<br/> MEIS2,PHF1D2,PHF1L1,<br/> H1D12,PHF1L1,POUR3D,NUDT<br/> RRC49,NUDT21,DOG1,<br/> 21,LOG61,LEFTUD2,TPX2,RIF<br/> ,DMTTP1,TPX2,KCTD1,<br/> 1,NPAT,GRWD1,ZFP64,B3G<br/> 3,EM12,RPF1,DMNT1,<br/> ALT6,SETD8,CHEBP,FBXK8,N<br/> NPAT,GRWD1,EFSEC,<br/> ME7,FTSID1,ER2,KT112,ERN<br/> ZFP64,MAPRE1,IRX3,Z<br/> 1,ELK3,ZSCAN12,EMEL,HIRI<br/> SCAN20,B3GALT4,SM<br/> P3,ADNP,PABPC1,PABPC4,K<br/> UG1,B3GALT6,TCOF1,<br/> RRL,EXOSC3,EXOSC5,HCCS,<br/> CICN2,RHESD,CB83,SE<br/> SR59,CCT7,MEIS1,RCDN3<br/> TDB,CHEBP,PROSER1,<br/> D,PO1,R3H,CTNNB1,POE5A<br/> DOX49,FBXK8,WDR55,<br/> GAR1,RLH35,SIRT6,BLM,U<br/> NMET7,TTB,FTSID1,ERN<br/> BA2,MN67P,ANPC2,POUR<br/> LA0103,CBP3,EF59A,TP<br/> 2,KT1D2,IRH1,ELK3,NT<br/> 2H5,CE9A6,WASP,MAT1PA<br/> K2,NR6A2,SP92,UBRCP4,<br/> HLL,ZSCAN12,EMEL,1H<br/> LB2,SHQ1,NUPT15,PHF5A,C<br/> ,DDX39A,NEDD1,INVS,C<br/> HBP3,TRIM39,ADNP,D<br/> NTROB,RRP15,NUIT2,RFCA,<br/> CAND,PABPC4,GAPOH<br/> RFCA,CIOBP,PANCD2,DNA<br/> AP1,SC36A1,SMC6,CD<br/> 2,SRP2,SLC,<br/> POLR2H,CBP<br/> CA3,OVC42,RPE,LSM1L,<br/> ,GT3C1,POUR1,C,KRR<br/> F2,POH,CEP164,MCC3,NE<br/> 36A1,SMC,<br/> F,H5H1,RRS<br/> IMD2,DXK37,CENPO,TY<br/> 1,EXOSC3,RRM19,DHX<br/> DD1,NOCL,MASTL,CXSB1,T<br/> 6,PSM2,<br/> 1,PRDS,GA<br/> MP,RRS1,LRPC2,C17orf<br/> 37,HCCS,WDR46,SRF,<br/> RADO,TMNT6,FANCF,F1IR,<br/> MFSO9,AT<br/> POHSHANK<br/> 80,CEP41,MT6,PIK4M<br/> 37,HCCS,WDR46,SRF,<br/> RADO,TMNT6,FANCF,F1IR,<br/> M,NUP107,<br/> 2,ACYP1,CD<br/> CM7,MTNP,UNC130,IFI<br/> FTUD2,PMVE1,POR3<br/> ASRP,PUS1,NUP107,RRS1E<br/> ,SUPT16H,<br/> CA3,TYMP,PI<br/> 30,ZNF73,POLR2H,PCGF<br/> H1BP1L,PDE5A,GAR1,<br/> FNAS,DAB2P,DPH2,FAM96<br/> C17orf80,T,TX2,PREDU1,<br/> 1,JAG1,RRM45,HIRA,PT<br/> ED30,NUPT5,SIRT6M<br/> B,INQ2,CHRNA1,EBNA1BP2,<br/> MX1,RRM,<br/> WRAP53,CD<br/> HLH,MEITIS,NUPT7,UB<br/> E3D,NUPT5,BLM,UB<br/> SEMA3F,PPAN,DCAD,ANK4,<br/> 45,GPR155,C45,PTTH1,C<br/> EF2,PTM2C,BANF1,SLC3<br/> A2,HIFC4,CCP110,NK<br/> SF3B4,BANF1,CCG45,NV16<br/> SGGGAAG,FTSID1,CD<br/> UIZ,CXK6A1,<br/> SBR,PRKACB,CDC45,TM<br/> 1671P,PTNP2,GARTAP<br/> B,POA1,UTP9,FRCC1,CEP5<br/> _V\$E2F1,OC45,FBXO3,<br/> JAG1,DH3<br/> EMT297,AT5L,ILTRAG<br/> TX,POLR2H,SLC39A6,T<br/> 5,GEN1,PREDU1,NUPT7,EF<br/> _N\$E2F1,OC45,FBXO3,<br/> JAG1,DH3<br/> EMT297,AT5L,ILTRAG<br/> NK2,INSP,POLIM1,WF<br/> 251,UBOX5,PTNR23,BAVER </p> |



5 B5 B



|      |       |       |       |        |     |     |         |       |   |       |       |     |   |       |        |     |      |      |       |    |     |      |      |      |         |       |    |    |      |        |    |         |       |         |     |      |      |      |      |       |       |       |       |        |       |      |       |        |       |   |      |       |       |         |       |        |      |      |      |    |      |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |  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    |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     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  |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |     |     |        |       |      |   |        |         |   |    |       |       |    |    |       |         |    |     |       |      |    |      |      |      |     |     |        |      |      |    |       |      |     |      |       |      |       |   |      |        |       |       |         |      |    |       |       |       |     |    |     |      |      |    |         |     |   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| AAAS | HAUS3 | NUD21 | SEMA6 | CCDC94 | DIN | MT1 | FAM110A | ZC3H1 | 0 | GNVD1 | PRIM2 | TUT | 1 | ZFP64 | MAPRE1 | ZSC | AN20 | GF1R | TCOF1 | CL | CN2 | WIP1 | CHB3 | RAE1 | SYNCRIP | WDR55 | NM | EL | SPK3 | PRPM12 | ME | TNFSF11 | LCMT2 | RINODCA | D26 | EXR3 | IMD1 | BP42 | ADNP | SF3B4 | TGIF2 | HOKX4 | HIRP3 | TRIM39 | ISG20 | CTT7 | SGOL2 | PRPM12 | RINQ4 | Z | EDC3 | NDNG1 | LEH9A | AACTP23 | NCOM1 | INDBRE | POLL | SIS9 | CTT7 | CM | FUT1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 | SGOL2 | HAUS3 | POOLR2H | HBE6 | GR | HERC4 | SART3 | PPIN2 | WD1 | AF | CA1 | ING2 | CSF1 | MA | TNFSF11 | LEP | NIP | DES | PR137B | CD79B | NCOM | 1 | LARAP1 | ARHGEF6 | N | DN | PIK3G | PILRA | TN | N2 | LMND2 | SLC39A6 | NU | PV2 | GSPT2 | ALP3 | CP | YSL3 | FGD2 | SPN1 | ZCC | VE1 | CEP164 | WHDH | LEK3 | AS | PMH1E | POU4 | GAR | ERH1 | MEB26 | NOCL | SNF59 | 1 | TCF7 | INMPS1 |
|------|-------|-------|-------|--------|-----|-----|---------|-------|---|-------|-------|-----|---|-------|--------|-----|------|------|-------|----|-----|------|------|------|---------|-------|----|----|------|--------|----|---------|-------|---------|-----|------|------|------|------|-------|-------|-------|-------|--------|-------|------|-------|--------|-------|---|------|-------|-------|---------|-------|--------|------|------|------|----|------|--------|------|------|----|-------|------|-----|------|-------|------|-------|---|------|--------|-------|-------|---------|------|----|-------|-------|-------|-----|----|-----|------|------|----|---------|-----|-----|-----|--------|-------|------|---|--------|---------|---|----|-------|-------|----|----|-------|---------|----|-----|-------|------|----|------|------|------|-----|-----|--------|------|------|----|-------|------|-----|------|-------|------|-------|---|------|--------|-------|-------|---------|------|----|-------|-------|-------|-----|----|-----|------|------|----|---------|-----|-----|-----|--------|-------|------|---|--------|---------|---|----|-------|-------|----|----|-------|---------|----|-----|-------|------|----|------|------|------|-----|-----|--------|------|------|----|-------|------|-----|------|-------|------|-------|---|------|--------|-------|-------|---------|------|----|-------|-------|-------|-----|----|-----|------|------|----|---------|-----|-----|-----|--------|-------|------|---|--------|---------|---|----|-------|-------|----|----|-------|---------|----|-----|-------|------|----|------|------|------|-----|-----|--------|------|------|----|-------|------|-----|------|-------|------|-------|---|------|--------|-------|-------|---------|------|----|-------|-------|-------|-----|----|-----|------|------|----|---------|-----|-----|-----|--------|-------|------|---|--------|---------|---|----|-------|-------|----|----|-------|---------|----|-----|-------|------|----|------|------|------|-----|-----|--------|------|------|----|-------|------|-----|------|-------|------|-------|---|------|--------|-------|-------|---------|------|----|-------|-------|-------|-----|----|-----|------|------|----|---------|-----|-----|-----|--------|-------|------|---|--------|---------|---|----|-------|-------|----|----|-------|---------|----|-----|-------|------|----|------|------|------|-----|-----|--------|------|------|----|-------|------|-----|------|-------|------|-------|---|------|--------|-------|-------|---------|------|----|-------|-------|-------|-----|----|-----|------|------|----|---------|-----|-----|-----|--------|-------|------|---|--------|---------|---|----|-------|-------|----|----|-------|---------|----|-----|-------|------|----|------|------|------|-----|-----|--------|------|------|----|-------|------|-----|------|-------|------|-------|---|------|--------|-------|-------|---------|------|----|-------|-------|-------|-----|----|-----|------|------|----|---------|-----|-----|-----|--------|-------|------|---|--------|---------|---|----|-------|-------|----|----|-------|---------|----|-----|-------|------|----|------|------|------|-----|-----|--------|------|------|----|-------|------|-----|------|-------|------|-------|---|------|--------|-------|-------|---------|------|----|-------|-------|-------|-----|----|-----|------|------|----|---------|-----|-----|-----|--------|-------|------|---|--------|---------|---|----|-------|-------|----|----|-------|---------|----|-----|-------|------|----|------|------|------|-----|-----|--------|------|------|----|-------|------|-----|------|-------|------|-------|---|------|--------|-------|-------|---------|------|----|-------|-------|-------|-----|----|-----|------|------|----|---------|-----|-----|-----|--------|-------|------|---|--------|---------|---|----|-------|-------|----|----|-------|---------|----|-----|-------|------|----|------|------|------|-----|-----|--------|------|------|----|-------|------|-----|------|-------|------|-------|---|------|--------|-------|-------|---------|------|----|-------|-------|-------|-----|----|-----|------|------|----|---------|-----|-----|-----|--------|-------|------|---|--------|---------|---|----|-------|-------|----|----|-------|---------|----|-----|-------|------|----|------|------|------|-----|-----|--------|------|------|----|-------|------|-----|------|-------|------|-------|---|------|--------|-------|-------|---------|------|----|-------|-------|-------|-----|----|-----|------|------|----|---------|-----|-----|-----|--------|-------|------|---|--------|---------|---|----|-------|-------|----|----|-------|---------|----|-----|-------|------|----|------|------|------|-----|-----|--------|------|------|----|-------|------|-----|------|-------|------|-------|---|------|--------|-------|-------|---------|------|----|-------|-------|-------|-----|----|-----|------|------|----|---------|-----|-----|-----|--------|-------|------|---|--------|--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[illegible]







[illegible]



F1\_Q6

### 3. EKRPI











|           |      |      |      |      |      |          |   |
|-----------|------|------|------|------|------|----------|---|
| VSMF2_01  | 4.46 | 7.20 | 3.02 | 2.90 | 2.60 | VSMF2_0  | MDR1, BAG2, NUDCD1, POT1, RIN1, HSPA9, TIN AG1L, EPHA2, KBTBD8, ATKXN12, MAFF, PHLD A2, TLL, PRRT, CMAS, A                      |
|           |      |      |      |      |      |          | MDR1, CO15A3, SNX10, T BGR6, BCL2A, DOCK2A,5  |
|           |      |      |      |      |      |          | UBAC1, GHRP2, NDN, GA, RC, SPAT52, PRK3, GAP, L1, EPHA2, ASS1, ATKXN12, M   |
|           |      |      |      |      |      |          | MDR1, RIN1, PDH, PRP28, C, PSMD2, C, DH, ENOT, NUDT11, GC, AFF, PHLD, KBTBD8, S10A, CO15A1, ANK3, CO15A                         |
|           |      |      |      |      |      |          | GAPDH, REL, MAS, FH3, GSTP1, WDR8, AT, BNP3, OMG, SIC2, 2, DOCK2A, SRC, SPAT52, ENO1, 3, EFF1A2, ILK, USP13, H                  |
|           |      |      |      |      |      |          | 2, PHL3, GSTP1, 1, MAPK12, REL2, GEF11, A18, NOTCH4, METAP1, 1, VASP, BNP3, 3, OMG, NOTCH4, CLS1, HSGST2, ARCD1, S              |
|           |      |      |      |      |      |          | 1, MAPK12, F, 1, BNP3, 1, HOG, SCNT, LEN, D, 1, PSMD1, REL2, L2, LD, 1, RIN1, LBP, MS, IL6, PT, RN, PA, MPX, ANGP1, L, CST7, BT |
|           |      |      |      |      |      |          | GF11, O1, PKA6, BCL3, ELMO3, K6, BCL3,  |
|           |      |      |      |      |      |          | PRR3, ADNP, CTC1, EPH   |
|           |      |      |      |      |      |          | A2, RUNC3A, PRPD1A  |
|           |      |      |      |      |      |          | PRK5, PRK4, PRELID, R   |
|           |      |      |      |      |      |          | IPK4, GSK3, NOC4, ARL   |
|           |      |      |      |      |      |          | 4D, SEMA3, MAFF, ELA  |
|           |      |      |      |      |      |          | V1L, AREG, CCNA2, DDX   |
|           |      |      |      |      |      |          | 51, MBP, WNT10A, AFR  |
|           |      |      |      |      |      |          | 4, ANAPC10, PARDBA, V   |
|           |      |      |      |      |      |          | PS37B, CNTRB, ZC3H1   |
|           |      |      |      |      |      |          | 0, ELI2, FLT1, TRAF4, LD  |
|           |      |      |      |      |      |          | HA, PFAS, RNM1T1, INT   |
|           |      |      |      |      |      |          | WISPI, ADNP, CTC1, EPHA2, R   |
|           |      |      |      |      |      |          | 57, UMPS, LTRP1, DNTT   |
|           |      |      |      |      |      |          | UNDC3A, RBK5, PRP4, PRELID  |
|           |      |      |      |      |      |          | IP1, CENPE, SUV39H2, Y, 1, RPRK4, NOC4, ARL4D, SEM  |
|           |      |      |      |      |      |          | THOC2, JIR2BP, PLK4, AIC, MAFF, FLT1, AREG, CCNA  |
|           |      |      |      |      |      |          | PLCD3, NUP12, GTF3C1, 2, MBP, PACRG, DDX51, VPS   |
|           |      |      |      |      |      |          | THOC1, RAD51C, MRB, 37B, CNTRB, ELI2, TRAF4, LD   |
|           |      |      |      |      |      |          | F, PTBRU, SUT4A1, SRB, HA, PFAS, RNM1T1, INTS7, LU  |
|           |      |      |      |      |      |          | M4, PRRT15A, SARNP, M05, CENPE, SUV39H2, MCA  |
|           |      |      |      |      |      |          | PACRG, ANP1L, ARCE1, M, PLK4, PLCD3, RAD51C, SGI  |
|           |      |      |      |      |      |          | IGF2, P1, WNT10A, ARCE1, TGF2,  |
|           |      |      |      |      |      |          | CDN1, ADNP, BCL11A  |
|           |      |      |      |      |      |          | , ANOT1, IMPD4, IERF, P   |
|           |      |      |      |      |      |          | RELD1, PDPR, MBP, M   |
|           |      |      |      |      |      |          | PP2, PTHH, IIR, ZBP1, LN  |
|           |      |      |      |      |      |          | FL3, WEE1, ZSCAN20, S   |
|           |      |      |      |      |      |          | TK35, PMEPAL, RCC2, E   |
|           |      |      |      |      |      |          | PMEPAL, SUL, MEPAL, PTHH, PRELID, TV4, TRIM8, SARNP, CRI  |
|           |      |      |      |      |      |          | M1, RNF145,   |
|           |      |      |      |      |      |          | PRK3, ELAVL1, CTC1, EP  |
|           |      |      |      |      |      |          | HA2, RUNC3A, RPRD1  |
|           |      |      |      |      |      |          | A, RBK5, PRP4, GSK8, NO   |
|           |      |      |      |      |      |          | CAL, ARL4D, SEMAC,  |
|           |      |      |      |      |      |          | MAFF, FLT1, AREG, CCN   |
|           |      |      |      |      |      |          | A2, DDX51, GTF3C1, ZH   |
|           |      |      |      |      |      |          | X2, WNT10A, AFR4, AN  |
|           |      |      |      |      |      |          | APC10, PARDBA, VPS37  |
|           |      |      |      |      |      |          | B, ZC3H10, PHC1, ELI2,  |
|           |      |      |      |      |      |          | WISPI, CTC1, EPHA2, RUNC  |
|           |      |      |      |      |      |          | TRAF4, LDHA, PFAS, RN   |
|           |      |      |      |      |      |          | MTL1, INTS7, UMPS, LT   |
|           |      |      |      |      |      |          | 3A, RBK5, PRP4, NOC4, ARL4  |
|           |      |      |      |      |      |          | BP1, DNTT1P, CENPE, S, D, SEMAC, NCAM1, MAFF, FL  |
|           |      |      |      |      |      |          | UY39H2, YTHOC2, IIRF2, T1, AREG, CCNA2, ZH2, PACR   |
|           |      |      |      |      |      |          | BP1, R, CDS, NUP12, TH, GL, DDX51, VPS37B, PHC1, EL   |
|           |      |      |      |      |      |          | OC1, RAD51C, MRB, SY, L2, TRAF4, LDHA, PFAS, RNM1T  |
|           |      |      |      |      |      |          | NCN1P, PPR1, SUT4A, L1, INTS7, UMPS, CENPE, SUV   |
|           |      |      |      |      |      |          | 1, SRNP4, PPR1, TRISAP, 39H2, M, CDM, PLCD3, RPD051   |
|           |      |      |      |      |      |          | AICGGL, ANP1L, ARCE1, T, C, SGPI, WNT10A, ARCE1, TG   |
|           |      |      |      |      |      |          | GF2,  |
|           |      |      |      |      |      |          | AUTS2, EMCK, TREM1, IF2,  |
|           |      |      |      |      |      |          | BCL11A, BBOX2, PITX1  |
|           |      |      |      |      |      |          | , 50M6, RRB1, DENND2  |
|           |      |      |      |      |      |          | C, PRICKLE3, H3SS1, LM  |
|           |      |      |      |      |      |          | AML13, GRHL2, CENPE1, C   |
|           |      |      |      |      |      |          | SRNP2, JINBA, NF13, S   |
|           |      |      |      |      |      |          | OX5, CNOT7, DKL1, MO  |
|           |      |      |      |      |      |          | RC4, CAMK1G, PRSS12,  |
|           |      |      |      |      |      |          | WRAP53, FGR2, NASP,   |
|           |      |      |      |      |      |          | EZF1, GZL3, NANOS1,   |
|           |      |      |      |      |      |          | MX1L, VAV3, PCOH7, KR   |
|           |      |      |      |      |      |          | T14, HOXA2, STCL, PTC   |
|           |      |      |      |      |      |          | HL, KIF20B, TDP2, CCN   |
|           |      |      |      |      |      |          | 1,  |
|           |      |      |      |      |      |          | KLHL13, NCAM1, JAM3   |
|           |      |      |      |      |      |          | , RASSF2, CDR2L, MNOT   |
|           |      |      |      |      |      |          | , EBF1, KBTBD10, FSTL1  |
|           |      |      |      |      |      |          | , ANGP1, NRP1,  |
| VSSOX5_01 | 1.50 | 4.17 |      |      | 1.85 | VSSOX5_0 | CTGF60, INH   |
|           |      |      |      |      |      |          | BA, WRAP53,   |
|           |      |      |      |      |      |          | PPR2R2B,  |



















|           |      |      |      |      |           |                |  |
|-----------|------|------|------|------|-----------|----------------|--|
| V\$AP1_Q2 | 7.37 | 6.63 | 4.40 | 6.25 | V\$AP1_Q2 | 5.88 Q2        | <p>MDR1, FHOD</p> <p>1.SYNPO,UB MDR1,FHOD1,CYP2A4,1</p> <p>ECG,RINI,GA TUBA1C,CHP2,SGTB,6</p> <p>PDR,REL2,F APDR,REL2,NMR3,GN</p> <p>H3,LANC2, AS,PHI3,PARB2,ZA,SCRN1</p> <p>LANB3,FGH1,ZNF23,NCDN,LANC2,U</p> <p>1, BEC2,TAGLN2,FGF11,</p> <p>MDR1,N1,P,CDCL1,EPH</p> <p>A2,UCN2,LANB3,ATX</p> <p>ES2,CWAS,NH5,MAMP</p> <p>E3,PM2,XPOT,PNK3,E MDR1,UZ3A,PICD1,EPHA2,IL</p> <p>FNAL,GAPDH,DSN1,6,UCN2,LANB3,ASS1,ATXN</p> <p>MDR1,UBEC2 PDH,TXN,TUBA1C,FAP,C</p> <p>UFU,LANC2,PAV9,EN 712,SLC9A5,TRIM8,CO,27A</p> <p>DOU,OMG,IL10,UBR2 1,XPOT,PAAPA,SUFU,LANC</p> <p>3,ZIC1,LANC EV28,UCHI3,CYP2A4,1</p> <p>EL2,SFN,EK3,MMP9,UBEC2,RINI,SFN,EK3,MMP</p> <p>2,LANB3,FG,UBEC2,REL2,NMR3,SFN,PAK6,KOV3A,FAM178</p> <p>9,PTFRN,PAK6,FAM178B,PI C,MRP1,</p> <p>FN1, ,NCDN,</p> <p>MDR1,SLC4A11,RINI,17</p> <p>MAGL,EPHA2,RUNDC</p> <p>3A,LANA3,RIPIK4,UCN MDR1,SLC4A11,NFATC4,IL23</p> <p>2,KRTBDB,ATXN712,P A,TIMAQ1,EPHA2,RUNDC</p> <p>H1D2,TLL1,TRIM8,PI A,LANA3,RIPIK4,UCN2,KRTB</p> <p>C4,HS97,FE,FI,2,NE</p> <p>RT,GMAS,GNM1,SPAT</p> <p>DS,V5SP,PHL02,SLC9A5,T</p> <p>K6,KRTBDB,MYBP,FA</p> <p>MDR1,YWHAZ,NMR3,JS</p> <p>S2,XPOT,PNK3,FNAL, RIM8,ATXN712,CO,27A,1,TS</p> <p>P5,PAK6,CDKX,CO,2</p> <p>MDR1,PA,GAPOH,REL2, GAPDH,DSN1,PICD1,</p> <p>KU,XPOT,PAAPA,ENO1,PLC 7A,1,DMNK,ABCD,1,IG</p> <p>MDR1,UBEC2 PSMD2,SFN,PHI3,ENO1, AMC2,OMG,BMP2,EN</p> <p>D1,LANC2,SCOC,SPAT,52,UC FBR2,PAAPA,FERMT3,</p> <p>H,REL2,FHL BEC2,TAGLN2,CMA5,1M</p> <p>U1,UBEC2,PSMD1,RE H13,OMG,BMP2,UBEC2,RIN</p> <p>KRTBD10,VAMP5,DCN</p> <p>3,LANC2, EW54,UCHI3,</p> <p>AG,KOV3A,PTPNC1, AK6,PTPNC1,</p> <p>MESDC1,QRTRD1,AS8</p> <p>16,FAM128,TRAF4,JS</p> <p>EMA6D,NADRO1,PGF,</p> <p>PTK7,SIX5,WNT10B,1</p> <p>MPDH,REP1,INDUF A</p> <p>PTK7,SIX5,WNT10B,1</p> <p>4L2,CCDC18,WNT7B,E</p> <p>RBB3,TCF7,DDIT4,SUV QTRTRD,PTK7,TRAF4,SEMA</p> <p>POLIM4,TGFRB2,OBSC</p> <p>3,9H2,GLT5,CHL,IFR2BP 6D,5GPI1,PGF,PRICKLE1,SIX</p> <p>N,TGFRB3,DES,PA5,12,</p> <p>L,DLL4,TSEN54,GRP21 5,REP1,INDUF,PA12,CCDC18</p> <p>ASB5,FLUP1,JHEF2,KCN</p> <p>A,RTB2,PCYT1B,EZF1, DDIT4,SUV39H2,DBCL,DLL</p> <p>MA1,DBC1,PRICKLE1,</p> <p>TAP4,IL11,STOML2, 4,SLC25A2,TSEN54,PCYT1</p> <p>MYBP1,ENQ3,ITGB1B</p> <p>PTK7,RTKN5,PGF,PTK7,TAP4,NCDN,1,WNT4,PRAT,CASKIN2,</p> <p>B,TAP4,IL11,WNT4,PRAT,C</p> <p>P2,GPM6B,TMEM182,</p> <p>UC26A10,CU MPDH1,WDR81,SLC25A</p> <p>WNT9A,PHF7,PAK6,9P ASKIN2,WNT9A,PHF7,PAK6</p> <p>TMEM100,CD9B,AM</p> <p>NEP1,</p> <p>MYL6B,</p> <p>MESDC1,ASB16,TME</p> <p>M125,EPHA2,SLC25A3</p> <p>5,TRAF4,NES,PGF,TNN</p> <p>T2,PTK7,SIX5,INDUF A</p> <p>TMOD3,HOXCA,NES,PGF,PR</p> <p>ICKE1,1,TNNT2,PTK7,SIX5,PP</p> <p>OBSCN,PRICKLE1,FBX</p> <p>1,KONQ4,SUV39H2,GI</p> <p>M,UL,CACNA1G,INDUF,PA12,7</p> <p>ORQ,MAP2,ASB5,OLF</p> <p>TSOR1,CNNM2,NINJA4,MEIM25,TRAF4,KCNQ4,SU</p> <p>WILL,HEF2,KCNMA1,C</p> <p>BTR2,PCYT1B,CO,7A,1,</p> <p>V39H2,EPHA2,CNNM2,AP0</p> <p>ACNA1G,TMEM182,M</p> <p>TAP4,NANOS1,STOM</p> <p>LD1,NINJA,PCYT1B,CO,7A,1,7</p> <p>YBP,FLUP1,CBK6,FA</p> <p>SEG,FLA,RTK</p> <p>B,PHI3,PRICKO,PTPNU,1</p> <p>L2,WNT4,WNT9A,XPN</p> <p>FAP4,WNT4,KCH12,WNT9</p> <p>MP2,TMEM100,NES,R</p> <p>N,PTK7, CK,</p> <p>AMNT6B,</p> <p>AS112,</p> |
| V\$AP1_Q6 | 3.74 | 6.86 | 3.73 | 8.12 | V\$AP1_Q6 | 9.53 V\$AP1_Q6 | <p>MDR1,UBEC2</p> <p>PSMD2,SFN,PHI3,ENO1, AMC2,OMG,BMP2,EN</p> <p>D1,LANC2,SCOC,SPAT,52,UC FBR2,PAAPA,FERMT3,</p> <p>H,REL2,FHL BEC2,TAGLN2,CMA5,1M</p> <p>U1,UBEC2,PSMD1,RE H13,OMG,BMP2,UBEC2,RIN</p> <p>KRTBD10,VAMP5,DCN</p> <p>3,LANC2, EW54,UCHI3,</p> <p>AG,KOV3A,PTPNC1, AK6,PTPNC1,</p> <p>MESDC1,QRTRD1,AS8</p> <p>16,FAM128,TRAF4,JS</p> <p>EMA6D,NADRO1,PGF,</p> <p>PTK7,SIX5,WNT10B,1</p> <p>MPDH,REP1,INDUF A</p> <p>PTK7,SIX5,WNT10B,1</p> <p>4L2,CCDC18,WNT7B,E</p> <p>RBB3,TCF7,DDIT4,SUV QTRTRD,PTK7,TRAF4,SEMA</p> <p>POLIM4,TGFRB2,OBSC</p> <p>3,9H2,GLT5,CHL,IFR2BP 6D,5GPI1,PGF,PRICKLE1,SIX</p> <p>N,TGFRB3,DES,PA5,12,</p> <p>L,DLL4,TSEN54,GRP21 5,REP1,INDUF,PA12,CCDC18</p> <p>ASB5,FLUP1,JHEF2,KCN</p> <p>A,RTB2,PCYT1B,EZF1, DDIT4,SUV39H2,DBCL,DLL</p> <p>MA1,DBC1,PRICKLE1,</p> <p>TAP4,IL11,STOML2, 4,SLC25A2,TSEN54,PCYT1</p> <p>MYBP1,ENQ3,ITGB1B</p> <p>PTK7,RTKN5,PGF,PTK7,TAP4,NCDN,1,WNT4,PRAT,CASKIN2,</p> <p>B,TAP4,IL11,WNT4,PRAT,C</p> <p>P2,GPM6B,TMEM182,</p> <p>UC26A10,CU MPDH1,WDR81,SLC25A</p> <p>WNT9A,PHF7,PAK6,9P ASKIN2,WNT9A,PHF7,PAK6</p> <p>TMEM100,CD9B,AM</p> <p>NEP1,</p> <p>MYL6B,</p> <p>MESDC1,ASB16,TME</p> <p>M125,EPHA2,SLC25A3</p> <p>5,TRAF4,NES,PGF,TNN</p> <p>T2,PTK7,SIX5,INDUF A</p> <p>TMOD3,HOXCA,NES,PGF,PR</p> <p>ICKE1,1,TNNT2,PTK7,SIX5,PP</p> <p>OBSCN,PRICKLE1,FBX</p> <p>1,KONQ4,SUV39H2,GI</p> <p>M,UL,CACNA1G,INDUF,PA12,7</p> <p>ORQ,MAP2,ASB5,OLF</p> <p>TSOR1,CNNM2,NINJA4,MEIM25,TRAF4,KCNQ4,SU</p> <p>WILL,HEF2,KCNMA1,C</p> <p>BTR2,PCYT1B,CO,7A,1,</p> <p>V39H2,EPHA2,CNNM2,AP0</p> <p>ACNA1G,TMEM182,M</p> <p>TAP4,NANOS1,STOM</p> <p>LD1,NINJA,PCYT1B,CO,7A,1,7</p> <p>YBP,FLUP1,CBK6,FA</p> <p>SEG,FLA,RTK</p> <p>B,PHI3,PRICKO,PTPNU,1</p> <p>L2,WNT4,WNT9A,XPN</p> <p>FAP4,WNT4,KCH12,WNT9</p> <p>MP2,TMEM100,NES,R</p> <p>N,PTK7, CK,</p> <p>AMNT6B,</p> <p>AS112,</p>   |
| V\$AP1_Q5 | 2.82 | 1.33 | 3.58 | 3.58 | V\$AP1_Q5 | 6.38 V\$AP1_Q5 | <p>MDR1,SLC4A11,RINI,17</p> <p>MAGL,EPHA2,RUNDC</p> <p>3A,LANA3,RIPIK4,UCN MDR1,SLC4A11,NFATC4,IL23</p> <p>2,KRTBDB,ATXN712,P A,TIMAQ1,EPHA2,RUNDC</p> <p>H1D2,TLL1,TRIM8,PI A,LANA3,RIPIK4,UCN2,KRTB</p> <p>C4,HS97,FE,FI,2,NE</p> <p>RT,GMAS,GNM1,SPAT</p> <p>DS,V5SP,PHL02,SLC9A5,T</p> <p>K6,KRTBDB,MYBP,FA</p> <p>MDR1,YWHAZ,NMR3,JS</p> <p>S2,XPOT,PNK3,FNAL, RIM8,ATXN712,CO,27A,1,TS</p> <p>P5,PAK6,CDKX,CO,2</p> <p>MDR1,PA,GAPOH,REL2, GAPDH,DSN1,PICD1,</p> <p>KU,XPOT,PAAPA,ENO1,PLC 7A,1,DMNK,ABCD,1,IG</p> <p>MDR1,UBEC2 PSMD2,SFN,PHI3,ENO1, AMC2,OMG,BMP2,EN</p> <p>D1,LANC2,SCOC,SPAT,52,UC FBR2,PAAPA,FERMT3,</p> <p>H,REL2,FHL BEC2,TAGLN2,CMA5,1M</p> <p>U1,UBEC2,PSMD1,RE H13,OMG,BMP2,UBEC2,RIN</p> <p>KRTBD10,VAMP5,DCN</p> <p>3,LANC2, EW54,UCHI3,</p> <p>AG,KOV3A,PTPNC1, AK6,PTPNC1,</p> <p>MESDC1,QRTRD1,AS8</p> <p>16,FAM128,TRAF4,JS</p> <p>EMA6D,NADRO1,PGF,</p> <p>PTK7,SIX5,WNT10B,1</p> <p>MPDH,REP1,INDUF A</p> <p>PTK7,SIX5,WNT10B,1</p> <p>4L2,CCDC18,WNT7B,E</p> <p>RBB3,TCF7,DDIT4,SUV QTRTRD,PTK7,TRAF4,SEMA</p> <p>POLIM4,TGFRB2,OBSC</p> <p>3,9H2,GLT5,CHL,IFR2BP 6D,5GPI1,PGF,PRICKLE1,SIX</p> <p>N,TGFRB3,DES,PA5,12,</p> <p>L,DLL4,TSEN54,GRP21 5,REP1,INDUF,PA12,CCDC18</p> <p>ASB5,FLUP1,JHEF2,KCN</p> <p>A,RTB2,PCYT1B,EZF1, DDIT4,SUV39H2,DBCL,DLL</p> <p>MA1,DBC1,PRICKLE1,</p> <p>TAP4,IL11,STOML2, 4,SLC25A2,TSEN54,PCYT1</p> <p>MYBP1,ENQ3,ITGB1B</p> <p>PTK7,RTKN5,PGF,PTK7,TAP4,NCDN,1,WNT4,PRAT,CASKIN2,</p> <p>B,TAP4,IL11,WNT4,PRAT,C</p> <p>P2,GPM6B,TMEM182,</p> <p>UC26A10,CU MPDH1,WDR81,SLC25A</p> <p>WNT9A,PHF7,PAK6,9P ASKIN2,WNT9A,PHF7,PAK6</p> <p>TMEM100,CD9B,AM</p> <p>NEP1,</p> <p>MYL6B,</p> <p>MESDC1,ASB16,TME</p> <p>M125,EPHA2,SLC25A3</p> <p>5,TRAF4,NES,PGF,TNN</p> <p>T2,PTK7,SIX5,INDUF A</p> <p>TMOD3,HOXCA,NES,PGF,PR</p> <p>ICKE1,1,TNNT2,PTK7,SIX5,PP</p> <p>OBSCN,PRICKLE1,FBX</p> <p>1,KONQ4,SUV39H2,GI</p> <p>M,UL,CACNA1G,INDUF,PA12,7</p> <p>ORQ,MAP2,ASB5,OLF</p> <p>TSOR1,CNNM2,NINJA4,MEIM25,TRAF4,KCNQ4,SU</p> <p>WILL,HEF2,KCNMA1,C</p> <p>BTR2,PCYT1B,CO,7A,1,</p> <p>V39H2,EPHA2,CNNM2,AP0</p> <p>ACNA1G,TMEM182,M</p> <p>TAP4,NANOS1,STOM</p> <p>LD1,NINJA,PCYT1B,CO,7A,1,7</p> <p>YBP,FLUP1,CBK6,FA</p> <p>SEG,FLA,RTK</p> <p>B,PHI3,PRICKO,PTPNU,1</p> <p>L2,WNT4,WNT9A,XPN</p> <p>FAP4,WNT4,KCH12,WNT9</p> <p>MP2,TMEM100,NES,R</p> <p>N,PTK7, CK,</p> <p>AMNT6B,</p> <p>AS112,</p>   |
| V\$AP1_Q6 | 2.44 | 1.38 | 2.35 | 4.55 | V\$AP1_Q6 | 5.67 V\$AP1_Q6 | <p>MDR1,SLC4A11,RINI,17</p> <p>MAGL,EPHA2,RUNDC</p> <p>3A,LANA3,RIPIK4,UCN MDR1,SLC4A11,NFATC4,IL23</p> <p>2,KRTBDB,ATXN712,P A,TIMAQ1,EPHA2,RUNDC</p> <p>H1D2,TLL1,TRIM8,PI A,LANA3,RIPIK4,UCN2,KRTB</p> <p>C4,HS97,FE,FI,2,NE</p> <p>RT,GMAS,GNM1,SPAT</p> <p>DS,V5SP,PHL02,SLC9A5,T</p> <p>K6,KRTBDB,MYBP,FA</p> <p>MDR1,YWHAZ,NMR3,JS</p> <p>S2,XPOT,PNK3,FNAL, RIM8,ATXN712,CO,27A,1,TS</p> <p>P5,PAK6,CDKX,CO,2</p> <p>MDR1,PA,GAPOH,REL2, GAPDH,DSN1,PICD1,</p> <p>KU,XPOT,PAAPA,ENO1,PLC 7A,1,DMNK,ABCD,1,IG</p> <p>MDR1,UBEC2 PSMD2,SFN,PHI3,ENO1, AMC2,OMG,BMP2,EN</p> <p>D1,LANC2,SCOC,SPAT,52,UC FBR2,PAAPA,FERMT3,</p> <p>H,REL2,FHL BEC2,TAGLN2,CMA5,1M</p> <p>U1,UBEC2,PSMD1,RE H13,OMG,BMP2,UBEC2,RIN</p> <p>KRTBD10,VAMP5,DCN</p> <p>3,LANC2, EW54,UCHI3,</p> <p>AG,KOV3A,PTPNC1, AK6,PTPNC1,</p> <p>MESDC1,QRTRD1,AS8</p> <p>16,FAM128,TRAF4,JS</p> <p>EMA6D,NADRO1,PGF,</p> <p>PTK7,SIX5,WNT10B,1</p> <p>MPDH,REP1,INDUF A</p> <p>PTK7,SIX5,WNT10B,1</p> <p>4L2,CCDC18,WNT7B,E</p> <p>RBB3,TCF7,DDIT4,SUV QTRTRD,PTK7,TRAF4,SEMA</p> <p>POLIM4,TGFRB2,OBSC</p> <p>3,9H2,GLT5,CHL,IFR2BP 6D,5GPI1,PGF,PRICKLE1,SIX</p> <p>N,TGFRB3,DES,PA5,12,</p> <p>L,DLL4,TSEN54,GRP21 5,REP1,INDUF,PA12,CCDC18</p> <p>ASB5,FLUP1,JHEF2,KCN</p> <p>A,RTB2,PCYT1B,EZF1, DDIT4,SUV39H2,DBCL,DLL</p> <p>MA1,DBC1,PRICKLE1,</p> <p>TAP4,IL11,STOML2, 4,SLC25A2,TSEN54,PCYT1</p> <p>MYBP1,ENQ3,ITGB1B</p> <p>PTK7,RTKN5,PGF,PTK7,TAP4,NCDN,1,WNT4,PRAT,CASKIN2,</p> <p>B,TAP4,IL11,WNT4,PRAT,C</p> <p>P2,GPM6B,TMEM182,</p> <p>UC26A10,CU MPDH1,WDR81,SLC25A</p> <p>WNT9A,PHF7,PAK6,9P ASKIN2,WNT9A,PHF7,PAK6</p> <p>TMEM100,CD9B,AM</p> <p>NEP1,</p> <p>MYL6B,</p> <p>MESDC1,ASB16,TME</p> <p>M125,EPHA2,SLC25A3</p> <p>5,TRAF4,NES,PGF,TNN</p> <p>T2,PTK7,SIX5,INDUF A</p> <p>TMOD3,HOXCA,NES,PGF,PR</p> <p>ICKE1,1,TNNT2,PTK7,SIX5,PP</p> <p>OBSCN,PRICKLE1,FBX</p> <p>1,KONQ4,SUV39H2,GI</p> <p>M,UL,CACNA1G,INDUF,PA12,7</p> <p>ORQ,MAP2,ASB5,OLF</p> <p>TSOR1,CNNM2,NINJA4,MEIM25,TRAF4,KCNQ4,SU</p> <p>WILL,HEF2,KCNMA1,C</p> <p>BTR2,PCYT1B,CO,7A,1,</p> <p>V39H2,EPHA2,CNNM2,AP0</p> <p>ACNA1G,TMEM182,M</p> <p>TAP4,NANOS1,STOM</p> <p>LD1,NINJA,PCYT1B,CO,7A,1,7</p> <p>YBP,FLUP1,CBK6,FA</p> <p>SEG,FLA,RTK</p> <p>B,PHI3,PRICKO,PTPNU,1</p> <p>L2,WNT4,WNT9A,XPN</p> <p>FAP4,WNT4,KCH12,WNT9</p> <p>MP2,TMEM100,NES,R</p> <p>N,PTK7, CK,</p> <p>AMNT6B,</p> <p>AS112,</p>   |



|              |      |       |      |      |              |         |   |
|--------------|------|-------|------|------|--------------|---------|---|
| VSCORE_Q2    | 3.70 | 1.42  | 7.34 | 5.07 | VSCORE_Q     | 2       | CHRF,PLSCR<br>3,RUSCL,PRE,SLC8A1,WISPL,PIK4,C<br>LUD1,PTTX2J, OLSA3,PRELUD1,GTFTZ4I<br>AG1,SE2612, MAF,TAGLUN2,JAG1,<br>2,MRRF,<br>58,<br>ONMAD1,TRIM39,DDX<br>51,ELAVL1,MESDCL,C<br>TC1,EPHA2,RUNDC3A,<br>RPRD1A,SLC25A37,PK<br>P4,PRELUD1,RIPIK4,PA<br>NCD2,CBX8,NOCL,AR<br>L4D,WDHD1,CBX3,MA<br>FF,SEMA4C,NR6A1,W<br>NT10A,FAM167A,PRR<br>3,LSM12,VPS37B,CNT<br>ROB,CZ3H10,CEP57,M<br>RRE,MSX2,JAG1,LDHA<br>ONMAD1,WISPL,PABPC1,EP<br>PFAS,INTS7,LTBP1,SL<br>HA2,RUNDC3A,SLC25A37,P<br>CB8A2,KIF7,IRX3,YTH<br>KP4,PRELUD1,RIPIK4,FANCD2<br>DC3,IRE2BP,PIK4,CA<br>NOCL,AR,4D,WDHD1,CBX<br>SC5,THOC1,POLC1,DN<br>NT10A,DDX51,LSM12,VPS3<br>AC9,PTPRU,BBBR8,IT<br>NT10A,DDX51,LSM12,VPS3<br>HG2,GTFR3,CL,ERF,PPP<br>TB,CNTROB,CTCL,JAG1,LDH<br>R5A,KIF17,SAHP1P<br>APPAS,INTS7,SLC8A2,PIK4<br>M4,NPTXL,ALKRH5,TG<br>CJGSG,DPH3,DNAIC9,ERF,S<br>IF2,ELMO3,<br>GPI,KIF17,TGIF2,   |
| VSCORE_Q4    | 2.86 | 13.44 | 7.72 |      | VSCORE_Q     | 4       | CHRF,RUSCL<br>J,PRELUD1,PT<br>X2,JAG1,SEZ<br>612,<br>ONMAD1,TRIM39,ELAVL1<br>J,MESDCL,CTCL,HSY9<br>J,BCL11A,EPHA2,RUNDC<br>3A,RPRD1A,ERF,RIPIK<br>4,TPM4,CBX8,NOCL,<br>AR,4D,SEMA4C,CBX3,<br>MAFF,FLT1,DDX51,JBC<br>L2L13,WNT10A,FAM1<br>677A,AF4,KCNK1,VP53<br>ONMAD1,CTCL,EPHA2,RUN<br>78,CNTROB,CZ3H10,E<br>DCA,ERF,RIPIK4,NOCL,ARL<br>LL2,MSX2,NPTXL,LTBP<br>4D,SEMA4C,CBX3,MAFF,FLT<br>1,SLC8A2,SUV9H21,<br>1,WNT10A,DDX51,KCNK1,C<br>R72BP,FLT1,TR3,MRP51<br>NTR0B,VPS37B,ELI2,SLC38<br>88,PTPRU,BBBR8,ITG6<br>A2,SUV9H21,MRP51,88,FLR<br>2,PTPR1,SL5A,GSTCD1,<br>T3,MCM4,DPH3,SGP1,GST<br>GF2,<br>CD,TGIF2,<br>AGB15,SYNPO,JAR102,<br>BEND4,MDM1,NR6A1<br>SEMA7A,TFAP2C,KCN<br>K7,DDX3,KIF5,DDCA<br>P1,PHC1,KIF7,DXL1N<br>KAIN1,CNSPUD1,RN6A1<br>1,LTBP1,KRT14,CD44,<br>SYNPO,PABPC1,JAR102,PRIC<br>ERS1,SETD8,WETT121,<br>KLE1,NR6A1,CACNA1G,CDC<br>D,PHF7,P2RY2,GCA1,<br>A3,KIF5,PHC1,BEND4,IERG1<br>PRICKLE1,TGFR4,MB,<br>MTERD3,UBE23,SNR<br>SETD8,WETT121,SD1,MID<br>ARHGFF6,SIPR2,FLI1,<br>PDI,RIN1,CDK2,MRB6<br>M1,SEMA7A,SNRPD1,RIN1,<br>OD,RHOC,C6,<br>ACTN3,CASQ1,ANKRD<br>2,CHRN1,NEB,MYLK<br>2,JUNC5B,CNN1,GFRA<br>1,TTN,DMPK,FSTPDP1,<br>XIRP1, |
| VSCORE_P1_Q2 | 2.23 | 6.52  | 4.10 |      | VSCORE_P1_Q2 |         | PITD2,RUSCL<br>SE2612,THIC<br>HPF,  |
| VSWB_Q6      | 2.97 | 3.23  | 2.30 |      | VSWB_Q       | 1.96 6  | ZNF746,SYN<br>PO,SOCS2,T<br>PS313,RIN1,<br>CDCA3,<br>PDOFB,RIN1,<br>HNL1,TNFRSF<br>21,FLIM1,S<br>LC26A10,GA<br>UNT2,  |
| VSWMOD_Q6    | 3.89 |       |      |      | VSWMOD_Q     | 3.00 Q6 |   |







|                    |      |      |      |          |                    |                                    |   |
|--------------------|------|------|------|----------|--------------------|------------------------------------|---|
| VSMEF2_03          | 1.64 |      |      | VSMEF2_0 | 12.72 3            | AR181.SHA<br>NR2.PMEFA<br>1.TPM4.2 | SSPN,THMP2,ACTG1,T<br>NNC2,MYL1,ITGB1BP<br>2.TBON,CASQ1,SIPR1<br>,HFE2,THBS2,LYN,COL<br>8A1,ADP1,TSC2D1,G<br>NBA,MYO22,ENOS3,SY<br>NPO2L,XBP1,ADOC2,S<br>MPXJ51,MFE2CATP<br>1A2,PTPRN,RRX1, |
| VSANNT_01          | 2.92 | 2.71 | 4.67 | 4.30     | 1                  | VSANNT_0                           |   |
| VSNGFC_01          | 1.55 | 3.23 |      |          | VSNGFC_01          | VSNGFC_01                          | ETV1,GRNEM2,CDC80,<br>CD36,LOB2,CNK14,HS<br>6572,ZIC1,CD798,SLA,<br>MMP14,FHBP14,ARM<br>CQ3,ARMC2,SULF1,P<br>RRX1,  |
| VSOC1_07           | 1.43 |      |      |          | VSOC1_0            | VSOC1_0                            |   |
| VSXBP7_01          | 2.51 | 1.57 |      |          | VSXBP7_0           | VSXBP7_0                           |   |
| VSIMQZCOM_01       | 4.55 | 1.79 | 4.91 | 3.44     | VSIMQZCOM_01       | VSIMQZCOM_01                       |   |
| VSXFX1_01          | 1.54 |      | 2.63 | 3.65     | VSXFX1_0           | VSXFX1_0                           |   |
| CCANNAGRGCC_UNKNOW | 1.80 | 1.47 | 2.02 | 3.35     | CCANNAGRGCC_UNKNOW | CCANNAGRGCC_UNKNOW                 |   |



|             |      |      |       |             |                                    |   |
|-------------|------|------|-------|-------------|------------------------------------|---|
| V\$VFAC2_01 | 1.52 | 3.08 | 3.55  | V\$VFAC2_01 | PITG2,INHBA<br>,GREN1,PPP<br>ZNR6, | MMP13,DIOC3,BCL11<br>A,CDC41,BRP1,NDR<br>G1,MAFF,KLF12,CNPE<br>1,MAB213,INHBA,NR<br>G1,WEE1,CADM1,KCN<br>MMP13,HOKC4,CDC41,AD<br>OS,NGEF,EXTL,RAD21<br>AM12,NDRG1,BRP1,MAFF<br>,TET2,MCM7,DSTUN<br>KLF12,CNPE1,MAB213,PDE<br>UTD18,CNPI,EGN1,L,P<br>EXT1,RAD21,KCNOS<br>PAPPA,EMP21,MRGPR,NRA<br>CC,STOM2,MTP,BG,<br>JMC07,NGEF,EGN1,BMP2,<br>P,ADAM12,GREN1,G<br>9,PCDH18,UN54,PTP<br>TFAR4,MTP,CNPI,PTNKC1<br>NCL1,ATN1,<br>,<br>TME88,TREB1,GNA<br>O1,CELF4,BCL11A,M5<br>S76,IGL1,LABB3,MAF<br>F,DENNDC,MAN13,2<br>H42,CNPE1,MES2,2C<br>3H1D,ANGPT2,CADM1<br>JUK1,BUB3,TG86,EF<br>N45,MRP518B,MCM7<br>ENNDC,ZHX2,CNPE1,NRG1<br>O40,DCN,CDKN1C,NT<br>NRG1,METTL21D,MMP<br>ARTN,BUB3,TG86,EFNA5,<br>N1,FAP,C1QTNF6,MIR<br>DHL,LRH1,ETV4,TFAP4<br>MRP518B,PAPPA,MCM7,AN<br>GRNF,FSTLL,LRHGAP3<br>TIMM9,PPP<br>R2B,MCM7,CNPI1,BRM5<br>,CCDC12,ZBTB40,TRI<br>GPT2,METTL21D,ETV4,LRH1<br>O,AGPAT3,GRFA1,MYL<br>M8,HOOAA,BCL9,HOK<br>TFAP4,C1QTNF6,TRIM8,CD<br>128TB20,PAPPA,MYC<br>A2,CDK6,ARTN,<br>K6,<br>N1,ZEB2,  |
| V\$VFAC3_01 | 3.00 | 5.73 | 4.01  | 2.70        | V\$VFAC3_01                        | GPR1,BCL11B,TFAP4,BU<br>B3,TG86,C1QTNF6,FAP<br>,NRG1,METTL21D,MMP<br>ARTN,BUB3,TG86,EFNA5,<br>N1,FAP,C1QTNF6,MIR<br>DHL,LRH1,ETV4,TFAP4<br>MRP518B,PAPPA,MCM7,AN<br>GRNF,FSTLL,LRHGAP3<br>TIMM9,PPP<br>R2B,MCM7,CNPI1,BRM5<br>,CCDC12,ZBTB40,TRI<br>GPT2,METTL21D,ETV4,LRH1<br>O,AGPAT3,GRFA1,MYL<br>M8,HOOAA,BCL9,HOK<br>TFAP4,C1QTNF6,TRIM8,CD<br>128TB20,PAPPA,MYC<br>A2,CDK6,ARTN,<br>K6,<br>N1,ZEB2,   |
| V\$VHNR_01  | 2.64 | 1.62 | 1.41  | 2.79        | V\$VHNR_0                          | ETV1,INHBA,EMP2,BUB3,TFAP4,BG<br>ARTN,ANRP<br>11B,GTG2A,LLCP2,PPP2<br>JPP2NR2B,<br>R2B,ARTN,<br>TME88,STN1,LAB1<br>D2,EPH42,PRSS,ANR3<br>ZE,SOX5,TLL,NMDO3,<br>GHRH1,3,ZHX2,CNPE1,P<br>VRL1,RBM14,ZBTB5,5<br>XO4,NMDO3,LEK3,P,DD2,C<br>P<br>PIGB1,NAGBD1,FAP<br>H3RF1,SGOL,NKRF,P<br>NE1,WSP1,CNPI,PVRL1,CO<br>HSPG2,PKACD,SPARC<br>AK1P1,CONTR,P2RY1,<br>LBA1,SH3RF1,SGOL1,EPHA2<br>L1,LMRGPR,NR2P1,6<br>SOX21,IGFBP3,LEK3,H<br>,NKRF,PAK1P1,P2RY1,APOL<br>FBP3,TEK,FAM6C,SUL<br>OXA2,MRP145,PHF6,D<br>DL1,IGFBP3,PCDH12,ZHX2,M<br>F1,ZIC1,IGALS1,AMIC<br>LL4,TBP2,<br>RP45,PHF6,DLL4,<br>A1,RAS12,<br>SCN1G,CELF4,BRP1,<br>ATXN2,YES1,KLF12,<br>S1C10A7,NR6A1,MMP<br>KLF12,CELF4,TFAP4,BUB3,R<br>H2,H12,INHBA,CADM<br>AD21,CNPI,ORCA,KCNOS,<br>EVL1,NIN1,ILR1,L,PRO<br>1,BUB3,RAD21,KCNOS<br>HOKC4,MMPD2,FH2,PMC<br>M3,C1QTNF3,FLU1,ST<br>J,MCH1,ERT3,TFAP4,<br>H,ERT3,COIL3A1,NR6A1,Y<br>L,LRHGAP3,DD,SIT3,C<br>GND1,IRCC,COIL3A1,<br>ES1,BRP1,ATXN2,1,TOPIA<br>XKX3,CBM6,GRAL,H<br>S1C3S1,ARTN,<br>TME88,STN1,LAB1<br>D2,EPH42,PRSS,ANR3<br>ZE,SOX5,TLL,NMDO3,<br>GHRH1,3,ZHX2,CNPE1,P<br>VRL1,RBM14,ZBTB5,5<br>XO4,NMDO3,LEK3,P,DD2,C<br>P<br>PIGB1,NAGBD1,FAP<br>H3RF1,SGOL,NKRF,P<br>NE1,WSP1,CNPI,PVRL1,CO<br>HSPG2,PKACD,SPARC<br>AK1P1,CONTR,P2RY1,<br>LBA1,SH3RF1,SGOL1,EPHA2<br>L1,LMRGPR,NR2P1,6<br>SOX21,IGFBP3,LEK3,H<br>,NKRF,PAK1P1,P2RY1,APOL<br>FBP3,TEK,FAM6C,SUL<br>OXA2,MRP145,PHF6,D<br>DL1,IGFBP3,PCDH12,ZHX2,M<br>F1,ZIC1,IGALS1,AMIC<br>LL4,TBP2,<br>RP45,PHF6,DLL4,<br>A1,RAS12, |
| V\$WAT_06   | 2.28 | 1.86 | 3.93  | 7.80 6      | V\$WAT_0Q                          | PITG2,PDGF<br>B,FLTA,SULF<br>1,ZC1,<br>NUTF2,STN1,HSF4,P<br>TK7,SMAD7,EPHA2,A<br>NARC10,PH1D2,CELF<br>4,SRF,PIGW,KPNB1,EX<br>OC55,UB,KLF10,SKIS,<br>EIF3B,NAT81,ZEP1,CA<br>TSPR2,STT12,TSEN2<br>WEE1,EPHA,HNRNP,D<br>AC1,SPK1,KHL35,TC<br>AHCTF1,PABPC1,SMAD7,EP<br>OF1,ASCL2,ENOPH1,N<br>H42,PH1D2,CELF4,PIGW,5<br>PM1,IR2BP1,PPP2,VE<br>OX4,EXOS5,UB,SIX5,NAT8<br>GRABIN,PHF7,SENA<br>L,ZFR1,JHNRNP,ACT1,KHL<br>7A1,TAPC,OSBPL1D,35,<br>ENOPH1,NR6A1,NODC1,P<br>BR2,NDNA,TFAP4,3<br>DP2,VEGFA,ATL4,PHF7,SE<br>OC53,CNPI,RANBP1,<br>MAY1,OSBPL1D,TFAP4,SO<br>C<br>LRP8,NSUN2,NANDP1,<br>53,CNPI,RANBP1,LRP8,KP<br>TRIM8,P,CD1,NCL,SEN<br>NB1,TRIM8,P,CD1,NCL,DLL<br>B1,DLL4,UBE2S,ABCE<br>4,UBE2S,ABCE1,TGIF2,TGIF<br>1,TGIF2,<br>ZDHHC15,STN1,MB<br>1,<br>LAC2,JUNB,GEN1,SH3<br>BP4,POLR3G,RBK5,KIF<br>7,IGF2BP3,RHEB1,IGR<br>HL2,BHLHE40,CNPE1,<br>NR2F6,MES2,PRR7,JU<br>P,NAV2,NHS,RRM14,F<br>BK19,INR207,JHNRNP<br>JUNB,H2ARY,GEN1,SH3BP<br>D,BCL2A,ZBTB5,LSM5,<br>4,RBK5,GRH12,BHLHE40,NA<br>MRP5,METTL6,VEG<br>T8L,CNPE1,INR207,BGALT<br>FAD1X5,THOCL,NAT8<br>2,JHNRNP,LSM5,MRP5,VE<br>L,IGFBP3,SYNCRIP,MT<br>GEA,DUX5,CDBB,UTP18,MT<br>HD21,TFAP4,MAPRE1,<br>HSD2,TFAR4,METTL6,RRP<br>A1D,FLTA,PD<br>SND2,RAB10,WN15A,B<br>GRB,<br>40ALT2,IGF2BP3,<br>ALB,<br>TSA,ALB,  |
| V\$WCMAX_B  | 1.48 | 2.17 | 11.83 | 11.62       | V\$WCMAX_X_B                       | TBX2,HENMT1,TFAP4,B<br>HN1,PDGFR,<br>CL11B,HNL,PE51,GTFA<br>SEZ6A,2,PIV7<br>1,PTC7,CTC5,MANBP1,E<br>FSA,<br>ZDHHC15,STN1,MB<br>1,<br>LAC2,JUNB,GEN1,SH3<br>BP4,POLR3G,RBK5,KIF<br>7,IGF2BP3,RHEB1,IGR<br>HL2,BHLHE40,CNPE1,<br>NR2F6,MES2,PRR7,JU<br>P,NAV2,NHS,RRM14,F<br>BK19,INR207,JHNRNP<br>JUNB,H2ARY,GEN1,SH3BP<br>D,BCL2A,ZBTB5,LSM5,<br>4,RBK5,GRH12,BHLHE40,NA<br>MRP5,METTL6,VEG<br>T8L,CNPE1,INR207,BGALT<br>FAD1X5,THOCL,NAT8<br>2,JHNRNP,LSM5,MRP5,VE<br>L,IGFBP3,SYNCRIP,MT<br>GEA,DUX5,CDBB,UTP18,MT<br>HD21,TFAP4,MAPRE1,<br>HSD2,TFAR4,METTL6,RRP<br>A1D,FLTA,PD<br>SND2,RAB10,WN15A,B<br>GRB,<br>40ALT2,IGF2BP3,<br>ALB,<br>TSA,ALB,   |
| V\$ZT5_B    | 1.64 | 1.65 | 6.43  | 4.56        | V\$ZT5_B                           | PITG2,SLC26<br>TFAR4,LSM5,FAP,MAZ,P<br>A1D,FLTA,PD<br>SND2,RAB10,WN15A,B<br>GRB,<br>40ALT2,IGF2BP3,<br>ALB,<br>TSA,ALB,   |







|  |      |      |      |      |           |        |
|--|------|------|------|------|-----------|--------|
| V\$SX02_B1                                       | 2.35 | 1.67 | 6.53 | 3.40 | V\$SX02_B | 5.39 1 |
| ETV1,INHBA,RL1,ERN2,CCO92,BCL1,2,HOXA2,PTPN12,ST |      |      |      |      |           |        |
| ZIC1,PLSC03,18,NAVA1,BASP1,NG53P                 |      |      |      |      |           |        |
| PPPR2B,PPR2B,TOP2A                               |      |      |      |      |           |        |
| K38L,CCN1,LFZ                                    |      |      |      |      |           |        |
| K38L   |      |      |      |      |           |        |
| FR1  |      |      |      |      |           |        |
| STX1A,WN13A,RRAD                                 |      |      |      |      |           |        |
| TNEM125,HIF1A,SLC4                               |      |      |      |      |           |        |
| A11,ITGB3BP,POLR1D                               |      |      |      |      |           |        |
| LRN4,BCL9L,LAMB3,5                               |      |      |      |      |           |        |
| RSF7,SAMD12,IVPD3,STX1A,SLC411,RRAD,HIF1         |      |      |      |      |           |        |
| GRHL2,TFAP2A,CCDC1A,POLR1D,LRN4,LAMB3,SR         |      |      |      |      |           |        |
| 4,ZC3H10,UPP,5100A9,SPT7,SAMD12,LYPO3,GRHL2,     |      |      |      |      |           |        |
| ,RBMX2,DSG3,PAQR9,TFAP2A,CCDC14,RBMX2,DS         |      |      |      |      |           |        |
| ANKRD1,USP1,S1PR1,                               |      |      |      |      |           |        |
| LNW2,CRB3,EHF,DLL4,GS,TNEM125,LYNX,MCAH,         |      |      |      |      |           |        |
| CLDN5,SIC7A11,MCA                                |      |      |      |      |           |        |
| B,HN1,ZIC11,PL1,SLC411,HN1,S100A                 |      |      |      |      |           |        |
| AMC2,SLC6  |      |      |      |      |           |        |
| 9,LAMC2,DSG3,SLC6A11                             |      |      |      |      |           |        |
| COH7,STK35,TTG3BP                                |      |      |      |      |           |        |
| D1,SPR2,LLG2,ETV4,PCDH                           |      |      |      |      |           |        |
| PR12A,C10A,CXK5,ZI                               |      |      |      |      |           |        |
| AM6,NXPH4,                                       |      |      |      |      |           |        |
| TNEM88,USP1,SLC6A                                |      |      |      |      |           |        |
| 9,KCNQ3,POLR1D,IGI                               |      |      |      |      |           |        |
| 2,SRF7,SAMD12,ZHX                                |      |      |      |      |           |        |
| 2,WN1T08,KRT8,ZC                                 |      |      |      |      |           |        |
| 3,H1D,PLA2G4D,KCNIP                              |      |      |      |      |           |        |
| 4,FRB3,ITGA3,LYN2                                |      |      |      |      |           |        |
| D,IGF2,SOX4,HNFB1,SRF7,                          |      |      |      |      |           |        |
| ROCD1,SHRNF1,IRF28                               |      |      |      |      |           |        |
| SAMD12,ZHX2,CNIE1,KRT8                           |      |      |      |      |           |        |
| PLEH,DLU4,ERNAL1A,DS,PDFA,LYNX2,NQCD1,SH9        |      |      |      |      |           |        |
| MC2,OMG,USP37,EGF,RP1,DLU4,UCH15,OMG,PLA2        |      |      |      |      |           |        |
| N3,LLG2,GDNF,WN1T                                |      |      |      |      |           |        |
| G4D,EGN1N3,LLG2,GDNF,W                           |      |      |      |      |           |        |
| 9A,CNIE1,  |      |      |      |      |           |        |
| NT9A,  |      |      |      |      |           |        |
| PMEP1,MMP15,TPM                                  |      |      |      |      |           |        |
| TVASH1,TPSNB3,SEC                                |      |      |      |      |           |        |
| 14,2,SMAO6,ITGA3,T                               |      |      |      |      |           |        |
| BCCNR2,CAIP,CSRNIP                               |      |      |      |      |           |        |
| 2,KLF7,DV13,IRF22BP1,                            |      |      |      |      |           |        |
| PRICKLE1,WN1SP1,VASH1,M                          |      |      |      |      |           |        |
| MP15,ITGA3,METS1,IGIC1,K1                        |      |      |      |      |           |        |
| PRICKLE1,TEK,EMILIN                              |      |      |      |      |           |        |
| F7,TPSNB3,PMEP1,ZWILC                            |      |      |      |      |           |        |
| 1,0,TFHML1,WN1SP1,NR2                            |      |      |      |      |           |        |
| F7,LD83,CBR6,AXL,                                |      |      |      |      |           |        |
| H,WN1SA,FAM126A,                                 |      |      |      |      |           |        |
| THRENF1,KIK13,MEN2,                              |      |      |      |      |           |        |
| SOX15,SNARCAS,EIF5                               |      |      |      |      |           |        |
| A,UBP,PAN2,PTK7,BHL                              |      |      |      |      |           |        |
| HEAD,CCT7,ATXN712,F                              |      |      |      |      |           |        |
| UF,PTK7,KIK13,CCT7,SMAR                          |      |      |      |      |           |        |
| BKL19,CASKIN2,XPOL,                              |      |      |      |      |           |        |
| CAS,UB,BHHE40,SOX15,A                            |      |      |      |      |           |        |
| SRE,ARGGEH15,VGGA                                |      |      |      |      |           |        |
| TXN12,XPOL,GREMI,ARH                             |      |      |      |      |           |        |
| ITENS4,MED26,FGR                                 |      |      |      |      |           |        |
| GEH15,VGGA,ITENS4,MED                            |      |      |      |      |           |        |
| 26A10,IGRE                                       |      |      |      |      |           |        |
| OX15,BCL11B,TBZ2,GT                              |      |      |      |      |           |        |
| H7,KRT13,HOKX4,STC                               |      |      |      |      |           |        |
| 1,PCDH7,PMN1J,CASKIN2,5                          |      |      |      |      |           |        |
| ATP1A2,EBF1,KRT8D1                               |      |      |      |      |           |        |
| MI1,PTK7,  |      |      |      |      |           |        |
| ZALF15A,   |      |      |      |      |           |        |
| TCL,   |      |      |      |      |           |        |
| 0,NQAM1,LDAC73,                                  |      |      |      |      |           |        |
| GNQ1,LYNS,CNIE1,R                                |      |      |      |      |           |        |
| COR2,FAM83H,IGL1,R                               |      |      |      |      |           |        |
| RN1,DDO1,TPH4,EIF                                |      |      |      |      |           |        |
| 5A,PGF,KLF2,SAMD1                                |      |      |      |      |           |        |
| 2,MAM13,FMNL2,WN                                 |      |      |      |      |           |        |
| FANCD2,PTK7,ZDHHC12,LIN                          |      |      |      |      |           |        |
| T10B,IST13,PTK7,NRG                              |      |      |      |      |           |        |
| 5,KCOR2,FAM83H,IGL1,RR                           |      |      |      |      |           |        |
| 1,NDUPAL12,HNRPD                                 |      |      |      |      |           |        |
| M1,CUEC1,PGF,KLF2,SA                             |      |      |      |      |           |        |
| ,ERBB3,FRAS1,PRMT1,                              |      |      |      |      |           |        |
| MD12,FMNL2,CNIE1,NR01,                           |      |      |      |      |           |        |
| MIRP51,8B,VGGA,LAM                               |      |      |      |      |           |        |
| NDUPA12,UTP18,HNRPD,                             |      |      |      |      |           |        |
| C2,COL7A1,PRDM10,                                |      |      |      |      |           |        |
| TRAF4,ARHGFE17,PRMT1,M                           |      |      |      |      |           |        |
| PMP22,HSR92,CCDC1                                |      |      |      |      |           |        |
| 111,LRP8,METTL4,FA                               |      |      |      |      |           |        |
| RPS18B,VGGA,LAMC2,UCH                            |      |      |      |      |           |        |
| 02A,MAGED1,FEFMP                                 |      |      |      |      |           |        |
| 8,TPM2,LLA                                       |      |      |      |      |           |        |
| C12,WDR81,PRDX5,ARH                              |      |      |      |      |           |        |
| M126A,CASKIN2,CHK6                               |      |      |      |      |           |        |
| 13,COL7A1,111,LRP8,FAM1                          |      |      |      |      |           |        |
| 2,CERN4,DGKH,SLIT3,                              |      |      |      |      |           |        |
| MC2,LMAN2  |      |      |      |      |           |        |
| GEF17,RGS14,FU12,NM                              |      |      |      |      |           |        |
| ,DLL4,PTCH1,TGIF2,SH                             |      |      |      |      |           |        |
| 26A,CASKIN2,CHK6,DLL4,TG                         |      |      |      |      |           |        |
| FF5,CXK5,NTN1,S100                               |      |      |      |      |           |        |
| L  |      |      |      |      |           |        |
| FLAMC2,UCH13,EF5A,                               |      |      |      |      |           |        |
| 3BP1,  |      |      |      |      |           |        |
| IF2,   |      |      |      |      |           |        |
| A4,  |      |      |      |      |           |        |







|                 |      |      |      |               |           |                       |   |
|-----------------|------|------|------|---------------|-----------|-----------------------|---|
| VSFOXL_02       | 1.63 | 4.07 | 2.29 | 4.14 02       | VSFOXL_02 | PITGLAMC<br>ZJAGLETVY | <p> TRENF,MMPI3,GNA<br/> O1,HOKA2,NDRG1,SE<br/> MA6D,SIC25A39,MAF<br/> F,KUF12,SIC0A7,WD<br/> R46,RAD21,MES2,NR<br/> G1JAG1,CADM1,WNT<br/> 28,TCF7,LUK1,DDIT4,5<br/> HRE1,TET2,DLL1,LA<br/> MC2,BMP2,TPA4,TB<br/> CC,BRX1,TRIM8,STC3<br/> J,HOKA1,DHXC1,PCDH<br/> 18,TC1H,PTNCL1,MT<br/> DING,LSHMAD,JAG1,MAF<br/> PTNCL1,KIT20A,<br/> 1,<br/> MMPI4,ETV1,AMCA<br/> 1,MSRB3,NR4P,GPC3,<br/> FIBIN,A2M,<br/> </p>  |
| VSNOX_01        | 1.38 |      |      | 1.75 VSNOX_01 | VSNOX_01  | MMPI4,ETV<br>1,ITGA3  | <p> PHID2,MOAP2,POCI<br/> A,BHLHE40,GAP1,D<br/> OC2A,CDH24,IR2BP,<br/> FLRT3,GPA21,COL7A,<br/> ELK3,BTB25,FAM122<br/> B,ADNP,FRS3,ITGA7,T<br/> NFRSF12A,SERPINE1,X<br/> POL,PLXNB1,RUVBL2,<br/> CNE2,MST1,PCDH84,<br/> SYT12,RAPHL,ANGPT2<br/> ,KCNP4,HOKA2,HOKA<br/> 1,RPUSD4,DSTN,ARLN<br/> ,PMP2,SMTN12,INHA,<br/> GSL,ETV4,TPA4,CO<br/> X18,PDH17,PHF6,EL<br/> MO3,TRP2,NXPH4,V<br/> SNL1,RCOR2,KRT7,SH<br/> 3BP,LCR6A,DCIN4,GN<br/> A11,CEP164,DFFB,KCD<br/> H812,DUSP9,DUSP8,P<br/> CHB15,RNF152,CITE<br/> D1,JARID2,ENOPH1,IE<br/> RS1,NUDT14,OMG,NU<br/> P54,TRCC,RELI2,TWTC<br/> 2,CDK6,RNF45,PRND<br/> 2,JOVNB,BC11A,BC9L<br/> J,PGF,KLF12,KLF10,PR<br/> 7,DV13,IPCAT4,KCNK3<br/> ,NRG1,WNT3B,OTOP2<br/> AP1,TGIF2,TGIF1,NXPH4,<br/> B2D,FAM5C,<br/> </p> |
| CTGCAGY_UNKNOWN | 4.97 | 2.44 | 6.38 | 4.78          | 8.25 N    | CTGCAGY_UNKNOWN       | <p> ETV1,PGFP<br/> DGF8,ADAM VSNL1,HRA5,GTF2A1,C1<br/> TS2,TUBA1A 9orf66,POCIA,ADAMT15<br/> J,FGF11,RTN2,CNE2,CAP1,COT11,F<br/> R2B,FLH3,R AP4,PP2R2B,OSBP7,R<br/> USCL,BAU25 BM46,HIRA,CALM1,REL<br/> LC6A10,SE 12,NCN4,RNF45,LOK,P<br/> RPINEL, PP2R5C,<br/> </p>   |
| VSNNK62_02      | 1.63 | 1.63 | 2.22 | 1.96          | 5.30 02   | VSNNK62_02            | <p> PHDX5,ZIC1, TNFSF10,PHDX5,MTIOB<br/> J,CAP1,SOX15,UNC13D,C XDC1,PHF5A,ARTN,8T<br/> 15orf41,BTB03,ARTN,<br/> B03,<br/> </p>  |
| VSBAK12_01      | 4.47 | 6.56 | 4.99 | 7.10          | 1.42 01   | VSBAK12_01            | <p> SCA11,SYNPO,RIN1,<br/> TINAGL1,NCG1,RUND<br/> CA,LAAMA3,TAF15,JC<br/> N2,BCL9,BTB011,PHL<br/> DA2,XPO7,SAMD12,T<br/> NFRSF12A,DSG2,CSRN<br/> P1,KBTBD8,CMA5,HBE<br/> GFP,PRSS36,MARE3,G<br/> DNE,SPAT32,CNNAL1<br/> J,ITGB4,PRN3,EFNA1,G<br/> 2,NCG1,REL 2,SRN,KRT16,SCRN1,ZN<br/> C2,FGF11,M 14,TG1G2,BTB011,FGF<br/> MP1, 11,COL5A3,MMPI1,<br/> 9,KDM3A,<br/> </p>  |







|                 |      |      |      |                    |  |  |
|-----------------|------|------|------|--------------------|--|--|
| V\$ANNT_02      | 3.03 | 5.16 | 4.83 | 2.13               | V\$ANNT_0<br>2                               | <div>STMN1,GAPDH,HIF1A,<br/>OLFNL2,FEN1,NPTX1,C<br/>BXS,DCN4,TOPORS,T<br/>HUMPD2,AF4,VP537<br/>BAPEX1,CDKSR1,MAF<br/>F,BKL19,LONP1,HOX<br/>A1,GT2H1,PSME3,JIR<br/>AL1,GT2H1,PSME3,JIR<br/>D2,GT2B3,PAZGA,SY<br/>PREL01,THUMP02,NGRFA<br/>8,RAB31,H19A,HP3,GA<br/>NCRP,HSP9A1,RCOR<br/>P1,HOXA1,SNV,VS37B,GT<br/>2,SNV,ZBTB40,PTPRG,<br/>2H1,PSME3,HIF1A,PAZGA<br/>LTPB2,SQC32,PDH,SIC6GAL,PRDM4P<br/>GAPDH,REL E31,THUMP02,PREL01,<br/>SME1,NCCL,DEPDC7,PA<br/>PEX1,RCOR2,FEN1,DEPDC7,<br/>ID1,ZIC1,SLC BAX,ITR02,KNAU03,IG<br/>SA,AVP11,PREL01,EM<br/>IFR02,NCCL,UTP16,EWEL1,IG<br/>Z6410,<br/>F2BP3,<br/>E1,1GF12,PPCS,NRP15,<br/>F2,MAAF,RRP15,</div>   |
| V\$WYCMAX_03    | 1.56 | 1.52 | 5.03 | 4.16               | V\$WYCMA<br>2.00 X_03                        | <div>TGBF2,AF4,STMN1,F<br/>KBP11,PPIC1,PARPC4<br/>QTRTD1,JOE,M2,NPTX<br/>1,CB8,CB5,ODC,D<br/>CTN4,TOPORS,XPOL1,T<br/>RIM37,NOP58,KCNIG,<br/>SLC38A2,VP537B,RBM1<br/>TGBF2,PKBP11,PABRC1,TRI<br/>15B,FBX19,DUSP7,H<br/>M37,QTRTD1,ADAM12,ODC<br/>NRNPD,GAL1,HNRNP4<br/>1,XPOL1,NOP58,VP537B,DUS<br/>3,SMYD4,PD2,MCQ2<br/>P7,HNRNPD,PDN2,SIC38A<br/>NPM1,SHMT1,SYNCR<br/>2,HNRNP43,PP2,MCQ2,N<br/>P,TEAP4,RLF,DEPDC7,<br/>PM1,SHMT1,GAL1,PARPC4,<br/>H3B1,PMU1,HEXA,AD<br/>N2,SEZ612,ZI BAX,NRP3,PRDM4,NEU<br/>HOXA1,PTCH1,EME1,<br/>TPAP,DEPDC7,HOXA1,EME<br/>AM12,GRG3,ZIC1,CBX<br/>C1,<br/>R12,GT2A1,MCN2,<br/>TGF2,PPCS,<br/>1,TGF2,GPR176,<br/>6,5ASB3,GPR176,</div>  |
| V\$FOXM1_01     | 1.60 | 3.45 | 3.53 | 1.60               | V\$FOXM1<br>2.51_01                          | <div>VSNL1,PKT7,CDCC5,CE<br/>GEN1,SAHNP,SYNCRP<br/>CL,HNRNP90,CASQ2,PRMT<br/>3,CFHML1,FSTL1,MFC<br/>P41,PRDYS,NCN,SGTB,<br/>ABTB2,RBS12,RCZP,<br/>6,HOKA,GEN1,MAFCA,DLX<br/>3,CGRMB5,BEFL,LMFC<br/>SMO11,IMB06,PIH3,<br/>5,JAMBID2,NCAM1,OGG4,PI1<br/>N1,ZBTB70,NCAM1,F<br/>7,MAFS,CRIM1,<br/>5,<br/>MESDC1,NUDCD1,FO<br/>XP4,KCNQ3,GNAO1,S<br/>MAO6,EPHA2,TP11,IG1<br/>1,KLF12,TNNT2,ZHX2,<br/>WNTT08,KNTC1,CSRN<br/>NUDCD1,POP4,EPHA2,TP1<br/>P2,KLF5,RBM14,ELI2,<br/>1,OVQ12,TRA4,KLF12,TNN<br/>ELMO3,IGF1R,TRA4,E<br/>T2,ANKRD1,ZHX2,KNTC1,CA<br/>CHST11,TGBF3,ANKR<br/>XT1,DLI4,STC1,TA5,C<br/>CNAIG,KLF5,ELI2,IGF1R,CY<br/>D1,TSC22D1,MAGED1<br/>NNM2,TBCC,SRMA,T<br/>R61,EXT1,DLI4,SCMH,ARO<br/>VCAN,EFEMP2,ARMC<br/>RIM8,MMP9,PLAGL2,<br/>LDI,TAF5,CNNM2,TRIM8,M<br/>X3,AMOT,MEFAP5,DOK<br/>CAMK2N2,WNT5A,LIN<br/>M9,STC1,WNT5A,PP2B5B<br/>1,ANGPT11,SORBS2,L<br/>5A,OVQ12,<br/>JG1,<br/>NUTF2,FAM122A,PAP<br/>LN,DOCK3,LINS,SCRP<br/>1,ATNNT12,RREB1,ZBT<br/>B12,TIMEL,ES,CSRP<br/>1,CKSR1,FOSL1,NDU<br/>FAL2,HOXA2,PMIEP4<br/>1,ERBB3,TCF7,TRA4,<br/>ROCD1,IER5L,LSM05,<br/>CHP1,ATNNT12,ZBTB12,IT1<br/>ACTN3,FYND1,TSC22D1<br/>MELESS,HNF1B,FOSL1,NDU<br/>1,SLC7A7,PTHR,CD<br/>NR2C1,LEAP2,CNTRF,<br/>MELESS,HNF1B,FOSL1,NDU<br/>1,SLC7A7,PTHR,CD<br/>PMEPA1,BAI 7A7,CD,C8B8,NCN,P<br/>HAT1,WN1,STOML2,P<br/>A1,NR2C1,IER5L,HAT1,RRP<br/>NR2F2,PRG4,SLIT3,M<br/>2,PDGFB,RT<br/>MEPA1,MAA20,MAF,FI2<br/>CDH7,MTTP,GDNF,ST<br/>MS,PCDH7,MTTP,GDNF,STK<br/>VUF,SEC16B,ZBTB70,<br/>PRRX2,NRP1,DUSP3,<br/>K39,BTB03,<br/>39,</div> |
| V\$GCM_Q2       | 1.62 | 3.66 | 4.90 | V\$GCM_Q<br>4.10 2 | <div>PIEZO1,PDG<br/>FB,FGH1,TP<br/>M2,</div> |  |
| V\$HNFAL_PHA_Q6 | 1.47 | 2.58 | 3.04 | 2.00               | V\$HNFAL<br>7.07 PHA_Q6                      | <div>AGP3,SCNN1,CDG19,SLC<br/>GART,PCHEB3,USP37,<br/>FAH2,TRA4,RCOD1,PMIE<br/>PMEPA1,BAI 7A7,CD,C8B8,NCN,P<br/>MEPA1,MAA20,MAF,FI2<br/>CDH7,MTTP,GDNF,ST<br/>MS,PCDH7,MTTP,GDNF,STK<br/>VUF,SEC16B,ZBTB70,<br/>PRRX2,NRP1,DUSP3,<br/>K39,BTB03,<br/>39,<br/>FAM122A,SOK5,EMC<br/>N,H2AFX,BMP,PRB,RRP<br/>M4,EF5A,SNYS,UBAS<br/>H3B,KIFS,TUT1,EDNZ,<br/>DUX1,CADMI,LTBP1,R<br/>PP25,PIR43,HNTL,IG1<br/>EMCN,H2AFX,HOKA,BMPR<br/>1,EPAR,ZIC1,CAQNA,IS,<br/>PRXPI1,WHY2,ANKR1<br/>P1,CN3,KONB,MEF2A<br/>N1E1K3,STC1,CNMT4,NRP4,<br/>185,</div>  |
| V\$HOKA_Q2      | 2.14 | 2.18 | 2.09 | 2.37               | V\$HOKA_<br>7.86 Q2                          | <div>COL10A1,MMP14,CSNK<br/>PIT2,AMP 14L1,PHD1,LMGA2,FA<br/>2,STOML2,PR3,STNE 5,HNLL,SLVW,COU,TAL1,NU<br/>P1,CN3,KONB,MEF2A<br/>N1E1K3,STC1,CNMT4,NRP4,<br/>185,</div>   |















|                   |      |      |      |         |                   |  |
|-------------------|------|------|------|---------|-------------------|--|
| V\$SMADL_Q6       | 1.63 | 2.51 | 2.49 | 3.68    | V\$SMADL_Q6       | <p> AGBL5,NUDCD1,HMG<br/> NS,EPHA2,RUNC3A5<br/> LC3A35,LEPRE4,IGI<br/> 1,TFNFSF12A,FAM83F<br/> ADAMTS4,ADORA2B, NUDCD1,NEATC4,FRBP10,E<br/> MEIS2,ATYN12,KLF7, PHA2,RUNC3A,LEPRE4,L<br/> CADM1,TF72,SUV39H, GIL,ATYN12,ADAMTS4,L12<br/> 2,PRKC2,MAGROD2,TS,3A,CACNA1G,KLF7,SUV39H, ADAMTS4,POGFRAL0<br/> ENSLAMC2,ETV4,PA, 2,PRKC2,TSERK5,LANC2,P8, N13,NEATC4,FRBP10,P<br/> O1,SULF1,PP,RS1,ING33,LANC2,MAR6, ASIN2,CDB6,IL17AC,SKIN2,CDB6,MT1DB1,PAM112, FL3,CACNA1G,MER2C,<br/> AM12B4,CMTN4, 6A,CMTN4, DOCK1,<br/> SAR62,TNEM88,MES<br/> 2,FRP4,IRPK4,TFNFSF<br/> 12A,SAMD12,F208,CP<br/> NE1,PTHLH,STY12,INH<br/> BA,DUSP9,NPM3,JAG, SAR62,H2AF2,PCSK5,PKP4,<br/> 1,DX1,CADM1,JAR5A, RBP4,SOD4,SAMD12,CASQ<br/> QP3,MRP117,SEPHS1, 2,CPIIE1,THBS2,PTHLH,DUS<br/> FLRT3,METTL21D,UHR P9,BCAR3,JAG1,JAR5,MRPL MYH2,STAC2,MYL1,T<br/> F1,BCAR3,BACE2,STO 17,FLRT3,METTL21D,UHHR1 HB52,PCSK5,TNEM11<br/> MHBA,ZIC1, CDB6,GORAB,MAR69,C<br/> M2,TWTC2,GORAB, NPM3,HOMAS,GORAB,WDR 9,GRP3,MYBPCL,ZIC1,<br/> WDR93,CHIM1, 73,<br/> SMRX,NRP1,PTTRD,<br/> STX1A,TRERF1,CRLFI,<br/> KIK13,HSP9A,SWTN,H<br/> IF1A,SRRM4,RPBD1A,<br/> RCOR2,SC2A37,POX<br/> PATNY12,KLF12,BHE<br/> BL1,MAM13,KCNK7,6 STX1A,NEATC4,FOXP4,KIK1<br/> RMD1,IMPDH2,PVRL1, 3,HOKA,HIF1A,RCOR2,SIC<br/> JUP,DUSP8,FOXQ4, 25A37,PDXP,PVRL1,ATYN71, C4,DPR512,EYD1,ACT<br/> MAO1,SPAL12,PDE5A, 2,KLF12,IMPDH2,HNF1B,GR, CL,CACNB1,HSPG2,AR<br/> DMM73B,TNF4,IPN8 WDI,ACT1,TGFB1,13,PA1, HGP40,TNEM119,C<br/> 1,IRB2BP,PD2,MAR9, L2,PDE5A,GRMN1,TNAT4,AP ORO1A,SUT3,BIGALT<br/> 18B,PH1DB3,LRB,DC, NB1,MAR918B,PD2,BIGAL, 23,NPO21,TGFB11,T<br/> AAD1,LRER,FB,CB, 12,LRB9,DCAORDER,BC1B, NS1,FUNC,CLDN5,MVL<br/> C1B6,PRKD2, PRKD2,<br/> STMN1,REW2,BCL11A<br/> J,PTHLH,SPK2,IL24RR<br/> M1,STIP1,DONSON,PA<br/> N2,WNT10A,TFAP2C,C<br/> NKSR1,SMCA,GEN1,NI<br/> D2,KLF5,SKA2,MAR6, LIF,NEATC4,REH2,TNFSF11,<br/> IRK5,NDUFAL2,SOX5, PTHH,GEN1,L24,RRM1,NC<br/> S1C7A1,CADM1,FAM9 AM1,PRICKLE1,WNT10A,CN OBSCN,TM6SF1,TNFS<br/> 8A,IRNF43,SRH,HNL,R KSRI,SMCA,MES1,MID2,KF, FL1,NEATC4,BATF,TSC<br/> NF26,TAFS,TERT,CDC2, 5,SKA2,MAR6,NDUFAL2, 22D1,HSPG2,AOC3,IL<br/> 7,CAMSA2,PRH11,P1, LC7A1,HOKA,HNL,RNF26, 16,FAM5C,PRICKLE1,<br/> AG12,MIR17HG,ESM1, TA65,CAMSA2,PRH11,MIR GR66,MYBPCL,ZIC1,<br/> NRP4,<br/> ANKRD138,TRERF1,SL<br/> CGA9,S1C7A1,DYRK3,1<br/> L24,SEMA6D,ADAMTS<br/> 4,MPL2,2,SMOX,HAUS<br/> 3,ING1,ANP72,DUX5, HOKA,S1C7A1,DYRK3,L24,<br/> CTED1,DOCK,LEPR110, SEMA6D,ADAMTS4,MPL22,<br/> AB2P,IRNG1,STC1,P2A, HAU53,APOLDJ,INHB,ANG, ETV1,ADAMTS4,PTH1<br/> G4,P2A2GE,TA65,NU PTZ,DUS,ORC4,HNRP40, R,MYH11,MYH11,TSZ<br/> P54,IL10,MX1,MICAL, DAB2P,IRNG1,P2G4,TA65, 201,C10C,ARHGFB,5<br/> L2,RINI,SRRM4,LEK3, NUP54,MICAL2,RINI,PTPR TARDB3,TGFB3,TN1LD<br/> HOKA2,CAMK2N2,PTI, G,ELK3,STC1,PTPNC1,NXPH B3,ABCD1,PRRXL,BTK,<br/> PNC1,NRP4, 4, ZEB2,<br/> </p> |
| V\$SHMGV_Q6       | 1.59 | 4.47 | 5.14 | 3.98_Q6 | V\$SHMGV_Q6       | <p> PITD2,STK32<br/> C,PTHLH,ZIC<br/> 1,<br/> </p>   |
| V\$P53_DECAMER_Q2 | 1.54 | 2.91 | 3.65 | 4.38_2  | V\$P53_DECAMER_Q2 | <p> V\$P53_DECAMER_Q2<br/> ETV1,ANKRD<br/> 138,FGT1,LR<br/> INI,<br/> </p>   |







|            |      |      |      |         |            |                                  |  |
|------------|------|------|------|---------|------------|----------------------------------|--|
| V\$SRAP_Q3 | 1.53 | 2.57 | 2.88 | 4.91_Q3 | V\$SRAP_Q3 | KRT17,TFAD<br>2,GERM1,PT<br>HLH, | NUDCD1,KLK13,HS9A<br>9,BCL11A,HIF1A,PTHL<br>HRCOR2,FAM83H,ME<br>X3D,KIF12,SET,GRHL2<br>JAMHR2,MST1L,CDKL3<br>NUDCD1,NFATC4,KLK13,HO<br>GREM2,PDGFRB,GRE<br>PVR1L,HBEGF,ST7,GN<br>XCA,HIF2A,RCOR2,FAM83H,<br>MI,NFATC4,DPS12,F<br>AO1,REBP1,DGSG1DN,<br>KLF12,SET,GRHL2,PTHH,<br>CD,XO1,HS9G2,SICZAT1<br>MT3B,KRNB1,MRP518,<br>K13,PVR1L,HBEGF,REEP1,<br>DS,CLOTN7,ARHGAP40,<br>BLD4,TNNT2,IERSL,<br>G3,GREM1,KPNB1,LMR518<br>G72BP3,IEF1L,LR8,TB<br>B,PDP2,TNNT2,IERSL,<br>MREX3,PF,KANK2,PHLP1,<br>TRI<br>C,CDP1,CDP2,CDP3,<br>CDP4,CDP5,CDP6,<br>CDP7,CDP8,CDP9,<br>CDP10,CDP11,CDP12,<br>CDP13,CDP14,CDP15,<br>CDP16,CDP17,CDP18,<br>CDP19,CDP20,CDP21,<br>CDP22,CDP23,CDP24,<br>CDP25,CDP26,CDP27,<br>CDP28,CDP29,CDP30,<br>CDP31,CDP32,CDP33,<br>CDP34,CDP35,CDP36,<br>CDP37,CDP38,CDP39,<br>CDP40,CDP41,CDP42,<br>CDP43,CDP44,CDP45,<br>CDP46,CDP47,CDP48,<br>CDP49,CDP50,CDP51,<br>CDP52,CDP53,CDP54,<br>CDP55,CDP56,CDP57,<br>CDP58,CDP59,CDP60,<br>CDP61,CDP62,CDP63,<br>CDP64,CDP65,CDP66,<br>CDP67,CDP68,CDP69,<br>CDP70,CDP71,CDP72,<br>CDP73,CDP74,CDP75,<br>CDP76,CDP77,CDP78,<br>CDP79,CDP80,CDP81,<br>CDP82,CDP83,CDP84,<br>CDP85,CDP86,CDP87,<br>CDP88,CDP89,CDP90,<br>CDP91,CDP92,CDP93,<br>CDP94,CDP95,CDP96,<br>CDP97,CDP98,CDP99,<br>CDP100,CDP101,CDP102,<br>CDP103,CDP104,CDP105,<br>CDP106,CDP107,CDP108,<br>CDP109,CDP110,CDP111,<br>CDP112,CDP113,CDP114,<br>CDP115,CDP116,CDP117,<br>CDP118,CDP119,CDP120,<br>CDP121,CDP122,CDP123,<br>CDP124,CDP125,CDP126,<br>CDP127,CDP128,CDP129,<br>CDP130,CDP131,CDP132,<br>CDP133,CDP134,CDP135,<br>CDP136,CDP137,CDP138,<br>CDP139,CDP140,CDP141,<br>CDP142,CDP143,CDP144,<br>CDP145,CDP146,CDP147,<br>CDP148,CDP149,CDP150,<br>CDP151,CDP152,CDP153,<br>CDP154,CDP155,CDP156,<br>CDP157,CDP158,CDP159,<br>CDP160,CDP161,CDP162,<br>CDP163,CDP164,CDP165,<br>CDP166,CDP167,CDP168,<br>CDP169,CDP170,CDP171,<br>CDP172,CDP173,CDP174,<br>CDP175,CDP176,CDP177,<br>CDP178,CDP179,CDP180,<br>CDP181,CDP182,CDP183,<br>CDP184,CDP185,CDP186,<br>CDP187,CDP188,CDP189,<br>CDP190,CDP191,CDP192,<br>CDP193,CDP194,CDP195,<br>CDP196,CDP197,CDP198,<br>CDP199,CDP200,CDP201,<br>CDP202,CDP203,CDP204,<br>CDP205,CDP206,CDP207,<br>CDP208,CDP209,CDP210,<br>CDP211,CDP212,CDP213,<br>CDP214,CDP215,CDP216,<br>CDP217,CDP218,CDP219,<br>CDP220,CDP221,CDP222,<br>CDP223,CDP224,CDP225,<br>CDP226,CDP227,CDP228,<br>CDP229,CDP230,CDP231,<br>CDP232,CDP233,CDP234,<br>CDP235,CDP236,CDP237,<br>CDP238,CDP239,CDP240,<br>CDP241,CDP242,CDP243,<br>CDP244,CDP245,CDP246,<br>CDP247,CDP248,CDP249,<br>CDP250,CDP251,CDP252,<br>CDP253,CDP254,CDP255,<br>CDP256,CDP257,CDP258,<br>CDP259,CDP260,CDP261,<br>CDP262,CDP263,CDP264,<br>CDP265,CDP266,CDP267,<br>CDP268,CDP269,CDP270,<br>CDP271,CDP272,CDP273,<br>CDP274,CDP275,CDP276,<br>CDP277,CDP278,CDP279,<br>CDP280,CDP281,CDP282,<br>CDP283,CDP284,CDP285,<br>CDP286,CDP287,CDP288,<br>CDP289,CDP290,CDP291,<br>CDP292,CDP293,CDP294,<br>CDP295,CDP296,CDP297,<br>CDP298,CDP299,CDP300,<br>CDP301,CDP302,CDP303,<br>CDP304,CDP305,CDP306,<br>CDP307,CDP308,CDP309,<br>CDP310,CDP311,CDP312,<br>CDP313,CDP314,CDP315,<br>CDP316,CDP317,CDP318,<br>CDP319,CDP320,CDP321,<br>CDP322,CDP323,CDP324,<br>CDP325,CDP326,CDP327,<br>CDP328,CDP329,CDP330,<br>CDP331,CDP332,CDP333,<br>CDP334,CDP335,CDP336,<br>CDP337,CDP338,CDP339,<br>CDP340,CDP341,CDP342,<br>CDP343,CDP344,CDP345,<br>CDP346,CDP347,CDP348,<br>CDP349,CDP350,CDP351,<br>CDP352,CDP353,CDP354,<br>CDP355,CDP356,CDP357,<br>CDP358,CDP359,CDP360,<br>CDP361,CDP362,CDP363,<br>CDP364,CDP365,CDP366,<br>CDP367,CDP368,CDP369,<br>CDP370,CDP371,CDP372,<br>CDP373,CDP374,CDP375,<br>CDP376,CDP377,CDP378,<br>CDP379,CDP380,CDP381,<br>CDP382,CDP383,CDP384,<br>CDP385,CDP386,CDP387,<br>CDP388,CDP389,CDP390,<br>CDP391,CDP392,CDP393,<br>CDP394,CDP395,CDP396,<br>CDP397,CDP398,CDP399,<br>CDP400,CDP401,CDP402,<br>CDP403,CDP404,CDP405,<br>CDP406,CDP407,CDP408,<br>CDP409,CDP410,CDP411,<br>CDP412,CDP413,CDP414,<br>CDP415,CDP416,CDP417,<br>CDP418,CDP419,CDP420,<br>CDP421,CDP422,CDP423,<br>CDP424,CDP425,CDP426,<br>CDP427,CDP428,CDP429,<br>CDP430,CDP431,CDP432,<br>CDP433,CDP434,CDP435,<br>CDP436,CDP437,CDP438,<br>CDP439,CDP440,CDP441,<br>CDP442,CDP443,CDP444,<br>CDP445,CDP446,CDP447,<br>CDP448,CDP449,CDP450,<br>CDP451,CDP452,CDP453,<br>CDP454,CDP455,CDP456,<br>CDP457,CDP458,CDP459,<br>CDP460,CDP461,CDP462,<br>CDP463,CDP464,CDP465,<br>CDP466,CDP467,CDP468,<br>CDP469,CDP470,CDP471,<br>CDP472,CDP473,CDP474,<br>CDP475,CDP476,CDP477,<br>CDP478,CDP479,CDP480,<br>CDP481,CDP482,CDP483,<br>CDP484,CDP485,CDP486,<br>CDP487,CDP488,CDP489,<br>CDP490,CDP491,CDP492,<br>CDP493,CDP494,CDP495,<br>CDP496,CDP497,CDP498,<br>CDP499,CDP500,CDP501,<br>CDP502,CDP503,CDP504,<br>CDP505,CDP506,CDP507,<br>CDP508,CDP509,CDP510,<br>CDP511,CDP512,CDP513,<br>CDP514,CDP515,CDP516,<br>CDP517,CDP518,CDP519,<br>CDP520,CDP521,CDP522,<br>CDP523,CDP524,CDP525,<br>CDP526,CDP527,CDP528,<br>CDP529,CDP530,CDP531,<br>CDP532,CDP533,CDP534,<br>CDP535,CDP536,CDP537,<br>CDP538,CDP539,CDP540,<br>CDP541,CDP542,CDP543,<br>CDP544,CDP545,CDP546,<br>CDP547,CDP548,CDP549,<br>CDP550,CDP551,CDP552,<br>CDP553,CDP554,C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P1674,<br>CDP1675,CDP1676,CDP1677,<br>CDP1678,CDP1679,CDP1680,<br>CDP1681,CDP1682,CDP1683,<br>CDP1684,CDP1685,CDP1686,<br>CDP1687,CDP1688,CDP1689,<br>CDP1690,CDP1691,CDP1692,<br>CDP1693,CDP1694,CDP1695,<br>CDP1696,CDP1697,CDP1698,<br>CDP1699,CDP1700,CDP1701,<br>CDP1702,CDP1703,CD 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[illegible]







|                       |      |        |      |          |                               |                               |   |
|-----------------------|------|--------|------|----------|-------------------------------|-------------------------------|---|
| WTTGKCTG_UNKNOWN      | 2.61 | 2.42   | 7.81 | 6.90     | 8.03 W/N                      | WTTGKCT<br>G_UNKNOWN          | MDR1, TDO2, C25C, UBEC2, HMGA2, CA, 2C, MADK1, SFN, RND, NXX, HIST2H2AB, HIST, 2C, PP2R2B, LUTSS1, FAR1, GTF2A1, ALDIXC, HES1, LEFT1, E2C, SFN, PRRL1, HOXA1, PNN, E10A, ZEB2, CN3, AKA, LAMC2, TEA, AMC2, DIEU1, HIST2H2A, E1, PTPN1C, MACROD, D2, LMAN2L, CTDO2, FAM83D,  |
| WYMAANNRNNNGG_UNKNOWN | 1.46 | 2.94   | 2.47 | N        | WYMAANN<br>RNNNGG<br>_UNKNOWN | WYMAANN<br>RNNNGG<br>_UNKNOWN | MAP2B, MDR1, PRRL1, CD, RIP, PCTY1B, PHC1, UBE, NDC1, HMGA2, LSM1, IER5L, R124, SLIT3, PRELP, AN, 1, PRRL1, PCDH17, HOX, NXX, HIST2H2AB, PCTY1B, UB, NR2F2, EBF1, ZEB1, PD, 2, MESDC1, LUK1, VASH1, AHON2, SMAD6, BRX1, E2B8, ELK3, BFB, STK35, MRB2D, NDUF4L2, R, V12, FEF, E2B8, KCOR2, HOXA, CON2, 5, NDUF4L2,   |
| YCATTA_UNKNOWN        | 2.42 | 2.14   | 4.00 | 9.46 N   | YCATTA,<br>_UNKNOWN           | YCATTA,<br>_UNKNOWN           | TME88, POLA1, PHN1, IP1, TREB1, DUX1, SF, 3B4, CELF4, EPHA2, HA, US3, SH3BP4, SLC5A2, NUDT21, LODG6, SOD5, A, DANT132, NOB1, ZHX2, JTAAP2, CTIMELESS, VP, 537B, LSM11, AARP19, SLC5A10, NDNU2, KCN1, POLA1, PTC2, MRP5188, DUO, PA, HNRPND, HOKA2, E, X1, S3B4, CELF4, EPHA2, HA, ITGA9, PDGFRA, ACTC1, RBB3, ACP12, ART4, KC, US3, SH3BP4, NUDT21, SGP1, , RASSF2, CELF2, KCNM1, N15, JTGB6, IRR4, EF, , CDG6, ZHX2, TGF1, TIMELES, A1, PRG4, P2RY12, HOX, M45, PMEPA1, MSH5, E, 5, VP537B, LSM11, COL12A1, DB, NR2F2, TRDN, PTGE, HF, DLL1, PAK1P1, MRP, NOB1, TTYH1, NDNU2, CKAP4, R1, CCK4, FSTL1, STAP, 5188, PAX9, NPM3, DD, , HNRPND, ACP12, KCN15, IT, 1, SOUTF1, TNS1, KHLH3, X49, RBPR8, ILG12, SHC, G86, EFNA5, PMEPA1, DLL1, P, , STAC2, FTL1, MCAM1E, BPL, ROBO1, TIMEF1, U, AKIUP1, MCAM1A, G13, PAV9, NR1, RHOF, PTPRO, KB, BR2C, PCDH17, SFN, WTT, , NPW3, ILG12, SHCBP1, SOX4, TRD10, PAT171, ZEB1, CX, P, BC19, POLE2, HOXA1, , ROBO1, TIMEF1, UBEC2, PC, C13,4, SGCA, CNR8, CI, GNRH1, GNL3, PTC1, D17, SFN, WTTP, POLE2, HOX, QIN7, HSG572, SMPX, TUBE1, A1, ACTC1, TUBE1, , NR1, COL12A1, FES, |
| YCATTA_UNKNOWN        | 2.42 | 2.14   | 4.00 | 9.46 N   | YCATTA,<br>_UNKNOWN           | YCATTA,<br>_UNKNOWN           | ZDHHC15, TME88, YS, NL1, NCS1, RIBC1, AON, P, TOPORS, HAUS6, CPN, E1, NOP56, SPS9, LSM, 11, SVT12, KNS3, EBF5, PDCL3, VSNL1, HAUS6, CPNE, A, PAQ9, ASC12, HMG, 1, NOP56, SPS9, RIBC1, LSM1, AYA6, MAGED1, DUF, CLL, CPT10, SEENAV7A, 1, HMGCLL1, SEENAV7A, SLC39, M13, CDK14, HGF, FGR, , SLC39A6, ATP13A1, A6, ADNP, 1,  |
| YGCANTGCR_UNKNOWN     | 1.71 | 3.65   | 1.79 | 1.46 W/N | YGCANTGC<br>R_UNKNOWN         | YGCANTGC<br>R_UNKNOWN         | STEAR4, PDGFRA, SDR, ,NFATC4, PDLIM3, MY, H8, ARMC4, IRS1, SUL, F1, NR2F2, MEF2C, PTP, RD, TTN, EBF1, DLCL1, PY, GM, AMOT,  |
| YACATT_UNKNOWN        | 1.44 | 4.53 N |      |          | YACATT<br>_UNKNOWN            | YACATT<br>_UNKNOWN            | STK32C, BAI2, ,SUT1, PPP2, R2B,   |



[illegible]







[illegible]



|                    |      |      |      |          |   |      |      |      |      |        |  |
|--------------------|------|------|------|----------|---|------|------|------|------|--------|--|
| RTAACA_V\$REAC2_01 | 2.05 | 5.63 | 6.26 | 14.96_01 | RTAACA_V\$REAC2_01  |      |      |      |      |        |  |
|                    |      |      |      |          | ETVL,ENPEP,<br>PDGB,SRE<br>MLSTNOJC<br>7of60,SULF<br>1,PP2R2B,I<br>NHBA,PTX2,   |      |      |      |      |        |  |
| GATAAGR_V\$GATA_C  | 1.35 |      |      |          | GATAAGR_7.73_V\$GATA_C<br>PTX2,FHL3,<br>ETVL,RAP1B,   |      |      |      |      |        |  |
|                    |      |      |      |          | TGM4,PHH2D,TM1,SE<br>MAC,RRREB1,NHBA,<br>METTL18,PTIRN1,IRX<br>5,EDN2,MAPRE3,BRC<br>A1,ERBB3,EFH,MACR<br>OD2,CACNA2D3,PAFA<br>H1B3,BRD3,JAG1,SHR<br>OON2,ROBO4,CEP70,<br>SOX5,EMCN,ITGA3,TR<br>IM37,GTFC1,CTNN1,<br>TERT,MEB2,RHBD2,<br>KCNIP4,CDC35A,SICO<br>2A1,TFAP4,DEPDC7,W<br>NTSA,TFP2,ANKRD1<br>3B,VSNL,SMAD6,DIE<br>X,FRB5,TAIF5,MCIP<br>2,TLL1,MP2L2,NRBA1,<br>ZHX2,DUSP8,CITF1,C<br>ADN1,ASC2,JARID2,E<br>FNA5,TNTE,FMA1,M<br>AST4,HST1,H1B,SEMA<br>3C,OMG,PPAT,FAM17<br>13B,TUBA1A,RDX1,BCL11B,<br>JTG43,PPP2_A1,MP2L2,<br>R2B,KRT17,J_AGLN2,BGAL12,<br>NHBA,FAM1_068,LINC13D,<br>764,ZIC1,PT_TRM44,PP2R2B,<br>X2,JAG1,TEA_IAG1,TFAP4,<br>D4,   | 3.85 | 2.64 | 5.29 | 5.27 | 6.78_6 | TGTTGV_V\$NH3_Q<br>TGTTGV_V\$NH3_Q6  |
|                    |      |      |      |          | SYNPO,ASB16,LINS,M<br>AFF,RRREB1,SAMD11,F<br>AM110A,I,NHBA,NOB1<br>J,MC,GFR,NGEF,EXT<br>1,SIC38A2,WNK2,FLR<br>T3,PCOT1B,BMP3,BM<br>P2,ROBO1,CCND1,STA<br>RD1D,ADNP,MMP13,D<br>OCK3,KCNB3,PASSF6,<br>FEN1,NBRG1,SIC3A3,13,<br>JUNB,LINS,XOXC,CCDC<br>UNK559,CKN1,CTN1<br>9,MAM13,WDR46,ELK<br>41,PCSK5,SHROOM1,FEN1,<br>3,CTCF,BUB1,BUB3,<br>SEMA6B,CTH,ATXN7L2,MA<br>HSD17B1,CDK14,AB1<br>KCNQ3,PMCH,ZBTB5,<br>FF,CAO,MDK,KCNJ15,SAMD<br>3BP,MN1L,GPR137B,N<br>CN1,GALNT3,GAL1E<br>11,CUEC1,CNNE1,SIC3A2<br>RAP,BINI,XAL,DCNM<br>GNTL1,RPS6KA5,TFAP4,<br>CTN1,MEB1,MAP21L3,FHL<br>DK,ABTB05,TEK,ARHG<br>TRIM8,MTTP,STK35,P<br>2,NID2,NOB1,COR61,NR61,<br>E6F,BMP1P,STK1P1,DE<br>CCH18,ALKBH5,TFDP2<br>NIDF,AL2,ELK3,HOKAS,GO<br>KHH2,SURF1,PKC,G5,<br>BTD3,ATXN1,TREFF<br>NE,GFR18,GREM1,GMPNAT1<br>TAP1,GRRC,FS1L1,<br>1,CCDC4,SHROOM1,<br>EXT1,PAO21,KCNQ5,DAB2<br>GMEF,DICI,GREM1,P<br>CTH,ATXN7L2,SIC1D4<br>P,BUB1,PAPPA,BUB3,KIF12,<br>DUM3,ENPEP,FULM<br>7,RBM8A,ZH2,ING1,<br>FERT3,METTL21D,MGCN7<br>P,RGFR,PA2PA,TSPAN<br>FHL2,GNAO1,CADM1,<br>EYA,TRIM8,MYC,GALNT3,<br>G4,AMR8A,HMCN1,PCS<br>K5,ETVL,NIN,POU4F4<br>LONR1,TTT2,DAB2IP,<br>ALSGN1,PCOT1B,BMP3,B<br>KS,ETVL,NIN,POU4F4<br>NODT18,WEE1,TRCC,<br>MAP2,TFAP4,ROBO1,PTPNC<br>1,NYN1,CTCONE6,NKI<br>HOXA1,ISG20,SIC3SD<br>J,CTCONE6,ADAM12,NOTE<br>A1,IL6,IBD5,ARHGAP3<br>1,KIF20A,JUNB,BCL11<br>H4,ZH2,DDIT4,MYT1P,BTD<br>O,CTCONE6,CTCFC1,COX<br>A1,IGF1,DD174,SEMA6B<br>B,XOXA1,ISG20,CCND1,<br>CPN1,C5,CCTDIN3,CSMP3<br>P,CAOK,FTJ2,SMOX,BCL1,<br>PMCH,TGFR,INT20A,<br>DETA,<br>SOX11,ADPH11,SLC7<br>A7,PKA,BIN1,MC1CH,CH<br>RNB1,STPR2,CDK4,G<br>REN2,LTV1,FULL,FERM<br>T3,IGFBP5,FGF7,ITPR1<br>ETVL,TACCL1,W02,C<br>CDC80,IRS1,MF2C,PT<br>PRC, |      |      |      |      |        | BAZ,ANKRD_V\$NL1,ITGA3,<br>13B,TUBA1A,RDX1,BCL11B,<br>JTG43,PPP2_A1,MP2L2,<br>R2B,KRT17,J_AGLN2,BGAL12,<br>NHBA,FAM1_068,LINC13D,<br>764,ZIC1,PT_TRM44,PP2R2B,<br>X2,JAG1,TEA_IAG1,TFAP4,<br>D4, |



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|                    |      |      |      |       |                                  |
|--------------------|------|------|------|-------|----------------------------------|
| GCANTGNY_VSNF00_06 | 6.53 | 4.87 | 6.17 | 14.29 | GCANTG<br>NY_VSNF<br>00_06       |
| TGCCAAR_VSNF1_06   | 1.35 | 2.14 | 3.22 | 4.70  | TGCCAAR_<br>16.51_VSNF1_06       |
| TOASTMAGC_VSNF2_01 | 4.51 | 5.12 | 4.07 | 4.27  | TOASTMA<br>GC_VSNF<br>1.87 2_01  |
| GGGNTTTC_VSNF06_01 | 3.44 | 2.08 |      |       | GGGNTT<br>TTC_VSNF<br>8.13 06_01 |

|  |  |
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| ETV1, BAI2, P<br>DGB, TPV2,<br>C19orf55, P<br>O13, RIN1, G<br>APPH, C12orf<br>15, HNL, TNFR<br>SF21, RTKN, F<br>BLIM1, BASG<br>ETIA, TEAD2<br>FCG11, JAG1,<br>LIMAN2L,<br>CULP1, LTBAR2, HSP90,<br>PCKA, PKP4, PRK7, AB<br>M19B, WNT10A, EMI5,<br>IRX5, MYC, DOCA, ERB<br>B3, GFI1, DOTT4, ANK8<br>D42, WNK2, MRP56, WI<br>P11, FRT3, CACNA2D3,<br>TSPAN9, ABCB9, COL7A<br>1, RFX1, CPNE1, LAMBT<br>12, PLAG12, ZBTB25, M<br>MP15, NGF, RRAD, TBC<br>F4, COL8A1, PCSK1, SOX15, PR<br>B93, TNNC2, NC272, M<br>CTGA3, CEF1, GAPDH, ICKE1, ADAM12, PR4, SMA<br>CAM, NCAM, LILRP2L,<br>JTGAF, ADAMTS12, CC<br>RGS, LAMN5, XPO1, MYH3, H<br>TGB1P2, MYH3, ABT8<br>NE2, SOX15, ATKYD12,<br>ETLCONE2, WNT10A, CPNE1,<br>DS, MYH9, APOBEC2,<br>TNNC2, CTCF, MYT1, KCN<br>ATXN12, AARS1, LPM11E<br>ABHGF6, ZEB1, CACN<br>Q5, IGFBR3, VEGFA, PHL<br>M3, PDEFA, LAMBT12, NR61<br>B1, HFE2, THBS3, XIRP1<br>D83, SNTN12, JNHA, EG<br>R6312, NDJFA42, JAG1, DO<br>TNN12, SLIT2, DMPK, A<br>LNI, GUA4, UBE2O, NAD<br>C2A, TFAP4, GFI1R, ENOPH1,<br>NGPT1, NR1H3, ACTN3<br>K01, CASKIN2, MPP2, A<br>DOTT4, TGB4, TAP1, ANKRD<br>COL8A1, DES1, V1L, FG<br>GBL5, TREF1, LEIF2B3, 5<br>42, ODC1, WIP1, DAB2P, DB<br>D2, PKN1, DBCL1, GFBP<br>H38P1, HOVA2, SLCA4B<br>C1, EF2B3, IGFBR3, FLRT3, YE<br>3, ENO3, KRTBD10, IGF<br>JWDR25, S100A8, TAP<br>GFA, MCAM, KCNOS, TSEN54<br>BR5, SYNE1, LGALS1, SL<br>1, DNHD1, LAMAS, ENO<br>WDR25, TSPAN9, CDEB, MY<br>C43A3, CAC14, FGR1,<br>PH1, DAB2P, FENAL, DI<br>C, G1A5, PIGW, FAM3, EGN1<br>ETV1, G1A5, LDB3, C1Q<br>L1, DILA, TSEN54, FSCN<br>NCAM1, COL2A1, ARID5A, D<br>TNE2, TAC1, LINC458,<br>2, METT18, FAM3A, RGS<br>L11, NC019, INHA, RIN1, ERF<br>R, PLEKHA4, CHRNBL, GF<br>12, TFAP4, RIN1, BC17A<br>PA3, RGDH12, PRP25B, HOX<br>B41, MAGEF1, SMDX<br>AUTS2, MORG4, ERF, EZ<br>AS, CTRN, CASKIN2, COL12A1<br>MYO7A, PDE1A, COL12<br>H2, SMC6A3, SOX5, KL<br>JDL4, KLF12, TIGR2, TIGR1,<br>AL1, MYH7F,<br>RANGRF, FRT43, PHYHIP<br>L1, GMA1, EMCN, ACTG2<br>RRAD, GNM1, MED27<br>CSRP1, SLC25A3, RC<br>OR2, TP11, RNF183, PTK<br>7, TSL, P, MOND1, LRRC4<br>8, RALGAP1, TSL, VSNL,<br>KLF12, TSPAN9, AP1X, S<br>AMD12, SMOX, TRIM8,<br>SRE, WNT10A, CPNE1,<br>MEIS2, GIB6, PVAL, RT<br>MIRP1, MOAP1, ABCG6,<br>RANGRF, FRT43, PTK2, EMCN,<br>ADAM12, FABP3, HOX<br>ARTN, RBM14, IRX5, CA<br>ACTG2, RRAD, EPHA3, FTS13,<br>DB, SORBS2, PRXPL, N<br>MKMT, PAPLN, DLX1, PI<br>RCOR2, TP11, TMSB1D, TSLP,<br>CAM1, MYH2, MYH3, M<br>15, TSSK6, DOTT4, CDK6,<br>MXOD1, CTRN61, ARID5A, NCA<br>VHL, EPHA3, ARHGFB6,<br>IL19, KCNO4, TGA7, V<br>M1, SOKA, VSNL1, MYH3, P1X<br>FAP, CACNA1C, SLIT3, C<br>WAL, EFH, LAMC1, F1R<br>NB1, SAND12, PTK7, CUEDC1<br>48, PRELP, FMO2, P116,<br>T3, P1XNB1, LMAST4, PE<br>WNT10A, CPNE1, CACNA1C,<br>CLIC5, HSPB2, LITB2, P<br>UP1, MB21D2, TTC39B,<br>PTNH, GIB6, PVAL1, SLOCAM<br>ODN, SRPZ2, ENP2, DB<br>GPR22, CACNA2D3, GP<br>OAP1, SRPZ2, CMAP, P115, D<br>C1, SDPR, HGF, ST6GAL<br>R21, MANOS1, SNTN12,<br>DIT4, KLF12, KCNO4, HNG42<br>NACS, OC14, HRC, ZE<br>X1, TP11, TMSB1D, WDR8<br>ETV4, SNGRP, LNS4,<br>DBCL, VMA1, FRT3, MAST4,<br>B2, STP2, DCLK1, CN<br>BNC1, SP9B, KAS, ROBO<br>CIN1, TSPAN9, OSBP, L, SRP<br>1, KAP2, EMI1N1, C1<br>PTK7, PTHH, AP, PTHH, JON<br>SL, GAT11, 1, KRP24, RUF<br>RIS2, PCD, 2, IL13, BNC1, ETV4<br>ROBO1A, QTNF3, C1QNTF1, JMS1<br>KR17, PTK1X2, ARTN, SERP<br>N1B3, JHNG, H7, WE1, KLF7, HOXA2,<br>DAM12, PCDH7, TRIM8, KLF7,<br>JL16, WSP2, COLEC12,<br>J, FBLN1, LIT, A2, PRP2R2, OSBP, L, PC<br>E1F, EBP3, PTHH, PTHC<br>MAPEK35, CDK6, TSPAN6, AR<br>MYB6, ABR4, TUBA<br>4, ARTN, GF1, HIRA, CALM1,<br>1, RRP15,<br>MDF1, BAG2, SYNPO, JS<br>PAG, TINAQ1, GAPDH,<br>LAMA3, PHLD2, TLL1,<br>PRP7, CMA5, FOSL1, AB<br>C86, FT11, LMK1, DLX1,<br>MAREP3, PROCR, SPAT<br>S2, XPT, G044, ENO1,<br>1, LAMA3, ASS1, PHLD2, FOS<br>MDF1, SYNPO, HRF2, LMK1, GAPDH, PP<br>NUDT11, PLCD1, BNP3<br>L1, FT11, LMK1, S100A2, SPA<br>J, LMK1, GAP, P2R2, PSMO2, CMA5, EN<br>JOM6, SLCA22A8, PSM<br>TS2, XPT, ENO1, PLCD1, VAS<br>DH, REL2, G5, O1, GSTP1, REL2, NCN1,<br>D11, REL2, MMP9, PAK<br>P, BNP3, OMG, IL6, MMP9, PT<br>PRN, PAK6, PROCR,<br>6,<br>ETV1, FHL3, J<br>URB1A, GRE<br>M1, WBP43, PRS6K4, TREC, CCL5, CD<br>C27, FHL3, JANG, SJANR8,<br>, | ETV1, BAI2, P<br>DGB, TPV2,<br>C19orf55, P<br>O13, RIN1, G<br>APPH, C12orf<br>15, HNL, TNFR<br>SF21, RTKN, F<br>BLIM1, BASG<br>ETIA, TEAD2<br>FCG11, JAG1,<br>LIMAN2L,<br>CULP1, LTBAR2, HSP90,<br>PCKA, PKP4, PRK7, AB<br>M19B, WNT10A, EMI5,<br>IRX5, MYC, DOCA, ERB<br>B3, GFI1, DOTT4, ANK8<br>D42, WNK2, MRP56, WI<br>P11, FRT3, CACNA2D3,<br>TSPAN9, ABCB9, COL7A<br>1, RFX1, CPNE1, LAMBT<br>12, PLAG12, ZBTB25, M<br>MP15, NGF, RRAD, TBC<br>F4, COL8A1, PCSK1, SOX15, PR<br>B93, TNNC2, NC272, M<br>CTGA3, CEF1, GAPDH, ICKE1, ADAM12, PR4, SMA<br>CAM, NCAM, LILRP2L,<br>JTGAF, ADAMTS12, CC<br>RGS, LAMN5, XPO1, MYH3, H<br>TGB1P2, MYH3, ABT8<br>NE2, SOX15, ATKYD12,<br>ETLCONE2, WNT10A, CPNE1,<br>DS, MYH9, APOBEC2,<br>TNNC2, CTCF, MYT1, KCN<br>ATXN12, AARS1, LPM11E<br>ABHGF6, ZEB1, CACN<br>Q5, IGFBR3, VEGFA, PHL<br>M3, PDEFA, LAMBT12, NR61<br>B1, HFE2, THBS3, XIRP1<br>D83, SNTN12, JNHA, EG<br>R6312, NDJFA42, JAG1, DO<br>TNN12, SLIT2, DMPK, A<br>LNI, GUA4, UBE2O, NAD<br>C2A, TFAP4, GFI1R, ENOPH1,<br>NGPT1, NR1H3, ACTN3<br>K01, CASKIN2, MPP2, A<br>DOTT4, TGB4, TAP1, ANKRD<br>COL8A1, DES1, V1L, FG<br>GBL5, TREF1, LEIF2B3, 5<br>42, ODC1, WIP1, DAB2P, DB<br>D2, PKN1, DBCL1, GFBP<br>H38P1, HOVA2, SLCA4B<br>C1, EF2B3, IGFBR3, FLRT3, YE<br>3, ENO3, KRTBD10, IGF<br>JWDR25, S100A8, TAP<br>GFA, MCAM, KCNOS, TSEN54<br>BR5, SYNE1, LGALS1, SL<br>1, DNHD1, LAMAS, ENO<br>WDR25, TSPAN9, CDEB, MY<br>C43A3, CAC14, FGR1,<br>PH1, DAB2P, FENAL, DI<br>C, G1A5, PIGW, FAM3, EGN1<br>ETV1, G1A5, LDB3, C1Q<br>L1, DILA, TSEN54, FSCN<br>NCAM1, COL2A1, ARID5A, D<br>TNE2, TAC1, LINC458,<br>2, METT18, FAM3A, RGS<br>L11, NC019, INHA, RIN1, ERF<br>R, PLEKHA4, CHRNBL, GF<br>12, TFAP4, RIN1, BC17A<br>PA3, RGDH12, PRP25B, HOX<br>B41, MAGEF1, SMDX<br>AUTS2, MORG4, ERF, EZ<br>AS, CTRN, CASKIN2, COL12A1<br>MYO7A, PDE1A, COL12<br>H2, SMC6A3, SOX5, KL<br>JDL4, KLF12, TIGR2, TIGR1,<br>AL1, MYH7F,<br>RANGRF, FRT43, PHYHIP<br>L1, GMA1, EMCN, ACTG2<br>RRAD, GNM1, MED27<br>CSRP1, SLC25A3, RC<br>OR2, TP11, RNF183, PTK<br>7, TSL, P, MOND1, LRRC4<br>8, RALGAP1, TSL, VSNL,<br>KLF12, TSPAN9, AP1X, S<br>AMD12, SMOX, TRIM8,<br>SRE, WNT10A, CPNE1,<br>MEIS2, GIB6, PVAL, RT<br>MIRP1, MOAP1, ABCG6,<br>RANGRF, FRT43, PTK2, EMCN,<br>ADAM12, FABP3, HOX<br>ARTN, RBM14, IRX5, CA<br>ACTG2, RRAD, EPHA3, FTS13,<br>DB, SORBS2, PRXPL, N<br>MKMT, PAPLN, DLX1, PI<br>RCOR2, TP11, TMSB1D, TSLP,<br>CAM1, MYH2, MYH3, M<br>15, TSSK6, DOTT4, CDK6,<br>MXOD1, CTRN61, ARID5A, NCA<br>VHL, EPHA3, ARHGFB6,<br>IL19, KCNO4, TGA7, V<br>M1, SOKA, VSNL1, MYH3, P1X<br>FAP, CACNA1C, SLIT3, C<br>WAL, EFH, LAMC1, F1R<br>NB1, SAND12, PTK7, CUEDC1<br>48, PRELP, FMO2, P116,<br>T3, P1XNB1, LMAST4, PE<br>WNT10A, CPNE1, CACNA1C,<br>CLIC5, HSPB2, LITB2, P<br>UP1, MB21D2, TTC39B,<br>PTNH, GIB6, PVAL1, SLOCAM<br>ODN, SRPZ2, ENP2, DB<br>GPR22, CACNA2D3, GP<br>OAP1, SRPZ2, CMAP, P115, D<br>C1, SDPR, HGF, ST6GAL<br>R21, MANOS1, SNTN12,<br>DIT4, KLF12, KCNO4, HNG42<br>NACS, OC14, HRC, ZE<br>X1, TP11, TMSB1D, WDR8<br>ETV4, SNGRP, LNS4,<br>DBCL, VMA1, FRT3, MAST4,<br>B2, STP2, DCLK1, CN<br>BNC1, SP9B, KAS, ROBO<br>CIN1, TSPAN9, OSBP, L, SRP<br>1, KAP2, EMI1N1, C1<br>PTK7, PTHH, AP, PTHH, JON<br>SL, GAT11, 1, KRP24, RUF<br>RIS2, PCD, 2, IL13, BNC1, ETV4<br>ROBO1A, QTNF3, C1QNTF1, JMS1<br>KR17, PTK1X2, ARTN, SERP<br>N1B3, JHNG, H7, WE1, KLF7, HOXA2,<br>DAM12, PCDH7, TRIM8, KLF7,<br>JL16, WSP2, COLEC12,<br>J, FBLN1, LIT, A2, PRP2R2, OSBP, L, PC<br>E1F, EBP3, PTHH, PTHC<br>MAPEK35, CDK6, TSPAN6, AR<br>MYB6, ABR4, TUBA<br>4, ARTN, GF1, HIRA, CALM1,<br>1, RRP15,<br>MDF1, BAG2, SYNPO, JS<br>PAG, TINAQ1, GAPDH,<br>LAMA3, PHLD2, TLL1,<br>PRP7, CMA5, FOSL1, AB<br>C86, FT11, LMK1, DLX1,<br>MAREP3, PROCR, SPAT<br>S2, XPT, G044, ENO1,<br>1, LAMA3, ASS1, PHLD2, FOS<br>MDF1, SYNPO, HRF2, LMK1, GAPDH, PP<br>NUDT11, PLCD1, BNP3<br>L1, FT11, LMK1, S100A2, SPA<br>J, LMK1, GAP, P2R2, PSMO2, CMA5, EN<br>JOM6, SLCA22A8, PSM<br>TS2, XPT, ENO1, PLCD1, VAS<br>DH, REL2, G5, O1, GSTP1, REL2, NCN1,<br>D11, REL2, MMP9, PAK<br>P, BNP3, OMG, IL6, MMP9, PT<br>PRN, PAK6, PROCR,<br>6,<br>ETV1, FHL3, J<br>URB1A, GRE<br>M1, WBP43, PRS6K4, TREC, CCL5, CD<br>C27, FHL3, JANG, SJANR8,<br>, |
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|                   |      |      |       |       |                      |
|-------------------|------|------|-------|-------|----------------------|
| GGGTGGR_V\$PAM_03 | 7.62 | 5.14 | 12.02 | 12.39 | 28.28_03             |
| GGGTGGR           |      |      |       |       | GGGTGGR<br>R_V\$PAM4 |
| GGATTG_V\$PMT2_Q2 | 4.80 | 2.51 | 7.93  | 4.90  | 5.79 \$PMT2_Q2       |
| GGATTG_V          |      |      |       |       | GGATTG_V             |
| GGAGGAA_V\$PUI_06 | 4.72 | 7.76 | 2.31  | 5.10  | 19.75_06             |
| GGAGGAA           |      |      |       |       | GGAGGAA<br>R_V\$PUI  |

WNT3A,PECK,CHE11,K LF, RIK13,LINS,CURL,SOX1 CD38,CW4,CLMP,GP  
 LK12,KIK13,LINS,HAU 5,TNNC1,RAVEF3,SEMA4C M6B,PBX1,CAV3,AX  
 S3,EFNB1,PAPEF3,SE\_MAF,KLF7,FNNL3,CACNA LDCN,PTGER1,CACNA  
 MAAC,MAFF,COCA2,E 16,DDIT4,ARHGFL5,STRAB 16,DMPK,ABCD1,PYG  
 M12,MPP2,SOX15,FA\_7RIM27,VWAL1,SC25A245 M,TRPV2,ENTD1,STR  
 M110A,MARPE,RESS EMAW2,PA2G4,PTPN12,H2A AG,FLI1,TPN,ANA,SHAB  
 36,MAB213,DDIT4A\_FKLEK3,NFATC4,ADNP\_RBA GRL,FGFR1,NIN,SCAR  
 RHGEF15,HK2,STRAB\_ D,ITGA2,CELA,ITGA5,HIF1A F1,MAGED1,MAGED2  
 5P2,TRIM27,RZAP11\_SC25A27,MIS12,SERPINE1\_PIVA,VIM,PIERHA4,P  
 R2TRBL,VWAL1,EHF,NB JUB,SC9A5,HAUS4,HAUS3\_RRX1,CSRP2,DDA42,N  
 G1,SEMA2A,PA2G4,SY ITG66,PNR1L,NIN2,CDCA2 5 FATC4,HSRQ2,TMEM1  
 NCIP,PRR7,KCQR2,PT AND1,BAG,AT2,PROCK,KC 19,ARMC4,KRTBDS,MY  
 PNT2,H2AR,PNKL,ELN\_NQ3,PIGSS,CG9A6,RP56K\_BPT1,THSS3,TTN1,NS1,  
 3,DLL4,SHBBP1,ME5D\_A4,TNIM8,EHFEHP1,WNT5A\_BAG4,IT2,DPS12,NAS  
 C1,TRIM39,ADNP\_RBA\_RALB,PPP2R5B,ASDHPPT, L1B1,IGFBP3,ZEB1,PT  
 D,DCAKD,ITGA2,CE1FA WNT3A,ENB1,HDA6G,ACT\_RN6,MMP22,CDB7,SLC  
 ITGA5,HIF1A,SC25A3 C1,RCOR2,SHROOM1,ADA\_O2B1,INF125,FLNCB  
 7,PNM2,SERPINE1,EPF5\_MTS12,FBXO5,CBX3,A2M\_F\_TK,ACTC1,ADAMTS12,  
 A10,CDKAP\_0,UBEPF,MSA41,YWH4Z\_AJUB,HAUS4,AF4,M L17,2HQ,NATB1,KNTC1,CS\_C079B,A2M,PODNLH  
 1,H5CB,RASI\_CCN2A,SOX15,G1B6,CD\_E5Z,PNR1L,NIN2,JUP\_ 18,H8EGF,BCAR3,DSG3,UPT\_C1,FLIPL,CACNB1,HS  
 P1,SERPINE1\_C42,PHL3,RAB10,SLC6A\_SAMD1,CCL25,DLLX1,P 18,RBL1,DAB2IP,BAEPK,H PA218,SPARC,PH1,P  
 ,PHL3,RTKN\_ 11,E1F5A,C17G662,APF\_RCCR,KCNQ5,PTGES,P\_OXCA,DLL4,MAB213,UNG\_ RELP,PAASF2,CDB9,N  
 FGG11,PDGF\_C2,NGS14,PP2R2B,COL\_HUDB3,SIC\_39A6,RP56\_EMOD1,CO117A1,LRNA,DC\_LNA,GNB4,FERMT2,CO  
 B,PPP2R2B\_ 5A3,MITS1,SLC2A24,D\_K44,PRDM10,SMTN12\_AKD16,HOXA5,CO113A1,C\_LSA3,FES,AR18BP\_SCA  
 WRAP53,SEZ,S63,S100A16,H157H2A\_7RIM8,KRT14,KRT13\_DK4,CD66,PRKD2,PHF16,FU R2,EMULIN,NTNL,IR  
 612,FHOD1\_C,FHOD1,TAX1BP3,BIG\_WNT5A,KDM3A,RALB\_NCC3A,PTV7,IGSF3,ERE\_OV\_S116,AGPAT4,AMOT  
 BMD,KRT17\_A172,PR56A4,H2AFXN\_ATTN1,HDA1,TMEM1\_O12,IG2,SPRRTA,DCLE1A\_TGFB3,EEF1A2,VCAN,  
 CDK4,TMM1\_R193,GRP2,EHFEHP1,NC\_88,AGRL5,DPT1,ANR\_K1512,CNM2,IMP2,H2,G1B6\_C0R01A,ELN,FBN1C1  
 9,  
 D1,CDK4,CD0B43,LOC\_HST1HC,FAM122A4,  
 MGN5,PPP2C,ADNP\_CAMK1G,TMEM88,XL  
 K12,KIK13 ITGA3,JARIN  
 D2,MITD1B,IGF3,SHR,  
 5,PNV2,SLC4A7,PRELID  
 1,IG1,1,ITF43,DMAAF2,  
 SOX15,TEFT,PBK1,PGF  
 ,ADAMTS4,TEPP,NAN  
 OG,MAML3\_AHC12,E  
 HF,GNEL,KHSRP,TAT  
 DNL,IMPDH1,CDK12,G  
 U2,KLE5,CXCR7,FOXF2  
 ,IRK5,PHCL,ENQ2,CNO  
 T7,IRX3,MCTP2,TCF7\_HST1HC,WNT3A,ADNP,IFT  
 BRCA2,EPHA2,ARHG\_43,KIK13,SUF,U,ARID2,MY  
 F15,LTBP1,SHR1,ST\_O1B,IGF3,SLC4A7,PRELID,  
 R46,RNF43,MRF51B8\_LG1,DMAF2,PGF,ADAMTS  
 BSRP1,SCAF1,IGFRR3\_F\_4,NANOG,ITGA3,CASQ2,CP\_SICA47,DNM1,GNM6  
 LRT3,DLL4,CASC5,SUF\_NET,SOX5,G12,KLE5,CXCR\_8,FBXP1,ADAMTS4,T  
 U,CITR1,GP2B3,AN\_7,CDCA2BP4,SPR2,PHCL,H\_MEN10,DG4,MVG  
 O1,WNT3A,ANKRD29\_NINPD,BRCA2,EPH42,ARH\_PDE1A,SULE1,TNIEV  
 BRD3,PWCH1,PCTT1B1\_GEF15,SHR1,STRAB,ORCA\_182,DMPK,TN1,LOC  
 C2,ITGA3,T\_P3,CNGB1,NTSC,ITGA3\_LG12,PRDM10,NUP54\_MRP51B8,BR551,PWCH1,FR\_NA15,DSF93,SBRX2,5  
 PM2,SULE1\_SOX15,MOT1B,SULE11,ROBO1,HNRNP,DS1C5\_13,DLL4,CASC5,STCL,LANC\_TRA6,USP13,TCF47,K  
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 M176A,MMP MC2,PRELID1,IGF2BP3\_BP2,SRM4,LANC2,ES\_FAM101B,CTBP2,MV1B,EL5\_3,MYBPCL,ANGPT12,C  
 K9,  
 MAPK9,  
 M1,ATYNL,  
 M1,  
 XXCS,PRRX1,FAM5C,  
 RASGRP3,TMPO,EMC  
 N,PTK7,SRCL,SM12,PP  
 RCL,LINS,MSH5,SPRE  
 D2,SLC7A1,HAUS3,EF  
 NA1,OVO2,SOX5,TLL  
 1,SMOX,PCCB,ARHG  
 EF4,TIMELESS,MER2,F\_TNFSF11,EMCN,PTV7,PAAP  
 AM10A,NAV2,MARK\_C1,LINS,US,SPRED2,PCSK5\_P13GCG,CIOTN15,STA  
 3,ANGPT2,FAM176A,5\_OVO12,NCAM1,CUEC1,PR1\_P1,TMEM204,GPR137  
 RPT2,PUS7L,EBR83,CT\_CUE1,TNOD3,POC1B,HOX\_8,CD200R1,LNW,ANGP  
 TIMPRESS1D,VWHA2,DO\_BP2,ARHGFT5,SHRPF\_C4,TIMELESS,HAUS3,CACNA\_T1,DCL1,GN721Y1,  
 PTG7,IMPDH1,S100A10  
 RASP1,PTV7\_K2,EV2B,ITGA,CCDC68\_1,KONOS,IERL,ROD1\_1G,MARK3,ANGPT2,SLC7A1\_OXK5,FQD2,PRNT,TR  
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 17RE,SECH42,ESM1\_MMP9,PTH1H,CTBP2,ESM1,NC,  
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 SEC1B8,CACNA16,CD  
 798,NCAM1,PIVAP,P  
 RICKET1,EV2B,CTH4,  
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 PIK3CG,CIOTN15,STA  
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 TNFSF11,CNVA5,PCSK  
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 SEC1B8,CACNA16,CD  
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 RICKET1,EV2B,CTH4,  
 ARAP1,TRORP,NDN,  
 PIK3CG,CIOTN15,STA  
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 T1,DCL1,GN721Y1,  
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 SEC1B8,CACNA16,CD  
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 TH1L1,TPW2\_NEURD2,FAM176A,LYN\_H1,TRIP3,STC2,TNK1\_15,SHRPF,JOBC,KONQ5,IE\_A17RHD1,LRNP,TRIM6  
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|      |      |      |          |          |
|------|------|------|----------|----------|
| 5.80 | 5.99 | 2.13 | YSEL1_02 | YSEL1_02 |
| 3.48 | 3.49 | 6.83 | 9.71     | 10.07 Q6 |
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|           |      |      |      |                    |  |
|-----------|------|------|------|--------------------|--|
| VSTFE_Q6  | 1.89 | 2.13 | 3.31 | 4.40 VSTFE_Q6      | <p>FAM122A,TRERF1,SPR<br/>V2,ERF,RIPIKA,CRIM1,K<br/>LF12,TRIM8,SCNN1G,<br/>PELO,KCNJ3,DJX5,CA<br/>DM1,IGFIR,BUB3,WIP<br/>11,MRP518B,PAK1P1,<br/>X4,XL,F12,ROBO1,CCDC14,P<br/>PAX1,SIC20A1,CNOD1,<br/>TRCC,ROBO1,COL13A,<br/>BUB3,WIP1,MRP518B,PAK<br/>TGA1,OLEFM13,CELF2,<br/>FAM5C,DIPYD2,TTN,P<br/>2R2D,UNC13D,RG53,KKA<br/>3,ATXN1,TTDP2,NHEP<br/>1,TRIM8,COL13A1,LSM1,UB<br/>RAC4,EGF7,CDX6,LO<br/>AOT1,<br/>TIN43,TPM4,CTCLS<br/>E25,NHEP2,LOP1,<br/>XOPNCSB,NRP12EB2,<br/>MAD6,SPRED2,RUND<br/>CA,BRKS,HAND1,CBX<br/>8,TRERF12A,MARF,FL<br/>11,AREG,NR6A1,NEDD<br/>1,CNPE1,AF4,PAR6B<br/>A,HOX44,NFIL3,ELF21,<br/>CTCL,SPRED2,RUND,CA,LY<br/>DHA,PPAS,RNP51,DNT<br/>R33,HAND1,MARF,FLT1,ARE<br/>TIP1,CEPNE,SUV39H2,<br/>G,NR6A1,NEDD1,CNPE1,WI<br/>HRE2BP1,PAR6B,ZNMC<br/>SP1,PPM11,CACNA1G,ELL2,<br/>B4,MAGED1,WISPL,M<br/>H,PTPRU,SULT1A1,CC<br/>NAN5,LDHA,PPAS,CEPNE,SU<br/>CAM,CACNA1G,LMCD<br/>A,NEDD1,CEPNE,WISPL,<br/>NOD,DYRK3,ERF,MBD<br/>TH,MAF,ZWILCH,COR06<br/>6,GDNF,STC2,SRNM4,<br/>PP2RBC,<br/>TGIF2,<br/>GPR176,<br/>176,</p>  |
| VSAFTL_Q6 | 2.65 | 5.99 | 5.75 | VSAFTL_Q<br>4.33 6 | <p>MMP15,ELAVL1,ACTG<br/>2,ITGA3,FRS3,LEPREL1<br/>,MPP2,MEI52,HLI2,PE<br/>LO,NKRF,IRX5,CDH3,8<br/>C17A,HOX2,LIAMA3,5<br/>MMP15,ACTG2,ITGA1,ITGA<br/>RE,GPR19,CDK25B,KC<br/>3,MESI,FIN2,PELO,NRIF,C<br/>TSRAN,EPHA1,LRP15,<br/>CDK25B,KCNQ4,PIEPA1,<br/>HSP92,HOB8,ACTG2,<br/>VWHAZ,CDK25B,TFAP4,<br/>NOD,PIEPA1,MCM7,<br/>DH3,ANXA3,LIAMA3,TRIM28<br/>TGM28A,COL15A1,<br/>TGAI,CCDC38B,ITGA3,5<br/>TSRAN,EPHA1,LRP15,<br/>CDK25B,KCNQ4,PIEPA1,<br/>HSP92,HOB8,ACTG2,<br/>DOCK93,PIEPA1,MCM7,<br/>NUP54,CNOD1,TRCC1,<br/>CNMT,TFAP4,VASH1,NUP54,<br/>1,CERMANIN,SGGA,G<br/>DEP2,CDH3,BTB03,JMS<br/>ER2,ILU5TK35,NOD1,<br/>CNOD1,HER2,DIOL,XOBER1,<br/>PC3,CNN1,CBX6,ANG<br/>B1B03,ATXN1,<br/>CQAP4,<br/>PTL,CD248,AXL,<br/>HOAC1,ITGA3,VSNL1,C1<br/>7,OTR80,CNCE1,CCDC92,<br/>NAV1,NCN5,SPC24,<br/>ITGA3,CELF4,RIPIKA1R<br/>RC48,FZD10,SIC10A7,<br/>ZHX2,SRCH4D,JUP,H<br/>OX44,NRG1,CADM1,P<br/>AQR9,KCNQ3,ITGB6,K<br/>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p> |
| VSHH4_Q1  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/>1,CRTV1,RNF207,PI15,CYR61,<br/>WISP2,C1QTNF6,SILA,<br/>TNF6,SULF1,DOCK2,WDR<br/>M4,RN1,MMIP9,PIH6<br/>RBL1,KNNB1,PAPA,NO19,D<br/>FLT1,VIM,PAPPA,AGP<br/>81,SCRN1,PTPN7,LOCKE1,<br/>JL17RE,PTCH1,PTPNC<br/>LX5,BCAR3,ARLR,RNLS,SGI<br/>AT4,MVP22,SULF1,IE<br/>F5A,<br/>P1,MMIP9,PIH6,PTPNC1,<br/>VIZA,RAMP2,SSB3,</p>  |
| VSHH4_Q0  | 1.65 | 1.48 |      | VSHH4_Q<br>2.75 1  | <p>COL1D1A1,DING1,ITGB6,N<br/>CQD5,JNLLC,CNOD1,T<br/>CDN,ITGA3,BCL11B,PRK<br/>BCC,COL13A1,PCDH17<br/>ACB,CD68,<br/>SCHP1,CNN1,<br/>ADAMTS4,POLAI,ETV4,PTK<br/>ADAMTS4,STAC2,HIC<br/>7,AC13,JAIRID2,SKA2,PPAR<br/>D,PRR11,BCL3,<br/>MEF2C,<br/>BRCA1,OVGPI,CCDC7<br/>5,NR6A1,LTBP1,HMG<br/>B2,TRCC,SOX15,MRP5<br/>18B,MED26,ERF,ST7Y<br/>BRCA1,OVGPI,NR6A1,HMG<br/>EGF,AODNF,FRD2,BCL<br/>B2,SOX15,MRP5,18B,MED26<br/>9,ILHES1,PMK6,NOS1A<br/>,ERF,VEGFA,GDNF,FRD2,HE<br/>P1,PC3,SOX5,<br/>S1,PMK6,<br/>F11,TGNR4,REN2,ZBT<br/>B25,ERF2B3,PCSK4,ERF<br/>5A,PGF,GHIL3,CNPE1,<br/>FOXF2,RBM14,RNF20<br/>7,SOX5,PI15,TGTF,FGD<br/>1,RBL1,KNNB1,RNF43,<br/>LIF,C1QTNF6,REN2,ERF2B3,<br/>NEK6,BATF,CTSK,CYG<br/>NOL9,PGV,DLX5,BCA<br/>PCSK4,FGD1,FLT1,PGF,CNPE<br/>B,CCDC102A,PDLIM3,<br/>R3,PRX1,APLR,CNN<br/></p>  |







|                        |      |      |      |                                   |                                   |  |
|------------------------|------|------|------|-----------------------------------|-----------------------------------|--|
| VSP1_Q2_Q1             | 2.94 | 4.95 | 3.57 | VSP1_Q2                           | 1.68_Q1                           | AGBL5, ENAH, PPRC1, U<br>NS, ADAM10, RCOR2, P<br>TPN2, BCL9, PHA3, J<br>UB, KLF16, TPM4, TIME<br>LESS, PTH, CSNP2, K<br>LF7, IRF2BP1, CDKSR1,<br>FBXL19, NDUFAL2, CA<br>ENAH, LINS, PTHH, RCOR2, C<br>DM1, FRB3, ASG1, 2, PR<br>HKA, PH, DA3, LUB, F2D2, KLF<br>MT1, CDH4, SRP, PCGF, 16, TIMELESS, CRY1, KLF7, ND<br>1, BCL6, BCL3, NRP4, CL3, NRP4,<br>PIGA, CNNM2, STMN1,<br>RML2, SUV39H1, MACR<br>OD2, CTT, ADAM10, C<br>DCA3, IUP, PCDH17, ST<br>K35, IFRD2, HES1, MSX2, PIGA, CNNM2, SUV39H1, CTT<br>NOL6, RAD51, C, DCA3, LIG1, IFRD2, HES1, Y<br>CN, LIG1,<br>NUTT2, PCYT1B, PRDM<br>10, PTK7, ASCL2, SIK5, C<br>SRNP2, CDC20, PVRL1,<br>PANK2, PTK7, CENPF, CDC, KCNIP4, CENPF, RP9K,<br>20, TMSB10, MAF, JAG1, S, AS, MEX3D, JAG1, DLX1<br>F, MS12, MEX3D, JAG1,<br>SOX5,<br>IRF2BP1, PDLIM7, POC<br>1A, CTFL1, STA3, MARS,<br>STOML2, CSNP2, POL,<br>HHAT, NEATC4, POCIA, POLR<br>P, LHM7, POCIA, LINS, CE<br>R1B, ANP32E, MRP1, SO<br>18, HXC4, HOKA5, POLIM7,<br>P4, SCNA1, TGFBI, C150<br>NOP16, DLX1, OGG1, P1<br>MRP150, NOP16, TGFBI, OGG<br>1, H1,<br>1, PHL5,<br>AGBL5, NUDC1, MYC<br>DCMO, E2F1, CBL1, S<br>MANC3, DRG2, AUR<br>KAWEE1, SUV39H1, DI<br>S3, GART, UBE2S, RBBP<br>SMARCA5, CSTF1, DCAK, NC<br>8, SNRPD, CD, C7, CST<br>AM1, BANF1, DUS, AURKA, P<br>HF7, UBE2S, MYC, UTP18, FA<br>M126A,<br>ZEB1, ZEB2, CYP1B1, NC<br>AM1, YIM,<br> |
| MCATNNNNNGCG_UNKNOWN   | 2.57 | 5.65 | 3.39 | MCATNN<br>NNNGCG_<br>UNKNOW<br>N  | MCATNN<br>NNNGCG_<br>UNKNOW<br>N  | ADAM10, CCA3, IFRD2,<br>MAF, CEN2, S, QLE,<br>   |
| MYATNNNNNNNGCG_UNKNOWN | 3.18 | 1.98 | 1.80 | MYATNN<br>NNNNNG<br>C_UNKNOW<br>N | MYATNN<br>NNNNNG<br>C_UNKNOW<br>N | PANK2, PTK7, CENPF, CDC, KCNIP4, CENPF, RP9K,<br>20, TMSB10, MAF, JAG1, S, AS, MEX3D, JAG1, DLX1<br>F, MS12, MEX3D, JAG1,<br>SOX5,<br>IRF2BP1, PDLIM7, POC<br>1A, CTFL1, STA3, MARS,<br>STOML2, CSNP2, POL,<br>HHAT, NEATC4, POCIA, POLR<br>P, LHM7, POCIA, LINS, CE<br>R1B, ANP32E, MRP1, SO<br>18, HXC4, HOKA5, POLIM7,<br>P4, SCNA1, TGFBI, C150<br>NOP16, DLX1, OGG1, P1<br>MRP150, NOP16, TGFBI, OGG<br>1, H1,<br>1, PHL5,<br>AGBL5, NUDC1, MYC<br>DCMO, E2F1, CBL1, S<br>MANC3, DRG2, AUR<br>KAWEE1, SUV39H1, DI<br>S3, GART, UBE2S, RBBP<br>SMARCA5, CSTF1, DCAK, NC<br>8, SNRPD, CD, C7, CST<br>AM1, BANF1, DUS, AURKA, P<br>HF7, UBE2S, MYC, UTP18, FA<br>M126A,<br>ZEB1, ZEB2, CYP1B1, NC<br>AM1, YIM,<br>   |
| RACTNNRTTNC_UNKNOWN    | 2.27 | 1.31 | 1.86 | RACTNNRT<br>TTNC_UNK<br>NOVN      | RACTNNRT<br>TTNC_UNK<br>NOVN      | PDLIM7, POCIA, LINS, CE<br>R1B, ANP32E, MRP1, SO<br>18, HXC4, HOKA5, POLIM7,<br>P4, SCNA1, TGFBI, C150<br>NOP16, DLX1, OGG1, P1<br>MRP150, NOP16, TGFBI, OGG<br>1, H1,<br>1, PHL5,<br>AGBL5, NUDC1, MYC<br>DCMO, E2F1, CBL1, S<br>MANC3, DRG2, AUR<br>KAWEE1, SUV39H1, DI<br>S3, GART, UBE2S, RBBP<br>SMARCA5, CSTF1, DCAK, NC<br>8, SNRPD, CD, C7, CST<br>AM1, BANF1, DUS, AURKA, P<br>HF7, UBE2S, MYC, UTP18, FA<br>M126A,<br>ZEB1, ZEB2, CYP1B1, NC<br>AM1, YIM,<br>  |
| RRCGTTA_UNKNOWN        | 2.42 | 6.34 | 4.88 | RRCGTTA<br>_UNKNOW<br>1.58 N      | RRCGTTA<br>_UNKNOW<br>1.58 N      | HENN1, SNRPD1, CDC2<br>F1, BANF1, PHEF, STC2,<br>7, MAZ, BANF1, TAGLN2,<br>FAM126A,<br>ZEB1, ZEB2, CYP1B1, NC<br>AM1, YIM,<br>   |
| TCGATTW_UNKNOWN        | 2.07 | 2.83 | 2.98 | TCGATTW<br>_UNKNOW<br>2.16 N      | TCGATTW<br>_UNKNOW<br>2.16 N      | VSNL1, GNAO1, ENAH,<br>PABPC4, CACNA2D3, D<br>CLRE1A, PLXNB1, CCDC<br>92, NOB1, MAPK6, AUR<br>KA, CKR7, SOX5, DLX1,<br>BCL7A, SPAT2, JARID2<br>VSNL1, ENAH, JARID2, CDRL2,<br>SPAG5, RNF43, CORT, P<br>SOX4, DCLE1A, PLXNB1, CAS<br>WIP2, GART, SYNCRIP, N<br>Q2, NOB1, MAPK6, AURKA, CX<br>OLFM1, 3, DPISL2, TACC<br>DCG2, NAV1, PH1, 3, GTF2<br>AS, OMG, BWP2, CSTF<br>CR7, SPAT2, PARP4, SPAG5<br>1, H5RG2, CDRL2, SHWD<br>A1, FGF1, CNT2, PPR2B<br>1, TMT2, BCL6B, TDP<br>TSPAN6, PMP2, NASP, OMG<br>1, 1, 6FRP4, KRTB10, M<br>2, LINS, ILF2,<br>BMP2, CSTF1, BCL6B, LINS,<br>YL1, SORBS2, FGFR1,<br>  |
| TGTNNNNNNNGCMM_UNKNOWN | 1.79 |      |      | TGTNNN<br>M_UNKNOW<br>4.38 WN     | TGTNNN<br>M_UNKNOW<br>4.38 WN     | SEMA4B, NCDN, S, DIT1, P<br>TIF, PPR202B,<br>  |



|                |      |      |      |                |            |  |
|----------------|------|------|------|----------------|------------|--|
| WTGAAT_UNKNOWN | 1.98 | 4.30 | 4.34 | WTGAAT_UNKNOWN | 776 N      | PTG2,STINL1,MOAP1,TREBF1,JARID2,HIF1A,IMPDH1,SHBP4,KP4,RIPK4,RAD1,CBX8,TMPRSS11A,FZD10,KBTBD8,CBX3,PBP4,DGGL,DICER1A,LRR1,CCNA2,MAML1,SOX6,CPNE1,GRWD1,FAM35A,PELO,CXK6,MED30,NLN2,TUBD1,MSX2,ONX,RGS12,TMTC2D,NMT7B,BEND4,CTNNB1,PTG2,PTC2,MOAP1,IL23A1,AL1,EFEFBP3,BUB3,S,EHPA3,WIP1,LINP4,3C,AMR4,SSGAL,PAKAP1,PRP4,OGG1,DICER1A,MOK1,LATIN,GRH2,PROGE,R1,MNAT1,PART1,PAAX,WDI,KBTBD8,PELO,NDNL2,9,STC2,SMNL2,BHD3,TUBD1,BEND4,BUB3,WIP1,OMG,MTHFD2,NUP54,HMG62,PAPPA,SSGAL,PAK35,ITGA1,HMG62,IMPDWNT2B,KIF23,WNT4,H1,KIF23,CCM2,SP110E,IFAEBP1,UCHL3,MAF,XD,ELR2,PTMHH,FGF11,BCL11B,SQLE,BTBD3,26,SC25A13,ESM1,BTB26,ESM1,0,SMMPX,WMPF1,FOXQ1,PLIN17,GIN4,ACTG2,DLL1,SLC16A1,TEAP2C,WIP1,HBEFG,IMPDH2,ING2,BHLHE41,ING2,BHLHE40,PAK2B,IMP0,PIK2B,DYDOL2,GRH2,DH2,ACTG1,CNN1,VASP,NC6,STP1,PIK2B,COL1A1,2,CNN1A,NRBD10,BOR3,KCNQ5,ILQ2,NR6A1,BKX1,SMO11,NUP54,LIN5,TPL1,LINE52,TRIM8,ITGB3BP,APUN,PLAIG2,WNT16,C13,RA22B,TNFSF10,PAPER,ST11,PP2R2B,TPL1,CCK1,13,FAH2,FLT13,P15,FAH2,FLT13,P15,ME3DC1,DPF1,GNAO1,JUNG1,ARID2,PTMHH,8,C9L,FLT1,ADAMTS12,ADAMTS4,KIF10,EIK3,JST13,HBEGF,FBX119,ELI2,DLL1,TRAF4,TO,M111,COL18A1,NRF4,3,PSME3,PCGF2,DLL4,PIGW,TRIM8,PCFTTB,CALM1,CA2,NGDN,PTHL,H,MN5S1,SMARCE1,RGS3,RAB10,FGF11,RHOG,ACTG2,HIF1A,MOC53,LAMA3,FEN1,BCL9,LEI,F51,ATXN12,D,CTNA4,TOPORS,KIF12,TPR1B,ZDHHC13,AFK4,SAE1,APBL1,LRRC4,DUSP8,MATF,SOX5,DLL1,BCL7A,HOUA2,SRG,OTOP2,JOR66,GTH21,SPV3,ENPEP,SLC38A2,TFAP4,AC2,JOR66,MAF,SIDT1,AB22A,BAX,CHN1,MEU,R12,SLC36A1,HP53,TME,M199,GRN,TM4SF19,RC,CZ,FLUC2,S100A16,1,PPCS,VAL1,WDR19,EMEL,TGIF1,TDUSP3,SRPN,SCN7A,ITGA1,M,TLD,CLL1,SPARC,LL,HP,GRN6B,LOX,FBL,N5,ITGB1B2,NE6,CL,EC5A,HEF2,P2RY12,PL,CNA15,ENTPD1,MDK,PNX1,PAPPA,LDB2,IGFBR5,NRP1,TMEV47,GFH,CIQTNF7,METPC,STAR08,NMWT,ZBTB20,SMMPX,WMPF1,HSR37,HOR08,ACTG2,CIQTNF3,PHK1,MIR6,GRF,NR27,CNN1,D,MFK,ACTC1,NEATC4,NCAM1,MNT3,FAF,NUTD4,EPSTIL,LD3,ZEB2,3,CEB2, |
| WTGAAT_UNKNOWN | 1.45 | 1.35 | 5.45 | WTGAAT_UNKNOWN | 5.41 DOWN  | PTG2,STINL1,MOAP1,TREBF1,JARID2,HIF1A,IMPDH1,SHBP4,KP4,RIPK4,RAD1,CBX8,TMPRSS11A,FZD10,KBTBD8,CBX3,PBP4,DGGL,DICER1A,LRR1,CCNA2,MAML1,SOX6,CPNE1,GRWD1,FAM35A,PELO,CXK6,MED30,NLN2,TUBD1,MSX2,ONX,RGS12,TMTC2D,NMT7B,BEND4,CTNNB1,PTG2,PTC2,MOAP1,IL23A1,AL1,EFEFBP3,BUB3,S,EHPA3,WIP1,LINP4,3C,AMR4,SSGAL,PAKAP1,PRP4,OGG1,DICER1A,MOK1,LATIN,GRH2,PROGE,R1,MNAT1,PART1,PAAX,WDI,KBTBD8,PELO,NDNL2,9,STC2,SMNL2,BHD3,TUBD1,BEND4,BUB3,WIP1,OMG,MTHFD2,NUP54,HMG62,PAPPA,SSGAL,PAK35,ITGA1,HMG62,IMPDWNT2B,KIF23,WNT4,H1,KIF23,CCM2,SP110E,IFAEBP1,UCHL3,MAF,XD,ELR2,PTMHH,FGF11,BCL11B,SQLE,BTBD3,26,SC25A13,ESM1,BTB26,ESM1,0,SMMPX,WMPF1,FOXQ1,PLIN17,GIN4,ACTG2,DLL1,SLC16A1,TEAP2C,WIP1,HBEFG,IMPDH2,ING2,BHLHE41,ING2,BHLHE40,PAK2B,IMP0,PIK2B,DYDOL2,GRH2,DH2,ACTG1,CNN1,VASP,NC6,STP1,PIK2B,COL1A1,2,CNN1A,NRBD10,BOR3,KCNQ5,ILQ2,NR6A1,BKX1,SMO11,NUP54,LIN5,TPL1,LINE52,TRIM8,ITGB3BP,APUN,PLAIG2,WNT16,C13,RA22B,TNFSF10,PAPER,ST11,PP2R2B,TPL1,CCK1,13,FAH2,FLT13,P15,FAH2,FLT13,P15,ME3DC1,DPF1,GNAO1,JUNG1,ARID2,PTMHH,8,C9L,FLT1,ADAMTS12,ADAMTS4,KIF10,EIK3,JST13,HBEGF,FBX119,ELI2,DLL1,TRAF4,TO,M111,COL18A1,NRF4,3,PSME3,PCGF2,DLL4,PIGW,TRIM8,PCFTTB,CALM1,CA2,NGDN,PTHL,H,MN5S1,SMARCE1,RGS3,RAB10,FGF11,RHOG,ACTG2,HIF1A,MOC53,LAMA3,FEN1,BCL9,LEI,F51,ATXN12,D,CTNA4,TOPORS,KIF12,TPR1B,ZDHHC13,AFK4,SAE1,APBL1,LRRC4,DUSP8,MATF,SOX5,DLL1,BCL7A,HOUA2,SRG,OTOP2,JOR66,GTH21,SPV3,ENPEP,SLC38A2,TFAP4,AC2,JOR66,MAF,SIDT1,AB22A,BAX,CHN1,MEU,R12,SLC36A1,HP53,TME,M199,GRN,TM4SF19,RC,CZ,FLUC2,S100A16,1,PPCS,VAL1,WDR19,EMEL,TGIF1,TDUSP3,SRPN,SCN7A,ITGA1,M,TLD,CLL1,SPARC,LL,HP,GRN6B,LOX,FBL,N5,ITGB1B2,NE6,CL,EC5A,HEF2,P2RY12,PL,CNA15,ENTPD1,MDK,PNX1,PAPPA,LDB2,IGFBR5,NRP1,TMEV47,GFH,CIQTNF7,METPC,STAR08,NMWT,ZBTB20,SMMPX,WMPF1,HSR37,HOR08,ACTG2,CIQTNF3,PHK1,MIR6,GRF,NR27,CNN1,D,MFK,ACTC1,NEATC4,NCAM1,MNT3,FAF,NUTD4,EPSTIL,LD3,ZEB2,3,CEB2, |
| WTGAAT_UNKNOWN | 1.81 | 1.94 | 1.90 | WTGAAT_UNKNOWN | 2.05 WN    | PTG2,STINL1,MOAP1,TREBF1,JARID2,HIF1A,IMPDH1,SHBP4,KP4,RIPK4,RAD1,CBX8,TMPRSS11A,FZD10,KBTBD8,CBX3,PBP4,DGGL,DICER1A,LRR1,CCNA2,MAML1,SOX6,CPNE1,GRWD1,FAM35A,PELO,CXK6,MED30,NLN2,TUBD1,MSX2,ONX,RGS12,TMTC2D,NMT7B,BEND4,CTNNB1,PTG2,PTC2,MOAP1,IL23A1,AL1,EFEFBP3,BUB3,S,EHPA3,WIP1,LINP4,3C,AMR4,SSGAL,PAKAP1,PRP4,OGG1,DICER1A,MOK1,LATIN,GRH2,PROGE,R1,MNAT1,PART1,PAAX,WDI,KBTBD8,PELO,NDNL2,9,STC2,SMNL2,BHD3,TUBD1,BEND4,BUB3,WIP1,OMG,MTHFD2,NUP54,HMG62,PAPPA,SSGAL,PAK35,ITGA1,HMG62,IMPDWNT2B,KIF23,WNT4,H1,KIF23,CCM2,SP110E,IFAEBP1,UCHL3,MAF,XD,ELR2,PTMHH,FGF11,BCL11B,SQLE,BTBD3,26,SC25A13,ESM1,BTB26,ESM1,0,SMMPX,WMPF1,FOXQ1,PLIN17,GIN4,ACTG2,DLL1,SLC16A1,TEAP2C,WIP1,HBEFG,IMPDH2,ING2,BHLHE41,ING2,BHLHE40,PAK2B,IMP0,PIK2B,DYDOL2,GRH2,DH2,ACTG1,CNN1,VASP,NC6,STP1,PIK2B,COL1A1,2,CNN1A,NRBD10,BOR3,KCNQ5,ILQ2,NR6A1,BKX1,SMO11,NUP54,LIN5,TPL1,LINE52,TRIM8,ITGB3BP,APUN,PLAIG2,WNT16,C13,RA22B,TNFSF10,PAPER,ST11,PP2R2B,TPL1,CCK1,13,FAH2,FLT13,P15,FAH2,FLT13,P15,ME3DC1,DPF1,GNAO1,JUNG1,ARID2,PTMHH,8,C9L,FLT1,ADAMTS12,ADAMTS4,KIF10,EIK3,JST13,HBEGF,FBX119,ELI2,DLL1,TRAF4,TO,M111,COL18A1,NRF4,3,PSME3,PCGF2,DLL4,PIGW,TRIM8,PCFTTB,CALM1,CA2,NGDN,PTHL,H,MN5S1,SMARCE1,RGS3,RAB10,FGF11,RHOG,ACTG2,HIF1A,MOC53,LAMA3,FEN1,BCL9,LEI,F51,ATXN12,D,CTNA4,TOPORS,KIF12,TPR1B,ZDHHC13,AFK4,SAE1,APBL1,LRRC4,DUSP8,MATF,SOX5,DLL1,BCL7A,HOUA2,SRG,OTOP2,JOR66,GTH21,SPV3,ENPEP,SLC38A2,TFAP4,AC2,JOR66,MAF,SIDT1,AB22A,BAX,CHN1,MEU,R12,SLC36A1,HP53,TME,M199,GRN,TM4SF19,RC,CZ,FLUC2,S100A16,1,PPCS,VAL1,WDR19,EMEL,TGIF1,TDUSP3,SRPN,SCN7A,ITGA1,M,TLD,CLL1,SPARC,LL,HP,GRN6B,LOX,FBL,N5,ITGB1B2,NE6,CL,EC5A,HEF2,P2RY12,PL,CNA15,ENTPD1,MDK,PNX1,PAPPA,LDB2,IGFBR5,NRP1,TMEV47,GFH,CIQTNF7,METPC,STAR08,NMWT,ZBTB20,SMMPX,WMPF1,HSR37,HOR08,ACTG2,CIQTNF3,PHK1,MIR6,GRF,NR27,CNN1,D,MFK,ACTC1,NEATC4,NCAM1,MNT3,FAF,NUTD4,EPSTIL,LD3,ZEB2,3,CEB2, |
| WTGAAT_UNKNOWN | 1.30 | 1.87 | 2.27 | WTGAAT_UNKNOWN | 9.72 FL_01 | PTG2,STINL1,MOAP1,TREBF1,JARID2,HIF1A,IMPDH1,SHBP4,KP4,RIPK4,RAD1,CBX8,TMPRSS11A,FZD10,KBTBD8,CBX3,PBP4,DGGL,DICER1A,LRR1,CCNA2,MAML1,SOX6,CPNE1,GRWD1,FAM35A,PELO,CXK6,MED30,NLN2,TUBD1,MSX2,ONX,RGS12,TMTC2D,NMT7B,BEND4,CTNNB1,PTG2,PTC2,MOAP1,IL23A1,AL1,EFEFBP3,BUB3,S,EHPA3,WIP1,LINP4,3C,AMR4,SSGAL,PAKAP1,PRP4,OGG1,DICER1A,MOK1,LATIN,GRH2,PROGE,R1,MNAT1,PART1,PAAX,WDI,KBTBD8,PELO,NDNL2,9,STC2,SMNL2,BHD3,TUBD1,BEND4,BUB3,WIP1,OMG,MTHFD2,NUP54,HMG62,PAPPA,SSGAL,PAK35,ITGA1,HMG62,IMPDWNT2B,KIF23,WNT4,H1,KIF23,CCM2,SP110E,IFAEBP1,UCHL3,MAF,XD,ELR2,PTMHH,FGF11,BCL11B,SQLE,BTBD3,26,SC25A13,ESM1,BTB26,ESM1,0,SMMPX,WMPF1,FOXQ1,PLIN17,GIN4,ACTG2,DLL1,SLC16A1,TEAP2C,WIP1,HBEFG,IMPDH2,ING2,BHLHE41,ING2,BHLHE40,PAK2B,IMP0,PIK2B,DYDOL2,GRH2,DH2,ACTG1,CNN1,VASP,NC6,STP1,PIK2B,COL1A1,2,CNN1A,NRBD10,BOR3,KCNQ5,ILQ2,NR6A1,BKX1,SMO11,NUP54,LIN5,TPL1,LINE52,TRIM8,ITGB3BP,APUN,PLAIG2,WNT16,C13,RA22B,TNFSF10,PAPER,ST11,PP2R2B,TPL1,CCK1,13,FAH2,FLT13,P15,FAH2,FLT13,P15,ME3DC1,DPF1,GNAO1,JUNG1,ARID2,PTMHH,8,C9L,FLT1,ADAMTS12,ADAMTS4,KIF10,EIK3,JST13,HBEGF,FBX119,ELI2,DLL1,TRAF4,TO,M111,COL18A1,NRF4,3,PSME3,PCGF2,DLL4,PIGW,TRIM8,PCFTTB,CALM1,CA2,NGDN,PTHL,H,MN5S1,SMARCE1,RGS3,RAB10,FGF11,RHOG,ACTG2,HIF1A,MOC53,LAMA3,FEN1,BCL9,LEI,F51,ATXN12,D,CTNA4,TOPORS,KIF12,TPR1B,ZDHHC13,AFK4,SAE1,APBL1,LRRC4,DUSP8,MATF,SOX5,DLL1,BCL7A,HOUA2,SRG,OTOP2,JOR66,GTH21,SPV3,ENPEP,SLC38A2,TFAP4,AC2,JOR66,MAF,SIDT1,AB22A,BAX,CHN1,MEU,R12,SLC36A1,HP53,TME,M199,GRN,TM4SF19,RC,CZ,FLUC2,S100A16,1,PPCS,VAL1,WDR19,EMEL,TGIF1,TDUSP3,SRPN,SCN7A,ITGA1,M,TLD,CLL1,SPARC,LL,HP,GRN6B,LOX,FBL,N5,ITGB1B2,NE6,CL,EC5A,HEF2,P2RY12,PL,CNA15,ENTPD1,MDK,PNX1,PAPPA,LDB2,IGFBR5,NRP1,TMEV47,GFH,CIQTNF7,METPC,STAR08,NMWT,ZBTB20,SMMPX,WMPF1,HSR37,HOR08,ACTG2,CIQTNF3,PHK1,MIR6,GRF,NR27,CNN1,D,MFK,ACTC1,NEATC4,NCAM1,MNT3,FAF,NUTD4,EPSTIL,LD3,ZEB2,3,CEB2, |
| WTGAAT_UNKNOWN | 3.20 | 1.67 | 1.35 | WTGAAT_UNKNOWN | 2.27 BP_01 | PTG2,STINL1,MOAP1,TREBF1,JARID2,HIF1A,IMPDH1,SHBP4,KP4,RIPK4,RAD1,CBX8,TMPRSS11A,FZD10,KBTBD8,CBX3,PBP4,DGGL,DICER1A,LRR1,CCNA2,MAML1,SOX6,CPNE1,GRWD1,FAM35A,PELO,CXK6,MED30,NLN2,TUBD1,MSX2,ONX,RGS12,TMTC2D,NMT7B,BEND4,CTNNB1,PTG2,PTC2,MOAP1,IL23A1,AL1,EFEFBP3,BUB3,S,EHPA3,WIP1,LINP4,3C,AMR4,SSGAL,PAKAP1,PRP4,OGG1,DICER1A,MOK1,LATIN,GRH2,PROGE,R1,MNAT1,PART1,PAAX,WDI,KBTBD8,PELO,NDNL2,9,STC2,SMNL2,BHD3,TUBD1,BEND4,BUB3,WIP1,OMG,MTHFD2,NUP54,HMG62,PAPPA,SSGAL,PAK35,ITGA1,HMG62,IMPDWNT2B,KIF23,WNT4,H1,KIF23,CCM2,SP110E,IFAEBP1,UCHL3,MAF,XD,ELR2,PTMHH,FGF11,BCL11B,SQLE,BTBD3,26,SC25A13,ESM1,BTB26,ESM1,0,SMMPX,WMPF1,FOXQ1,PLIN17,GIN4,ACTG2,DLL1,SLC16A1,TEAP2C,WIP1,HBEFG,IMPDH2,ING2,BHLHE41,ING2,BHLHE40,PAK2B,IMP0,PIK2B,DYDOL2,GRH2,DH2,ACTG1,CNN1,VASP,NC6,STP1,PIK2B,COL1A1,2,CNN1A,NRBD10,BOR3,KCNQ5,ILQ2,NR6A1,BKX1,SMO11,NUP54,LIN5,TPL1,LINE52,TRIM8,ITGB3BP,APUN,PLAIG2,WNT16,C13,RA22B,TNFSF10,PAPER,ST11,PP2R2B,TPL1,CCK1,13,FAH2,FLT13,P15,FAH2,FLT13,P15,ME3DC1,DPF1,GNAO1,JUNG1,ARID2,PTMHH,8,C9L,FLT1,ADAMTS12,ADAMTS4,KIF10,EIK3,JST13,HBEGF,FBX119,ELI2,DLL1,TRAF4,TO,M111,COL18A1,NRF4,3,PSME3,PCGF2,DLL4,PIGW,TRIM8,PCFTTB,CALM1,CA2,NGDN,PTHL,H,MN5S1,SMARCE1,RGS3,RAB10,FGF11,RHOG,ACTG2,HIF1A,MOC53,LAMA3,FEN1,BCL9,LEI,F51,ATXN12,D,CTNA4,TOPORS,KIF12,TPR1B,ZDHHC13,AFK4,SAE1,APBL1,LRRC4,DUSP8,MATF,SOX5,DLL1,BCL7A,HOUA2,SRG,OTOP2,JOR66,GTH21,SPV3,ENPEP,SLC38A2,TFAP4,AC2,JOR66,MAF,SIDT1,AB22A,BAX,CHN1,MEU,R12,SLC36A1,HP53,TME,M199,GRN,TM4SF19,RC,CZ,FLUC2,S100A16,1,PPCS,VAL1,WDR19,EMEL,TGIF1,TDUSP3,SRPN,SCN7A,ITGA1,M,TLD,CLL1,SPARC,LL,HP,GRN6B,LOX,FBL,N5,ITGB1B2,NE6,CL,EC5A,HEF2,P2RY12,PL,CNA15,ENTPD1,MDK,PNX1,PAPPA,LDB2,IGFBR5,NRP1,TMEV47,GFH,CIQTNF7,METPC,STAR08,NMWT,ZBTB20,SMMPX,WMPF1,HSR37,HOR08,ACTG2,CIQTNF3,PHK1,MIR6,GRF,NR27,CNN1,D,MFK,ACTC1,NEATC4,NCAM1,MNT3,FAF,NUTD4,EPSTIL,LD3,ZEB2,3,CEB2, |











|                   |      |      |                        |
|-------------------|------|------|------------------------|
| V\$SRV_01         | 2.14 | 2.99 | 5.73 V\$SRV_01         |
| V\$SRM1_01        | 1.50 |      | V\$SRM1_5.90 01        |
| V\$CGRV_01        | 2.74 | 1.98 | V\$CGRV_03.06 1        |
| V\$SRV_02         | 3.23 |      | 1.96 V\$SRV_02         |
| V\$OCT1_05        | 2.41 | 2.32 | V\$OCT1_07.55 5        |
| ATCOWTCGV_UNKNOWN | 2.32 |      | ATCOWTC CGV_UNKN NOVEN |
| V\$SR_06          | 3.34 | 3.63 | 2.18 V\$SR_06          |

STMN1,IG11,SOX6,AT  
 XN712,SOX5,MP212,R  
 BMB8,MAB2113,PVRL  
 1,METTL8,MAG13,TE  
 A04,NOS1,AP,CADMI1, 2,MF212,MAB2113,PVRL, NCAM1,ENTP1,LOK  
 BRN05,D01T,ASC12,P METTL8,MAG13,SPONT,IE N1C,SIPL1,PIK3D,1TH  
 RMT6,ENAI,EHF,DFE N05,CN61,PMT6,DFB,LA B53,MSR83,PDE3B,A  
 BLAMC2,FL1R,PUSD MC2,FL1R,NCAM1,TSEN15, MCAL,GRAL1,PRRX1,  
 4,NXU1,TRIM8,BCLD, SGIP1,TRIM8,DEPDC7,CKAP NMR48,CSR9,5,TBGA  
 EPDC7  
 HST1HC,FAM122R,A 4,  
 OC2,ISPN,HSP9,JA81  
 D2,SLC47,AFG12,CT  
 H1A0D48,SOX15,CCD  
 C32,HSPD1,CTP39AL,  
 TCF7,DCUNID4,CNIF  
 R2DHHQ21,ILTRF,CD  
 HR1,BC19,SARNP,PHF  
 5A,PCDH18,STFAP2,E  
 ME1,BTBD3,  
 NUDCD1,VSNL1,GSTA  
 4,JARID2,SLC25A35,O  
 LFM2,YTHDF1,OVOL2,  
 EDNRB,OBFC1,SOX5,D  
 DXS2,PVRL1,FAHD15  
 100A9,RBM14,ANGPT  
 2,CADMI1,LTBP1,ANKR NUDCD1,NFATC4,VSNL1,G5  
 D42,KCNQ4,TBCLD88, TM4,JARID2,OBFC1,OVOL2,E  
 RNF43,ARVAD1,DLL1, DNRA,DDX52,PVRL1,ANGPT TTGB1BP2,CACNB1,AR  
 PAK1P1,CACNA2D3,B 2,ANKRD2,KCNQ4,ARAD NCX4,FLU1,PDE3B,AN  
 C4R3,PRDM10,UBE2O 1,DLL1,PAK1P1,ADMB,BCAR GPT12,GNGT2,MYRBC  
 ,STOM12,MAGH,PALL 3,ARMC4,SGIP1,NUP155,T 1,IGFBP5,EVD2A,NRAT  
 D,FAM170A,NUP155, GTF1,  
 PHT16,EMCK,CAMK1  
 GGNV01,SLC7A1,RBP  
 GEF3,CSNP2,SOX6,S  
 OX5,SRF7,HSS1T,AM  
 AML3,MAD5B,CNIE1,  
 CDCG2,KLEF,INHBA,  
 MAG3,CADMI1,LUK1,  
 RNF43,MCM7,DLL1,N  
 UDT11,FGR2,RBM8A,  
 E2F1,TFAP4,NANOS1,  
 MXL,METTL21D,KRT1  
 3,STC1,CCN1,ATYNT1,  
 ADNP,TRENF1,REM2,  
 MIR17HG,IG11,HST1  
 H2AC,SOX5,MAM13,G  
 RHL3,ZHX2,SEMA7A,C  
 PNE1,MAB2113,UG4,  
 PRDM10,NG1,CCCA7,  
 DUX1,CADMI1,PIW2,EH ADNP,REM2,MIR17HG,IG11 DPY35,ARMC4,SLC7  
 F,PTPN2,ESRR2,HST2 ,HST1H2A,CLUG,ZHX2,SEM A11,ENP1,IL6,PRRX1  
 H2AC,CNNM1,METTL A7A,CNIE1,H0X5,MAB211, PROKR2,LP,SLIT3,BT  
 8,TFAP4,TOPBP1,LEK3 3,MNF1B,PROKR2,CCNA7, KMTBRC1,SNRP2,BT  
 ,CDM2,NEL3,MST3H2 GFR2,TOPBP1,TFAP4,ANMC B2,DEB1,ILN1,CDL12  
 A,  
 5SRF7,NBL1,ATAO2,W  
 X4,IL6,LEK3,CDK2,CDL12A1, ALIGRCS8,  
 DNR8,CNMG,MIBD6,S  
 TK35,CAMK2N2,KDM  
 3A,MAM13,  
 DRG2,HMGNS,AUTS2,  
 ADNP,FOXQ4,PABPC4,  
 MEIS2,RCOR2,PIR4,S  
 CHIP1,MOAP1,CCDC1  
 26,DIG5,RUVBL2,BHL  
 HE4D,HAUS3,KIF5,G0 ADNP,TM0D3,PABPC4,GNB  
 T2,DLL1,H0X4,LYSM 1L,PIR4,CHIP1,NCAM1,M  
 D2,SLC38A2,PTPDC1, OAP1,CCDC136,FOXQ4,RUV  
 GYS1,FR13,METTL21 BL2,BHL,HE4D,HAUS3,KIF5,L  
 D,PAK1P1,GIPPC2,SYN Y5MD2,SLC38A2,MCM7,FLR FAM5C,CQCL14,NCX  
 GRP1,BR1,GNB1,NO 13,METTL21D,PAK1P1,GIP MLJPH2,PRRX1,PRG4  
 TCH4,WNT4,GNF,M C2,LR1,RCOR2,NOTCH4,W FSLAMB1,CSR9,LO  
 CM7,PCDH18,KCNV1, NT4,GDNF,TGIF1, X,BT,ZEB2,



|             |      |      |                |          |
|-------------|------|------|----------------|----------|
| VSOCTL_Q6   | 1.38 | 2.02 | 8.46 6         | VSOCTL_Q |
| VSP1_Q6     | 3.83 | 2.28 | VSP1_Q6        |          |
| VSCBP_QC    | 1.71 |      | 4.44 VSCBP_QC  |          |
| VSOCTL_QC   | 1.42 | 2.99 | 5.27 VSOCTL_QC |          |
| VSTATL_QC   | 1.75 | 2.99 | 8.76 VSTATL_QC |          |
| VSMF2_Q2    | 1.35 | 2.89 | 22.59 2        | VSMF2_Q  |
| VSMHRANT_Q1 | 3.39 | 2.58 | 1.73 NT_Q1     | VSMHRAR  |

|  |  |  |  |                         |
|--|--|--|--|-------------------------|
| VSNL1,TTRF1,SLC25A35,GNBL,SRE,ATXN7L     |  |  |  | GRRCB,ANKRD1,PIK3       |
| F12,ITPRP,GRH3,ZHX,UF,VSNL1,GNBL,ATXN7L2 |  |  |  | CD,DOX3,PROKR1,LYN      |
| 2,CCOC7,DLX1,IRX3,C                      |  |  |  | DIC1,STAC2,DPPX1,3,J    |
| ADNL1,PMI2,EHF,FIAT                      |  |  |  | ZHX2,HNF1B,PROKR2,CDCA  |
| 3,HST1,H3BA,RTTN,HI                      |  |  |  | 7,HST1H2B,RTTN,HI       |
| 5,STH2AC,PCOT1B,PRD                      |  |  |  | BA,RTTN,PCOT1B,RAR2,AR  |
| MD1,RAR2,CDI2,CD                         |  |  |  | MC4Q,CDI2,CDI6,PKM6,CO  |
| 16,PKM6,H3BA,RTTN,HI                     |  |  |  | 1,CDI12,1A1,PRRX1,2B    |
| AGRS,STN1,PTT7,5                         |  |  |  | 1,1241,                 |
| MARCA5,KAT2A,RCOR                        |  |  |  | 1820,1,PMR5C,IRTK,      |
| 2,PTPRD2,NDRG1,PRM                       |  |  |  |                         |
| 15B,PRICOLE3,TIMBLE                      |  |  |  |                         |
| SSDAK,COMS1,CDCA                         |  |  |  |                         |
| 7,CD25A,IRX3,CAOM                        |  |  |  |                         |
| 1,WN12B,EBB83,PRM                        |  |  |  |                         |
| 1,1281B5,ASCL2,KCN                       |  |  |  |                         |
| Q4,PHS12,HSP99,DC                        |  |  |  | SLBP,PTC7,KAT7A,RCOR2,N |
| UN1D4,PIGV,ANF24,I                       |  |  |  | DRG1,SMARCA5,TIMELESS,  |
| NG2,PCGF2,CNNM4,U                        |  |  |  | CRY1,DAK,CHKA,CDCA7,UT  |
| BE2D,TIRM27,ROD1,8                       |  |  |  | P18,CDK25A,PRMT1,TIRM2  |
| CL6B,PI,EKHA8,NYPH4                      |  |  |  | 8,KCNQ4,TIRM27,ANF24,IN |
| G2,PCGF2,BCL6B,NYPH4,                    |  |  |  |                         |
| TGM3,RRM1,P2RY1,8                        |  |  |  |                         |
| CL2L3,WN110B,KIF5,                       |  |  |  |                         |
| DXL,MRRL12,EHF,VE                        |  |  |  |                         |
| GFA,UNG,CACNA2D3,                        |  |  |  |                         |
| SERPIN2,SEMA7A,PT                        |  |  |  |                         |
| PRU,CRIM1,ATD05,PT                       |  |  |  |                         |
| PN12,RIF,ROBO4,SAR                       |  |  |  |                         |
| N,P,PLG12,STCJ,UNS                       |  |  |  |                         |
| 4,                                       |  |  |  |                         |
| ADNP,HEM2,JARID2,5                       |  |  |  |                         |
| LC2A3,5,MIR17HG,SR                       |  |  |  |                         |
| F,HST1H2AC,VSNL1,G                       |  |  |  |                         |
| RHL3,ZHX2,SEMA7A,I                       |  |  |  |                         |
| NG1,PRD10,DLX1,C                         |  |  |  |                         |
| MIR17HG,HST1H2A1,HST1                    |  |  |  |                         |
| ADNL1,PMI2,EHF,HIST                      |  |  |  |                         |
| H2AC,VSNL1,ZHX2,SEMA7A                   |  |  |  |                         |
| SRRP2,ETV1,DPPX12,D                      |  |  |  |                         |
| 1H3C,GFGR2,HISTH2H                       |  |  |  |                         |
| HNF1B,PROKR2,CIR61,HST                   |  |  |  |                         |
| PS1,3,SH3BG,LRM                          |  |  |  |                         |
| AC,HST1H2BK,ABTB2,                       |  |  |  |                         |
| 1H3B,HST1H3C,HST1H2BB                    |  |  |  |                         |
| C4,CDK14,LD2,PRR                         |  |  |  |                         |
| PCOT1B,TT12,RAB26,C                      |  |  |  |                         |
| ,fGFGR2,HST1H2BK,SRRP2,P                 |  |  |  |                         |
| X1,PROKR2,LR,CDR2L                       |  |  |  |                         |
| DK2,CNNM4,UBE2S,HI                       |  |  |  |                         |
| CTTB,SCOC,RAB26,ARMCX                    |  |  |  |                         |
| 1,MBPC1,SNPX,PATZ                        |  |  |  |                         |
| 5,TRH2A,                                 |  |  |  |                         |
| 4,CDK2,UBE2S,                            |  |  |  |                         |
| 1,2BTRB20,EBF1,LYN,                      |  |  |  |                         |
| TGFB2,MMP10,MMP1                         |  |  |  |                         |
| 3,JARID2,GEN1,GT3C                       |  |  |  |                         |
| 1,PRPF4,SOX5,ZC3H10                      |  |  |  |                         |
| ,NDNL2,CTED1,BNIP3                       |  |  |  |                         |
| TGFB2,MMP10,MMP13,AR                     |  |  |  |                         |
| POGFRB,TGFB3,MVH1                        |  |  |  |                         |
| ,MAREI,HAS2,CCDC3                        |  |  |  |                         |
| ID2,HOXCA,GEN1,BMIR1B,                   |  |  |  |                         |
| 1,MVH1,LOX,BIN1,ITG                      |  |  |  |                         |
| 8,SRE,ITBP1,MNP5,188                     |  |  |  |                         |
| PRPF4,MVH3,NDNL2,TAGLN                   |  |  |  |                         |
| B1BP2,MVH2,MVH3,                         |  |  |  |                         |
| ,FHF,HN1L,LEAP2,STC                      |  |  |  |                         |
| ,HAS2,CO13A1,CCDC38,CYR                  |  |  |  |                         |
| MVH1,ASB5,NRAP,AG                        |  |  |  |                         |
| 1,SNRPF,PA2G4,ENDO                       |  |  |  |                         |
| 61,HNRNP40,MNP5,188,HN                   |  |  |  |                         |
| PAT4,SLT3,CO,8A1,R                       |  |  |  |                         |
| U,PRX1,TOBP1,H2AF                        |  |  |  |                         |
| 1L,STR3,SNRPF,PA2G4,BIN                  |  |  |  |                         |
| AS111B,LD2,SDPR,TA                       |  |  |  |                         |
| X,BMIR1B,STR3,CYB                        |  |  |  |                         |
| P3,GAJ6,TOBP1,H2AF,ST                    |  |  |  |                         |
| GUN,GAJ6,LMO2,KNU                        |  |  |  |                         |
| 561D2,ELMO3,                             |  |  |  |                         |
| CL,                                      |  |  |  |                         |
| 8,MVH2,TIMP2,CRM,                        |  |  |  |                         |
| MYO12,TIMP2,CRM,                         |  |  |  |                         |
| ACTC1,ADAMTS12,TN                        |  |  |  |                         |
| NC2,MVH1,TRDN,KOT                        |  |  |  |                         |
| BD5,CGD1,LOMNL1,5                        |  |  |  |                         |
| 1PRL,PHF2,TNFR1B2                        |  |  |  |                         |
| ,TNM12,STOD4,LYN,C                       |  |  |  |                         |
| OLB1,FBXO40,ADP1,                        |  |  |  |                         |
| TS2C2D1,GNB4,SNPX,                       |  |  |  |                         |
| X2,KCNQ5,PMEP1,HI                        |  |  |  |                         |
| 4A,CTNN1,TNNC1,SLC9A5,T                  |  |  |  |                         |
| ADAM23,NBTD10,SY                         |  |  |  |                         |
| STH3A,DL4,HST1H2                         |  |  |  |                         |
| NN2,CASQ2,ZHX2,CO18A1,                   |  |  |  |                         |
| NPOZ1,STG6,ALUACS,                       |  |  |  |                         |
| BA,CACNA2D3,GABRB8                       |  |  |  |                         |
| KCNQ5,PMEP1,HST1H3A,                     |  |  |  |                         |
| GRI153,ADCY2,CMYT                        |  |  |  |                         |
| 3,PACSL1,DZIP1L,CO1                      |  |  |  |                         |
| DL4,HST1H2BA,GABRB3,P                    |  |  |  |                         |
| 2,IRSI1,MEF2C,CTGF,A                     |  |  |  |                         |
| 3A1,PLAGL2,PAK6,PTC                      |  |  |  |                         |
| ACS1,ADAMTS12,DZIP1L,CO                  |  |  |  |                         |
| TP1A2,ABRA,MYO2Z,                        |  |  |  |                         |
| HL,                                      |  |  |  |                         |
| USP1,PRRC1,BCL11A,C                      |  |  |  |                         |
| NTNAP1,ATXN7L2,LUB                       |  |  |  |                         |
| ,KIF10,CXSB1,STT12,G                     |  |  |  |                         |
| NAO1,AGL1,HK2,DL4,                       |  |  |  |                         |
| ABTB2,TAP4,MX11,W                        |  |  |  |                         |
| LUB,TFA9L,USP1,CXSB1B,WN                 |  |  |  |                         |
| NT4,ELK3,PCDH17,CD                       |  |  |  |                         |
| T4,ELK3,HOXAS,DL4,SOX4,                  |  |  |  |                         |
| 2,CTGF,CSRP3,ZBTB20                      |  |  |  |                         |
| 16,HES1,STC1,PTTNC                       |  |  |  |                         |
| CDK6,PARPC,HES1,JAG1A                    |  |  |  |                         |
| 2,CTGF,CSRP3,ZBTB20                      |  |  |  |                         |
| 1,                                       |  |  |  |                         |
| TAN12,PTTNC1,                            |  |  |  |                         |
| ZEB,                                     |  |  |  |                         |



|                  |      |      |                  |
|------------------|------|------|------------------|
| V\$AHARNT_02     | 1.63 |      | V\$AHARNT_02     |
| CATRRAGC_UNKNOWN | 3.48 | 2.64 | CATRRAGC_UNKNOWN |
| V\$GFR3_01       | 3.60 | 3.15 | V\$GFR3_01       |
| V\$GFR2_01       | 5.49 | 4.13 | V\$GFR2_01       |
| V\$RREB1_01      | 1.55 | 1.43 | V\$RREB1_01      |
| V\$HUF_01        | 2.97 | 2.32 | V\$HUF_01        |
| V\$OLF_01        | 2.47 | 1.71 | V\$OLF_01        |
| V\$P53_02        | 2.68 | 3.71 | 2.86 V\$P53_02   |

HES1,MAPRE1,MEIS2,REL2,  
 SNA6,TCERG1,FAM83H,MIR17HG,PUNB1,RAVER1,RADS4B,WNT10A,AF4,TFAP2E,FBXU9,KCND4,TGFB4,JAR,PUNB1,RAVER1,RADS4B,W102,EFNA5,PCGF2,AUD,NTIOA,EFNA5,JARID2,H0KC,OC,SATIN1.2,ABTB2,PC4,PCGF2,POCTB,MIR17HG,YT1B,SICR4BD,STC2,H,AUDOC,FAM83H,KCND4,HTT1B,R1B,ITGB4,  
 FAM122B,UBASH3B,TTA,SWDS,KCNQ3,MAST,LSHRNA,PRK3,CS,ENOPH1,FUS,KCNQ3,MASTRNP1,COMAS,ER,KLF5,L,ERF,CELF4,KLF5,VEGFA,NVEGFA,NDUPA12,EN,DUF412,GPR176,RANBP1,OPH1,RANBP1,CELF4,ETV4,FAM122B,CELF4,PABP,CA,ERF,IGT1,SLC25A39,SMARCA5,UBASH3B,ZHX2,EIF3B,PRK3,MA5,TL,CSRNPL,CMA5,KLF5,KLF4,FBXL19,NDUFA4L2,DOCA,TFAP4,KCNO5,SRF,ROCD1,NUP1,SMARCA5,S0X4,ZHX2,MA107,ENOPH1,SWDS,STL,KLF5,NDUPA12,DOCA,VEGFA,PTGES,USP37,,ENOPH1,ROCD1,NUP107,H SYNCRIP,ETV4,VASH1,ZAP72,KCNQ3,VEGFA,PTGES,SRNA4,PA10AC1,SH5,ETV4,TFAP4,VASH1,GPR13BP1,AUTS2,ADNP,TRERF1,MMPT13,GNAO1,CELF4,ITGAS,PH1D2,CDK8,KLF12,CNIE1,IMPH1,KLF12,CELF4,NFATC4,ADNP,P3,G5972,FLUP1,FLU1,S77,NNG1,DDX1,COI0,MMP13,PRN13,HNRNP40,THBS3,VIM,PPH2,FE5,M1,RBL1,KPNB1,DLL4,KPNB1,ITGAS,PH1D2,DLL4,EBF1,IGFBP5,SYNPO2,S656,WMI1,TBC1BCL1,SASS6,NKG1,BCL6B,CNIE1,RBL1,NCARL4C,  
 WNT3A,OXNAD1,ADNP,PAVO1,MEIS2,ERF,PNP,TX1,PDXP,SENA6Q,SPR1B,GRHL2,BHLHE40,MMP2,PTHLH,ING1,IRF2BP1,NFIL3,DUX5,DLC1,CADM1,HNRNP43,XC4,ERF,PDXP,SPR1B,SEMF,CACNA2D3,SHMT2,RC,ASD,PRICKLE1,GRHL2,BHLH,C2,ETV4,ROBO1,ATAD4,F40,PTHLH,DUX5,HNRNP43,1,NR2F2,H56572,PRK2,TRIM8,H0XA,STK3,SHMT2,RC2,DPH3,ETV4,R,GI,TNMC2,TCEALZ,SLU5,TTTC39B,CRIM1,HIST,OBOL1,ATAD2,TRIM8,MYL6B,T3LOX,PDGFRL,ANGP3H2A,ATXN1,RANRF,MEIS2CL1,MW1,P15,REW2,PRCL,ARI,D2,MEIS2,S0X5,GRW,D1,RAVER1,TFAP2C,C,RIET,PTHLH,LUP,BRE2B,P1,FLT1,ZSCAN20,YOENTPD7,MMP15,KCNQ3,CY,PDGFRB,NFATC4,ENTR6,ACT1,ENTPD7,S0K1,KCNQ3,ARF4,SETM,R61,RAVER1,JANGF,SNK1,PD1,CD9B,MAGEDD,AR,ASCL2,PRMT1,S1C,L11,REW2,PRMT1,JARID2,P,OUTM13,NUD1A,LIXL6A9,PIGW,AUDCSN,THLHEK3,GRWD1,H2AY7,,GFRAL1,ATP1A2,SONB,N,LI1,LEK3,PTPNM2,,COL23A1,PIGW,NFATC4,AL52,CWKIR1,PTPN6,DUPTCH1,DOC,ACT1,FLT1,SP3,ZEB2,  
 NUDCD1,TRER1,BCL11A,FAM83H,SH3BP1,S0X5,ADAMTS4,ZHX2,CNIE1,MEIS2,KRTB08,FOSL1,NRG1,CITED1,,NUDCD1,FAM83H,S0X4,ADTTAF4,NUP93,DA62IP,AMTS4,ZHX2,CNIE1,PPM11,METT121D,MMP28,C,KRTB08,JNHB8,FOSL1,NRG1,CPT10,SEMA7A,PLA2,,TTAF4,MOK,HNRNP40,DAB,ETV1,ADAMTS4,PTH1,G4E,NUP54,TMEFF1,V,2IP,METT121D,MMP28,SE,R,MYH1,HIC1,MOK,T5AV3,SRNA4,NRBP2,EL,MATA,NUP54,TMEFF1,PTPR,C22D1,MWH11,ENP2,K3,MBO6,TNCC7,TDPP,G,ELK3,PTPNCL1,TNCC7,PPP,AMOT,STARDB,FLUP12,PTPNCL1,NRPH4,,2B5B,NRPH4,,PRRCL,







|            |      |      |                 |  |
|------------|------|------|-----------------|--|
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | AGR15,TRERF1,JUNB,<br>BCL11A,MSH5,PRK4,L<br>G12,BC19,PCDH7,XPO<br>1,KLF12,NR6A1,ARPP1<br>9,KCNK5,NOC2L,MEIS<br>2,KLF7,RAD51AP1,KIF<br>5,IRX5,NDUF412,WN<br>5,IRX5,NDUF412,WN<br>72B,EBR3,IGF1R,ITB<br>PLEFNA1,SLC20A1,R<br>NP2,GART,DEFS,OM<br>G,MN1,WN74,HOK42<br>J,PAUG2,ADN3A,<br>BCL11A,BEND4,MNDX<br>1,OO61,SOX5,WAB52<br>MEI52,SKA2,PCDH13<br>,CABLES1,TNEM117,R<br>FAANK,SEPHS1,PRSS1<br>2,DLL4,ZDHHC21,PBX<br>1,SLC16A9,BACE2,IBR<br>1,PRDM10,STOM12,C<br>EP290,STC1,PTCH1,FA<br>M126A,<br>ERCC8,GNAO1,FBXO5,<br>NDUF4F2,PTPN8,KLF<br>10,SAMD11,TMIGD1,<br>KLF7,KLF5,NR61,CNO<br>T2,BEND4,PIW2,KCNQ<br>5,PSME3,LR73,TNKS1<br>BPI,PCID1,GCAT,MEF<br>T1.8,MBO6,HOX1,P1A<br>G12,IL7RC1,IGF2,CM<br>TM4,<br>KLF12,BEND4,OTOP2,<br>PDLIM1,TPAK4,SAMD<br>11,TPA2A,KCNQ5B1A<br>RID2,SKA2,MIR518B,<br>LRT3,PRK11,GP422,C<br>NOT2,IRX3,<br>TWIEW8,AOC21,IGF47<br>,MIR127,HG,IG1,FAW8<br>3F,SOX5,SAMD11,TUT<br>1,AAER52,CADMT1,RBB<br>P8,RNF43,ANGPT2,ME<br>TT121D,FGFR2,RNF15<br>2,SLC20A1,LLGL2,UBE<br>2C,STOM12,PPA3,TIR<br>M8,BBS12,TWTC2,WN<br>T7A,<br>HIST1H4C,POLAI,EMC<br>NPTK7,GNAO1,JARID<br>2,DSG3,SLC5A37,CNT<br>N1,CAGNA2D3,ODC1,<br>SOX5,MAM13,RAD54<br>B,HAUS3,IMPDH2,MA<br>G13,MAR13,CNOT7,C<br>NOT7,MAO9,KCNQ5,<br>PHN7B,GCA1,CCCH2,<br>CNNM2,CANSL,MN1,X<br>A1NB1,YSWD11,DNRK<br>3,5FN,WIB6,SARNP,PL<br>AG12,WN716,LIN54,T<br>FDP2,CNTM4,<br>SLC20A1,JMID6,TRER<br>F,LEIF3B,JUNB,OMGA<br>NKRD39,PBX1,<br>EFN1B,HMGB2,CEIF4,<br>BCL11A,SEMA6D,GNA<br>11,ADAMTS12,SRSF7,<br>MAM13,SAMD11,HAU<br>54,MEI52,ARPP19,SF3<br>B4,BEND4,NDNL2,PG<br>M1,MIR518B,DLL4,PA<br>KIP1,PIWEPAL,PICD1<br>RNF7A,SYNCRIP,SLC20<br>A1,CND1,TRCC,WDR<br>76,GDNF,STR39,<br>1, |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | SIN,COI8A1,HSPB2,LS<br>NEATC4,JUNB,COI8A1,PRP4<br>T1,GNR4,FAP,OLEFM13<br>LG12,PCDH7,SOX4,XPO1,KL<br>CRYAB,CLMP,PDZEB3<br>CTGF,FES,SLC7A11,TR<br>D51AP1,KLF5,NDUF412,IG<br>AF3P3,MATCG,CNKL<br>B2,<br>ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,  |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C10orf6,MSRB3,PAP<br>PA,MEF2C,KHL13,PT<br>PRC,PRRX1,<br>1,   |
| V\$MRE6_04 | 3.64 | 2.36 | V\$MRE6_6.28 04 | ETV1,CORP22,COL11A1<br>POU2AF1,LARMC3,W<br>ISPL,MYLX2,MIR6RF,<br>NCAM1,ARHGAP20,C<br>TSX,CXCR5,SNRPX,AR3<br>CD246,NRP<br>1,<br>MYH2,PDGFRA,MVH1,<br>C1   |



|  |      |      |           |           |
|--|------|------|-----------|-----------|
| V\$FACL_01   | 2.19 | 2.34 | 4.53 1    | V\$FACL_0 |
| TME88.FENB1.EMC<br>NUJNB.BCL1A.CCNG<br>2.SOX5.RHEB1.JAOS<br>4B.KLF7.TMEZ09.HA<br>52.BRC41.ACVB2B.ITG<br>BRC41.SAT1.FENB1.EMCN<br>FIUP1.PDGFRB.OLNUL<br>A3.PIM2.JARID2.FFNA<br>RAD54B.ROBOT1.TMEFF1.H<br>3.CACNA1G.LIK1L.HFE<br>1.HRIL1.OLAT1.CSN1CA<br>NINPAO.JUNB.JARID2.PAPB<br>2.GNG11.KCNMA1.EP<br>1.ROBOT1.TMEFF1.PFX<br>A.KLF7.NR1L1.CONG2.ITGA3<br>58.ZIC1.FBLN2.SORBS<br>1.GDNE.WNT9A.CAM<br>GONE.WNT9A.TMBB29.C<br>3.MR22.MECOM1.PAP<br>1CN3.NR122<br>KCNB.NR122<br>IFIT3.CTDS.NUDCD1.5<br>VINO.HSFA.MIR7HG<br>PRELID2.SEMAD.ATX<br>N72.0GG1.ITTT1.PAN<br>2.KONK4.CPNE1.SMC4<br>IF743.TNFSF11.NUDCD1.NF<br>BATF.TNFSF11.C1QTN<br>J.NOBI.KLP4.PHCL1.R8<br>ATCA.HS4.TMOD3.TSPAN6<br>F1.JNATCA.CCL5.DIF<br>C29.RBM14.TUT1.MA<br>JUF.MIR17HG.PRELID2.SIN<br>M11.OLFHL13.SERPIN<br>FF.DGKA.PDIIM1.ADA<br>PO.SEMAD.ATX.N72.DOG<br>G1.ADAWTS4.PAP.HF<br>M7S4.NFL13.PMCH.PP<br>1.ITTT1.ADAWTS4.CPNE1.5<br>E2.PC.DICE.LAMA2.EN<br>AHD.RF2BP1.DLL4.IN<br>MC4.NOBI.PHCL1.MAF.F.PDL<br>P22.TSPAN4.TMEI10<br>G2.CORT.TMEI163.P<br>M11.PMCH.PPABD.DLL4.CTP<br>O.MRP1.GPR153.GRB1<br>ALLO.MTTP.HOX425T<br>5.APOLO1.ING2.SGIP1.MTT<br>O.KCNB8.TIR7.WIPF1.<br>P.STCL1<br>CLUNE4.   |      |      |           |           |
| V\$STAT5A_01   | 4.35 | 5.94 | 9.07 _01  | V\$STAT5A |
| IF743.SYNPO.MIR17H<br>G.MAF.F.LUB.PAN2.W<br>NTIDA.SMC4.NOBI.K1<br>IF743.JUF.SYNPO.TMOD3.TN<br>RPING1.NER6.ADAWTS<br>FA.PHCL.OGG1.RBM1<br>FSF11.MIR17HG.MAF.F.JUB<br>54.FAP.HFE2.CCL5.PC<br>4.TUT1.DGKA.BEND4<br>ADAWTS4.ADAWTS6.WNT1<br>OLCE.CLDN5.LAMA2.E<br>PDIIM1.ADAWTS4.NF<br>O4.SMC4.NOBI.PHCL1.OGG1<br>NP2.TSPAN4.TMEI10<br>I3.PMCH.PPABD.DLL4<br>BEND4.PDIIM1.PMCH.PPA<br>100.NRP1.ZEB2.GRB1<br>CORT.PALUD.MTTP.8<br>RD.TSPAN6.STCL1.MTTP.DLL<br>O.KCNB8.TIR7.WIPF1.<br>ADNP.NC3.MIR17H<br>G1G11.HISTH2AC.NR<br>EB1.SNSF7.SAND1.LT<br>FAP2C.CARLES1.ZSC4<br>N20.DX1.CADML1.SIC<br>2A43.HISTH3C.PAKI1<br>SRP2.SNSF7.ADMC.CRN61A<br>P1.MDM1.GPR12.LING<br>DNP.ACTG2.SAND11.CAHS<br>1.TAMM41.PTCH1.RR<br>AP2.UPTB8.MIR7HG.HOXC<br>SRP2.OLFHL2B.ACT<br>DM10.CANSA2.HOX<br>4.HISTH3C.PAKI1P1.LG11.H<br>G2.DCN.NAGE22.CCD<br>AA1.TMTC2.NEIL3.DXND<br>ISTH2B8.DXND1.MDM1.G<br>CB0.PDE3B.ME.F2C.CX<br>C1.GAS2<br>AS2.PRB3.HISTH2AC<br>XCS.FGF7.LOX.ZEB2.<br>ZDHHC15.PHYHIP.AD<br>NP.KLK13.EPNA1.EFN<br>B1.GBL1.BC9L.JANKR<br>D39.EFSA.ADAWTS4.<br>POCIA.ZHX2.CPNE1.P<br>ARDB4.SVARC5.RB<br>M14.NRG1.NKAIN1.EF<br>ADAWTS4.CPNE1.FENB1.CY<br>N45.DNH01.ERBL.NU<br>R61.ADNP.BMPL.ZHX2.KLK<br>EYD6.ADAWTS4.BM<br>DT11.MAST1.SERPINB<br>13.EFN45.ERBL.WNT4.ATN<br>P1.TSC22D1.VIM1.PH2<br>2.NT50C2.PBX1.TNKS<br>1.ANRD09.NRG1.MAST1.P<br>RH01.SERPINF1.HMC<br>1BP1.WNT4.FANC1.AT<br>AK6.NT50C2.SMARCA5.FAN<br>N1.CSMP3.AMYO21.PD<br>N1.NR29<br>TME88.AOC2.ASR16<br>P.ASGRP3.CELF4.TGFA<br>7.ITGB3BP.SCHIP1.LGI<br>1.SERBA48.SOX2C3H<br>10.ZDB.NAT8L.CPNE<br>1.HIS7H2AC.FH12.HB<br>EGF.TMEI17.NOS1A<br>PWEPA1.B3GALT6.AOC2.PA<br>P.B3GALT6.CTNNA1<br>K6.NAT8L.CPNE1.WP1.L7H<br>GPR153.TRON.FYND1.<br>WP11.PMEPA1.HIST1<br>B52.HOX4.MEIS1.CELF4.PH<br>DES.AQP1.TSC22D1.T<br>H2BA.HIST2H2AB.HIS<br>L2.HBEGF.CO13A1.SCHIP1<br>HBS2.AMYH8.AS85.FU<br>TH1HA.NANOS1.CO11<br>HIST1H2BAL.GIT1.SEN44B.H<br>1.ANRD23.DMPC.PA<br>3A1.PLAG2.PAK6.ATX<br>IS7H2AB.HISTH1A.TMEI10<br>N1.<br>TME88.LCCDC41.PASS<br>F6.NDRG1.MAF.F.KLF1<br>2.S1C10A7.MAM13.ZH<br>X2.CPNE1.MEIS2.LMP<br>DH2.JNHBA.PELO.PCD<br>M12.NDRG1.MAF.F.KLF12.E<br>TG41.ENPP2.CO1A1.<br>DITA.EXT1.TAF5.KDM3.XT1.ZH2<br>CPNE1.LMPDH2.D<br>FST11.ARHGAP30.AD<br>A.EVY4.MN11.TBCC.KC<br>DITA.PELO.NRG1.CO1BA1.C<br>AM12.TABE4201.TSP<br>NUE5.PTGH1.PTHNCL1<br>YR61.KCNJ5.ORG4.TAF5.ET<br>AM4.C1QNTF3.LDB2.G<br>NIF20A.<br>VA1.GR1.JPTTHNCL1.NIF20A.<br>PR137B.CSRP3. |      |      |           |           |
| V\$P2MEP_01  | 5.28 | 3.51 | 3.74 _01  | V\$P2MEP  |
| V\$P2MEP<br>V\$P2MEP   |      |      |           |           |
| V\$P2MEP_02  | 1.36 | 1.64 | 2.32 _02  | V\$P2MEP  |
| V\$P2MEP<br>V\$P2MEP   |      |      |           |           |
| V\$STAT5B_01   | 1.61 | 2.79 | 11.52 _01 | V\$STAT5B |
| V\$STAT5B<br>V\$STAT5B   |      |      |           |           |
| V\$STAT5A_01   | 4.35 | 5.94 | 9.07 _01  | V\$STAT5A |
| V\$STAT5A<br>V\$STAT5A   |      |      |           |           |
| V\$FOXO4_01  | 1.69 | 2.89 | 4.08 01   | V\$FOXO4_ |
| V\$FOXO4_  |      |      |           |           |







|                |      |      |             |                |  |
|----------------|------|------|-------------|----------------|--|
| V\$STAT6_01    | 2.96 | 2.75 | 3.69 01     | V\$STAT6_01    | <p>HMGN5,STIMM1,EMC2,NPTK7,SF3B4,TGFA2,CELF4,BCL11A,SIC7A1,SFN2,PROSER1,STIP1,SEPRINEL,WARS2,SKA2,MARPK6,IRIS,CNOT2,IRX3,PCDH17,PRR11,C75F3B4,TGFA2,CELF4,HOK,SIC3B42,PRH43,HNU1,C4,SIC7A1,SEPRINEL,THBS2,TGALPN,GNM4,H9G6,F,IRTS3,DLX5,CACNA2,LSMT12,SKA2,MARPK6,CNOT2,THBS2,C10NTN6,PCD3,TG77,MRRF,LSM1,2,SL,C3B42,HNU1,LEU13,DXF,ESR1P,ADAM23,TC2,HOKX4,POLE2,STC1,5,C10NTN6,PRH11,POLE23,CLIPPS2,FUNC,FAM35D,HLA-DRA,HLA-DQB1,HLA-DQA1,HLA-DPA1,HLA-DPB1,TRER1,ARSB2,JARID2,MIE3,PR3A,SPN2,CACNA2D3,ANRDB3,MCTP2,ECT2,GRH3,2,H92,H4U9A,SMC4,IMS,X2,FOXZ2,CNOT2,LMTC,X2,DLX1,HAS2,WIPI1,SEMA3,CNLS1,DLA4,GRPR,SERPINB2,CITE01,BACE2,MNF1,PLAUG2,HOM4,FAM176A,HOM4,1,STEA1,STC1,CFN,XA1,1,VENTA1,STC1,CFN,ANRDB3,WNT7A,CFN1,H3,AMVBC1,ZIC1,HGF,FAS2,DOCK3,DEFB1,ITGA5,5,LC25A35,ITGB3BP,SFX,N2,SEMA6D,SPRR1,BD,DKX2,WNT10B,S100A9,KCNK3,NDUFAL2,P15,SDXL,CELF4,INTS5,CAMK1MT,MRP518B,TNKS1BP1,GPR22,CACNA2D3,PA66,FAM19A,RPR18,RPAS,SANRP,CDK6,STC15,STC2,PTCH1,E6,CHD2,</p> |
| V\$CBPDELTA_06 | 2.80 | 1.43 | 2.60 UTA_06 | V\$CBPDELTA_06 | <p>WNT3A,FAM122A,AMHR2,DEF6,HSTH14C,JARID2,MHS5,IGSF3,SLC6A2,PTX1,MCTP2,JIU8,MAM13,SAMD11,XHSP,SOX15,CXCR7,IRX5,MKX2,PGF,TCF7,ITBP1,BCL11A,MOH1,64L,HST,THMC,SAMD11,JAR2,LDB2,PRK4,CLIP,GPRI1,TM6A2,ILLG12,RP43,WDR8,OSTD,1X5,GSTCD,CKCR7,LSM1,RP,PAS,STNE1,TG77,ABR8,MBO5,SANRP,CIBP2,E,AS3,CIBP2,VASP,WNT3A,M,OADP1,ADTS2,VSNL1,SLC6A9,JARID2,SENNC2,JIU8,3BP,SMURF1,TNFI,KLF7,ZCHH10,HOKX2,ELF,NAS,TPW1,DAB2P,GRPR,SOX21,SYNCRIP,PTCH1,EP1,LMX1,MICAL12,FAM176A,PCDH17,CFN1,ILNS4,GFSM2,TFP2,RTBD3,</p>   |
| V\$DBP_06      | 1.42 |      | V\$DBP_06   | V\$DBP_06      | <p>TRIM39,KDM3A,REN2,ALMS1,GF3C1,RRM1,1,RRB1,NEK2,FAM167A,AMHR2,WARS2,M,ELS2,PRME1,TNEM20,9,XPOT,DY30,LSM6,V,EGFA,HEI3,GPRI22,CA,CNA2D3,SLC7A1,EBN1,ATBP2,PCCTB,IRIS2,M,ET,HOKX4,PCDH17,Z8,TB48,TNKS1BP1,PAK6,PTCH1,CKNG,BTB2,BBCA1,SLC4A11,NIND,CD1,MET,ATAD5,STO,M12,RINDCA,MIE32,METTTD,VGFA,PR,SSB,STC2,PCDH7,HAS2,ZATVNL,</p>   |
| V\$FCR_06      | 2.58 |      | V\$FCR_06   | V\$FCR_06      | <p>HSR2,PRLEA,FEFNP2,C10NTN7,PAK3,G,FE5ZC1,ITPR1,</p>  |
| V\$FR_03       | 1.50 | 2.74 | V\$FR_03    | V\$FR_03       | <p>HMGN5,STIMM1,EMC2,NPTK7,SF3B4,TGFA2,CELF4,BCL11A,SIC7A1,SFN2,PROSER1,STIP1,SEPRINEL,WARS2,SKA2,MARPK6,IRIS,CNOT2,IRX3,PCDH17,PRR11,C75F3B4,TGFA2,CELF4,HOK,SIC3B42,PRH43,HNU1,C4,SIC7A1,SEPRINEL,THBS2,TGALPN,GNM4,H9G6,F,IRTS3,DLX5,CACNA2,LSMT12,SKA2,MARPK6,CNOT2,THBS2,C10NTN6,PCD3,TG77,MRRF,LSM1,2,SL,C3B42,HNU1,LEU13,DXF,ESR1P,ADAM23,TC2,HOKX4,POLE2,STC1,5,C10NTN6,PRH11,POLE23,CLIPPS2,FUNC,FAM35D,HLA-DRA,HLA-DQB1,HLA-DQA1,HLA-DPA1,HLA-DPB1,TRER1,ARSB2,JARID2,MIE3,PR3A,SPN2,CACNA2D3,ANRDB3,MCTP2,ECT2,GRH3,2,H92,H4U9A,SMC4,IMS,X2,FOXZ2,CNOT2,LMTC,X2,DLX1,HAS2,WIPI1,SEMA3,CNLS1,DLA4,GRPR,SERPINB2,CITE01,BACE2,MNF1,PLAUG2,HOM4,FAM176A,HOM4,1,STEA1,STC1,CFN,XA1,1,VENTA1,STC1,CFN,ANRDB3,WNT7A,CFN1,H3,AMVBC1,ZIC1,HGF,FAS2,DOCK3,DEFB1,ITGA5,5,LC25A35,ITGB3BP,SFX,N2,SEMA6D,SPRR1,BD,DKX2,WNT10B,S100A9,KCNK3,NDUFAL2,P15,SDXL,CELF4,INTS5,CAMK1MT,MRP518B,TNKS1BP1,GPR22,CACNA2D3,PA66,FAM19A,RPR18,RPAS,SANRP,CDK6,STC15,STC2,PTCH1,E6,CHD2,</p> |







|  |      |      |           |                                |
|--|------|------|-----------|--------------------------------|
| VSCBP_Q3   | 2.49 | 2.07 | 5.08 3    | VSCBP_Q                        |
| <p> TME88,TGFB2,GSTA<br/> 4.GNAO1,JUNB,BCL11<br/> A,SLC35A5,DYRK3,O<br/> VOL2,EDNR,RUVBL2<br/> WNT10B,MES2,SUV3<br/> 9H1,IRX5,NDUFAL2,C<br/> ADMT1,IL19,ASCL2,JAR<br/> IL19,TGFB2,WNT5A,CYR61,<br/> PDGFRB,NFATC4,MYH<br/> 102,EFNA5,GYS1,HERC<br/> RUVBL2,SUV39H1,CDC138<br/> 1,NCCAM1,HSGS12,AK<br/> 4,NUTL18,SYNCRIP,M,<br/> FENAS,LUNB,ARID2,HOXC<br/> AP2,ADAMTS3,MYH8,<br/> XU1,CDC138,CLOTNF,<br/> 4,GSTA4,HOXA5,NFATC4,O<br/> DGK4,NR3C2,RTN1,P<br/> VOL2,NUP155,WIN<br/> 4,PALUD,NUP155,WIN<br/> TSA,NR61,<br/> ANDUFAL2,NAB1,NCCAM1,<br/> 28TB20,P8BAP1,TLR8,<br/> GSTT1,HSP9A,LINS,BE<br/> ND4,MXD3,RREB1,AP<br/> OL1,PAN2,PRK3,UG4,C<br/> DCA3,KLF5,AURKA,FO<br/> XK2,CNOT2,SOX5,CAD<br/> CSTF1,LINS,MXD3,XPOL1,KIF<br/> M1,CHRSPD1,LAMMA3,<br/> 12,CACNA1G,LIG4,CDC43,K<br/> FRAS1,LTBP1,KIF12,W<br/> LF5,AURKA,ACTC1,CNOT2,B<br/> PRICKLE1,LC15,TSC22<br/> IP1L1,IERSL,PHF7,P2RY<br/> END4,LAMA3,PRICKLE1,WIP<br/> D1,ACTC1,FIL1,PRK3C<br/> 2,GCAT,SEMA7A,SHM<br/> 11,HMG2,IERSL,PHF7,SEM<br/> 6,ARHGFB,MYO18B,<br/> T1,TAF5,OMG,ETV4,RI<br/> A7A,SHMT1,TAF5,OMG,ETV<br/> CAB,GMFG,MYOZ2,LY<br/> NL,CDC2,MBD6,STC1,<br/> 4,RINI,CDC2,STC1,WNT5A,<br/> N,CACNA1G,SECT16B,C<br/> WNT5A,ZBTB26,<br/> MYL6B,ZBTB26,COU2A1,<br/> OL12A1,PA5A3,<br/> SMUG1,GYS1,TRIM39<br/> BMS1,MOC53,TRMT1<br/> 1,RUVBL2,DYX55,BOD<br/> IN3D,BANF1,E2F4,IGH<br/> TRMT11,E2F4,MOC53,RUVB<br/> MBP2,PARYA,GINI,EI<br/> 12,CLASP,RCIN3D,BANF1,<br/> F53,LEBNA1BP2,DPM<br/> IGH4BP2,PARYA,GINI,EIF2<br/> 1,<br/> S1,EBNA1BP2,<br/> FAM122A,TMEM88,G<br/> MAO1,TGA3,IGL1,BRI<br/> PLATNY12,NR6B1,XL<br/> F7,SCID1P,ZHX2,MA<br/> B2L13,PVAL1,METTL1<br/> 8,NR61,DEPDC7,CEIF<br/> PVRL1,KONOS,CYR61,ZHX2,<br/> 4,KONOS,IRK5,FLT3,F<br/> COL13A1,TGA3,FLT3,ATX<br/> ARHGAP30,TGFB3,IL1<br/> OXN1,BDH1,STOML2,<br/> N712,PTPRG,METTL18,KIF7<br/> 6,MERZF6,GFRAL,ANG<br/> KCNK4,COL13A1,PCD<br/> ,CELF4,IGL1,NR61,BRIP1,M<br/> P11L,MVLL,SNRP,SLIT<br/> H17,TDP2,SNX25,<br/> AB2113,FOXL1,DEPDC7,<br/> 3,<br/> NUTF2,FAM122A,DPE<br/> 1,STNN1,CLSPN,PHF1<br/> 3,SP2,SIC16M,ZFR1,C<br/> EP290,IRF2BP1,FEN1,<br/> NUTF2,SAMD12,CLSPN,ZEP<br/> NFATC2IP,SAMD12,IN<br/> 1,CACNA1G,FEN1,NFATC2IP<br/> O80E,CZCAN20,PAZG4,<br/> JINORDE,PAZG4,PP2R5B,HI<br/> RASSF2,CACNA1G,FES<br/> RIP3,<br/> J1TRP1,UGG71,ZEB2,<br/> PHF16,STNN1,WNT5<br/> A,ANO1,SLC35A5,DY<br/> RK3,SEMA6D,PCDH7S<br/> PRR18,SOX5,KIF12,RU<br/> VBL2,HIGH,WNT10B,<br/> MLH3,PCDH4,FAHD1<br/> ,KUF51,DOCK3,CAMKMA<br/> T,WEE1,DXL1,CDKN1L<br/> BEND4,IL19,ASCL2,NH<br/> KIF12,PHF16,CYR61,CUEDC<br/> L3,GYS1,HERC4,CTED<br/> 1,SPRR18,RUVBL2,WNT5A,<br/> DCN,SDPR,FBXO4,A<br/> 1,NDUFAL2,SYNCRIP,<br/> DYRK3,BEND4,HOXC4,PCDH<br/> DAMTS2,TSC22D1,SU<br/> ER,ATAD2,MTPR,H0<br/> 7,IL19,ERF,KLF5,MTPR,HOX<br/> LF1,CDKN1C,RTN1,P<br/> XK2,HOXA1,STC1,STC<br/> A1,STC1,SEMA6D,ATAD2,H<br/> RNG1,TNMC2,SLIT3,ZB<br/> 2,CRIM1,<br/> OXAS,NDUFAL2,<br/> TB20,ANGPT1,TLR8,<br/> PRR3,HSP9A,BEND4,P<br/> ZNF2,SEMA6D,MXD3,<br/> RREB1,XPO1,KIF12,N<br/> R6A1,CNIE1,AF4,LI6<br/> 4,CDC43,KLF5,RBM14,<br/> NNG1,SOX5,SLC6A9,C<br/> ACTC1,SEMA6D,MXD3,XPO<br/> ADMT1,CRSPD1,FRAS<br/> 1,KIF12,NR6A1,CNIE1,UG4<br/> 1,LTBP1,KIF7,WIP1,P<br/> ,CDCA3,KLF5,NR61,BEND4,<br/> PRICKLE1,CC15,ARHG<br/> GM1,METT21D,GPR2,<br/> PRICKLE1,TWIP1,HMG2,RG<br/> EF6,ACTC1,FAP,FIL1,C<br/> 2,MDM1,SEMA7A,SH<br/> M1,METT21D,MDM1,SEM<br/> DK14,PRK3G,RHOC<br/> MTI,OMG,ETV4,BIN1,<br/> A7A,SHMT1,OMG,ETV4,BIN<br/> MYO18B,FMOD,GMF<br/> CXK2,MBD6,WNT5A,Z<br/> 1,CDC2,WNT5A,MYL6B,ZBT<br/> G,MYOZ2,SECT6B,PDE<br/> B,TB26,NR13,NR20A,<br/> B26,PP2R5B,NR20A,<br/> 38,PA5A3,<br/> </p> |      |      |           |                                |
| V\$HNF3_Q6   | 3.22 | 2.41 | 1.95 6    | V\$HNF3_Q                      |
| <p> GGAMTNN<br/> NNNTCCY_<br/> UNKNOWN<br/> </p>   |      |      |           |                                |
| GGAMTNNNNNTCCY_UNKN  | 2.46 | 1.64 | 1.59 N    | GGAMTNN<br>NNNTCCY_<br>UNKNOWN |
| VSCBP_Q2_Q1  | 4.44 | 1.79 | 3.14 2.01 | VSCBP_Q                        |
| <p> PRR3,HSP9A,BEND4,P<br/> ZNF2,SEMA6D,MXD3,<br/> RREB1,XPO1,KIF12,N<br/> R6A1,CNIE1,AF4,LI6<br/> 4,CDC43,KLF5,RBM14,<br/> NNG1,SOX5,SLC6A9,C<br/> ACTC1,SEMA6D,MXD3,XPO<br/> ADMT1,CRSPD1,FRAS<br/> 1,KIF12,NR6A1,CNIE1,UG4<br/> 1,LTBP1,KIF7,WIP1,P<br/> ,CDCA3,KLF5,NR61,BEND4,<br/> PRICKLE1,CC15,ARHG<br/> GM1,METT21D,GPR2,<br/> PRICKLE1,TWIP1,HMG2,RG<br/> EF6,ACTC1,FAP,FIL1,C<br/> 2,MDM1,SEMA7A,SH<br/> M1,METT21D,MDM1,SEM<br/> DK14,PRK3G,RHOC<br/> MTI,OMG,ETV4,BIN1,<br/> A7A,SHMT1,OMG,ETV4,BIN<br/> MYO18B,FMOD,GMF<br/> CXK2,MBD6,WNT5A,Z<br/> 1,CDC2,WNT5A,MYL6B,ZBT<br/> G,MYOZ2,SECT6B,PDE<br/> B,TB26,NR13,NR20A,<br/> B26,PP2R5B,NR20A,<br/> 38,PA5A3,<br/> </p>   |      |      |           |                                |
| V\$HNF_Q5_Q1   | 4.44 | 4.53 | 4.16 5.01 | V\$HNF_Q                       |







|                               |      |      |   |
|-------------------------------|------|------|---|
| GKCGNNNNNNNGTGA_G_UN<br>KNOWN | 5.90 | 4.06 | GKCGNN<br>NNNNNTG<br>AVG_UNK<br>NOVN    |
| GTCGYATGR_UNKNOWN             | 1.35 | 2.20 | GTCGYAT<br>GR_UNKN<br>OWN               |
| GTTGNVNRGNAC_UNKNOW<br>N      | 1.75 |      | GTTGNV<br>NRGNAC<br>_UNKNOW<br>N        |
| GTTNVYNN<br>GGTAA_U<br>NKNOWN | 2.16 |      | GTTNVYNN<br>GGTAA_U<br>NKNOWN           |
| KCCGNSWTTT_UNKNOWN            | 3.43 | 1.57 | KCCGNSW<br>TTT_UNKN<br>OWN              |
| RAAGTTGT_UNKNOWN              | 3.06 | 6.42 | RAAGTTGT<br>_UNKNOW<br>1.62 N           |
| RTTGCNWVSGNR_UNKNOWN<br>N     | 2.89 |      | RTTGCNW<br>TSGNR_U<br>NKNOWN            |
| SNACANNVSYAGA_UNKNOW<br>N     | 1.71 | 2.97 | SNACANN<br>NYSAGA_<br>UNKNOW<br>N       |
| SVATTGTG_UNKNOWN              | 1.87 | 2.39 | SVATTGTG<br>_UNKNOW<br>N                |
| WCTCNATGGY_UNKNOWN            | 3.86 | 4.55 | WCTCNAT<br>GGY_UNK<br>NOVN              |
| VAAFNANNNNNKAG_UNKNOW<br>N    | 2.39 | 2.43 | VAAFNAN<br>NNNNKAG<br>_UNKNOW<br>1.42 N |

QTRTD1,RNP51,ADPG  
 K,NEK1,REF1,CCD86,  
 PSME3,NUP155,TRMT  
 61B,NUP12,PHF7,PWP,QTRTD1,ADPGK,REF1,CCDC  
 1,PHF5A,COO7,ABCE1,86,PSME3,PIRX1,NUP155,P  
 1,CNOT7,ANAC10,  
 HET7,PHF5A,PWP1,ABCE1,  
 DOC2A,OXNAO1,WDR  
 54,BRAD,STOM12,PTP  
 DC1,YNITA,ERF,PRG4,  
 CDC3A,HOKA2,GPIN1,  
 JPHC1,ODC1,  
 RPP38,NME7,GRHL2,C  
 IIP,ABHD14A,STOM1,  
 2,ING2,ATN1,TMTCZ,  
 MPP2,SEMA4B,KCNP  
 4,EBNA1BP2,BTBD3,C  
 ADM1,  
 DIS3,PIW2,TRER1,JUN  
 6,GTTC1,DNAIC21,R  
 FX1,PHID2,TG88BP,  
 FRA10A,CL,TMCM209,  
 KDM3A,MARE3,RRE  
 B1,  
 XP01,SYNCRIP,JAIF15,  
 LUN54,CNMA2ADNP,G  
 RHL3,JARID2,TRIM27,  
 BCL11A,MEIS2,SPRED  
 2,REF1,NHS,RX5,IGF2,  
 BR3,KDMA3,CBX3,CSN  
 P,TRIM27,JARID2,SPRED2,T  
 KIA1,  
 AF15,CBX3,NCAM1,  
 MOAP1,CE1F4,REF1,S  
 LCT5A37,FEN1,IGT1,R  
 RMI,ANGEL1,GRND1,  
 ECT2,TFAP2A,WNITD  
 SAT1,LEF,MOAP1,TM0D3,IT  
 A,PELO,HAUS1,KIF5,K  
 GAL,CE1F4,REF1,SC2A37,  
 U4,ESPL1,MIPR50M,  
 FEN1,IGT1,RMI1,GRND1,  
 5S2,JARID2,KCNO4,SL  
 C12,TFAP2A,WNITD,A,PELO,  
 C2A43,ATRN,GNR21,S  
 HAUS1,KIF5,MIPR50,ESPL1  
 VNCBP,LEWD1,ZBTB2,  
 JARID2,KCNO4,SCC1A,W  
 ETV1,RCN3,DPM513,JA  
 6,PSMD11,PCDH7,TM  
 1,ZBTB26,EDL3,PCDH7,PTP  
 M3,ITGA1,RASSF2,TM  
 TC2,MIR17HG,ALKBH4  
 RG,HOKA5,MIR17HG,ALKB8  
 EMI50A,CXCS,STGG  
 4,TOP3A,  
 KCNIP4,EPF1,WDR34,  
 MARE3,RIN1,JUNB,A  
 AASD1,STOM12,IERSL,  
 MET,ITG88BP,TNKS18  
 P1,GV11B,SEMA4B,  
 PIN1,POLL,TMCM107,  
 PAK6,BTBD3,  
 NURCD1,PR26,BUB1  
 B1,ARID2,DCAD,HAU  
 NIUDC1,ARID5A,BUB1B,JA  
 S1,DCUNDA,CBL1,W  
 RIO2,CHEFN,DCAD,HAUS1,  
 NTR4,UBXN8,TOP4A,  
 NOS3,UBXN8,WNIT9A,  
 TOR3  
 ATTN7D2,LRRC29,  
 AATXN7L2,  
 TRIM39,RECL11A,CXK8,  
 UCN2,FRA10A,C1,SIPT  
 6,TSU1,MAR6,IGL1N  
 F1A3,DUX1,BCT7A,AMH  
 GEF15,EXT1,TONS1,D1,  
 TFAP4,OMG,AHGEF15,EXT  
 L1,IFRO2,NAT8L,POLC  
 1,TSR1,NAT8L,TONS1,HOC  
 1,ETV4,OMG,TFAP4,U  
 4,MES1,SGP1,DLL1,SIPT6,  
 BEZO,BOP1,HOKA2,G  
 MARK6,IGL1,SUZ12,GRPDS,  
 DPM5,PIAG2,LDI,BAF  
 UCN2,IFRO2,LDI,BAF1,  
 SOX4  
 1,  
 ETV4,  
 PAN2,WDR54,GPIN1,B  
 CS1,OXNAO1,EIF251,  
 BRX1,IER2,CCT7,ZC3H  
 OXNAO1,DPH3,BRX1,EIF25  
 10,METT18,PKP4,CH  
 1,ERF,IER2,CCT7,PKP4,MET  
 ERF,RAO1,ERCC1,ERF,  
 TL18,WDR54,CHEP,GPIN1,  
 HNRNPD,  
 ERCC1,HNRNPD,  
 LRRL,NUSAP1,LOP5,TR  
 ERF,PGM13,MBT12,  
 NUSAP1,OP5,TM0D3,ORC4  
 HOKA2,MAR3,AARS2,  
 PGM13,MBT12,MAR3,FG  
 LD82,DCN,POE1A,GPR  
 ,PTTX1,GFTR2,CADMT1,  
 FR2,LRRL,  
 65,



|                         |      |      |                         |
|-------------------------|------|------|-------------------------|
| VATTNATC_UNKNOWN        | 3.96 | 5.73 | VATTNATC_UNKNOWN        |
| YRCCANNNGCCG_UNKNOWN    | 2.45 | 1.48 | YRCCANNNGCCG_UNKNOWN    |
| YRTCCANNR_CGC_UNKNOWN   | 2.45 | 2.08 | YRTCCANNR_CGC_UNKNOWN   |
| YTCGCCNNAGGY_UNKNOWN    | 2.08 | 1.30 | YTCGCCNNAGGY_UNKNOWN    |
| YTTCCNNNGGAMR_UNKNOWN   | 1.37 | 1.37 | YTTCCNNNGGAMR_UNKNOWN   |
| TTTCNRGNNNNTTC_VSHSF_Q6 | 3.25 | 4.98 | TTTCNRGNNNNTTC_VSHSF_Q6 |
| YTAATTAA_VSHX3_01       | 1.60 | 2.51 | YTAATTAA_VSHX3_01       |
| RTGCGNNNGAAC_VSMFT_01   | 2.25 | 1.69 | RTGCGNNNGAAC_VSMFT_01   |
| VATGNMAAT_VSOCT_C       | 3.33 | 5.04 | VATGNMAAT_VSOCT_C       |

|                    |                     |                     |                  |                   |                   |                   |                         |                     |                        |                         |                         |                        |                        |                          |                  |                         |                       |                  |                        |                          |                    |                        |                  |                     |                       |                    |                     |                      |                    |                      |                      |                    |                    |                     |                         |                   |                          |                    |                        |                  |                  |                   |                    |                    |                    |                       |                   |                       |                   |                        |                    |                       |                     |                         |                    |                     |                         |                    |                   |                          |                    |                    |                        |                     |                     |                        |                    |                  |                       |                    |                  |                 |             |
|--------------------|---------------------|---------------------|------------------|-------------------|-------------------|-------------------|-------------------------|---------------------|------------------------|-------------------------|-------------------------|------------------------|------------------------|--------------------------|------------------|-------------------------|-----------------------|------------------|------------------------|--------------------------|--------------------|------------------------|------------------|---------------------|-----------------------|--------------------|---------------------|----------------------|--------------------|----------------------|----------------------|--------------------|--------------------|---------------------|-------------------------|-------------------|--------------------------|--------------------|------------------------|------------------|------------------|-------------------|--------------------|--------------------|--------------------|-----------------------|-------------------|-----------------------|-------------------|------------------------|--------------------|-----------------------|---------------------|-------------------------|--------------------|---------------------|-------------------------|--------------------|-------------------|--------------------------|--------------------|--------------------|------------------------|---------------------|---------------------|------------------------|--------------------|------------------|-----------------------|--------------------|------------------|-----------------|-------------|
| THEF1,IGNA01,CELF4 | JMED27,UCN2,SIC5A2  | PP64,TPRC6,TAF15,M  | OXD1,BC9L,SMG5,O | VGP1,SAVD11,CPIE1 | JCXCR7,CSRP1,NOB1 | S77,MAG3,PRKG2,FB | SATI,LU23A,CELF4,BMPR1B | X119,DSG3,KCNQ4,IRX | PCSK5,UCN2,POIR3D,PP64 | 3,P1U5,BEND4,HNRNP      | TPRC6,TAF15,MOXD1,PRICK | AS1,NUDT2,RNF43,MR     | LET1,ONGP1,ADAMTS6,SAM | PS1,B8,EIF               | FUR3,IGF2        | D11,CPIE1,CXCR7,CRT1,NO | SSPN,PRICKLE1,FAM5    | BR3,GBR8B,SNRPFG | B1,MAG3,TTTH1,PRKG2,DS | C,MAG11B,NCPT1,P8        | PHI51,DMG6,EZF1,NA | G3,PH15,BEND4,HNRPY3,K | AMP1,SC9A3,CCD80 | NO51,MKI1,LRP8,BMP  | CNO4,IMR51B8,FER3,G4B | N,EB,CLQIN7,ZCCHC  | RB,WNT4,HOX2,HO     | RB3,SNRP,OSBP17,DMG1 | 24,PCSK5,APOBEC2,G | XA1,CTBP2,SEC14I2,PI | RP8,RBPMS,WNT4,HOX41 | PC3,ZIC1,SMYX,ENO3 | TPNCC1,NRP44       | CTBP2,PTTPNC1,NRP44 | DIC1,MYOG               | DCBP1,NR6A1,FRS3  | PIGO,PTPRF,FZD5,DLL      | 4,HOX42,HES1,AAE52 | NR6A1,DCTP1,SGRP1,DLL4 | NOL11,FBXO5      | FBXO5,HES1,NOL11 | FAM98B,SULT1A1,GN | AOL1,SUV39H2,NARG2 | PABD6,PELP1,NAAS   | 2,PTPR2,UBE25,PTPN | B,MAM13               | TAAC1,FUNC,DPS12  | NCAM1,GNM68           |                   |                        |                    |                       |                     |                         |                    |                     |                         |                    |                   |                          |                    |                    |                        |                     |                     |                        |                    |                  |                       |                    |                  |                 |             |
| ZDHHC15,PTPN23,CCT | 8,SRP2,TFAP4,TDG,PO | LR1B,IEB3,GRWD1,IRF | ZBP1,ZW10,IL17RC | SNAG1,SRFS,TPRP1  | JBRN3,WPHC1,ZC3H1 | 0,PMVE1,JAG1      | NUT2,LINC03,STIP1       | CBX3,HSR1A,APOLC    | C78,IMJ06,NOP58,G      | XPOL1,NUT2,NCC2,LMNB1,J | B2,CCT7,CCT4,PVRL1      | MID6,NOP58,HN1L,PARP16 | HS9D1,RANGAP1,HN1      | JLRP8,GJB2,H2AFY2,CCT7,C | PMP22,HSR2,NUDT4 | L,VEGFA,RCCL,LMNB2      | ACNA16,PVRL1,HSR1,INH | CGVAB,UNC5B,STAR | PARP16,LRP8,HOX42      | BB,VEGFA,PHF6,TSPAN6,PII | DB,MW1L,DPS12,CAC  | D,CBX3                 | NA16             | MAO6,FZD10,IER3,ITX | NL4B,RREB1,SRF7,TF    | AP2A,TMIGD1,RX5,LR | RQ4,SUC1G2,DLL4,BAC | E2,RP42,DNDC1,ALKB   | H5,WNT7A,TFDP2,PT  | PNC1                 | CCDC126,CEP350,WA    | RS2,CCDC1,FTUD2    | PMN1,IRF17,VEGFA,C | ACNA203,RNF138,BO   | CCDC126,CEP350,CCDC41,E | P1,PAK6,TOT1,KCNK | FTUD2,IRF17,VEGFA,BOP1,P | G                  | AK6,KORIG              | STMN1,ADNP,ACTG2 | REN2,TGFBP1,MR17 | HG,SRF,HISTH3CS   | OX5,TPRP1,RENF2,H  | X2,SEMA7A,TFAP2C,F | OXN1,PROM1,ING1    | ADNP,ACTG2,RENF2,MR17 | RX5,CNOT2,KCNP4,D | HG,HISTH2AH,CO23A1,HI | LX1,CADN1,PM2,NEI | STH2AC,FZD2,NR6A1,ZHYZ | L3,ABTB2,SIC2A3,SC | SEMA7A,CDK2,HNF1B,SCO | AF4,DLL1,DLL4,NR6A1 | C,PRODR2,CNOT2,UTP18,CY | ACTG2,SGCA,CD79B,G | ,GPR22,HIST2H2AB,HI | R61,DLL1,DLL4,HIST1H2BB | PRCS8,TRDN,CKN14,D | S7ZH2AC,HIST1H2BK | LLG12,ADN1,HIST2H2AB,FOX | OK3,PROKR2,LYN,ETV | BACE2,PCCT1B,LLG12 | N1,HIST1H2BK,SRP2,PCCT | 1,DPS13,LD92,LYL,SH | TT12,RA826,HIST1H3C | 18,NGRAP1,PARB2,HIST1H | 3BGR1,PAZ1,ZEB2,SF | ,CCND1,CDK2,GDNF | 3C,CCND1,HOX45,GDNF,W | RP2,NIN,DCN,CCDC80 | WNT9A,PHF6,UBE25 | NT9A,PHF6,UBE25 | PRRX1,FAM5C |



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|                        |      |                                    |
|------------------------|------|------------------------------------|
| V\$SRF_C               | 4.62 | 15.84 V\$SRF_C                     |
| CAGNKGMAAA_UNKNOWN     | 1.60 | CAGNKG<br>MAAA_UN<br>KNOWN         |
| V\$STAT3_01            | 1.74 | V\$STAT3_01                        |
| V\$PPARA_01            | 1.54 | V\$PPARA_01                        |
| CCATNNNNNNCGG_UNKNOWN  | 2.20 | CCATNNNS<br>NNNGCG_<br>UNKNOW<br>N |
| V\$TFH1_01             | 2.34 | V\$TFH1_01                         |
| V\$PPA8_B              | 1.93 | 1.78 V\$PPA8_B                     |
| V\$MES1BHOXA9_01       | 2.05 | V\$MES1B<br>4.59 HOXA9_01          |
| V\$AR_Q2               | 1.46 | V\$AR_Q2                           |
| V\$ROKZ_01             | 3.08 | V\$ROKZ_01                         |
| V\$WKK22_01            | 2.05 | V\$WKK22_01                        |
| V\$TF7_06              | 1.64 | V\$TF7_06                          |
| V\$CDX2_Q5             | 1.74 | V\$CDX2_Q5                         |
| V\$STAT_06             | 2.20 | V\$STAT_06                         |
| RITTNNNVTGGM_UNKNOWN   | 1.86 | RITTNNNV<br>TGGM_UN<br>1.54 KNOWN  |
| TTAWWNANTGGM_UNKNOWN   | 1.95 | TTAWWNA<br>NTGGM_U<br>1.44 KNOWN   |
| V\$CTCTGR_UNKNOWN      | 1.37 | V\$CTCTGR<br>UNKNOW<br>N           |
| VNTTTNNNANGCAM_UNKNOWN | 1.33 | VNTTTNNN<br>ANGCAM<br>_UNKNOW<br>N |

|  |  |
|--|--|
| MYH11,AOC3,ACTG2,CKM,ACTC1,RASFF2,JPH2,MOT18B,CD348,DACT3,MVY9,NR2F2L1,ACTG2,ACTC1JUNB,MYO18B,MCD1,DMPK,TGFB1L1,SIC7A1,TNINCL,RRM1,JHNF1,TAG1,NPDLIM4,CO18,18,AAARD1,MES1,PH2,F0,A1,TG81BP2,ANNA6,S11,TGFB111,CO18A1,PDIM,MCAAM,RHO1,MIRGPRF,7,CYR61,TG86,MCAAM,DLL1,ZEB2,CNN1,EMULN2,SCOT,CTG1,N,CNN1,IER2,H,LD83,JNCK45B,TNEM,OXAS,DNOC1,BHPT1,NNRPND,HGD18,TPI1,CLSTN2,GABRB3,CDH5,TGIF1,IFT43,TRAF4,MAFF,GEN1,PGF,SRC,KLF5,ATN1,PTPRG,ICCI,CAONB1,TN51,CD36,B  | MYH11,AOC3,ACTG2,CKM,ACTC1,RASFF2,JPH2,MOT18B,CD348,DACT3,MVY9,NR2F2L1,ACTG2,ACTC1JUNB,MYO18B,MCD1,DMPK,TGFB1L1,SIC7A1,TNINCL,RRM1,JHNF1,TAG1,NPDLIM4,CO18,18,AAARD1,MES1,PH2,F0,A1,TG81BP2,ANNA6,S11,TGFB111,CO18A1,PDIM,MCAAM,RHO1,MIRGPRF,7,CYR61,TG86,MCAAM,DLL1,ZEB2,CNN1,EMULN2,SCOT,CTG1,N,CNN1,IER2,H,LD83,JNCK45B,TNEM,OXAS,DNOC1,BHPT1,NNRPND,HGD18,TPI1,CLSTN2,GABRB3,CDH5,TGIF1,IFT43,TRAF4,MAFF,GEN1,PGF,SRC,KLF5,ATN1,PTPRG,ICCI,CAONB1,TN51,CD36,B  |
| XP01,TMPO1,TP18,CLSPN,MES1,MRP518B,HE5L,TES,SAT1,PCSK5,IJ24,I2F8,MAN,CTSK,TGFB3,HIC1,MB,PH12,NR61,MEED19,JAG1,BE,MAGED1,STPRL,CCDC,NDA,ITGB6,HNRNP40,DLL1,805PRAC1,PCSK5,CL1,ZDHHC11,PCCT1B,PERHG6,P3PRG4,BBFI,AB1BP,NME1,NUP54,COND1,SGRP1,ANGPT1,PI16,NRP1,B,ZH02,ESM1,TK,TAF5,IARS,RGS12,HNRNP40,GREN2,KO,HL13,HOD,BEND4,PA2PA,PAK1P1,NR8,PA2PA,TEK,MIRPCLG1,WN17,OSBP17,NP43,IL13,PDIM1,TFAP2A,SAMD1,PHY18,MOK,ACTN2A,I1,TT2,ANMCA,MRP23,HOK,NMCA4,INS,CDK14,PIQ4,MRP518B,SGP1,GNB1L,K3CG,NR2F2,CD79B,NMOK,ANNAT13,ADNP,RP1,STFA9,AMOT,ADNP,GRH12,ZH02,HOKQ4,TG46,GRND1,EIF4EBP1,WNT9A,SEMA6C,PAX9,APOLD1,RCOR2,TM1M50,NFRAP1,DISP7,CCDC126,POLA1,IFT43,ZHX,MYH2,SPON1,SDPR,5,2,NAT18,HNRNP40,CACNA1,CAR2,CACNA1C,CARM,CCT7,HOKQ4,PINCH,MAP,C2,CD36,STARDB,SUK6,SPON1,SCHIP1,FZD2,WN13,MTL1,ZBTB20,ITPR,T7A,PRK,TTYH1,1,DLCL1,WN13A,LRP8,KCNQA,SUV39H2,ARTN,NR17,AD1,LC1H5,MRTD4,ATXN12,CCZ7,CHST2,NR6A1,PWF1,GNB1L,ROBO1,HMG62,HNRNP40,PHY18,CXCL13,TSC22,CACNA1,CCOARD,HOK4,M,D1,CACNA1C,CTNNE51,PA2PA,NID2,NR6F,ELK,7,PA2PA,LP,SUT1LO,3,NIDUP412,JAG1,CDH7,U,XANGPT1,NR137R,BE2C,SOX4,AMOT1,NR6A1,MMP14,TNFSF1RANGRF,IFT43,TNFSF11,NF1,NFATC4,GJ45,PNICKATCA,SKA2,GEN1,MOKD1A,LE1,NR18,STPRL,KOU,TNAT12,PRICKEL1,GRH12,PT8,ENP2,JPR2,ARHGEH1U,HSPD1,TNMC4,TTYH1,T,FD6DKH,MVFP,ST6GRAF4,FLRT3,FGR2,JNG2,GJALVACS,TNEM100,FAAS,ER11,PRR11,MIR145,MSC,NGF,PCVT1B,IJ23A,CEP4,HOXCA,SICD2A1,PTPRG,KLF5,ETV1,AKAP2,CCDC80,NOS3,MAS7A1,MPPH2,GOR,PDGRL,ZIC1,F13A1,FA8,1SPAN6,HAS2,BUN5,LF,ADAMTS5,OMG,CNE1,EGFNT,CO112A1,ANKRD32,CNMT2,OLFML3,ANGTGIF1,SIC39A2,ANKRD2,MCAAM,JGSF3,PH12,ATN1,SEMA6D,H1STH1A,ESM1,SFRP2,CN13,CACNA1,SFRP2,CCDC14,OMG,CACN,CLDB2,MIRPCL3,MIPALC,HOKQ4,VWAL,PVNL1,XZEB2, | XP01,TMPO1,TP18,CLSPN,MES1,MRP518B,HE5L,TES,SAT1,PCSK5,IJ24,I2F8,MAN,CTSK,TGFB3,HIC1,MB,PH12,NR61,MEED19,JAG1,BE,MAGED1,STPRL,CCDC,NDA,ITGB6,HNRNP40,DLL1,805PRAC1,PCSK5,CL1,ZDHHC11,PCCT1B,PERHG6,P3PRG4,BBFI,AB1BP,NME1,NUP54,COND1,SGRP1,ANGPT1,PI16,NRP1,B,ZH02,ESM1,TK,TAF5,IARS,RGS12,HNRNP40,GREN2,KO,HL13,HOD,BEND4,PA2PA,PAK1P1,NR8,PA2PA,TEK,MIRPCLG1,WN17,OSBP17,NP43,IL13,PDIM1,TFAP2A,SAMD1,PHY18,MOK,ACTN2A,I1,TT2,ANMCA,MRP23,HOK,NMCA4,INS,CDK14,PIQ4,MRP518B,SGP1,GNB1L,K3CG,NR2F2,CD79B,NMOK,ANNAT13,ADNP,RP1,STFA9,AMOT,ADNP,GRH12,ZH02,HOKQ4,TG46,GRND1,EIF4EBP1,WNT9A,SEMA6C,PAX9,APOLD1,RCOR2,TM1M50,NFRAP1,DISP7,CCDC126,POLA1,IFT43,ZHX,MYH2,SPON1,SDPR,5,2,NAT18,HNRNP40,CACNA1,CAR2,CACNA1C,CARM,CCT7,HOKQ4,PINCH,MAP,C2,CD36,STARDB,SUK6,SPON1,SCHIP1,FZD2,WN13,MTL1,ZBTB20,ITPR,T7A,PRK,TTYH1,1,DLCL1,WN13A,LRP8,KCNQA,SUV39H2,ARTN,NR17,AD1,LC1H5,MRTD4,ATXN12,CCZ7,CHST2,NR6A1,PWF1,GNB1L,ROBO1,HMG62,HNRNP40,PHY18,CXCL13,TSC22,CACNA1,CCOARD,HOK4,M,D1,CACNA1C,CTNNE51,PA2PA,NID2,NR6F,ELK,7,PA2PA,LP,SUT1LO,3,NIDUP412,JAG1,CDH7,U,XANGPT1,NR137R,BE2C,SOX4,AMOT1,NR6A1,MMP14,TNFSF1RANGRF,IFT43,TNFSF11,NF1,NFATC4,GJ45,PNICKATCA,SKA2,GEN1,MOKD1A,LE1,NR18,STPRL,KOU,TNAT12,PRICKEL1,GRH12,PT8,ENP2,JPR2,ARHGEH1U,HSPD1,TNMC4,TTYH1,T,FD6DKH,MVFP,ST6GRAF4,FLRT3,FGR2,JNG2,GJALVACS,TNEM100,FAAS,ER11,PRR11,MIR145,MSC,NGF,PCVT1B,IJ23A,CEP4,HOXCA,SICD2A1,PTPRG,KLF5,ETV1,AKAP2,CCDC80,NOS3,MAS7A1,MPPH2,GOR,PDGRL,ZIC1,F13A1,FA8,1SPAN6,HAS2,BUN5,LF,ADAMTS5,OMG,CNE1,EGFNT,CO112A1,ANKRD32,CNMT2,OLFML3,ANGTGIF1,SIC39A2,ANKRD2,MCAAM,JGSF3,PH12,ATN1,SEMA6D,H1STH1A,ESM1,SFRP2,CN13,CACNA1,SFRP2,CCDC14,OMG,CACN,CLDB2,MIRPCL3,MIPALC,HOKQ4,VWAL,PVNL1,XZEB2, |



|                           |            |                                      |  |
|---------------------------|------------|--------------------------------------|--|
| TAAWVAATAG_VSRNFCA_Q<br>2 | 1.60       | TAAWVAAT<br>AG_VSRNR<br>11.91 FCL_Q2 | SIC9A5_LIF_POU1/MORC4,<br>ZHX2_DZIP1L_KCNQ5_PABRC,<br>4_CO.8A1_TNNC1,ACTC1,PN<br>F207_PACSL1,P15,<br>KMT2_SMPX,<br>HSR01_VSNL1,SEMA3F,HM<br>G83_RANBP1,CENH1,FAM69<br>B,KONK1,PCDH7,MYH18,RA<br>PGEF5,POU3D,CARD2,PAN<br>CD2,PHF5A,ZDHHC1,VASP,<br>MED26,SEMA7A,NRPH4,   |
| TGACCTTG_VSFF1_Q6         | 1.82       | TGACCTTG<br>_VSFF1_Q<br>6            | TRDN,PODUSDPH,AC<br>SIOC,ACTG2,ACTC1,UBE3C,<br>TG2,MYH11,CKM,ACT<br>AARSD1,PCDH7,TNNC1,DX<br>DC1,NPNA3,TAGLN,  |
| CCAWNNMAGG_VSRRF_Q4       | 2.10       | CCAWNN<br>MAGG_VSS<br>6.96 RF_Q4     | SSPN,LMCD1,PDGFRA<br>,TRDN,SYNP02L,FBN0<br>40,PH42,TSQ2D1,SIP<br>R1CKMT2,MEF2C,MY<br>OZ2,DPTSL3,CKM,TTY<br>H2,MTLSMPX,LYN,S<br>H3BGR1,TIMP2,<br>TFB3,KCNE4,NDNA,<br>RHGEF6,GSDMD,LD82  |
| VSMEF2_01                 | 11.22 1    | VSMEF2_0                             | TNEM47,LMO2,ACTC<br>1,NRP1,ADPRAL,<br>NEK6,NR2A,ADPRHL<br>1,ACTC1,LMO2,GN1A8<br>,CDKL1A,TNEM47,NRP<br>1,<br>PTN1R,NATCA,CELF2,<br>CD36,PRG4,LAMB1,F8<br>LN2,GRRCG,POE3B,C<br>LSTN2,TCAP,HOXD8,L<br>DB2,CKCL14,ZEB2,ETV<br>1,8MP1,CNN3,NRP1,<br>MEF2C,PRRX1,ZBTB20  |
| VSEVIL_05                 | 2.20       | VSEVIL_05                            | PTN1R,PRICKLE1,PDG<br>FRA,TNS1,CKM,EPHA3<br>,PLA1A,DAB2,ZBTB20,<br>NRP1,<br>USP13,FIL1,ZEB2,   |
| VS88_01                   | 8.54       | VS88_01                              | LOX1,NRP2,MEF2C,P<br>RRX1,CTGF,PRG4,ANG<br>PT12,SMYX,TRIM5A,C<br>SRP3,TRIM5A,BTK<br>MYH2,INSULIN,MEF2<br>C,NTN1,SMYD1,EBF1<br>,MTL1,<br>GSP72,AUPK3,SDPRLY<br>L1,PRN1,SIPR2,LMO2<br>,GFBP5,PKA,AGPAT4<br>,TACC1,DAB2,ANGPT1<br>,BIN1,ITGB1BP2,<br>MYH2,PTHR,TGFB3,<br>HSPG2,GFRA1,COLEC<br>12,XBTBD10,AB13BP,L<br>OX,HMCN1,<br>MYH2,STXBP1,CACNA<br>1G,KCNE4,ZIC1, |
| VSONE_C                   | 5.21       | VSONE_C                              | NEK6,SEPP1,ORSCNP<br>RRX2,NNAF,SELM,COL<br>15A1,FXD1,CO8A1,<br>NR2F2,GPR12A,PRG4,<br>SECT1B,SNAIL,DUSP3,   |
| VSNNKX25_01               | 1.97 01    | VSNNKX25_                            |  |
| VSIMODZCOM_02             | 4.02 OM_02 | VSIMODZC                             |  |
| VSIFREAC4_01              | 3.17 01    | VSIFREAC4                            |  |
| VSPK3_01                  | 4.29 1     | VSPK3_0                              |  |
| VSNNF4_01_B               | 3.89 1_B   | VSNNF4_0                             |  |



|                             |  |         |  |
|-----------------------------|--|---------|--|
| VSCHX10_01                  | VSCHX10_   | 3.34 01 | ETV1,MYH1,FBXO40,B<br>MP1,FIUP1,KCNMA1,<br>LDB2,GRK3,MYRBC2,Z<br>ICL,PRRX1,CNN3,GPB<br>CSC,<br>MYH2,PTHR,LXK12,<br>MYH8,CACNA1C,KCN<br>MA1,HS6T12,ZIC1,DL<br>C1,ZEB2<br>OR5CN1,GIAS,KCN18,E<br>NRP2,GNRC3,PTZ1,<br>BTK,<br>NKG6,ETV1,PTHR,CA<br>CNALC,MYH8,DTN1L<br>3,CEU2,FTILL,KCNM1<br>A1,USP1,LOXCL3,COX<br>CS,XBTBD10,C8K6,ZB<br>TB20,MDOG,NCAM1,<br>CTSK,<br>SSPN,PTM18,COXCL3,5<br>TAC2,CFB,CEP2,SULF<br>1,KCNMA1,LDB2,PRR<br>X1,PRKG1,MYL1,PTPR<br>O,FBUN2,ZBTB20,ANG<br>PT1,NRP1,ZEB2,<br>GREM2,PDGFRA,LY1,<br>HIC1,GPRI16,TACCL1<br>MO2,FUJ,IGFBP5,CN<br>N1,COXCL3,BIN1,AMO<br>T,<br>FHLIN1,CD36,PIGMA,<br>FES,TRIM63,FAM5CA<br>MOT,<br>LAMA4,CD66,PIGMA,P<br>RKL,FES,SMRX,LDXT<br>RIM63,COXCL4,<br>SPARC,BMP1,SONR52,<br>LXIL,C4B,<br>MYO18B,ZEB2,SLC43<br>A3,GPMA6B,<br>MMP14,PRELP,ACT3,L<br>AMA4,ZIC1,<br>PIB,MDK,M8,CD79B,<br>MEF2C,LDB2,RHOC,P<br>BXIP1<br>MYH2,HIC1,MYH8,NU<br>DTA,ZCHC2A,PCOLCE<br>JG17,ZEB1,XMRP1,<br>SPR9,DPR142,PK3CG,<br>TDR7,COL6A3,BIN1,<br>PRRX1,SMRX,CSMP3,T<br>SC22D1,ATP1A2, |
| VSMKXA_01                   | VSMKXA_  | 1.77 01 |  |
| VSTATA_02                   | VSTATA   | 1.71_02 |  |
| VSPU6F1_01                  | VSPU6F1  | 5.95_01 |  |
| VSUX3_01                    | VSUX3_0  | 6.39 1  |  |
| VS6ATA_06                   | VS6ATA_Q   | 3.88 6  |  |
| VSPR_01                     | 1.61 VSPR_01   |         |  |
| VSPR_02                     | 2.89 VSPR_02<br>RNCIGNY<br>RNCIGNY<br>Y_UNKNO<br>1.60 VN<br>RNTCANN<br>RNNVAATT<br>W_UNKNO<br>1.48 VN<br>RYAAAKN<br>NNNNNTT<br>GW_UNKN<br>1.64 OVN<br>RYCANNR<br>NNNCAG<br>UNKNOW<br>3.97 N<br>TAYNRN<br>NTC_UNK<br>2.20 NOVN<br>TNCATTC<br>CTR_UNKN<br>1.39 OVN |         |  |
| RYAAAKNNNNNTTGW_UNK<br>NOWN | RYAAAKN<br>NNNNNTT<br>GW_UNKN<br>1.64 OVN<br>RYCANNR<br>NNNCAG<br>UNKNOW<br>3.97 N<br>TAYNRN<br>NTC_UNK<br>2.20 NOVN<br>TNCATTC<br>CTR_UNKN<br>1.39 OVN  |         |  |
| RYCANNNNNNRNCAG_UNKN<br>OWN | RYCANNR<br>NNNCAG<br>UNKNOW<br>3.97 N<br>TAYNRN<br>NTC_UNK<br>2.20 NOVN<br>TNCATTC<br>CTR_UNKN<br>1.39 OVN   |         |  |
| TAANNNNNTTC_UNKNOWN         | TAANNR<br>NTC_UNK<br>2.20 NOVN<br>TNCATTC<br>CTR_UNKN<br>1.39 OVN  |         |  |
| TNCATTCCTR_UNKNOWN          | TNCATTC<br>CTR_UNKN<br>1.39 OVN  |         |  |
| YWATTWNNRGCT_UNKNOW<br>N    | YWATTWN<br>NRGCT_U<br>1.95 NKNOVN  |         |  |







H2AFX -0.672839 -0.324654 0.1142072 -0.616473 -0.715632 -0.567894 -1.064113 1.3816816 -0.764834 0.2229798 -0.443983 -0.092876 -0.010665 0.1744594 -2.811421 0.7813246 0.8211097 -0.616473 0.4597535 -0.550493 0.848658 -0.107862 -0.245092 1.6514568 0.9669249 2.1827494  
ENTPD7 -0.92134 -0.744252 -0.318244 -0.23503 -0.52038 -1.104978 -0.824812 -0.800029 0.688395 -0.815486 1.2291594 1.5147977 -0.692577 -1.093857 0.0439326 0.7772965 1.5886026 -0.929038 -0.640477 0.7368563 2.7566801 -0.211793 -0.547078 0.9291086 -0.284578 0.4216007  
ARRGAP1L -0.983711 0.5092425 -1.070192 -0.760244 -1.318133 -0.830952 -1.226571 1.3594099 0.1100641 0.5012417 -0.588574 -0.001669 -1.013168 -0.805345 0.9893222 0.1087071 0.858769 2.8249438 -0.762367 -0.601715 1.3869126 -0.579282 0.5426692 0.4659844 0.7335712 0.1516848  
HMGCN2 -1.833276 -0.770621 -0.869011 0.5053942 -0.025143 -0.313076 -1.628219 -0.137129 1.2300746 0.1091663 0.5262355 0.3695918 -0.120835 0.4817793 1.2121343 -0.018373 0.3609458 -1.10177 -1.710734 0.4894675 2.6735519 0.9182184 -0.19323 -0.496227 -0.448174 0.7902984  
C12orf75 -1.027236 -0.530103 -0.819085 -0.527212 -0.395848 -0.689794 -0.696901 -0.403552 -0.511121 -0.113384 0.2309213 2.1755171 -0.75443 -0.080661 0.5387841 -0.520722 0.2004486 -0.931729 -0.887015 1.0357388 -0.068406 2.3259313 -0.825623 2.5611638 0.3856972 -0.07124































|          |       |       |       |       |      |          |
|----------|-------|-------|-------|-------|------|----------|
| V9991_01 | 3.25  | 4.34  | 3.61  | 2.81  | 1.82 | V9991_02 |
| V9991_01 | 2.79  | 8.88  | 15.13 | 11.35 |      | V9991_01 |
| V9991_01 | 5.83  | 1.42  | 6.88  | 7.46  | 6.40 | V9991_01 |
| V9991_01 | 2.70  | 2.57  | 9.21  | 7.93  |      | V9991_01 |
| V9991_01 | 3.80  | 4.37  | 3.63  | 2.14  | 2.22 | V9991_01 |
| V9991_01 | 13.51 | 16.87 | 12.65 | 8.10  |      | V9991_01 |
| V9991_01 | 2.13  | 2.86  | 2.28  |       |      | V9991_01 |
| V9991_01 | 6.01  | 8.51  | 5.66  | 2.97  | 4.31 | V9991_01 |
| V9991_01 | 8.22  | 8.42  | 5.76  | 6.74  | 1.40 | V9991_01 |
| V9991_01 | 2.01  | 4.58  | 2.79  | 2.68  | 2.31 | V9991_01 |
| V9991_01 | 1.53  | 3.33  | 1.31  |       | 2.38 | V9991_01 |
| V9991_01 | 3.81  | 3.67  | 4.45  | 2.01  |      | V9991_01 |
| V9991_01 | 3.46  | 4.62  | 1.70  | 2.20  |      | V9991_01 |
| V9991_01 | 1.44  | 2.25  |       |       | 1.71 | V9991_01 |
| V9991_01 | 1.56  | 4.48  | 2.07  | 3.15  |      | V9991_01 |
| V9991_01 | 2.04  | 4.48  | 2.07  | 3.15  |      | V9991_01 |
| V9991_01 | 8.22  | 11.64 | 12.61 | 14.38 |      | V9991_01 |
| V9991_01 | 4.60  | 11.75 | 20.83 | 21.36 |      | V9991_01 |

|          |       |       |       |       |      |          |
|----------|-------|-------|-------|-------|------|----------|
| V9991_01 | 3.25  | 4.34  | 3.61  | 2.81  | 1.82 | V9991_02 |
| V9991_01 | 2.79  | 8.88  | 15.13 | 11.35 |      | V9991_01 |
| V9991_01 | 5.83  | 1.42  | 6.88  | 7.46  | 6.40 | V9991_01 |
| V9991_01 | 2.70  | 2.57  | 9.21  | 7.93  |      | V9991_01 |
| V9991_01 | 3.80  | 4.37  | 3.63  | 2.14  | 2.22 | V9991_01 |
| V9991_01 | 13.51 | 16.87 | 12.65 | 8.10  |      | V9991_01 |
| V9991_01 | 2.13  | 2.86  | 2.28  |       |      | V9991_01 |
| V9991_01 | 6.01  | 8.51  | 5.66  | 2.97  | 4.31 | V9991_01 |
| V9991_01 | 8.22  | 8.42  | 5.76  | 6.74  | 1.40 | V9991_01 |
| V9991_01 | 2.01  | 4.58  | 2.79  | 2.68  | 2.31 | V9991_01 |
| V9991_01 | 1.53  | 3.33  | 1.31  |       | 2.38 | V9991_01 |
| V9991_01 | 3.81  | 3.67  | 4.45  | 2.01  |      | V9991_01 |
| V9991_01 | 3.46  | 4.62  | 1.70  | 2.20  |      | V9991_01 |
| V9991_01 | 1.44  | 2.25  |       |       | 1.71 | V9991_01 |
| V9991_01 | 1.56  | 4.48  | 2.07  | 3.15  |      | V9991_01 |
| V9991_01 | 2.04  | 4.48  | 2.07  | 3.15  |      | V9991_01 |
| V9991_01 | 8.22  | 11.64 | 12.61 | 14.38 |      | V9991_01 |
| V9991_01 | 4.60  | 11.75 | 20.83 | 21.36 |      | V9991_01 |



























|           |      |      |       |       |       |           |   |
|-----------|------|------|-------|-------|-------|-----------|---|
| VSP00A_01 | 2.71 |      | 7.48  | 3.50  | 3.74  | VSP00A_01 | SSWAAKCNZ24RPPRANZC1<br>AASQDZJNZ2401101                |
| VSP00A_03 | 4.02 |      | 3.32  | 2.88  | 2.19  | VSP00A_03 | BBQZCCQZJNTRNKKRMS3711<br>TNNR001                       |
| VSP00A_03 | 4.71 | 1.51 | 6.75  | 4.13  | 2.02  | VSP00A_03 | STWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_02 | 3.40 | 3.26 | 6.34  | 6.86  | 3.09  | VSP00A_02 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_06 | 5.85 |      | 15.20 | 7.50  | 9.16  | VSP00A_06 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_06 | 5.75 |      | 7.23  | 1.59  | 2.57  | VSP00A_06 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_02 | 5.92 | 4.02 | 11.54 | 10.76 | 10.01 | VSP00A_02 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_06 | 3.27 |      | 6.37  | 2.73  | 1.44  | VSP00A_06 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_06 | 2.97 | 1.60 | 6.51  | 9.46  | 11.50 | VSP00A_06 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_06 | 4.01 |      | 5.64  | 5.02  | 2.32  | VSP00A_06 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_06 | 6.07 |      | 5.86  | 8.57  | 6.00  | VSP00A_06 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_04 | 6.50 | 2.20 | 7.28  | 3.32  | 2.15  | VSP00A_04 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_06 | 4.06 | 1.53 | 6.90  | 8.14  | 5.53  | VSP00A_06 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_06 | 4.02 |      | 3.52  | 3.18  | 2.66  | VSP00A_06 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_06 | 1.95 |      | 4.59  | 3.27  | 5.68  | VSP00A_06 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_06 | 5.50 | 1.54 | 9.66  | 3.27  | 5.60  | VSP00A_06 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |
| VSP00A_06 | 5.86 | 2.27 | 2.61  | 2.45  | 1.81  | VSP00A_06 | SSWAAKCNZ24RPPRANZC1<br>BBQZCCQZJNTRNKKRMS3711<br>137CL |















|                   |       |      |       |       |       |                   |  |
|-------------------|-------|------|-------|-------|-------|-------------------|--|
| VS2A_Q2           | 1.02  | 1.54 | 4.59  | 8.39  | 5.57  | VS2A_Q2           |  |
| GAIAITVQA_UNKNOWN | 4.10  |      | 3.36  | 2.70  |       | GAIAITVQA_UNKNOWN |  |
| VS1E_Q2           | 1.76  | 3.40 | 8.87  | 4.14  | 5.24  | VS1E_Q2           |  |
| VS1H_Q2           | 1.94  |      | 6.20  | 7.17  | 5.17  | VS1H_Q2           |  |
| VS1M_Q2           | 1.85  |      | 7.70  | 8.57  | 5.47  | VS1M_Q2           |  |
| VS1Q_Q2           | 3.11  | 5.68 | 11.69 | 7.93  | 7.86  | VS1Q_Q2           |  |
| VS1R_Q2           | 10.29 |      | 22.75 | 10.21 | 5.91  | VS1R_Q2           |  |
| VS1W_Q2           | 2.02  | 4.13 | 4.88  | 8.78  | 6.08  | VS1W_Q2           |  |
| VS1X_Q2           | 3.10  |      | 15.40 | 9.69  | 10.01 | VS1X_Q2           |  |
| VS1Y_Q2           | 3.10  |      | 15.40 | 9.69  | 10.01 | VS1Y_Q2           |  |
| VS1Z_Q2           | 3.10  |      | 15.40 | 9.69  | 10.01 | VS1Z_Q2           |  |
| VS2A_Q1           | 1.30  | 3.07 | 5.65  | 4.29  | 5.30  | VS2A_Q1           |  |
| VS2B_Q1           | 3.72  | 2.19 | 5.05  | 3.52  | 4.21  | VS2B_Q1           |  |
| VS2C_Q1           | 1.80  | 2.18 | 1.88  | 2.23  | 1.14  | VS2C_Q1           |  |
| VS2D_Q1           |       |      |       |       |       | VS2D_Q1           |  |
| VS2E_Q1           | 4.44  |      | 30.58 |       |       | VS2E_Q1           |  |
| VS2F_Q1           | 5.36  |      | 11.78 | 1.35  |       | VS2F_Q1           |  |
| VS2G_Q1           | 1.66  | 1.55 | 1.88  |       |       | VS2G_Q1           |  |
| VS2H_Q1           | 1.85  | 2.14 | 5.51  | 3.92  | 2.93  | VS2H_Q1           |  |
| VS2I_Q1           |       |      |       |       |       | VS2I_Q1           |  |
| VS2J_Q1           |       |      |       |       |       | VS2J_Q1           |  |
| VS2K_Q1           |       |      |       |       |       | VS2K_Q1           |  |
| VS2L_Q1           |       |      |       |       |       | VS2L_Q1           |  |
| VS2M_Q1           |       |      |       |       |       | VS2M_Q1           |  |
| VS2N_Q1           |       |      |       |       |       | VS2N_Q1           |  |
| VS2O_Q1           |       |      |       |       |       | VS2O_Q1           |  |
| VS2P_Q1           |       |      |       |       |       | VS2P_Q1           |  |
| VS2Q_Q1           |       |      |       |       |       | VS2Q_Q1           |  |
| VS2R_Q1           |       |      |       |       |       | VS2R_Q1           |  |
| VS2S_Q1           |       |      |       |       |       | VS2S_Q1           |  |
| VS2T_Q1           |       |      |       |       |       | VS2T_Q1           |  |
| VS2U_Q1           |       |      |       |       |       | VS2U_Q1           |  |
| VS2V_Q1           |       |      |       |       |       | VS2V_Q1           |  |
| VS2W_Q1           |       |      |       |       |       | VS2W_Q1           |  |
| VS2X_Q1           |       |      |       |       |       | VS2X_Q1           |  |
| VS2Y_Q1           |       |      |       |       |       | VS2Y_Q1           |  |
| VS2Z_Q1           |       |      |       |       |       | VS2Z_Q1           |  |
| VS3A_Q1           |       |      |       |       |       | VS3A_Q1           |  |
| VS3B_Q1           |       |      |       |       |       | VS3B_Q1           |  |
| VS3C_Q1           |       |      |       |       |       | VS3C_Q1           |  |
| VS3D_Q1           |       |      |       |       |       | VS3D_Q1           |  |
| VS3E_Q1           |       |      |       |       |       | VS3E_Q1           |  |
| VS3F_Q1           |       |      |       |       |       | VS3F_Q1           |  |
| VS3G_Q1           |       |      |       |       |       | VS3G_Q1           |  |
| VS3H_Q1           |       |      |       |       |       | VS3H_Q1           |  |
| VS3I_Q1           |       |      |       |       |       | VS3I_Q1           |  |
| VS3J_Q1           |       |      |       |       |       | VS3J_Q1           |  |
| VS3K_Q1           |       |      |       |       |       | VS3K_Q1           |  |
| VS3L_Q1           |       |      |       |       |       | VS3L_Q1           |  |
| VS3M_Q1           |       |      |       |       |       | VS3M_Q1           |  |
| VS3N_Q1           |       |      |       |       |       | VS3N_Q1           |  |
| VS3O_Q1           |       |      |       |       |       | VS3O_Q1           |  |
| VS3P_Q1           |       |      |       |       |       | VS3P_Q1           |  |
| VS3Q_Q1           |       |      |       |       |       | VS3Q_Q1           |  |
| VS3R_Q1           |       |      |       |       |       | VS3R_Q1           |  |
| VS3S_Q1           |       |      |       |       |       | VS3S_Q1           |  |
| VS3T_Q1           |       |      |       |       |       | VS3T_Q1           |  |
| VS3U_Q1           |       |      |       |       |       | VS3U_Q1           |  |
| VS3V_Q1           |       |      |       |       |       | VS3V_Q1           |  |
| VS3W_Q1           |       |      |       |       |       | VS3W_Q1           |  |
| VS3X_Q1           |       |      |       |       |       | VS3X_Q1           |  |
| VS3Y_Q1           |       |      |       |       |       | VS3Y_Q1           |  |
| VS3Z_Q1           |       |      |       |       |       | VS3Z_Q1           |  |
| VS4A_Q1           |       |      |       |       |       | VS4A_Q1           |  |
| VS4B_Q1           |       |      |       |       |       | VS4B_Q1           |  |
| VS4C_Q1           |       |      |       |       |       | VS4C_Q1           |  |
| VS4D_Q1           |       |      |       |       |       | VS4D_Q1           |  |
| VS4E_Q1           |       |      |       |       |       | VS4E_Q1           |  |
| VS4F_Q1           |       |      |       |       |       | VS4F_Q1           |  |
| VS4G_Q1           |       |      |       |       |       | VS4G_Q1           |  |
| VS4H_Q1           |       |      |       |       |       | VS4H_Q1           |  |
| VS4I_Q1           |       |      |       |       |       | VS4I_Q1           |  |
| VS4J_Q1           |       |      |       |       |       | VS4J_Q1           |  |
| VS4K_Q1           |       |      |       |       |       | VS4K_Q1           |  |
| VS4L_Q1           |       |      |       |       |       | VS4L_Q1           |  |
| VS4M_Q1           |       |      |       |       |       | VS4M_Q1           |  |
| VS4N_Q1           |       |      |       |       |       | VS4N_Q1           |  |
| VS4O_Q1           |       |      |       |       |       | VS4O_Q1           |  |
| VS4P_Q1           |       |      |       |       |       | VS4P_Q1           |  |
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| VS4S_Q1           |       |      |       |       |       | VS4S_Q1           |  |
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| VS4V_Q1           |       |      |       |       |       | VS4V_Q1           |  |
| VS4W_Q1           |       |      |       |       |       | VS4W_Q1           |  |
| VS4X_Q1           |       |      |       |       |       | VS4X_Q1           |  |
| VS4Y_Q1           |       |      |       |       |       | VS4Y_Q1           |  |
| VS4Z_Q1           |       |      |       |       |       | VS4Z_Q1           |  |
| VS5A_Q1           |       |      |       |       |       | VS5A_Q1           |  |
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| VS5C_Q1           |       |      |       |       |       | VS5C_Q1           |  |
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| VS5P_Q1           |       |      |       |       |       | VS5P_Q1           |  |
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| VS5U_Q1           |       |      |       |       |       | VS5U_Q1           |  |
| VS5V_Q1           |       |      |       |       |       | VS5V_Q1           |  |
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| VS5X_Q1           |       |      |       |       |       | VS5X_Q1           |  |
| VS5Y_Q1           |       |      |       |       |       | VS5Y_Q1           |  |
| VS5Z_Q1           |       |      |       |       |       | VS5Z_Q1           |  |
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| VS6X_Q1           |       |      |       |       |       | VS6X_Q1           |  |
| VS6Y_Q1           |       |      |       |       |       | VS6Y_Q1           |  |
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| VS7G_Q1           |       |      |       |       |       | VS7G_Q1           |  |
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| VS7J_Q1           |       |      |       |       |       | VS7J_Q1           |  |
| VS7K_Q1           |       |      |       |       |       | VS7K_Q1           |  |
| VS7L_Q1           |       |      |       |       |       | VS7L_Q1           |  |
| VS7M_Q1           |       |      |       |       |       | VS7M_Q1           |  |
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| VS7R_Q1           |       |      |       |       |       | VS7R_Q1           |  |
| VS7S_Q1           |       |      |       |       |       | VS7S_Q1           |  |
| VS7T_Q1           |       |      |       |       |       | VS7T_Q1           |  |
| VS7U_Q1           |       |      |       |       |       | VS7U_Q1           |  |
| VS7V_Q1           |       |      |       |       |       | VS7V_Q1           |  |
| VS7W_Q1           |       |      |       |       |       | VS7W_Q1           |  |
| VS7X_Q1           |       |      |       |       |       | VS7X_Q1           |  |
| VS7Y_Q1           |       |      |       |       |       | VS7Y_Q1           |  |
| VS7Z_Q1           |       |      |       |       |       | VS7Z_Q1           |  |
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| VS8G_Q1           |       |      |       |       |       | VS8G_Q1           |  |
| VS8H_Q1           |       |      |       |       |       | VS8H_Q1           |  |
| VS8I_Q1           |       |      |       |       |       | VS8I_Q1           |  |
| VS8J_Q1           |       |      |       |       |       | VS8J_Q1           |  |
| VS8K_Q1           |       |      |       |       |       | VS8K_Q1           |  |
| VS8L_Q1           |       |      |       |       |       | VS8L_Q1           |  |
| VS8M_Q1           |       |      |       |       |       | VS8M_Q1           |  |
| VS8N_Q1           |       |      |       |       |       | VS8N_Q1           |  |
| VS8O_Q1           |       |      |       |       |       | VS8O_Q1           |  |
| VS8P_Q1           |       |      |       |       |       | VS8P_Q1           |  |
| VS8Q_Q1           |       |      |       |       |       | VS8Q_Q1           |  |
| VS8R_Q1           |       |      |       |       |       | VS8R_Q1           |  |
| VS8S_Q1           |       |      |       |       |       | VS8S_Q1           |  |
| VS8T_Q1           |       |      |       |       |       | VS8T_Q1           |  |
| VS8U_Q1           |       |      |       |       |       | VS8U_Q1           |  |
| VS8V_Q1           |       |      |       |       |       | VS8V_Q1           |  |
| VS8W_Q1           |       |      |       |       |       | VS8W_Q1           |  |
| VS8X_Q1           |       |      |       |       |       | VS8X_Q1           |  |
| VS8Y_Q1           |       |      |       |       |       | VS8Y_Q1           |  |
| VS8Z_Q1           |       |      |       |       |       | VS8Z_Q1           |  |
| VS9A_Q1           |       |      |       |       |       | VS9A_Q1           |  |
| VS9B_Q1           |       |      |       |       |       | VS9B_Q1           |  |
| VS9C_Q1           |       |      |       |       |       | VS9C_Q1           |  |
| VS9D_Q1           |       |      |       |       |       | VS9D_Q1           |  |
| VS9E_Q1           |       |      |       |       |       | VS9E_Q1           |  |
| VS9F_Q1           |       |      |       |       |       | VS9F_Q1           |  |
| VS9G_Q1           |       |      |       |       |       | VS9G_Q1           |  |
| VS9H_Q1           |       |      |       |       |       | VS9H_Q1           |  |
| VS9I_Q1           |       |      |       |       |       | VS9I_Q1           |  |
| VS9J_Q1           |       |      |       |       |       | VS9J_Q1           |  |
| VS9K_Q1           |       |      |       |       |       | VS9K_Q1           |  |
| VS9L_Q1           |       |      |       |       |       | VS9L_Q1           |  |
| VS9M_Q1           |       |      |       |       |       | VS9M_Q1           |  |
| VS9N_Q1           |       |      |       |       |       | VS9N_Q1           |  |
| VS9O_Q1           |       |      |       |       |       | VS9O_Q1           |  |
| VS9P_Q1           |       |      |       |       |       | VS9P_Q1           |  |
| VS9Q_Q1           |       |      |       |       |       | VS9Q_Q1           |  |
| VS9R_Q1           |       |      |       |       |       | VS9R_Q1           |  |
| VS9S_Q1           |       |      |       |       |       | VS9S_Q1           |  |
| VS9T_Q1           |       |      |       |       |       | VS9T_Q1           |  |
| VS9U_Q1           |       |      |       |       |       | VS9U_Q1           |  |
| VS9V_Q1           |       |      |       |       |       | VS9V_Q1           |  |
| VS9W_Q1           |       |      |       |       |       | VS9W_Q1           |  |
| VS9X_Q1           |       |      |       |       |       | VS9X_Q1           |  |
| VS9Y_Q1           |       |      |       |       |       | VS9Y_Q1           |  |
| VS9Z_Q1           |       |      |       |       |       | VS9Z_Q1           |  |
| VS0A_Q1           |       |      |       |       |       | VS0A_Q1           |  |
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| VS0C_Q1           |       |      |       |       |       | VS0C_Q1           |  |
| VS0D_Q1           |       |      |       |       |       | VS0D_Q1           |  |
| VS0E_Q1           |       |      |       |       |       | VS0E_Q1           |  |
| VS0F_Q1           |       |      |       |       |       | VS0F_Q1           |  |
| VS0G_Q1           |       |      |       |       |       | VS0G_Q1           |  |
| VS0H_Q1           |       |      |       |       |       | VS0H_Q1           |  |
| VS0I_Q1           |       |      |       |       |       | VS0I_Q1           |  |
| VS0J_Q1           |       |      |       |       |       | VS0J_Q1           |  |
| VS0K_Q1           |       |      |       |       |       | VS0K_Q1           |  |
| VS0L_Q1           |       |      |       |       |       | VS0L_Q1           |  |
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| VS0N_Q1           |       |      |       |       |       | VS0N_Q1           |  |
| VS0O_Q1           |       |      |       |       |       | VS0O_Q1           |  |
| VS0P_Q1           |       |      |       |       |       | VS0P_Q1           |  |
| VS0Q_Q1           |       |      |       |       |       | VS0Q_Q1           |  |
| VS0R_Q1           |       |      |       |       |       | VS0R_Q1           |  |
| VS0S_Q1           |       |      |       |       |       | VS0S_Q1           |  |
| VS0T_Q1           |       |      |       |       |       | VS0T_Q1           |  |
| VS0U_Q1           |       |      |       |       |       |                   |  |



































[illegible]















|           |      |      |       |      |           |               |
|-----------|------|------|-------|------|-----------|---------------|
| VST32_01  | 2.19 | 3.54 | 8.07  | 8.02 | VST32_01  | 1.67 VST32_01 |
| VST32_02  | 1.58 |      |       |      | VST32_02  |               |
| VST32_03  | 1.42 | 3.98 | 3.81  | 3.11 | VST32_03  |               |
| VST32_04  |      |      |       |      | VST32_04  |               |
| VST32_05  | 5.25 | 3.95 | 12.53 | 7.25 | VST32_05  |               |
| VST32_06  |      |      |       |      | VST32_06  |               |
| VST32_07  |      |      |       |      | VST32_07  |               |
| VST32_08  |      |      |       |      | VST32_08  |               |
| VST32_09  |      |      |       |      | VST32_09  |               |
| VST32_10  |      |      |       |      | VST32_10  |               |
| VST32_11  |      |      |       |      | VST32_11  |               |
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| VST32_81  |      |      |       |      | VST32_81  |               |
| VST32_82  |      |      |       |      | VST32_82  |               |
| VST32_83  |      |      |       |      | VST32_83  |               |
| VST32_84  |      |      |       |      | VST32_84  |               |
| VST32_85  |      |      |       |      | VST32_85  |               |
| VST32_86  |      |      |       |      | VST32_86  |               |
| VST32_87  |      |      |       |      | VST32_87  |               |
| VST32_88  |      |      |       |      | VST32_88  |               |
| VST32_89  |      |      |       |      | VST32_89  |               |
| VST32_90  |      |      |       |      | VST32_90  |               |
| VST32_91  |      |      |       |      | VST32_91  |               |
| VST32_92  |      |      |       |      | VST32_92  |               |
| VST32_93  |      |      |       |      | VST32_93  |               |
| VST32_94  |      |      |       |      | VST32_94  |               |
| VST32_95  |      |      |       |      | VST32_95  |               |
| VST32_96  |      |      |       |      | VST32_96  |               |
| VST32_97  |      |      |       |      | VST32_97  |               |
| VST32_98  |      |      |       |      | VST32_98  |               |
| VST32_99  |      |      |       |      | VST32_99  |               |
| VST32_100 |      |      |       |      | VST32_100 |               |







[illegible]



[illegible]



[illegible]







CAGGTG\_V\$E12\_Q6

mRNA SCC-over-AK, up-regulated genes

mRNA SCC-over-NS, up-regulated genes

mRNA AK-over-NS,down

mRNA SCC-over-AK, down-regulated genes

mRNA SCC-over-NS, down-regulated genes

TGGAAA\_V\$NFAT\_Q4\_Q1

mRNA SCC-over-AK, up-regulated genes

mRNA SCC-over-NS, up-regulated genes

mRNA AK-over-NS,down

mRNA SCC-over-AK, down-regulated genes

STX1A,ANKRD13B,IP013,ITGA3,GAPDH,SERINC2,PRED1D1,MFAP2,MAPK12,FBLIM1,TEAD2,ZNF746,TEAD4,KRT17,CDK18,GJB2,PTHLH,SULF1,SHANK2,FHL3,FGF11,JAG1,LMAN2L,ETV1,ARTN,TYMP,PDGFBR,ITGB6,PPP2R2B,PMEPA1,C12orf5,GALE5,SMITN,LAMC2,CCM2,SLC26A10,GALNT2,STK32C,HHOD1,BAI2,RIN1,TNFRSF21,RELL2,HN1,SRM,GUCY1B3,SCG5,SIDT1,PLK4,MFAP2,PDCD10,SEMA4B,SOLE,MS4A1,POC1A,CALM1,CCDC88B,EML1,PIK3CD,CCDC92,CDH3,ZNF205,FAIM3,PPP2R2B,TNFRSF21,OSBPL7,PCGF1,MAZ,C1QC,SNF,ITC13,GUCY1B3,NETO2,ITGA3,TRIM37,GAPDH,FBLIM1,EIF5A,TUBA1C,INVS,SOX15,TAGLN2,S100A16,FAM98A,SGTB,PMEPA1,CCM2,F12,TRIM44,STK32C,TMEM65,UBE2F,GPX2,EIF4EBP1,TMEM199,BTBD3,STX1A,LCLAT1,TBX2,LAMC2,TMSB10,MAPK12,BTBD11,SKP2,SNX10,FHL3,RAB22A,S100A9,FGF11,ARTN,LRRGBD,CEPA1,UNC13D,SLC6A11,UCHL3,FHOD1,HIRA,ISP1,RELL2,HN1,CORO1A,SLAMF7,LPAR3,BCL11B,ADAM10,CD247,PRED1D1,WDR81,YWHAZ,CDK18,GJB2,PTHLH,SULF1,GJB6,RGS3,JAG1,ASF1B,RAC2,ITGB6,MCM7,MITS1,PRKCO,SELL,SLC7A11,NR1P3,TYMP,NCDN,FUC A2,FGFR11,PCK1,MTH14,CNTN4,FOXP4,PLA2G6,NTN4,TLE1,CBX8,PHF1,TRIM55,ERF,FST,TRIB1,ME3,BCAM,SORBS1,SORBS2,SPRY2,AXL,RGMA,PCP4,ANGPTL7,SLC27A6,GLI2,LYG2,SIK2,SOX10,DCD,FXVD1,RORC,PPARGC1A,NTRK3,PLEKHB1,RTN4,SLIT2,TNS1,NRG2,HS11B1,TMEM125,HMGCS1,ESRRG,SLC44A3,KIAA1324,STK40,PDLIM3,WNK2,PGM5,SFRP1,NGFR,DLI1,C8orf42,BARX2,KLK1,LPL,PALM,PPP1R13B,STC1,AKAP12,PREL,P,SEMA3A,STK32A,SEMA3B,PLEKHG6,AKAP1,LRI61,BNC2,TACC2,LRP5,SDC4,ITYH1,PDE2A,ATP6V0A4,NEED4L,KRT15,PHYHIP,SCARAS,FBXO32,COBL,ACLY,NFIX,LMOD1,POU2F3,SH3BGR12,CCDC64,PHF17,ADD3,ERBB3,ANKHD1,SMARCA2,IQGA2,SERTAD4,ZBTB16,DHRS9,AFF3,GATM,CADM1,RASGEF1B,CASZ1,DAAM1,ATP10B,NIPAL2,ZDHH C2,ABCA12,ARSG,CNTLN,FAM174B,GCH1,CD34A,RFK3,GFR1,PRDM1,PCDH1,FGFR11,DGAT7,SYTL1,CKB,PPARGC1A,CYPAF8,RAPGEF5,MFAP4,MKL2,WNK2,EGF,AXL,BCL6,DCN,PCK1,DLG2,PC,ZP1,DCD,FXVD1,RORC,DHRS3,NTRK2,NT RK3,KIF13B,ANKRD22,ELOVL3,GOLGA4,ITYH1,ARHGAP24,TMEM56,ENTPD2,IRX6,TLE1,IRX2,ERBB3,RTN4,CASZ1,BRP44,TSC22D1,DAAM1,CRB3,ATP1B1,SLC25A23,PER1,LPL,PALM,RBP5,GPT,TSPAN8,CXCL12,FDP5,KAZALD1,AKAP1,SOC3,CAMK2B,F2H,KIT,ANGPTL7,CDON,GFR1,GRB7,LMO1,ACLY,SFRP1,DDAH1,FBP1,CCDC64,VDR,ME3,PCN1,CRELD1,H6PD,MYLK,RASAL1,TRIB1,CNTN4,RFK3,LYG2,SOX10,TCPI1L2,PDLIM3,MEIS2,PPARGC1B,PLEKH81,GAT M,PHYHIP,SCNN1A,JMIDIC,TNS1,KCNIP2,NR1H3,STC1,PNPLA2,EPH86,STK40,FOS,UNC5B,PGM5,SPRR4,ITGA7,ARHGEF38,GADD45B,MANSC1,PARA,SL C26A9,CSRNP1,STK32A,ZDHH2C,LRI61,SH3BGR12,TMEFF2,DHRS9,SDC4,PTPC7,ATP6V0A4,KRT15,PZD2,FBXO32,ELOVL1,IL11RA,GRPD1L,NOV,EFCAB4A,RNF122,SNX25,TMEM88,PTGFR,MTH14,FOSB,EPHA2,MYLIP,PHF17,AKAP12,ADAMTS17,TRIM55,THRA,NCAM1,RGMA,PODN,ZBTB16,SIK2,KIAA1456,ALC AM,HBEF,C17orf28,DUSP5,DUSP4,PREL,HMGCS1,KIAA1324,DLI1,ZFP361,RNF152,ARSG,CITE2,SLC27A6,SLC27A2,SEMA3A,PHF1,SEMA3B,SYNR1,TACCL1,TACC2,HMBOX1,NTN4,CXXC5,COBL,PDE4B,C2orf55,LMOD1,USP54,SLC4A11,GCH1,OVOL1,C1orf210,USP2,GPD1,NGFR,KLK1,ANKHD1,SORBS1,AB TB2,SMARCA2,SORBS2,ELF5,IQGA2,SEMA6A,SCARAS,GJB4,GLI2,ACAA2,KIF4,SLIT2,NRG2,HS11B2,HS11B1,SLC44A3,ST3GAL5,NRA42,NRA43,NRA41,MFSD4,RTN3,ZNF295,PAD14,PIGV,SEPP1,CAT,NFIX,BNC2,PCDH1,PCP4,PDE2A,ANK2,CMTM8,ANK3,ATP6V1C2,NXPH4,POU2F3,CMTM4,

MMP14,PTK7,RASGEF1A,SLC4A3,S100A10,PTTX2,INHBA,LAMB3,CDK2AP1,DHX37,TIMM9,ARAP3,HSPH1,ADAMTS2,TUBA1A,TMNM2,SULF1,FHL3,ZIC1,JAG1,PDGFB,GREM1,RTKN,WRAP53,AKR1B1,SHANK2,ETV1,SOC32,GRB10,RIN1,KRT17,TYMP,FAM176A,GUCY1B3,MME,MMPI4,TP11,TNFSF10,VSNL1,PTK7,CCL5,TIMM37,TBX2,CHN1,COTL1,S100A10,C12orf35,CCNT2,TMEM117,SKP2,GDAP1,ADAMTS2,RACGAP1,FAP,SULF1,HIST2H2AC,FHL3,S100A8,RGS3,DSG3,DHX37,RAP2B,PIGB,IQGA2,NCDN,CEPA1,CD68,SMARCE1,SH2D2A,MITS5,EIF4H,SNVD2,CXCL10,CLEC11 A,C15orf41,CHST11,RCC2,JAG1,TFAP4,FN1,SLC16A1,PRMT5,CALM1,CALU,TMNM2,TYMP,PRR11,FAM176A,GUCY1B3,MME,WNT5A,MMP3,BTBD3,WDR81,FXYD6,KRT32,VPS37B,GSN,ADAMTS4,RORC,TINAGL1,KRTAP17-1,ENPP3,KRT25,LPL,HMGR,USP36,CAB39L,DNAJA1,CNN1,SOC52,ANGPTL7,VIT,PID1,STC1,IDA,DES,DCIK1,NDRG2,APOD,PPP1R1B,LYG2,SOX10,PAMR1,PPARGC1A,NFIL3,TNS1,TMEM125,ANGPTL1,PDLIM3,TMEM97,VEGFA,VEGFC,SLC26A7,PHLDB1,APOLD1,BCAR3,SH3BGR12,ARHGEF25,SDC4,CREM,BAIA P3,RCAN2,SPRY2,SPRY1,FST,CTNND2,ITIH3,SIK2,CACNB1,TMNM2,TPM1,ACLY,RNF152,PREL,SEMA3A,MERCE,LRP5,TACC2,KRTAP11-1,IRS2,ATP1A2,EGR2,LMOD1,EHFD1,SOX9,PTBN1,CABLES1,HS11B1,HSPB7,ESRRG,SLC44A3,STAC2,ISYNA1,TMPPRSS2,SLC25A4,NFIB,PTCH1,BNC2,NED DAL,PPP1R13B,NFIX,POU2F3,TGIF1,CCDC64,MAP3K8,PHF17,ADD3,ADCY2,ERBB3,CPEB4,ZNF407,AFF3,KRT25,PER2,PRDM1,MLIP,ANKHD1,DAAM1,SERTAD4,SMARCA2,CDK12,NDRG2,AGPA T9,CADM1,



FXVD6, ESPN, PPM1K, KRT32, CPE, ZFAND5, EGF, MAF, GSN, DCN, ADAMTS4, MAP3K8, DLG2, BHLHE40, GADD45B, RORC, DHRS3, IRX6, PDE4B, ERBB3, RCAN2, KRTAP17-1, CREB5, NFIL3, ATP1B1, LDB2, PER2, LPL, GLS2, HMGCR, SEMA7A, TNSI, USP36, ABHD5, CAB39L, NFAT5, ZNF675, CNN1, ACYP2, ADCY2, SLC25A4, CCDC80, ANGPTL7, ANGPTL1, P1D1, ACYL, ID4, ITGA8, CCDC64, CDKN1A, DES, DCLK1, ITGA7, C14orf43, STAC2, NDRG2, ADAMTS13, APOD, PPP11B, LYG2, GLDN, SOX10, FOS, PAMR1, PPARGC1A, CCL28, SCNN1A, JMD1C, IL22RA1, KCNIP2, VIT, PDLIM3, STC1, EHBP1, TMEM97, CCDC3, SLC26A7, ACO1, ITPR1, APOLD1, SH3BGR12, LMOD1, PDK4, SDCA, TTC18, PZDZ2, UBE2B, C20orf3, SNX25, NFATC1, PPARA, SPRY1, PHF17, ADAMTS17, ABL1, ZNF91, PODN, SIK2, CACNB1, ASPH, TPM1, CDKL2, ZNF430, RNF152, CITED2, PRELP, NFKBIA, KIAA1456, ZFP36L1, PDCD4, SEMA3A, TACC2, KRTAP11-1, IRS2, IL6, CTGF, ATP1A2, C9orf72, ZMIZ1, PDE4D, AGPAT9, ENPP1, EFHD1, USP2, MA2K3, SOX9, OVOL1, ANKHD1, MITF, SMARCA2, ELIF5, SPTBN1, SEMA6A, RER E, BC16, TOB2, PDE1B, TFAP2B, SLIT3, RGS2, DAAM1, CABLES1, HSD11B1, HSPB7, SLC44A3, CYR61, PGRMC2, NR4A2, NR4A3, TMPRSS2, NR4A1, IL11RA, CREM, GTPBP1, KRT25, CRA1, NFIB, NFIX, BNC2, GCNT2, CLIP, EGR2, RDH11, HAO2, PTC1, POU2F3, TGIF1,

mRNA SCC-over-NS, down-regulated genes

## TGANTCA\_V\$AP1\_C

mRNA SCC-over-AK, up-regulated genes

mRNA SCC-over-NS, up-regulated genes

mRNA AK-over-NS, down

mRNA SCC-over-AK, down-regulated genes

mRNA SCC-over-NS, down-regulated genes

## CTTGT\_V\$LEF1\_Q2

mRNA SCC-over-AK, up-regulated genes

mRNA SCC-over-NS, up-regulated genes

mRNA AK-over-NS, down

FXVD6, ESPN, PPM1K, KRT32, CPE, ZFAND5, EGF, MAF, GSN, DCN, ADAMTS4, MAP3K8, DLG2, BHLHE40, GADD45B, RORC, DHRS3, IRX6, PDE4B, ERBB3, RCAN2, KRTAP17-1, CREB5, NFIL3, ATP1B1, LDB2, PER2, LPL, GLS2, HMGCR, SEMA7A, TNSI, USP36, ABHD5, CAB39L, NFAT5, ZNF675, CNN1, ACYP2, ADCY2, SLC25A4, CCDC80, ANGPTL7, ANGPTL1, P1D1, ACYL, ID4, ITGA8, CCDC64, CDKN1A, DES, DCLK1, ITGA7, C14orf43, STAC2, NDRG2, ADAMTS13, APOD, PPP11B, LYG2, GLDN, SOX10, FOS, PAMR1, PPARGC1A, CCL28, SCNN1A, JMD1C, IL22RA1, KCNIP2, VIT, PDLIM3, STC1, EHBP1, TMEM97, CCDC3, SLC26A7, ACO1, ITPR1, APOLD1, SH3BGR12, LMOD1, PDK4, SDCA, TTC18, PZDZ2, UBE2B, C20orf3, SNX25, NFATC1, PPARA, SPRY1, PHF17, ADAMTS17, ABL1, ZNF91, PODN, SIK2, CACNB1, ASPH, TPM1, CDKL2, ZNF430, RNF152, CITED2, PRELP, NFKBIA, KIAA1456, ZFP36L1, PDCD4, SEMA3A, TACC2, KRTAP11-1, IRS2, IL6, CTGF, ATP1A2, C9orf72, ZMIZ1, PDE4D, AGPAT9, ENPP1, EFHD1, USP2, MA2K3, SOX9, OVOL1, ANKHD1, MITF, SMARCA2, ELIF5, SPTBN1, SEMA6A, RER E, BC16, TOB2, PDE1B, TFAP2B, SLIT3, RGS2, DAAM1, CABLES1, HSD11B1, HSPB7, SLC44A3, CYR61, PGRMC2, NR4A2, NR4A3, TMPRSS2, NR4A1, IL11RA, CREM, GTPBP1, KRT25, CRA1, NFIB, NFIX, BNC2, GCNT2, CLIP, EGR2, RDH11, HAO2, PTC1, POU2F3, TGIF1,

STX1A, MDF1, SYNPO, NCS1, SERINC2, MARK12, ST100A10, LAMB3, TPM2, FHL3, FGF11, GAPDH, SMTN, LAMC2, AKR1B1, PPP2R2B, DFNA5, C19orf55, UBE2C, RIN1, REL2, KRT17, GSTP1, NME, MMP1, MDF1, STX1A, SLC25A24, LTBR4R2, PSMD4, CHPF2, GAPDH, PSMD2, TPBG, WDR81, MAPK12, ST100A10, PRKCDBP, SPR1B, ARNTL2, BTBD11, YWHAZ, CMAS, MPZL2, STAT1, SNX10, TUBA1C, FAP, DSC2, XDH, AP2M1, FHL3, CEP135, RGS3, TAGLN2, LY6D, SLC38A1, BUB3, HK3, SMC6, PPP2R2C, PPP2R2B, COL5A2, COL5A3, PLAUC19orf33, LAMC2, DUSP14, SCRN1, CD68, RHOG, FGF11, DHNA5, RPS6K4, NME1, GZMB, ENO1, SPRY1A, FAM20A, UBE2C, MRP523, REL2, NRIP3, SFN, KRT16, GSTP1, NCDN, NME, TMAS19, RNF145, MMP3, MMP1, ACADVL, MYH14, TPM2, RCAN2, DCLK1, MCF2L, AQP5, FST, TRIB1, LGI3, NDRG2, TOB1, SLC9A1, PPARGC1A, NEK8, GLI2, DES, RIMS1, CCL27, HSPB7, ESRRG, TINAGL1, STK40, RTN4, AIF1L, KRT25, DLL1, PADI3, KCNN4, VEGFA, STC1, GABARAPL1, CIDECA, PTPRU, SEMA3B, AKAP1, NTN4, CAPN12, SNGG, KRT15, VIT, COB1, RBP4, TGIF1, CCDC64, JAK2, MAMDC2, MCF2L, CDC14A, CBFA2T2, PIK3C2G, PRDM1, LGI3, GFRA1, SMARCA2, KRT25, NDRG2, AGPAT9, OTUB2, ACADVL, SYTL1, LVE1, CSRNP1, ZFAND5, GADD45B, GRI183, DHRS3, CBFA2T2, PTP4A1, C2orf55, AQP5, CREB5, CRB3, ATP1B1, SLC25A23, KCNN4, PIK3C2G, AKA P1, ACSL3, MYLK, ANGPT14, GFRA1, VIT, STC1, CCDC64, YDR, SCEL, CDKN1A, DES, MAMDC2, C14orf43, TRIB1, NDRG2, ARNTL, PPP11R15A, PPARGC1A, ITPKC, IL22R A1, CLDN4, CCL27, GOS2, TMEM99, STK40, ANKRD22, SLC26A9, SNGG, ELOVL4, ELOVL1, MYH14, RCAN2, EPHA2, PODN, ASPH, HBEGF, C17orf28, CST6, RIMS1, DCL K1, ZFP36L1, DLL1, SEMA3B, IRRFIP2, SYNGR1, NTN4, MCF2L, IL6, COB1, PDE4D, AGPAT9, SLC4A11, C1orf210, USP2, LGI3, MITF, SMARCA2, RERE, TOB1, PDE1B, KR T15, GLI2, RGS2, SUOX, KLF9, HSPB6, HSPB7, VASN, RTN4, RTN3, PADI3, PADI4, GABARAPL1, LMNA, KRT25, CIDECA, PTPRU, PFKFB3, ANK3, TGIF1,

MMP14, ANKRD13B, PTK7, RAP1B, SERINC2, MEAP2, PITX2, TEAD2, LAMB3, HSCB, HSPH1, CDCA3, TUBA1A, FHL3, RTKN, ZIC1, PGF, RTN2, PPP2R2B, TNFRSF21, W RAP53, SEZ6L2, ETV1, PLSCR3, VASH1, HNF1, FAM176A, CHPF, MMP14, TNFSF10, PTK7, CCDC109B, SLC7A7, CCDC23, BCL11B, SAA1, MEAP2, PDCD10, COL3A1, SEMA4B, RAC2, MAFB, PGF, SFN, PANK2, SGTB, POC1A, C15orf4 1, CDCA3, CCNE2, FAP, PIK3CD, CAP1, CCDC92, GJB6, FHL3, RAB22A, HIRA, RGS3, RNF138, DSG3, CDH3, YWHAZ, SLC38A7, SLC38A1, HMGAA2, CEP41, PPP2R2B, SMA RCE1, COL5A3, TNFRSF21, RAB10, PSMD2, FTL, UCHL3, MCM7, TAX1BP3, TFAP4, CCOC132, SLC6A1, SLC2A6, SLC7A11, PAIP1, NRIP3, HNF1, BASP1, PRR11, FAM17 6A, ACT16A, MAF, KIF20A, CENPE, BTBD3, WDR81, FXYD6, MYH14, FOXP4, HMGCS1, CBX8, KRT35, CDO1, SPRY2, FST, TRIB1, CNTN4, LGI3, NDRG2, SORBS2, CGNL1, RGM A, ADAMTS4, APOD, TOB1, NEDD4L, SOX10, E GR3, PPARGC1A, TPM1, DNAB4, RTN4, NFIL3, RNF152, TRPV4, GSN, CDAN1, CAB39L, ESRRG, SLC44A3, MAT2A, STK40, WNK2, KRTAP17-1, TMPRSS2, DLL1, MEPC E, PALM1, CFL2, STC1, CNTRF, NXN, SH3BP5, BCAR3, SEMA3A, NFIB, DNAA1, LRP5, TACC2, BNC2, MCF2L, ANGPTL7, SNGG, SH3BGR, AKAP1 2, IL17RE, NFIX, TGIF1,



mRNA SCC-over-NS, down-regulated genes

V\$E2F\_Q6\_01

mRNA AK-over-NS, up

mRNA SCC-over-NS, up-regulated genes

GATTGGY\_V\$Nfy\_Q6\_01

mRNA AK-over-NS, up

mRNA SCC-over-NS, up-regulated genes

RyTTCCTG\_V\$ETS2\_B

mRNA AK-over-NS, up

mRNA SCC-over-AK, up-regulated genes

mRNA SCC-over-NS, up-regulated genes

FXYD6,SESTD1,LVE1,CKB,KRT35,CDO1,PARGC1A,ZFAND5,RASAL1,FBLN1,HPSE2,VASN,ADAMTS4,DHRS9,ZP1,MPP2,PTP4A1,ARHGAP24,ERBB3,W  
NK2,KRT23,CREB5,NFIL3,ATP1B1,LDB2,PALM,SEMA7A,CAB39L,KCTD12,CCDC80,RFX3,ANGPTL7,DDX5,CDON,GFRAL,STC1,C14orf43,BCHE,TRIB1,CNTN4,  
MAT2A,NDRG2,KIT,PANK1,APOD,SOX10,EGR3,PPM1K,MEIS2,RTN4,JMJD1C,CLDN4,RUFY3,CDAN1,STK40,FOS,SHF,CNTRF,RTN3,BTG2,ZDHHQ2,USP54,GC  
H1,SNCG,CDG37L1,MER2D,IL17RE,RNF122,MYH14,SORD,SH3BP5,CCNG2,PRKAR2B,AKAP12,STXBP6,ABL1,RGMA,ZBTB16,TPM1,C17orf28,RNF152,DUSP  
4,PDCC4,DUSP1,HMGCS1,ZFP36L1,SCAF4,DLL1,CITED2,CHMP1B,FRY,SEMA3A,SYNGR1,RAB15,TACCC,HMBOX1,MCF2L,IL6,CXXC5,ZMIZ1,PDE4D,PHF17,  
ANKH,JUND,IGI3,MITF,SMARCA2,SORBS2,ELF5,SEMA6A,LPHN3,HERPUD1,TOB1,GCNT2,MULT4,ANK2,TSC22D1,NEO1,SLT3,KRTAP17-  
1,TF,HSD11B2,RERE,SLC44A3,CYR61,NR4A2,NR4A3,TMPRSS2,PRICKLE2,CDCA2EP4,CFL2,PIGV,GFPT2,NFIB,BCL6,BNC2,PCDH1,PFKFB3,NOTCH2,CMTT8,  
ANK3,GPR133,SH3BGR,CGNL1,NFIX,TGIF1,

E2F7,HMGN2,MCM2,CDCA7,SASS6,SMC2,PLK4,ORC1,MELK,MCM4,MCM3,RRM2,CDCA5,DLEU1,ARHGAP11A,  
GAPDH,PKMYT1,RRM2,KIAA0101,CDG6,EIF5A,ADAMTS2,CDCA7,DLEU1,RANBP1,ORC1,MCM7,MCM4,MCM2,OSBPL7,MAZ,MELK,PLK4,ARHGAP11A,RAD  
51,CDCA5,SASS6,

HMGN2,BPGM,PLK1,USP1,ATM,LRRC20,HELB,BORA,TPX2,C12orf75,CDKN3,EA2,CKS2,C9orf85,DLEU1,TPX2A,ENTPD7,SEL1L,BUB1,ORC6,CENPF,PRMT5  
,CDCA5,MCM4,C12orf65,SLC7A11,KIF23,HOXA7,RACGAP1,ARHGAP11A,NCAPH,GORAB,  
HDAc1,WDR81,BPGM,PLK1,LCIAT1,FGF11,TOP2A,CALU,PPIL1,NUP37,TBCB,BORA,RACGAP1,YWHAZ,H2AFX,CDK18,PANK2,STAT2,CENPF,TUBA1C,NOP5  
6,INVS,CDG35C,MRPL51,CDKN3,RGS3,DLEU1,ACTL6A,CKS2,ASF1B,TROAP,RAP2B,CCDC51,TDO2,BUB1,ORC6,HMGGA2,CEP41,TPX2,PRMT5,MCM7,COL5A  
3,MCM4,GORAB,HIST2H2AC,C11orf82,PSMD4,CDH3,RNASEH2A,IFI6,UBE2C,MAZ,C1QTNF6,SLC7A11,KIF23,UBE2F,CDK1,PRR11,ARHGAP11A,NCAPH,CD  
CA5,CSE1L,PPP2R5C,BTBD3,KIF20A,

MAPK14,CAPZA1,FZD6,TFEC,S100A9,CLCN3,LSP1,CAB39,PIK3CD,GJB6,ARHGAP30,ARHGAP15,ARHGDIB,GPR132,RNF138,RAB10,LCP1,MS4A1,  
LTBR,PDGFB,RUVBL1,SLC2A9,PTK7,GRB10,RIN1,RTKN,SERINC2,MFAP2,PTX2,FBLIM1,TEAD4,TPM2,GALNT2,SLC35C1,  
FXYD5,WDR81,PTK7,S100A9,ITGA1,ADAM10,RGS14,CD247,MFAP2,PDCCD10,FBLIM1,PTPRC,EIF5A,LTBR,RUVBL1,FZD6,CLEC7A,PIK3CD,CAP1,GJB6,CMA5,  
NEUR1L,TAGLN2,LIMD2,JAK3,RGS3,RNF138,RAB10,LYN,MS4A1,LSP1,SLC35C1,CCDC51,ZNF205,TFEC,ARPC2,CAPZA1,SH2D2A,TNFRM209,PTPN7,COL6A3,  
CTSW,SLP1,RCC2,RPS6KA4,SLC2A9,FAM20A,TXNDC17,C1QTNF6,CASP8,LCK,ITGAL,PRKACB,KDELR3,SNX20,MMP3,PPP2R5C,



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LG13 0.8128775 2.072166 0.6953268 0.1139779 -0.50213 2.0747426 1.4589236 -0.586319 -0.636041 1.0822135 -0.315469 -0.587367 -0.226587 -0.507663 -0.829044 1.5606499 0.747131 -0.097252 0.1207317 -0.81094 -0.666433 -0.826544 -0.597083 -1.491211 -1.003988 -1.054669

SERINC2 -0.197487 -0.149152 0.1234429 -0.296907 -0.165123 -0.030117 -0.495465 0.105434 -0.383339 -0.205451 -0.133149 -0.209052 0.1818527 -1.578948 -3.220408 -0.265362 0.482983 -0.202802 -0.207379 -0.147302 0.61459 0.0350597 0.1238077 2.1528206 0.6134739 1.0268849

SPR1R13 -0.700843 -0.590811 -0.733745 -0.299976 -0.37731 -1.07807 -0.465002 0.2565742 -0.610099 -0.607599 0.3897324 0.2556338 -0.959593 -0.480212 -0.68014 -0.309002 0.2112234 -0.458918 -0.361156 0.372555 1.7642651 1.7083795 1.1773576 -1.296269 2.3285485 -0.257787

SPR1R14 -0.990074 -0.465182 -1.025913 -0.505481 -0.719825 -0.936181 -0.346849 1.1123783 -0.184498 -0.822847 0.5111997 1.0887697 -0.680183 -1.093837 -0.10562 -0.167625 0.6904109 -0.690871 0.3809714 -0.315965 1.110056 1.71237077 1.7123605 -1.363139 2.3855208 -0.367385

GPR183 -0.553925 0.5275598 1.225104 0.6906256 0.0273349 0.334361 0.6458966 1.9935156 -0.682094 -1.194662 -1.052016 0.2096477 1.5619505 2.3183687 0.2108647 -0.777709 -0.758552 -1.197828 -0.190015 0.7115068 -0.320519 0.0962394 -0.753657 -0.961851 -0.171397 -0.407976

PKFB3 -0.559243 -0.249173 0.5193152 0.1005931 0.6436234 -0.071678 2.4726918 1.5347374 -0.645992 -0.857794 -0.705003 0.0141095 1.1475564 2.6887011 -1.289241 -0.668547 -0.559621 0.2474157 -0.732126 -0.261324 -0.105152 -0.326396 -0.942716 -0.938431 0.072798 -0.529104

PKKCDP -0.141447 -0.303672 0.0551714 -0.026378 -0.120711 -0.937346 -1.205725 -0.350766 -0.121877 0.045761 -0.005163 -0.234427 -0.736792 1.8312668 -0.080037 0.4738637 -1.595393 -0.044387 -0.222373 0.0738673 0.4953776 0.5308956 0.8264705 -0.549327 1.944217 2.4353323

KRT15 2.5086115 0.743709 0.6870147 1.5865236 0.2964881 2.254426 0.9935477 -1.161616 -0.531591 0.413816 0.5661928 -1.113022 -0.442059 0.5114179 -0.653323 -0.300414 -0.441196 0.887051 -0.918283 -0.051621 -1.253066 -0.415816 -0.43332 -0.564963 -0.08554 -0.783943

SNPD 1.0644172 0.6493834 0.6634945 -0.166006 -0.660076 -0.536457 0.2593708 0.5409417 -0.616557 1.003849 -0.893926 -0.834276 0.415056 0.855193 -1.986387 -0.208652 -1.220131 0.4293784 0.0843701 -0.984715 2.471029 -0.447984 0.2445804 1.9583403 0.103339 0.841698

SNAC2 2.3433579 -0.479004 0.1754457 -0.146738 1.4088952 1.3198542 1.0704448 -0.608235 -0.75979 0.7747081 0.824614 0.643417 -0.551063 0.7490123 -1.354792 0.5001965 -1.16128 -0.735369 0.0750531 0.0717668 -0.83879 -0.480779 0.216274 -1.470049 1.9340287 -0.383669

RNCN 1.4365586 -0.609995 0.3934235 0.8196493 1.4952004 1.8339415 1.8286004 -1.130137 -0.084411 -0.087153 0.182419 -0.086029 2.0807794 1.4209411 -1.31981 -0.855488 -1.000079 -0.832442 1.0326756 -0.773431 -0.854481 -0.157931 -0.14884 0.229053 0.0411589 -0.883386

TRH1 -0.678921 2.2789977 0.5146732 0.3681329 1.6114636 0.3072518 2.4986256 0.22832 -0.456036 -1.327775 -0.715663 -0.248582 0.7140101 -0.106045 -0.225172 -0.819551 -0.289958 1.3965559 -0.985886 -0.356873 0.249278 -1.095724 -0.7598 -0.56073 -0.934268 -0.106872

HP8B7 -0.160686 -0.526082 2.1736215 0.4557948 0.8593775 0.8277314 3.1169613 -0.612439 -0.5557 -0.305447 -0.453993 -0.612439 0.6509143 0.1797312 -0.819877 -0.791049 -0.615452 -0.38831 1.1208619 -0.384566 -0.690028 -0.597963 -0.756973 -0.864653 -0.494243 -0.037914

POD1 1.4528523 -0.454712 0.7454608 0.3737513 0.6200561 0.4661945 2.0771698 -0.702738 -0.438358 0.109093 -0.134408 -0.480745 0.1234771 2.9746531 -1.28733 -0.495249 -1.008338 -0.660934 0.7930551 0.0481368 -0.686355 -0.450245 -0.882746 -1.359096 0.2844061 -0.607343

SLC2A9 -0.4512061 1.5604318 -0.763613 0.3295244 -0.374271 0.3642762 1.0369947 0.7191091 -0.07295 0.0673808 2.9562798 -0.633589 0.1292052 -0.830917 -0.259383 -0.923783 2.1170041 -0.786302 -0.584083 0.1463086 -0.677931 -0.831041 -0.36069 -0.993731 -0.641317 -0.838122

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CEP135 -0.198867 0.1297336 -0.996612 -1.250863 -0.352723 -0.892788 -0.844875 -0.064411 -0.772732 -0.251836 0.8304483 -0.4344399 -0.747333 -0.276226 2.7532279 -0.252652 -0.109392 2.155446 -0.341137 -0.094068 1.5341056 0.239712 -0.560742 -0.073219 -0.007984 -0.041246

UBE2C -0.773104 -0.638287 -0.573649 -0.21692 -0.67346 -0.765326 -1.364429 0.0074666 -0.432871 -0.506327 -0.405086 -0.259783 -0.466484 -0.705361 -0.807984 0.0009683 0.9211918 2.7049887 -0.713572 -0.474712 0.2505816 0.4178816 1.3217183 1.846714 -0.185094 1.4365704

DES 3.326268 0.737355 -0.351617 0.63774 -0.149351 0.5824864 2.250187 -0.591345 -0.591345 -0.349488 -0.118999 -0.369596 1.597426 -0.216304 -0.426878 -0.101987 -0.804203 -0.286535 -0.554163 -0.21474 -0.427316 -0.585321 -0.696796 -1.060387 -0.254536 1.3747005

PSMD2 -1.286193 0.6904875 -0.105308 -0.103782 -0.102562 -0.436386 -1.170625 0.6189157 0.1153841 0.7237181 -0.828665 0.0949575 -0.508751 -1.282802 1.2481646 -0.334852 0.1847378 2.2551243 0.708025 -0.337666 2.3741824 0.289186 0.7639256 -0.460904 -0.400177 0.6759063

CSM6 -0.325144 0.3507901 -0.412901 0.9293685 0.5142573 1.5518645 1.9926284 -0.588362 -0.407166 -0.192471 2.9246957 -0.349384 0.4406038 -0.84236 -1.089181 -0.820341 1.1235276 -0.587908 -0.21578 -0.215526 -0.54429 -0.495484 0.1603091 -1.10894 -0.879564 -0.913245

NRIP3 -0.953184 0.0637538 -0.92056 -0.569641 -0.515017 -0.564608 -0.20784 3.1346398 -0.621632 -0.704743 -0.164896 0.2572178 -0.807111 -0.501166 1.0496672 -0.580607 -0.597414 2.4022923 -0.450192 0.2069421 0.4145557 -0.77206 0.6490897 -0.506954 0.6219809 0.2719856

SFN -0.702953 -0.221609 -0.159584 -0.623355 -1.146674 -1.20114 -0.387184 0.9099971 -0.383583 -0.356414 -0.868924 0.1376207 -1.147283 0.1064366 -1.237978 2.150502 -0.581829 0.4882594 -0.346253 0.3228857 2.2630063 -0.008165 -0.041205 -0.2658 1.2416221 2.105052

RHOC -0.278642 -0.38857 -0.804211 -0.565194 -0.860835 -0.273485 -0.403748 1.591981 -0.663758 -0.298608 -0.635446 0.0264259 0.3029916 0.8251659 -2.982302 0.4446569 -0.137714 -0.622582 0.6718828 0.2383504 0.6202922 0.6324377 1.0911159 0.8169732 0.7797386 1.618409

TGF1 -0.603637 0.0433445 1.0786293 2.358443 0.6880307 0.3903705 2.0738049 -0.800311 -0.943408 -0.833547 -0.530528 -0.747107 0.8544288 2.1639077 -0.983151 -0.430281 -0.864633 -0.372399 -1.039832 0.0695972 0.7051476 -0.393577 -0.408541 -0.663893 -0.299922 -0.638139

MRF23 -1.553588 -0.582209 -1.57237 -0.651398 -0.180228 -0.27725 -1.130436 -0.818833 -0.509286 1.1596648 0.533777 0.3532996 -0.274134 -1.657693 1.1422951 -0.369711 0.2862085 0.1399037 -0.179901 0.5364677 1.6883126 1.8141656 1.0399922 1.669427 -0.258933 0.183815

CAPN12 -0.108826 -0.07802 0.5518303 -0.185789 -0.241599 0.4312505 1.0350879 0.2370142 -0.123522 -0.29617 -0.224324 -0.276576 -0.450417 -0.619326 -1.48445 -0.666453 -0.690848 0.3225763 -0.125699 -0.300089 0.0593857 -0.153349 -0.064491 0.4686916 -0.328633 -0.570828

FHL3 -0.49144 0.1154893 -0.593113 -0.414408 0.08726 -0.291616 -0.459308 1.1842712 -0.701211 -0.116496 -0.535595 0.212207 -0.964766 -0.60529 -2.425005 0.7723259 -1.325158 -0.354121 0.4327439 0.1617293 0.0828513 0.3092323 0.8276063 2.7573182 0.5781606 1.7563328

SMTN -0.470699 -0.597081 -0.37804 0.0013439 0.0942847 -0.813419 1.1229614 -0.626012 -0.732834 -0.364536 0.4230288 -0.290563 -0.880637 0.7566959 -1.482873 0.1039138 -1.477002 -0.38232 -0.517078 0.5820185 0.5350585 -0.125984 0.037863 0.5852792 0.8475996 1.0784799

ZFP36L1 0.1914642 0.2000336 2.3362698 1.3060243 -0.344267 0.2453473 0.6817095 0.749576 -0.215610 0.4711979 -1.017669 -0.891197 -0.22976 3.2354519 -0.647216 -0.216225 -0.79139 0.0865461 0.3004572 -0.755874 -0.490645 -0.937434 -0.43284 -0.795165 -0.701994 -0.538884

KRT16 -0.589533 -0.892916 -0.811641 -0.772164 -0.081493 -0.162079 -1.176951 0.3028523 -0.815436 -0.138387 -0.521605 0.5878727 -1.055428 0.1159668 0.4663466 1.8027285 -0.811639 0.242603 0.2888318 0.3727768 2.3514507 0.7695436 1.1405352 -0.8778034 1.6486513 1.0448052

MTF 1.0748726 -0.409174 2.3119645 1.7402281 0.0864116 -0.794097 0.013512 -1.275899 0.0079320 0.4048912 0.0951487 -1.372446 -0.803738 0.5569096 2.2084723 0.1694944 -0.276864 -1.171649 0.688949 0.469985 -0.850673 -0.661098 -0.834396 -0.96805 0.0106852 -0.422263

CIOC -0.318198 -0.41756 2.6315477 0.07863 0.9525319 1.534275 2.3916088 -0.41756 -0.41756 -0.38596 0.3117761 -0.41756 1.2425127 0.0324538 -0.797247 -0.827867 -0.41756 -0.41756 -0.41756 -0.41756 -0.41756 -0.41756 -0.41756 -0.41756 -0.41756 -0.41756 -0.41756

MAPK12 -0.734224 -0.827587 -0.875571 -0.796308 0.2683615 0.3441822 -0.65672 -1.160353 -0.469545 -0.822938 -0.422864 0.4808776 0.2634251 0.7211786 -1.650123 -0.114005 -0.081356 1.5383413 -0.030409 0.0107313 2.1950528 1.0004196 0.3163529 -0.778007 2.5036863 -0.278076

CLDN4 0.6290165 0.1813989 1.8942221 -0.27816 -0.095618 1.9433245 0.9410311 1.388091 -0.55363 0.1520336 -0.104845 -0.523095 1.948361 -1.249348 -1.637809 -0.12933 0.3779315 -1.069613 0.0139188 -0.131334 -1.072109 -1.00312 -0.142018 0.371447 -1.450194 -0.295711

STK40 -0.429607 2.009587 1.7302987 0.1824133 0.9321879 0.1364517 3.1413641 -0.458005 -0.707582 0.1289022 0.1321261 0.311332 0.347121 -0.456743 -0.94566 -0.513265 0.4962184 -0.053092 -0.73171 -0.502422 -0.660322 -1.326542 -0.405944 -0.678443 -0.766773 -0.641444

ESRRG 0.7171378 -0.920373 2.4987042 1.784974 0.8505488 -0.13735 -0.085071 -0.871649 -0.864901 -0.840367 0.059813 0.963435 -0.13735 -0.148406 0.1418903 0.0656356 -0.208136 2.6576287 -0.650161 -0.868103 0.915398 -0.947995 0.3746205 -0.161867 -0.208136 -0.107124

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MMP1 -0.524835 -0.512132 -0.516982 -0.522236 -0.511606 -0.589446 -0.651552 -0.474915 -0.498541 -0.520877 -0.450766 0.8071957 -0.490895 -0.634505 -0.599243 1.1225207 -0.613328 -0.395388 -0.524835 0.6638111 1.5852532 2.3377003 0.6893809 -0.581632 0.1838378 3.1980086

C2orf55 1.5860013 0.1394803 2.3945566 0.389041 -0.164551 -0.224434 0.3517796 -0.76464 1.5924461 0.9740048 0.871155 -1.728376 0.4432857 -0.652895 0.183783 -0.079434 0.1001378 -1.308786 -0.315511 0.3631839 -0.129539 -0.984803 -0.081498 -0.820255 0.6452183

LAMB3 -0.582538 -0.513786 -0.424398 -0.526219 -0.390448 -0.551781 -0.050356 -0.528108 -0.299364 -0.421907 0.311988 0.332951 -0.457053 -0.732557 0.736534 0.3250001 -0.788468 -0.484046 -0.447103 -0.3013 0.0485084 0.5872013 0.93396 0.5397132 -0.211624 1.7124738

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ASPH 0.6944222 1.9399258 -0.003467 1.8380804 1.5438157 -0.407582 -0.503922 -1.209827 -0.582397 -0.156895 0.8315887 -1.045263 -0.742074 1.565675 2.705706 -0.349609 -0.159036 -0.129681 -0.720315 -0.381374 -0.825158 -0.549853 -0.460575 -0.584007 -0.166372 -0.337759

TPM2 1.3035694 -0.564541 0.0428661 2.0170883 1.2599302 -0.007713 0.6452611 -1.274187 -1.176263 -0.854989 -0.623661 -0.395428 -0.632945 0.6388223 -0.74387 -0.534903 -1.598434 0.1688342 -0.897061 0.4601057 0.3348862 -0.417294 -1.006115 2.117591 1.071765 0.6669128

DLL1 0.0997879 -0.024179 1.6788939 -0.0029 1.1189189 0.7277544 2.6921833 -0.881788 -0.950749 -0.470224 -0.496355 -0.665532 0.110217 1.7456904 -1.268893 0.3910817 -0.556889 -0.689916 -0.343002 -0.488881 1.3263438 -0.564834 -0.57475 -1.365112 -0.558403 0.0115358

COL5A2 -0.752931 -0.66686 -0.44419 -0.223378 -1.104135 -0.956029 -0.814154 -0.606461 -0.084525 -0.317687 0.290687 -1.087582 1.0547947 -0.418265 0.8918278 -1.000334 -0.591841 -0.008258 2.567747 1.922906 -0.93456 -0.44801 -0.52205 2.0044884 0.2303752

KRT25 -0.480913 -0.023569 2.086554 2.7973128 -0.197159 2.843125 0.926659 -0.482749 -0.310588 -0.336033 0.128072 -0.644388 -0.231038 -0.337865 -0.563535 -0.550069 -0.247987 -0.481302 -0.480201 -0.47809 -0.480586 0.417363 -0.420181 -0.564274 -0.495642 -0.485136

VIT 1.5309953 -0.641621 2.6957416 0.231727 1.6852338 1.0602291 1.9133519 -1.08784 -0.398824 -0.632768 0.3408356 -0.940029 0.472837 0.2360997 -0.452715 -0.602349 0.0146746 -0.988584 -0.487166 -0.51774 -0.481755 -0.713752 -0.784063 -0.328296 -0.575432 -0.848793

LTBR42 -0.327191 -0.505613 -0.346723 -0.211598 -0.312278 -0.753105 -1.174912 0.083285 -0.069738 0.621662 0.161624 0.1966241 -1.381415 0.210288 -0.216573 2.0540182 -0.597457 -0.178 -0.190238 -0.129460 0.1397407 0.0104009 0.5211679 -0.970988 1.6409778 1.6842313

NCL21 2.9039842 -0.379851 -0.735577 0.4117417 0.2486889 2.3397231 1.2465462 -0.555749 -0.428485 1.2171651 -0.434872 -0.616893 -0.32647 1.0622888 -0.848407 -0.500227 -0.566735 -0.796699 -0.343098 -0.329095 -0.784707 -0.37



| human-EZF_OE_01.s |           |           |           |           |           |            |           |           |           |            |            |            |           |           |           |           |           |           |           |            |           |
|-------------------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|
| Groups            | NS        | NS        | NS        | NS        | NS        | NS         | NS        | NS        | NS        | NS         | NS         | NS         | NS        | NS        | NS        | NS        | NS        | NS        | NS        | NS         | NS        |
| Sample            | 2-NS      | 3-NS      | 4-NS      | 5-NS      | 6-NS      | 7-NS       | 8-NS      | 9-NS      | 10-NS     | 2-AK       | 3-AK       | 4-AK       | 4-AK-1    | 5-AK      | 6-AK      | 7-AK      | 8-AK      | 9-AK      | 10-AK     | 11-AK      | 12-AK     |
| OSRP17            | -0.43898  | -0.766712 | -0.365321 | -1.095439 | 0.329368  | -0.611882  | -0.515388 | -0.219994 | 0.1548948 | -0.863866  | -0.343457  | -0.722355  | 0.271075  | 2.108092  | -1.476798 | -0.939894 | -0.536522 | 2.2760451 | 1.070829  | 0.6025714  | -0.418689 |
| RAO51             | -1.364034 | -1.401419 | 0.4039345 | -1.134016 | -0.636932 | -1.238036  | -1.134040 | 0.676768  | 0.0780544 | -0.280689  | -0.402467  | 0.1875634  | -0.54192  | -0.515555 | -0.647746 | 1.4787387 | 0.5327029 | 1.4956756 | 0.4488327 | -1.280552  | 2.4971289 |
| MCN2              | -0.62638  | -0.739785 | -0.458392 | -0.971987 | -0.825041 | -0.461365  | -1.134040 | 0.676768  | 0.0780544 | -0.280689  | -0.402467  | 0.1875634  | -0.54192  | -0.515555 | -0.647746 | 1.4787387 | 0.5327029 | 1.4956756 | 0.4488327 | -1.280552  | 2.4971289 |
| ORC1              | -0.860894 | -1.061479 | -0.045872 | -0.779818 | -0.779818 | -0.779818  | -0.779818 | -0.779818 | -0.779818 | -0.779818  | -0.779818  | -0.779818  | -0.779818 | -0.779818 | -0.779818 | -0.779818 | -0.779818 | -0.779818 | -0.779818 | -0.779818  | -0.779818 |
| ADAMTS2           | -0.790267 | -0.015391 | -0.215448 | 0.2455513 | -0.432478 | -1.480258  | -1.217302 | 0.953763  | -0.621891 | -0.406113  | -0.107017  | 0.12104944 | -0.975231 | -0.865268 | 0.3154377 | -0.780468 | 0.4344257 | -0.115448 | 1.559127  | -0.128824  | -0.646094 |
| CD45              | -1.12781  | -0.798319 | -0.328307 | -1.079032 | -1.013136 | -0.766958  | -0.694509 | 1.056746  | 0.6069553 | -0.813384  | -0.805786  | -0.754157  | -0.178931 | -1.161178 | 0.5851771 | -0.154314 | -0.207573 | 2.0702542 | 0.8997248 | -0.896636  | 0.9153845 |
| CD65              | -1.131282 | -0.707984 | 0.8212165 | -1.113758 | -0.845191 | -1.026439  | -0.316718 | 2.9697929 | 0.3354759 | -0.010131  | -1.000087  | -0.394602  | -0.581677 | -0.467748 | 0.574807  | -0.43931  | -0.188959 | 0.4221258 | 0.539167  | -1.16144   | 1.7854732 |
| RAMBP1            | -1.068708 | 0.3558199 | -1.310425 | -0.63795  | -0.060074 | -0.753764  | -1.282716 | 1.0137441 | -0.489304 | -0.550331  | -0.29077   | 0.6471891  | -0.742183 | -0.504113 | 0.3001566 | 2.6191196 | -0.606457 | 0.550589  | -1.042392 | 0.4359867  | 2.5223221 |
| MA2               | -0.625909 | -1.243956 | -0.997415 | -0.301333 | -0.339754 | -0.802163  | -1.09726  | 0.191795  | 0.2804697 | -0.163988  | -0.451187  | 0.1608264  | -1.098211 | 0.2670377 | -1.393662 | 0.8016189 | -0.506412 | 0.5348439 | -0.61709  | -0.046664  | 1.4918793 |
| MCN4              | -1.433073 | -1.388113 | -0.054477 | -0.102034 | -1.22367  | -1.17139   | -1.211109 | -0.540725 | 0.3165204 | 1.195102   | 0.508977   | 0.8579903  | -1.280931 | -0.086098 | 2.3510359 | 0.289304  | -0.052475 | 0.0692691 | -0.704024 | -0.388903  | 0.6810093 |
| GADH              | -0.906228 | -0.404068 | -0.46876  | -0.378291 | -0.258492 | -0.76986   | -0.966358 | -0.546806 | -0.937704 | -0.676459  | -0.0973    | 0.17101232 | -0.849725 | -0.102957 | -0.190396 | 0.9995306 | -0.872398 | 3.3699469 | -0.274144 | -0.386699  | 0.6445766 |
| MCN3              | -1.011064 | -1.454658 | -0.714852 | -0.70803  | -0.694614 | -0.598554  | -0.934277 | 1.554965  | 2.0789336 | -0.054521  | -0.656419  | -0.023581  | -0.815648 | -0.390609 | 2.545104  | -0.193292 | 0.4845302 | 1.197686  | 0.4420852 | -1.035815  | 0.7048854 |
| PKMYT1            | -0.666172 | -0.160299 | -0.166008 | -0.80694  | -0.862542 | -0.364878  | -1.200397 | 1.0307997 | -0.165015 | -0.50655   | 0.1386684  | -0.152301  | -0.352969 | -0.745721 | -1.852521 | 0.304448  | 0.0446208 | 0.6511882 | 0.1453398 | -0.687188  | 0.8858115 |
| EFSA              | -1.411815 | 0.0489806 | -1.62715  | -1.228915 | 0.0016189 | -0.219397  | -1.097638 | 0.379665  | 0.0782777 | -0.582422  | 0.7314259  | 0.8509507  | -0.51508  | -1.16084  | -0.135288 | 0.5637683 | -0.66479  | -0.5705   | 0.9743328 | -0.97373   | 1.8278207 |
| SMC2              | 0.0295534 | -0.636154 | -0.103012 | -0.642003 | -1.562464 | -0.781772  | -0.952065 | 3.096322  | -0.488234 | 0.5937529  | -0.223489  | 0.268481   | -1.071704 | -0.463313 | 1.1281858 | 0.747643  | 0.9193628 | 1.4451774 | -0.111873 | -1.556859  | 0.4759561 |
| PLK4              | -1.974713 | -0.722788 | -0.085238 | -0.343993 | -1.062705 | -1.222424  | -1.129648 | 1.9754727 | 0.3400532 | 0.5925054  | 0.3385293  | -0.208988  | -0.761376 | -0.293122 | 0.002051  | 0.5222071 | 0.1966412 | 1.017995  | -0.330289 | -1.074428  | 1.8920603 |
| CDCA7             | -0.084402 | -1.005894 | -0.378106 | -0.83907  | -1.367044 | -0.3409363 | -0.984876 | 1.4778303 | 1.2532916 | -0.408028  | -1.138001  | -0.048669  | -0.321515 | -0.837889 | -0.82134  | 0.0411499 | 1.7934022 | 2.2766884 | 0.3466154 | -1.147759  | -0.81411  |
| SAS56             | 0.1398508 | -0.998657 | 0.1258293 | -0.959518 | -1.587232 | -1.065099  | -0.89156  | 1.6710182 | 1.8840469 | 0.11090475 | -1.156507  | -0.254851  | -0.906016 | -0.122588 | 2.2993378 | 0.2721575 | 0.939869  | 1.5778907 | 0.0270158 | -0.680798  | 0.5294189 |
| MEIK              | -1.597711 | -0.046718 | -0.379478 | -0.99932  | -1.113862 | -0.839522  | -1.112312 | 0.6886309 | 1.5124039 | -0.385995  | -0.529773  | -0.417122  | -1.025615 | -0.324895 | 0.5926703 | 0.2880513 | 0.3046182 | 1.436283  | -0.238198 | -0.790882  | 2.6789166 |
| E2F7              | -0.441536 | -0.852919 | -0.420591 | -0.850506 | -0.892119 | -0.386355  | -0.54061  | 1.3436865 | 1.6120544 | -0.54545   | -0.033733  | -0.756837  | -0.513698 | -0.209503 | 1.2286536 | -0.151756 | 0.3932367 | 3.6548462 | -0.508485 | -0.9308179 | 0.2142696 |
| KIAA0101          | -0.670144 | -0.659899 | 0.2634473 | -0.911754 | -0.76625  | -0.566357  | -0.794476 | 3.325065  | 0.5389912 | -0.611981  | -0.758341  | -0.692893  | -0.268071 | -0.497687 | -0.969781 | 0.2520416 | 0.6328714 | 0.6461591 | 0.5753922 | -0.897099  | 0.2052457 |
| RRM2              | 0.0484203 | -0.869184 | 0.4734502 | -0.957221 | -1.285047 | -1.248714  | -1.110206 | 1.0548961 | -0.007974 | -0.599144  | -0.595404  | 0.3621568  | -0.733832 | -0.569072 | 0.2189208 | 0.7564516 | 1.6514936 | 1.0317955 | -0.720196 | -0.881413  | 2.2795055 |
| DLEU1             | -1.109573 | -0.860901 | -0.170095 | -1.396491 | -1.461303 | -0.416285  | -1.001379 | 3.1966707 | 0.5206667 | 0.1760008  | -0.391942  | 0.8573152  | -0.646414 | -0.273684 | 1.0837386 | -0.128007 | 0.1520154 | 0.7975956 | 0.6178519 | -1.027405  | -0.287021 |
| ARRGAP11          | -0.983711 | 0.5092425 | -1.070192 | -0.760244 | -1.318133 | -0.830952  | -1.226571 | 1.3594099 | 0.1100641 | 0.5201247  | -0.5988574 | -0.001669  | -1.013168 | -0.805345 | 0.9893222 | 0.1087071 | 0.858769  | 2.8249438 | -0.762967 | -0.601715  | 1.3869126 |
| HMG2              | -1.833276 | -0.770621 | -0.869011 | 0.5052942 | -0.025143 | -0.313076  | -1.628219 | -0.137129 | 1.2300746 | 0.1019163  | 0.5262555  | 0.3695918  | -0.120885 | 0.4817793 | 1.2121343 | -0.018373 | 0.3600458 | -1.10177  | -1.710734 | 0.4894675  | 2.6735519 |



| human-TCF6_O6.5 |            |            |           |            |           |           |            |           |            |            |            |            |           |           |            |
|-----------------|------------|------------|-----------|------------|-----------|-----------|------------|-----------|------------|------------|------------|------------|-----------|-----------|------------|
| Groups          | 2-NS       | 3-NS       | 4-NS      | 5-NS       | 6-NS      | 8-NS      | 10-NS      | 2-AK      | 3-AK       | 4-AK-1     | 5-AK       | 6-AK       | 8-AK      | 12-AK     | 1-AK       |
| Simple          | NS         | NS         | NS        | NS         | NS        | NS        | NS         | NS        | NS         | NS         | NS         | NS         | NS        | NS        | NS         |
| TCF6            | -1.559795  | -1.886769  | 0.2612658 | -0.444462  | -0.120108 | -0.472367 | -1.091058  | -0.936198 | 0.1507557  | 0.03098628 | -0.0686402 | 0.9034418  | -0.909896 | 0.571936  | -1.145675  |
| TRG3            | -0.450646  | -0.228745  | -0.411048 | -0.615889  | -0.196839 | -0.818244 | -0.320569  | -0.682518 | -0.705073  | -0.548684  | 0.0245154  | 0.3045511  | -0.95349  | -0.373869 | -1.176798  |
| OSRP7           | -0.43888   | -0.766712  | -0.365321 | -1.095439  | 0.293368  | -0.611862 | -0.515086  | -0.196898 | -0.1861896 | -0.5889619 | -1.463316  | -1.182345  | -0.606645 | -0.499108 | 0.2481812  |
| EV1             | 1.84852022 | 0.7387316  | 0.9798228 | 0.4663249  | 0.7103001 | -0.943392 | -0.817194  | -0.6688   | -1.064091  | -1.463316  | -1.182345  | -0.606645  | -0.499108 | 0.2481812 | 0.1101161  |
| MYLP            | 0.0873027  | 0.743900   | 0.5320054 | 0.6412599  | 2.060244  | 0.6632137 | 1.6007367  | -0.15975  | 0.0418717  | 0.093381   | -0.087947  | 0.7979407  | 0.4848101 | 0.666168  | -0.597104  |
| PLKH6           | 0.0873027  | 0.743900   | 0.5320054 | 0.6412599  | 2.060244  | 0.6632137 | 1.6007367  | -0.15975  | 0.0418717  | 0.093381   | -0.087947  | 0.7979407  | 0.4848101 | 0.666168  | -0.597104  |
| MYK             | 1.592221   | 0.4003889  | 1.608861  | 0.2451188  | 0.285816  | 1.331172  | 1.0842614  | -0.65672  | -0.635423  | 0.2103958  | -0.752775  | -0.659432  | 0.2103958 | -0.752775 | -0.659432  |
| PCN             | 2.9105006  | -0.55655   | 2.9102054 | -0.313274  | 0.2949101 | 0.2248414 | 0.0880847  | -0.843425 | -0.733236  | 0.2949101  | -0.733236  | 0.2949101  | -0.733236 | 0.2949101 | -0.733236  |
| SEMA3B          | 1.5308076  | -0.154271  | 0.446198  | 1.173722   | 0.1852701 | 1.550138  | 1.069576   | -0.6831   | -0.506672  | 2.340285   | -0.256924  | -0.740615  | -0.506672 | 2.340285  | -0.740615  |
| NCN             | -0.339295  | -0.981684  | 0.3372692 | -0.374689  | -0.06093  | -1.411235 | -0.911419  | -1.00693  | 0.2801331  | 1.6280466  | -1.020121  | 0.2434371  | -0.34138  | -0.689799 | -2.002456  |
| PLEKH7          | -0.48761   | 0.0603148  | -0.216287 | 0.7507682  | 1.7485932 | 0.7619456 | -0.082409  | -0.78815  | -0.283536  | 1.639786   | -0.953308  | 1.7387049  | -0.178274 | -0.675356 | -1.022402  |
| NHR13           | -0.19857   | 0.905463   | 0.1028525 | -0.232704  | 0.7507682 | 1.7485932 | 0.7619456  | -0.082409 | -0.78815   | -0.283536  | 1.639786   | -0.953308  | 1.7387049 | -0.178274 | -0.675356  |
| TMVP            | -0.448132  | -0.282778  | -0.564825 | -0.39569   | -0.462093 | -1.220954 | -0.706731  | 0.1721945 | -0.198     | -0.47349   | -0.092947  | 1.6156343  | -0.326714 | 0.1905635 | -0.205467  |
| SLAMF7          | -0.435579  | -0.77177   | -1.188972 | -1.073567  | -1.166124 | -0.473593 | -1.108328  | 1.1335245 | -1.000332  | -0.73769   | -0.595876  | 1.6745163  | -0.888968 | -1.150428 | -0.747498  |
| USP10           | -0.942835  | -1.180451  | -0.861492 | -0.254357  | -0.054301 | -0.886974 | -0.86719   | -0.821268 | -0.19604   | 0.6286601  | -0.149926  | -0.595869  | -0.257556 | 1.7475567 | 0.2583937  |
| TM2B2           | -0.73682   | 0.2003217  | -0.143802 | 0.5697971  | 0.9032576 | 0.4935236 | 2.5332397  | -0.76471  | -0.382771  | 0.9367792  | -0.200521  | -0.659566  | 1.0453079 | -0.106911 | -0.200038  |
| BARX2           | -0.906979  | 0.4743052  | 1.217823  | 1.116696   | -0.093732 | 1.4166731 | 2.1259561  | -0.719039 | -0.414801  | -0.866056  | 0.6402133  | -0.712221  | 0.3501707 | -1.798328 | -1.4539    |
| BMX             | 1.186604   | 0.0168879  | 1.417929  | 0.3015046  | -1.283532 | 0.466343  | -0.410126  | 1.896576  | 2.340285   | -0.256924  | -0.740615  | -0.506672  | 2.340285  | -0.740615 | -0.506672  |
| HERP            | 2.4353565  | 0.1398243  | 1.7339845 | -0.072426  | 0.2614182 | 1.0436536 | 0.3898107  | 0.837492  | -0.185102  | 0.4880104  | -0.475303  | -0.758795  | 0.573292  | 2.065418  | -1.027014  |
| NEBDL           | 0.535276   | 0.2305027  | 0.8328993 | -0.252024  | 0.0656382 | -0.628173 | 1.21753105 | -0.34092  | -0.668466  | -0.951461  | -0.186956  | -1.030033  | -0.703914 | -0.420256 | 0.1559721  |
| ENTPD2          | 1.3111473  | 0.1467404  | -0.320813 | 0.2094081  | -0.087421 | 1.2731672 | 2.7485927  | -0.320813 | -0.090069  | -0.320813  | 0.0189042  | -0.279313  | 1.0317972 | -0.828808 | -1.807267  |
| PRMT1           | 0.4458     | 1.4967595  | -0.701387 | -0.407591  | -0.599818 | -0.407552 | -0.041353  | 3.507469  | -0.56235   | -0.006618  | -0.1180442 | 0.0651933  | 0.0487469 | -0.098642 | 2.106896   |
| LAMC2           | -0.588113  | -0.421076  | -0.549721 | -0.505388  | -0.443903 | -0.73995  | -0.359867  | -0.358173 | -0.3241    | -0.471113  | -0.171115  | 0.0655979  | -0.807157 | -0.693447 | -0.361495  |
| CAMK2B          | 1.1128641  | 2.7141899  | -0.61204  | -0.126082  | 0.1254659 | 0.742182  | 1.3696397  | -0.838133 | -0.7066    | -1.144143  | 0.912267   | -0.424446  | 2.0122916 | -0.431122 | -0.728192  |
| PIGV            | 2.4020908  | 0.6479402  | 1.4530005 | -0.611804  | 0.4747242 | 1.0593536 | 0.2404658  | -0.8767   | -0.007466  | -1.170201  | 0.6572707  | -0.69927   | 0.4895689 | -0.639667 | 2.078721   |
| GLI3            | 0.2170677  | -0.106183  | -0.506439 | -0.07714   | 0.1912944 | -1.080033 | -0.985191  | -1.418943 | -1.199742  | -0.27031   | -0.729433  | -0.166058  | -0.467893 | 0.1596605 | 0.0492922  |
| CHD3            | -0.846928  | -0.73659   | -0.597645 | -0.854159  | -0.69163  | -0.986435 | -0.948131  | 1.8131343 | -0.459705  | -0.879842  | -0.60723   | 0.314247   | -0.194749 | -0.435462 | 0.5513827  |
| DNMT2           | -0.03658   | 1.0428119  | -0.528182 | 0.1823875  | 1.4274852 | 1.658677  | -0.00689   | -0.64663  | -0.340289  | -0.376062  | 1.415179   | -0.555514  | 1.2361467 | -1.012353 | -0.9362    |
| NGN             | -0.442871  | 1.102085   | 0.965084  | 0.1174853  | 2.939131  | 0.7220672 | 2.920268   | -0.691038 | -0.665702  | 0.001864   | -0.09587   | -0.742619  | 0.6157247 | 1.1706502 | -1.267078  |
| CDON            | 1.557999   | 0.2689101  | 1.5276011 | 0.2779906  | 0.0075047 | -0.410591 | -0.493446  | -0.497318 | -0.098028  | 2.4703486  | -0.505096  | -1.322222  | 0.615424  | 0.287951  | -0.320763  |
| ERBB3           | 0.6027938  | 0.336832   | -0.803641 | 1.826705   | 0.0994784 | -0.335924 | -0.26348   | -0.135214 | -0.291415  | 1.791664   | 2.519724   | -0.190562  | -0.324881 | 0.5973458 | -0.539584  |
| MYLK            | 0.6385216  | 0.397948   | -0.117261 | 1.2747567  | 2.4702084 | -0.335924 | -0.26348   | -0.135214 | -0.291415  | 1.791664   | 2.519724   | -0.190562  | -0.324881 | 0.5973458 | -0.539584  |
| PRKDC           | -0.529195  | -0.699713  | -1.184067 | -1.1597349 | -0.490964 | -0.719383 | 2.996312   | -0.35447  | -0.804774  | -1.052371  | 0.717509   | -0.497869  | -0.382155 | 1.264854  | -0.657427  |
| ELOVL1          | -0.12828   | 0.2037645  | -0.858785 | 0.217156   | 1.537441  | 1.4342748 | 0.3535306  | -0.66766  | -0.337144  | -0.55182   | 0.696026   | -0.11434   | 1.326891  | -1.256423 | -1.147387  |
| EM1             | -0.543006  | -0.728971  | 0.2137681 | -0.826084  | -0.7504   | -0.872504 | -0.816583  | 0.170666  | -0.766304  | 1.3480001  | -0.683805  | -0.355332  | -0.945076 | 0.5331157 | 2.6427     |
| SIRT1           | -0.83694   | -0.927288  | -1.419953 | -0.46957   | -0.707484 | -0.36955  | -0.465836  | 2.8377189 | 0.7539098  | -0.02341   | -0.083805  | -1.3931222 | 0.501069  | -0.443352 | -1.842132  |
| DHR9            | -0.46063   | 1.5761571  | -0.167684 | 0.4123843  | 0.5387059 | 1.5768761 | 0.5149746  | 0.0399489 | -0.323248  | -1.108613  | 1.239642   | 1.6261742  | -0.172803 | -0.938076 | -0.00489   |
| GLU2            | 1.0450225  | -0.0116042 | 2.342062  | 2.2471272  | -0.737543 | 1.1021842 | 0.6822533  | -0.753829 | -0.480706  | -0.699728  | -0.73833   | 0.334638   | -1.047667 | -1.33736  | -1.204198  |
| TAD2            | -0.025129  | 0.175649   | -0.589395 | -0.414189  | 0.2801884 | -0.33275  | 0.37352409 | -0.70158  | -0.757033  | -0.699728  | -0.73833   | 0.334638   | -1.047667 | -1.33736  | -1.204198  |
| NEN4            | 1.575362   | -0.469912  | 1.444525  | 1.8120764  | 2.293839  | 0.349797  | 1.3009378  | -0.66411  | -1.531556  | -0.12673   | 0.1090051  | -0.118547  | 0.1714485 | 0.5071497 | -0.410112  |
| SEMA4           | -0.787682  | -0.44221   | -0.547186 | 0.6283112  | 0.763752  | -0.346692 | -0.061389  | -0.951341 | -1.531556  | -0.12673   | 0.1090051  | -0.118547  | 0.1714485 | 0.5071497 | -0.410112  |
| PHF17           | 2.7509897  | 0.371001   | 0.2255807 | 1.2674206  | -0.075044 | 0.2650194 | 0.2489723  | 0.0219793 | 1.387084   | -0.7353    | -0.371765  | -0.641928  | -0.474619 | -0.222246 | -0.551207  |
| CD10f5          | -1.0276588 | -0.383895  | -0.925798 | 1.5255449  | -0.41079  | -0.959515 | -0.65787   | -0.87248  | -0.867934  | -0.49252   | 0.147455   | 0.0886893  | -0.827467 | -0.970737 | -0.189025  |
| PCN1            | 2.3137504  | 0.1974343  | 1.3649848 | 0.2136655  | -0.220339 | -0.431092 | -0.3898    | 0.596115  | 1.6501673  | 0.3230309  | -0.43266   | -0.787767  | -0.4063   | -0.42746  | -2.7792754 |
| TNFI            | 1.2366461  | 0.664933   | 2.3610071 | 1.5621379  | 0.7066309 | 0.018626  | 0.529705   | -1.146976 | -0.44138   | 0.582799   | -0.413815  | -1.023246  | -0.758086 | 1.8062274 | 0.801573   |
| CD10A           | -0.423762  | 0.4441075  | -0.460649 | 0.3808419  | 1.7953479 | -0.476529 | -0.309512  | 1.2117324 | 0.81435    | -0.657391  | 1.824269   | -0.104046  | -0.594823 | -0.279355 | -0.564035  |
| NRX3            | 1.1013851  | 1.130948   | 1.9297712 | -0.432942  | 0.6703831 | 0.6176159 | 0.0759313  | -0.337564 | 1.102806   | 0.006274   | -1.020465  | -0.582732  | 0.5689314 | -0.1863   | 0.7861616  |
| SEMA3C2         | 1.867488   | 0.523804   | 1.4342968 | 1.48657    | 0.0753475 | 0.4076159 | 0.0359248  | -0.109777 | 0.3524236  | 0.0369377  | -0.09447   | -0.388887  | 0.2321808 | 0.6887064 | 1.7486191  |
| SEMA3C4         | -0.080916  | -0.064935  | 0.0210203 | 0.923803   | -0.686195 | -1.0378   | -0.75732   | -0.60763  | -0.518549  | 0.544499   | 2.6539798  | 1.305346   | -0.643535 | -0.217376 | 1.454678   |
| SEMA5           | -0.974873  | -0.479945  | -1.211394 | -0.24987   | -0.80678  | -0.68447  | -1.587488  | 1.2565689 | 0.693103   | -0.522821  | -0.086641  | 1.4586075  | -0.198931 | 0.2142192 | -0.343442  |
| PTHLH           | -0.560369  | -0.631017  | -0.648472 | -0.61563   | -0.669986 | -0.630106 | -0.616215  | -0.65848  | -0.648103  | -0.551207  | -0.172299  | -0.543006  | -0.759352 | -0.378528 | 0.4584178  |
| PPP1R13B        | 1.4796961  | 0.9188608  | 1.6924473 | -0.04485   | -0.094497 | 1.3121657 | 0.1199318  | -1.87659  | 0.6846182  | -0.520009  | -0.696051  | 0.812451   | -0.789761 | -0.33603  | -2.072618  |
| SIC1A1          | 0.8010711  | 2.1155987  | 0.0909488 | 0.2469344  | 0.1752928 | 1.150741  | 1.6999467  | -0.078439 | -0.273756  | -0.7909329 | -0.66531   | 1.0754105  | -0.425109 | -1.171409 | -0.97573   |
| SEMA6           | -0.400505  | 0.9748661  | 0.9676065 | 1.48670705 | 1.3852039 | -0.394356 | 0.8634661  | -1.14439  | -0.875488  | 0.53447184 | 2.216457   | -1.09825   | -0.6385   | 0.0467004 | 1.9349417  |
| UNC13D          | -0.715939  | -0.61654   | -0.861877 | -0.750742  | 0.1446073 | 0.267252  | 1.1086776  | -0.741226 | 0.1266725  | -0.671014  | 1.1138566  | 1.5935887  | -0.490705 | -2.719708 | -0.959575  |
| CRAT            | 0.1598841  | 1.2932017  | -0.479168 | 0.7305484  | 1.5027485 | -2.802595 | 0.466301   | -0.51702  | -0.252485  | -0.088823  | 0.5656741  | -0.500487  | 2.6485791 | -0.927064 | -1.013346  |
| SNRPA2          | 1.9453657  | -0.156727  | 3.0881336 | 0.2304669  | 1.0671769 | -0.278542 | -0.048508  | -0.802157 | -0.823143  | -0.416254  | -0.663881  | -0.8884924 | -0.42274  | -0.788066 | 1.6365351  |
| SNRPA5          | -0.640525  |            |           |            |           |           |            |           |            |            |            |            |           |           |            |



|          |           |            |           |            |           |           |           |            |            |           |           |            |            |           |            |           |            |            |            |            |            |            |           |           |            |           |           |           |           |
|----------|-----------|------------|-----------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|------------|------------|-----------|------------|-----------|------------|------------|------------|------------|------------|------------|-----------|-----------|------------|-----------|-----------|-----------|-----------|
| SOLE     | -0.81365  | -0.1413    | -0.83292  | -0.67348   | -1.00918  | -0.43202  | -0.52943  | 0.3860917  | -1.03726   | 0.0437621 | -0.013579 | 0.8716376  | -0.75042   | -1.01725  | 0.373928   | -0.207719 | 0.0537792  | 0.57021    | -0.066579  | 0.4779879  | 3.597188   | 0.543666   | 0.8922218 | 1.411026  | -0.914756  | -0.316306 |           |           |           |
| MYTH4    | -0.30624  | 0.1871762  | -0.72894  | -0.428042  | -0.883116 | -0.939343 | -0.373949 | 2.0041487  | -0.632981  | -0.001035 | -0.184639 | 0.9464763  | -0.143713  | -2.73955  | 1.2257059  | 1.5128657 | -0.00351   | -0.24895   | -0.423835  | 0.0864714  | -0.423835  | 0.5077322  | 0.5009302 | 0.7923436 | 0.2024558  |           |           |           |           |
| MYTH1A   | 0.3959544 | 0.5322149  | 1.6359539 | 0.7123070  | 0.996166  | 1.435311  | 1.959653  | -0.36474   | -0.195601  | 1.3370792 | 0.6060025 | -1.36695   | 0.1947606  | -0.608025 | -0.1967428 | -0.668025 | -0.774328  | 0.4442422  | -0.778802  | 0.7765242  | -0.930385  | -0.342605  | -0.81724  | -0.677809 | -0.810799  | 0.1440126 | -0.910307 | -0.801665 | -0.871394 |
| ATPB6M04 | -0.095459 | 2.1446175  | -0.214768 | 1.7437335  | 2.136484  | 0.407832  | 1.4462719 | -0.09042   | -0.66571   | -0.548202 | 1.0393468 | -0.706777  | 0.4927287  | -0.774328 | 0.4442422  | -0.778802 | 0.7765242  | -0.930385  | -0.342605  | -0.81724   | -0.677809  | -0.810799  | 0.1440126 | -0.910307 | -0.801665  | -0.871394 |           |           |           |
| CONL     | 1.1310154 | 1.597867   | -0.453593 | 1.3609471  | 0.8774624 | 0.9965229 | 2.1147424 | 1.1285876  | -1.140191  | -0.176768 | 0.1180391 | -0.817461  | -0.118746  | -0.103459 | -0.765097  | -0.122036 | 0.2367054  | -0.740336  | -0.62312   | -0.742616  | 0.0468916  | -1.0461    | -0.54459  | -1.666459 | -0.091121  | -0.848728 | 2.8978516 | -0.224511 | -1.550579 |
| STIXA    | -0.677794 | -0.29758   | -0.908689 | -0.49406   | -0.628915 | -0.02039  | -0.516596 | 0.0997091  | 0.0222997  | 0.193271  | -0.817461 | -0.118746  | -0.103459  | -0.765097 | -0.122036  | 0.2367054 | -0.740336  | -0.62312   | -0.742616  | 0.0468916  | -1.0461    | -0.54459   | -1.666459 | -0.091121 | -0.848728  | 2.8978516 | -0.224511 | -1.550579 |           |
| EPH6     | 1.343373  | -0.401539  | -0.584491 | 0.7615694  | -0.408069 | 1.0936569 | 0.6344263 | -0.76613   | -0.005053  | 2.239467  | 0.824205  | -0.82775   | -0.251009  | 0.181506  | -0.176639  | 1.2718638 | 0.3221058  | -0.113302  | 1.0589782  | 0.5150033  | -0.887079  | 0.33294    | -0.810929 | -1.852729 | -0.680663  | -0.441821 |           |           |           |
| CEP4     | 0.3817023 | 0.8232178  | -1.525314 | -0.959681  | -1.45031  | -0.915689 | -0.578658 | -2.02355   | 0.0546735  | 0.9324271 | 0.313187  | 0.3552471  | -0.740084  | 0.015663  | -0.196439  | 0.0109353 | 0.3212145  | -0.690296  | -0.708992  | 0.3262015  | -1.7770171 | 1.1373928  | 0.6823188 | 1.5362323 | -0.057132  | -0.564703 |           |           |           |
| CUNC18   | 1.1842023 | -0.6147149 | 1.6701336 | 0.6508783  | 0.6508783 | 1.4201012 | 1.0428792 | -1.73466   | -0.6279412 | 0.3417074 | -0.43206  | 0.829472   | -0.447001  | -0.972699 | 0.0748665  | -0.301793 | -0.859567  | -0.167843  | -0.084616  | -1.284912  | -0.49205   | -1.131395  | -1.656956 | 0.8481261 | -0.106996  |           |           |           |           |
| CUNC5    | -0.559669 | 1.5348247  | -0.672343 | 0.4688038  | 0.766765  | 1.1261075 | 1.586698  | -0.74246   | -0.665147  | 0.9142425 | -0.39353  | 1.3064165  | -0.824302  | -1.582705 | -0.619191  | 1.3316218 | -0.89546   | -0.231772  | -0.162615  | -0.048562  | -0.324695  | -0.985868  | -1.482776 | -0.018417 | -0.246996  |           |           |           |           |
| UNCL18   | 1.9462609 | -0.507551  | -0.133745 | -0.263438  | 0.9503719 | 0.2179858 | 3.2108827 | -0.65506   | -0.643916  | -0.02428  | -0.632694 | -0.500902  | 0.463705   | 0.7177646 | -0.2731946 | -0.775841 | -0.66135   | -0.395112  | -0.20734   | -0.48782   | -0.481992  | -0.165598  | -0.514013 | 0.6160271 | -0.627468  | -0.824921 |           |           |           |
| KZALD1   | -0.762216 | -1.128069  | -0.169893 | -0.655235  | -0.670559 | -0.89147  | -0.656794 | 1.2678274  | 0.509405   | -0.50101  | -0.07889  | -0.100922  | -0.893209  | -0.237847 | -0.7319465 | -0.252398 | -0.11188   | 2.7219354  | 1.585445   | -0.455949  | 0.0420592  | 0.165598   | -0.514013 | 0.6160271 | -0.627468  | -0.824921 |           |           |           |
| TRM47    | -0.681509 | 0.8538177  | 0.7270538 | 0.4994613  | 2.4282873 | 0.2950516 | 1.9897898 | 1.16262    | 0.0349715  | 0.950504  | 1.1201334 | -0.793484  | -0.026343  | -1.02046  | 1.553392   | -0.660138 | -0.474969  | -1.294213  | -0.547966  | -0.514408  | -0.860332  | -0.002225  | -0.882093 | -0.13096  | -0.932724  | -0.556472 |           |           |           |
| PNM6C1A  | 0.0532862 | 0.2537794  | 1.8128671 | 1.269194   | 1.3933635 | -0.239602 | -0.27703  | -0.734067  | -0.487836  | -1.074302 | -0.28461  | -0.507066  | 0.0012862  | -0.227735 | 0.7607279  | -0.511831 | 0.9712406  | -0.860943  | -0.902492  | -0.794967  | -0.747185  | -1.102566  | -0.670670 | -0.429279 | 0.0084637  | -0.58732  |           |           |           |
| ZR1B16   | 0.6016231 | 0.7028207  | -0.568642 | 1.5515583  | 0.46492   | 1.2978574 | 1.0607139 | 1.674635   | -0.640033  | -0.24716  | 1.059808  | -0.955642  | -0.132643  | -0.76199  | -0.108672  | 0.701344  | -0.1062937 | -0.794967  | -0.747185  | -1.102566  | -0.670670  | -0.429279  | 0.0084637 | -0.58732  |            |           |           |           |           |
| MANC1A   | 0.016366  | 1.8737461  | -0.096744 | 0.9264533  | 0.0657074 | 0.1740805 | 0.5317183 | -1.22688   | -0.135841  | 0.5666129 | 1.3611443 | -0.206522  | 1.5813505  | -1.090041 | -1.482468  | 0.343227  | 2.1750319  | -0.719645  | -0.192454  | -0.6534276 | -0.755627  | -1.11386   | -1.009026 | -0.040435 | -0.201092  | -1.111719 | -0.880062 |           |           |
| SCANS1   | 1.5105659 | 1.2013761  | -0.444013 | 0.7852539  | 0.3030175 | 0.9498083 | 0.1375945 | 0.980778   | -0.470853  | 1.0373017 | 1.6240047 | 0.5438129  | -0.481893  | -0.900125 | -0.708341  | -0.33105  | -0.746789  | -0.216478  | -0.6534276 | -0.755627  | -1.11386   | -1.009026  | -0.040435 | -0.201092 | -1.111719  | -0.880062 |           |           |           |
| RASL1    | 0.7435432 | 1.4475911  | 0.0301824 | -0.305536  | 0.0339364 | 1.7240137 | 1.5958468 | -0.1886208 | -0.449633  | -0.386851 | 0.980323  | -0.354899  | -0.920629  | -1.191934 | -1.830251  | -0.805848 | 1.2491143  | -1.140067  | -0.971279  | -0.881403  | -0.400593  | -0.818822  | -0.029820 | -0.721648 | -0.7142897 |           |           |           |           |
| VDR      | -0.047028 | 2.203245   | 2.4972005 | 0.3399704  | -0.101878 | 0.1272208 | 1.1216565 | 0.6713098  | -0.573757  | -0.13265  | 1.9903033 | -0.456189  | -0.920629  | -1.191934 | -1.830251  | -0.805848 | 1.2491143  | -1.140067  | -0.971279  | -0.881403  | -0.400593  | -0.818822  | -0.029820 | -0.721648 | -0.7142897 |           |           |           |           |
| GADH     | -0.960228 | -0.40686   | -0.46876  | -0.378291  | -0.256492 | -0.76668  | -0.963558 | -0.248806  | -0.791208  | -0.676459 | -0.0973   | 0.7101232  | -1.849725  | -0.102957 | -0.190096  | 0.9995306 | -0.872398  | 3.569469   | -0.27144   | -0.336699  | 0.6445756  | -0.2497245 | -0.296613 | 1.9624471 | 0.8562287  | 1.0793131 |           |           |           |
| PHI1     | 0.2798874 | -0.200251  | 1.8776992 | -0.174373  | 0.8601073 | 0.8764837 | 2.5632771 | -0.0675    | -0.791208  | -1.190004 | -0.518869 | -0.3812712 | -1.5748725 | -0.102957 | -0.190096  | 0.9995306 | -0.872398  | 3.569469   | -0.27144   | -0.336699  | 0.6445756  | -0.2497245 | -0.296613 | 1.9624471 | 0.8562287  | 1.0793131 |           |           |           |
| HMGCS1   | -0.050705 | 2.045407   | -0.641397 | 1.6408749  | 2.2088333 | 0.3793197 | 0.4811181 | -0.311446  | -0.60671   | -0.794408 | 1.0450751 | -0.612684  | 0.5693941  | -0.489727 | -0.413118  | -0.738184 | 1.5463354  | -0.635843  | -0.773368  | -0.787819  | -0.538307  | -0.805227  | 0.4761005 | -0.763946 | -0.724222  | -0.694564 |           |           |           |
| HEG1     | 0.054402  | 1.3883657  | 0.0584008 | 0.98671961 | 0.6211175 | 0.236269  | 2.973813  | 1.5692947  | -0.470066  | -1.015518 | -0.000484 | -0.444283  | -0.113906  | 0.0662223 | -0.964596  | -0.697169 | 0.1753896  | -0.969733  | -0.776425  | -0.667996  | -0.38027   | -0.6550273 | -0.505115 | -0.340233 | -0.794713  | -0.740262 |           |           |           |
| SCZ7V6   | 0.5114193 | 0.3585447  | 2.853842  | 0.9550327  | -0.133374 | 2.1065024 | 1.1939154 | -0.96055   | -0.550166  | 0.8362721 | -0.079167 | -0.935138  | -0.313844  | -0.131433 | -0.956158  | 0.640789  | 0.6388248  | -1.029208  | -0.882729  | -0.284476  | -0.99695   | -0.552532  | -0.409084 | -0.879393 | -0.652228  | -0.538779 |           |           |           |
| BLG6     | 1.6618083 | 0.9044869  | -0.365465 | 1.3010755  | 1.1683019 | 0.824709  | 1.1363125 | 0.8443697  | -0.85282   | -0.513936 | -0.332788 | -0.404010  | 0.3426502  | 2.7383917 | -0.618426  | -0.556244 | -0.326394  | -0.639499  | -0.579623  | -0.954855  | -0.931312  | -1.071182  | -0.438733 | -0.670926 | -0.600357  | -0.326754 |           |           |           |
| POCD10   | -1.133542 | -0.957569  | -0.990407 | -0.021297  | -0.448238 | -0.37139  | -0.509326 | -0.65805   | -0.865176  | -0.148485 | 0.2394051 | 0.1926945  | -0.533899  | -0.445253 | 3.0462374  | -1.14444  | -0.33632   | 0.8995599  | 2.8214454  | -0.1824721 | 0.4781417  | 0.81599    | -0.255057 | -0.179658 | -0.353043  | -0.279674 |           |           |           |
| LMANL1   | -0.426273 | -1.188211  | -0.515386 | -0.079562  | -0.369465 | 0.4759014 | -1.638861 | -0.177332  | -0.652793  | -0.508556 | -0.074264 | -0.6578395 | -0.961823  | -1.796028 | -0.543254  | -1.040087 | 0.7689939  | 2.4303767  | -0.5039571 | 1.2368297  | 0.1673931  | 1.8833694  | 0.2106693 |           |            |           |           |           |           |
| TRG6     | -0.616856 | -0.289847  | -0.391152 | -0.773816  | -0.006231 | -0.753749 | -0.629579 | -0.75161   | -0.380318  | -0.652441 | -0.415155 | 1.1832865  | -0.520766  | -0.642924 | -0.95628   | -0.045744 | -0.410606  | 0.1893917  | -0.815941  | 0.8447873  | 1.6776581  | 2.5059013  | 0.613344  | 0.3099954 | 1.2873114  | 0.1983804 |           |           |           |
| PCF1     | -0.206024 | 1.5786557  | -0.069029 | 1.7249153  | 2.0648584 | 1.1141945 | 0.956069  | -1.18031   | -0.82161   | -0.3132   | 1.7249153 | -0.787653  | 0.3277562  | -0.555528 | -0.56572   | -2.21847  | 0.6090214  | -0.053493  | -0.269679  | -0.347453  | 0.4959531  | -0.142468  | -0.688207 | 0.3264671 | -1.055485  |           |           |           |           |
| STR6A5   | -0.039509 | -1.193449  | 2.252099  | 1.5046249  | 0.1162636 | 1.3110542 | 0.4108379 | -0.147805  | -0.849322  | -0.29342  | 0.1267864 | -0.565313  | 1.8223341  | 0.0854314 | 0.4589399  | 1.365404  | -0.692271  | -0.540217  | -1.28842   | -0.535059  | 0.345852   | 0.2112751  | -0.548107 | -1.079417 | -0.187156  | -0.134082 |           |           |           |
| SIAM132A | 1.626371  | 0.475786   | 0.8847654 | 0.1970175  | 2.7020891 | 1.5450706 | 1.4681571 | -0.462511  | -0.702624  | -0.681173 | -0.528466 | -0.52379   | 1.4888569  | -0.291538 | -0.256149  | 0.6462108 | -0.781536  | -0.1133447 | -0.761625  | -0.761922  | -0.0320749 | -0.615747  | -0.675086 | -0.219944 | -0.684592  | 1.1939362 |           |           |           |
| KNM1     | -0.43638  | -0.255574  | -0.429357 | -0.159005  | 0.286368  | -0.664133 | -0.274054 | 0.069508   | -0.388989  | 0.1502187 | -0.270751 | -0.174483  | -0.19528   | -0.778842 | -0.30560   | 0.4462108 | -0.781536  | -0.1133447 | -0.761625  | -0.761922  | -0.0320749 | -0.615747  | -0.675086 | -0.219944 | -0.684592  | 1.1939362 |           |           |           |
| MMAP2    | -0.726364 | -0.787255  | -0.146003 | -0.2455    | -0.273136 | -1.00572  | -0.988778 | -0.88786   | -0.388882  | -0.64429  | 0.1174168 | 0.2210076  | -0.337074  | 0.6571763 | -0.465975  | 1.0362656 | -0.561738  | -0.192448  | -0.064697  | 2.7443653  | 1.6642369  | 0.1301684  | 0.0496904 | 0.1472702 | 1.8113109  | 0.3879455 |           |           |           |
| KDX8     | 0.5877734 | -0.730095  | -0.420262 | -0.974165  | -0.814761 | -0.120257 | -0.490748 | 0.4747958  | 0.673974   | -1.183801 | -0.701406 | -0.403099  | -0.357174  | -0.541706 | -1.718121  | -0.954179 | -0.9611    | 1.603207   | -0.20815   | 0.924557   | 1.6760968  | -0.301684  | 1.3636312 | 2.7349399 | 0.5179066  | 0.216247  |           |           |           |
| GALE     | -0.7023   | 0.0912351  | -1.231814 | -0.45501   | 0.060342  | 0.4284907 | -0.379382 | -0.97405   | -0.407331  | -1.0013   | -0.517085 | 0.6549046  | -0.19881   | -0.61139  | 2.04656    | 0.6139868 | 0.917967   | 1.616297   | -0.470887  | 0.7689939  | 2.4303767  | -0.5039571 | 1.2       |           |            |           |           |           |           |



|          |           |           |            |            |           |           |           |           |            |           |            |           |           |           |           |            |            |           |            |            |           |           |           |           |           |           |
|----------|-----------|-----------|------------|------------|-----------|-----------|-----------|-----------|------------|-----------|------------|-----------|-----------|-----------|-----------|------------|------------|-----------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| GC41     | -0.805208 | 0.909501  | 0.320928   | 0.311442   | 0.394976  | -0.222238 | 0.491085  | 0.975992  | 3.616207   | -0.163096 | -0.377523  | -0.163607 | 0.853644  | 0.5830091 | -1.343297 | -0.113103  | 0.094923   | -1.003777 | -1.177373  | 0.225806   | -0.38373  | -0.993628 | -0.126535 | -1.15038  | -0.526766 | -0.006683 |
| SCGA11   | -0.111819 | -0.321304 | -0.898945  | -0.549866  | -0.989555 | -0.86357  | -0.958597 | 1.8573474 | -0.62581   | -0.062859 | -0.35947   | 0.055932  | -0.945641 | -0.559092 | 1.057858  | 0.150286   | -0.787553  | 0.318579  | 0.467005   | 1.636241   | 0.2503157 | 0.5651922 | -0.312598 | 1.1667314 | 1.272354  | -0.006683 |
| EF5A     | -1.411815 | 0.049896  | -1.62715   | -1.228915  | 0.016189  | -0.219397 | -1.09738  | -0.37965  | 0.0782777  | -0.58242  | 0.731429   | 0.885007  | -0.51508  | -1.16084  | -0.135388 | 0.563766   | -0.66479   | 0.075025  | 0.9754328  | -0.075855  | 0.9473328 | -0.97373  | 1.827267  | 1.0004556 | -0.004118 | 1.1752395 |
| BRD3     | 0.0427681 | -1.756511 | -0.440068  | -0.147565  | -0.59396  | -1.36385  | -1.420267 | 2.301898  | -0.683217  | -0.04605  | -1.280088  | 0.30364   | -1.37061  | 0.241735  | 1.302831  | 0.292698   | 0.488941   | 1.133281  | 0.465171   | 0.664167   | 0.6286829 | 1.3553647 | -0.080382 | -0.72645  | 0.7937568 | 0.4687073 |
| RN3      | 0.0145117 | 0.0204582 | 1.2293569  | -0.22882   | 0.994806  | 1.359356  | -0.017142 | 0.3486806 | 0.939368   | 0.8485951 | 0.4865392  | -0.47563  | 0.033266  | -0.060745 | 2.110300  | -0.700738  | 0.7233932  | -0.545643 | -0.561093  | 0.005613   | -1.779947 | -1.557384 | -0.102569 | -0.186742 | -0.39063  |           |
| POD2     | 0.0952463 | 0.1070362 | 0.892109   | 1.584476   | 0.820765  | -0.4442   | -0.43046  | -0.20205  | -0.270549  | -0.25283  | 2.188130   | -1.400706 | 0.453266  | -0.200245 | 1.50646   | 0.1949208  | -1.09092   | -0.443758 | -0.382876  | -0.50106   | -0.338442 | -0.83146  | -0.79427  | 0.811879  | -0.347614 |           |
| RN12     | -0.484439 | -0.083309 | 0.361647   | 0.0307219  | 1.5710733 | 0.6680183 | 1.3657636 | -0.41258  | 1.315564   | -0.277547 | -0.146303  | -0.333338 | 0.367376  | 1.012347  | -1.50564  | 0.1949208  | -1.09092   | -0.443758 | -0.382876  | -0.50106   | -0.338442 | -0.83146  | -0.79427  | 0.811879  | -0.347614 |           |
| MEF12    | 1.9612894 | 0.5300021 | 1.895027   | 0.8902874  | -0.16504  | 0.4160235 | 0.3751548 | -1.873641 | -1.0737368 | -0.18333  | 0.360462   | -0.197891 | -0.797338 | 0.6910883 | 0.3653285 | 0.5824657  | -0.946698  | 0.618207  | -0.942873  | -1.274337  | -0.851042 | -1.384811 | -0.04247  | 0.5717313 | -0.697737 |           |
| NEF1     | 0.1404313 | 0.0965536 | 2.3669235  | -0.083817  | 2.578212  | -0.40465  | 1.404778  | -1.144835 | -0.762832  | 0.6531271 | -0.839396  | -1.197831 | -0.093468 | -0.577705 | 0.393096  | -0.1951668 | -0.469102  | 0.226711  | 0.26163    | 0.6699232  | -1.333552 | -0.296904 | -1.528681 | -1.245718 | 0.1861819 |           |
| FT       | -0.07659  | 0.9745347 | 0.3601083  | 0.5415615  | -0.251322 | 0.93451   | 1.2513379 | 0.5127895 | 2.1790317  | 0.27033   | -0.090519  | -0.652606 | 0.0931698 | -0.469102 | 0.226711  | 0.26163    | 0.6699232  | -1.333552 | -0.296904  | -1.528681  | -1.245718 | 0.1861819 | -0.07659  | 0.9745347 | 0.3601083 |           |
| CCM64    | 0.07659   | 0.9745347 | 0.3601083  | 0.5415615  | -0.251322 | 0.93451   | 1.2513379 | 0.5127895 | 2.1790317  | 0.27033   | -0.090519  | -0.652606 | 0.0931698 | -0.469102 | 0.226711  | 0.26163    | 0.6699232  | -1.333552 | -0.296904  | -1.528681  | -1.245718 | 0.1861819 | -0.07659  | 0.9745347 | 0.3601083 |           |
| FE5      | 1.2501011 | -0.13377  | 0.1914003  | 0.4689797  | 1.384914  | 0.0604262 | 0.4092932 | 3.94363   | -0.654334  | -0.597216 | -0.090519  | -0.652606 | 0.0931698 | -0.469102 | 0.226711  | 0.26163    | 0.6699232  | -1.333552 | -0.296904  | -1.528681  | -1.245718 | 0.1861819 | -0.07659  | 0.9745347 | 0.3601083 |           |
| FLM4     | 0.07659   | 0.9745347 | 0.3601083  | 0.5415615  | -0.251322 | 0.93451   | 1.2513379 | 0.5127895 | 2.1790317  | 0.27033   | -0.090519  | -0.652606 | 0.0931698 | -0.469102 | 0.226711  | 0.26163    | 0.6699232  | -1.333552 | -0.296904  | -1.528681  | -1.245718 | 0.1861819 | -0.07659  | 0.9745347 | 0.3601083 |           |
| FOY4     | 1.2511663 | 1.4129235 | -0.144623  | 0.59589819 | 0.368705  | 0.1938091 | 1.6693293 | -0.529323 | -0.654334  | -0.597216 | -0.090519  | -0.652606 | 0.0931698 | -0.469102 | 0.226711  | 0.26163    | 0.6699232  | -1.333552 | -0.296904  | -1.528681  | -1.245718 | 0.1861819 | -0.07659  | 0.9745347 | 0.3601083 |           |
| SCC6A0   | 0.3074021 | 0.5839143 | -0.082196  | -0.579886  | 0.3258174 | 0.426351  | 1.2806414 | -0.9528   | -0.95928   | -0.58686  | 0.2355946  | -0.438345 | -0.853823 | 0.0897088 | -1.29722  | 0.053997   | -1.12963   | 1.9985823 | -0.81547   | 1.912862   | 0.164157  | -0.937299 | 0.60209   | 0.7340693 | 1.5307007 |           |
| FOD1     | -0.141847 | 0.102382  | 0.01724629 | -0.957419  | -1.050601 | -0.826266 | 0.4683465 | -1.09674  | -0.571262  | -0.727447 | -0.80257   | -0.819355 | -0.494368 | -1.857348 | 1.5963017 | -0.768034  | -0.937513  | -0.580163 | 0.1347368  | -0.01957   | 1.7092607 | 0.1373151 | 0.6914653 | 1.626925  | 1.9812686 |           |
| SRP2     | 0.9312009 | 0.102382  | 0.01724629 | -0.957419  | -1.050601 | -0.826266 | 0.4683465 | -1.09674  | -0.571262  | -0.727447 | -0.80257   | -0.819355 | -0.494368 | -1.857348 | 1.5963017 | -0.768034  | -0.937513  | -0.580163 | 0.1347368  | -0.01957   | 1.7092607 | 0.1373151 | 0.6914653 | 1.626925  | 1.9812686 |           |
| RAGEF5   | 1.6281176 | 1.7611508 | -0.799639  | 1.793476   | 1.1802629 | -0.681597 | -0.631438 | -0.431716 | -0.681438  | -0.34071  | 0.3181223  | -1.039313 | -0.6665   | -0.44371  | 2.6684855 | 0.0502923  | -0.404512  | -0.3233   | -0.603307  | -1.016208  | 0.5913852 | -0.889525 | 0.619499  | 0.081549  | -0.68133  |           |
| CM2      | -0.526055 | -0.255799 | -0.907791  | -0.532335  | -0.591629 | -0.581669 | -1.304827 | -0.593651 | -0.088917  | -0.38774  | -0.28091   | 0.293257  | -0.495924 | 0.1400086 | -1.352466 | 0.8129245  | -0.67247   | -0.414859 | -0.363625  | 0.117503   | 0.688971  | 0.237662  | 2.2164602 | 0.3875952 | 0.4264603 |           |
| KL4      | 0.5267303 | -0.098609 | 2.7424328  | 0.0987101  | -0.43192  | 1.1937918 | 0.9682423 | -0.119272 | 1.400438   | -0.035994 | -0.74851   | 0.8042258 | 1.671619  | -1.176299 | -0.095644 | 0.1728456  | -0.146794  | -0.395418 | -0.7405033 | -0.502532  | -0.847432 | -0.803802 | -0.859598 | -1.528475 | -0.305746 |           |
| NOV      | -0.65667  | 0.30183   | 0.9537171  | 0.3517087  | 2.175487  | -0.314495 | -0.488326 | -0.143459 | -1.112732  | -0.190318 | -0.653954  | -0.515952 | 0.0812238 | 2.657305  | -1.176299 | -0.095644  | 0.1728456  | -0.146794 | -0.395418  | -0.7405033 | -0.502532 | -0.847432 | -0.803802 | -0.859598 | -1.528475 |           |
| IL19A    | 0.3030309 | -0.463159 | 0.1286934  | 0.59589819 | 0.368705  | 0.1938091 | 1.6693293 | -0.529323 | -0.654334  | -0.597216 | -0.090519  | -0.652606 | 0.0931698 | -0.469102 | 0.226711  | 0.26163    | 0.6699232  | -1.333552 | -0.296904  | -1.528681  | -1.245718 | 0.1861819 | -0.07659  | 0.9745347 | 0.3601083 |           |
| FOY4     | 1.2511663 | 1.4129235 | -0.144623  | 0.59589819 | 0.368705  | 0.1938091 | 1.6693293 | -0.529323 | -0.654334  | -0.597216 | -0.090519  | -0.652606 | 0.0931698 | -0.469102 | 0.226711  | 0.26163    | 0.6699232  | -1.333552 | -0.296904  | -1.528681  | -1.245718 | 0.1861819 | -0.07659  | 0.9745347 | 0.3601083 |           |
| SU1      | -0.882369 | -0.665172 | -0.801489  | -0.670293  | 0.227837  | -0.706755 | -0.756199 | -0.98628  | -1.00043   | -0.747399 | -0.5273282 | 0.0141613 | -0.650589 | -0.059494 | 1.0025137 | 0.0735145  | -0.790045  | 1.6956188 | -0.61771   | 2.268167   | 1.279412  | 2.285902  | 0.0598409 | -0.580725 | 0.696356  |           |
| POD23    | 2.1765374 | 0.0480809 | 1.5885402  | 1.0355821  | -0.231911 | 1.7299594 | 1.0195893 | -0.622476 | 0.621674   | 0.5488107 | 0.290056   | -0.389206 | -0.193793 | -0.27129  | -1.872728 | -0.561939  | 0.234951   | -1.427786 | 0.1115529  | 0.7251577  | -1.423776 | -0.702071 | -0.535579 | -0.7242   | -0.941565 |           |
| ADMD10   | 0.070239  | 0.1374101 | 0.0160137  | -0.136541  | -1.828359 | -0.876097 | -0.746058 | 0.3011263 | 0.0851883  | -0.52708  | -1.062364  | -0.667067 | 0.5487782 | 0.1581893 | 0.9891177 | -0.748714  | -0.817023  | -0.286532 | -0.347474  | -0.223337  | -1.396011 | -0.788238 | -1.674896 | -0.28518  | 0.1657659 |           |
| TACC     | 1.4860149 | 0.1304186 | 2.865411   | -0.051717  | 0.4894039 | -0.05411  | 1.8882803 | -0.746058 | 0.3011263  | 0.0851883 | -0.52708   | -1.062364 | -0.667067 | 0.5487782 | 0.1581893 | 0.9891177  | -0.748714  | -0.817023 | -0.286532  | -0.347474  | -0.223337 | -1.396011 | -0.788238 | -1.674896 | -0.28518  |           |
| DUP5     | 0.1543826 | 0.8973417 | -0.33163   | 0.4696271  | 0.8641984 | 0.728302  | 1.3299376 | -0.028104 | -0.523401  | -0.581435 | 0.3394876  | -0.426828 | 2.434423  | -0.087176 | -1.459777 | -1.051057  | 0.1810737  | -0.554428 | -0.286579  | -0.42048   | -0.477766 | -0.376386 | -0.523524 | -0.597634 | 0.8384312 |           |
| ARRGAP24 | 0.4997522 | 1.7166687 | 2.8974534  | -0.45320   | -0.83136  | -0.072596 | 0.4871401 | -1.268004 | -0.944374  | 0.607377  | 0.8234256  | -0.488043 | 0.2927066 | -0.246068 | 1.375747  | -0.348578  | 0.0928999  | 0.0244878 | 0.9025931  | -0.304824  | -0.141732 | -0.97322  | -0.796297 | -1.108584 | -0.884973 |           |
| RAGEF1B  | 0.9557399 | -0.230028 | -1.093616  | 1.7447825  | -0.335688 | -0.330962 | -0.05192  | 2.0538152 | -0.223827  | 0.3085243 | 1.4485488  | -0.324803 | -0.173381 | -0.022107 | 2.449666  | -0.524303  | -0.323382  | -1.737313 | -0.150665  | 0.918136   | -1.004256 | -0.813203 | -0.516347 | -0.95252  | 0.370276  |           |
| EGF      | 1.5938172 | 0.407087  | 0.2075412  | 0.602187   | 0.507802  | 0.984186  | 1.3511422 | 0.7493918 | 0.1459295  | -0.30065  | -0.30065   | -0.30065  | -0.30065  | -0.30065  | -0.30065  | -0.30065   | -0.30065   | -0.30065  | -0.30065   | -0.30065   | -0.30065  | -0.30065  | -0.30065  | -0.30065  | -0.30065  |           |
| RS3      | -1.475659 | -0.15368  | -0.391651  | -0.579898  | -0.262147 | -0.102621 | -0.766202 | 0.029953  | -0.30065   | -0.30065  | -0.30065   | -0.30065  | -0.30065  | -0.30065  | -0.30065  | -0.30065   | -0.30065   | -0.30065  | -0.30065   | -0.30065   | -0.30065  | -0.30065  | -0.30065  | -0.30065  |           |           |
| RBP5     | 1.2672192 | -0.15856  | 1.516519   | 0.8600772  | -0.97964  | 1.543615  | -0.11539  | -0.81851  | -0.273215  | -0.682187 | -0.547293  | 0.7796639 | 1.7716014 | 1.868133  | 0.665366  | -0.61652   | -0.772129  | -1.182763 | 1.502894   | -0.68398   | -1.04198  | -0.238391 | 0.240521  | 0.889304  | -0.703436 |           |
| SCC7A2   | 0.4957438 | 0.164643  | -0.706284  | 0.1746054  | 0.23593   | 1.440284  | -0.108059 | -0.759739 | 0.4277646  | -0.653364 | 1.053934   | -0.458658 | 1.7993362 | -0.611211 | -0.595936 | -0.623085  | 0.39851589 | -0.767302 | -0.185927  | -1.020799  | -0.699168 | -0.922159 | 0.286756  | -0.607739 | -0.580168 |           |
| ADMD17   | 0.5467593 | 0.7925391 | 1.1364767  | 0.66626    | -0.63032  | -0.111632 | -0.181804 | -0.004391 | 0.4277646  | -0.653364 | 1.053934   | -0.458658 | 1.7993362 | -0.611211 | -0.595936 | -0.623085  | 0.39851589 | -0.767302 | -0.185927  | -1.020799  | -0.699168 | -0.922159 | 0.286756  | -0.607739 | -0.580168 |           |
| NTRK3    | 0.962635  | 0.4920322 | -0.585859  | 0.8737026  | 1.4882257 | 1.6562156 | 2.197042  | 0.03638   | -0.201461  | -0.64717  | -0.642164  | -0.088888 | 0.2342038 | 0.524006  | -0.874596 | -0.65567   | -0.715334  | -0.289242 | -0.488001  | -0.414035  | -0.647957 | -0.540967 | -0.683427 | -0.555193 | -0.116158 |           |
| ARRG     | 1.2680936 | -0.90505  | 0.6885321  | 0.797323   | -0.229279 | -0.297878 |           |           |            |           |            |           |           |           |           |            |            |           |            |            |           |           |           |           |           |           |



|         |            |           |           |            |           |           |            |             |            |           |           |            |            |            |           |           |           |           |           |            |            |            |           |            |           |         |
|---------|------------|-----------|-----------|------------|-----------|-----------|------------|-------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|-----------|-----------|-----------|------------|------------|------------|-----------|------------|-----------|---------|
| NRA42   | -0.482032  | -0.114681 | 2.0722394 | 1.2303777  | 0.8198924 | 0.4790194 | 1.8996651  | -0.34175    | -0.476652  | -0.509689 | -0.412396 | -0.47507   | 0.4011628  | 2.9547931  | -0.735392 | -0.634384 | -0.669874 | -0.409294 | -0.494267 | -0.383692  | -0.510427  | -0.403252  | -0.764217 | -0.734923  | -0.699254 | -0.6108 |
| DDH1    | -0.220942  | 1.246757  | 2.3322654 | 0.6012975  | 1.785612  | -0.504495 | 0.1715696  | -1.363179   | -0.370915  | 0.1915258 | 0.5236427 | -0.390209  | -0.7216447 | 1.2573694  | 1.2640116 | -0.169212 | 0.3706694 | -1.150026 | -0.441591 | -0.691265  | -0.6124    | 0.057964   | -1.370724 | 0.725034   | 0.056445  |         |
| PGN5    | 3.555209   | -0.743051 | 1.4877418 | 0.3545904  | -0.437408 | 0.3489873 | 1.1141135  | -0.678752   | -0.1756975 | 0.1915756 | -0.285846 | -0.949994  | 0.0724444  | -0.172315  | 0.1660129 | 0.1158781 | -0.244923 | -0.160016 | -0.719189 | -0.190726  | -0.441959  | -0.50521   | -0.81378  | -0.916368  | -0.56146  |         |
| PDLM3   | -0.39662   | -0.609468 | 0.6433387 | 1.65532823 | 2.498662  | 0.555196  | 2.687863   | -0.76829    | -0.67804   | 0.041004  | -0.52324  | -0.668719  | 0.6514989  | 0.076648   | -0.708378 | 0.1634342 | -1.067272 | -0.526085 | -0.708874 | -0.023905  | -0.434808  | -0.527022  | -0.37981  | -1.033558  | -0.509531 |         |
| SONB32  | 1.0017536  | 0.6312809 | 1.5124862 | 3.0884407  | 0.8211032 | 0.609368  | 0.4421143  | -0.967354   | -0.473637  | -0.714593 | 0.0252    | -1.212187  | 0.740504   | -0.503825  | 1.1932407 | -0.261349 | 0.879636  | -0.759259 | 0.0023154 | -0.534706  | -0.893574  | -0.763288  | -0.983574 | -1.098348  |           |         |
| PANR618 | 0.629611   | 3.127065  | 1.310048  | 0.250664   | 0.1421032 | 0.4074059 | 1.8614035  | -0.195303   | -0.115832  | 0.0052    | -1.212187 | 0.740504   | -0.503825  | 1.1932407  | -0.261349 | 0.879636  | -0.759259 | 0.0023154 | -0.534706 | -0.893574  | -0.763288  | -0.983574  | -1.098348 |            |           |         |
| PPR2018 | -0.405821  | -1.759191 | -0.767214 | -0.840865  | 0.7424837 | -0.227361 | 0.51533408 | 0.4122248   | -1.55246   | 1.5198982 | 2.2782302 | 0.0332291  | 0.1775528  | -0.3647961 | 1.3240962 | -0.267344 | 0.944331  | -0.349584 | -0.759259 | -0.0023154 | -0.534706  | -0.893574  | -1.098348 |            |           |         |
| PCPD8   | 0.291451   | -0.131931 | -0.672141 | -0.948885  | 1.0873186 | -0.974837 | -0.208347  | 0.4191934   | -0.17294   | -0.062459 | -0.79238  | 0.9341416  | 1.3636706  | -0.89706   | -0.921838 | 2.1883983 | 0.251307  | -0.256383 | 0.8283373 | 0.32513    | -0.084151  | -0.250909  | -0.06443  | -0.323399  |           |         |
| MSM41   | -0.651664  | -0.646888 | -0.921838 | -0.921838  | -0.907962 | -0.1926   | 0.296219   | 0.3041416   | 1.3636706  | -0.89706  | -0.921838 | 2.1883983  | 0.251307   | -0.256383  | 0.8283373 | 0.32513   | -0.084151 | -0.250909 | -0.06443  | -0.323399  | -0.06443   | -0.323399  | -0.06443  | -0.323399  |           |         |
| FBMO32  | 1.1478394  | 1.2455526 | 0.4124737 | 2.3490818  | 0.478968  | 1.5247133 | 0.6934166  | -0.857399   | 0.3561807  | -0.90242  | 1.4925565 | -0.105099  | 0.96681816 | -0.58955   | -0.591984 | -0.079488 | -0.858123 | 0.2772288 | 2.3608214 | 0.0899699  | -0.045229  | -1.186889  | 0.168353  | -0.312356  |           |         |
| ERG     | 0.155056   | 0.181319  | 0.6722546 | 1.306669   | 2.8469059 | -0.738192 | -0.42131   | -1.133286   | -0.171809  | 1.1147885 | -0.284307 | -0.079488  | -0.858123  | 0.2772288  | 2.3608214 | 0.0899699 | -0.045229 | -1.186889 | 0.168353  | -0.312356  | -0.154571  | -0.094832  | 0.483187  | -0.87672   | 0.2712494 |         |
| KIT     | -0.030803  | 0.607961  | 1.942100  | 0.3814238  | 1.3033013 | -0.401304 | 0.6691535  | -0.529398   | -1.750875  | -0.10135  | -0.854782 | -0.079488  | -0.858123  | 0.2772288  | 2.3608214 | 0.0899699 | -0.045229 | -1.186889 | 0.168353  | -0.312356  | -0.154571  | -0.094832  | 0.483187  | -0.87672   | 0.2712494 |         |
| NMR2    | 0.29348    | 0.534305  | 0.864837  | 0.8303453  | 1.4205712 | 2.656748  | 0.530118   | 1.146467    | -0.972927  | 0.8490429 | 0.263747  | -0.093541  | 1.5225857  | -0.31565   | -0.518134 | -0.268526 | -0.144401 | -1.249633 | 1.010672  | -0.348856  | -1.1465    | -0.897144  | -0.138128 | -1.086411  | -0.622255 |         |
| TA6U12  | -1.620154  | -1.225384 | 0.368732  | -1.266484  | 0.1552427 | -1.009491 | -0.581368  | 0.3471656   | 0.1948811  | -0.670778 | -1.433344 | 0.0234968  | -0.870546  | 0.0776518  | 0.8682638 | 1.1279408 | -1.23464  | 0.308028  | -0.08473  | -0.645556  | 0.0465342  | -0.54165   | -0.715514 | -0.202146  | -0.620138 |         |
| STC1    | -0.558067  | -0.851931 | -0.451359 | 0.256286   | 0.1281272 | -1.009491 | -0.581368  | 0.3471656   | 0.1948811  | -0.670778 | -1.433344 | 0.0234968  | -0.870546  | 0.0776518  | 0.8682638 | 1.1279408 | -1.23464  | 0.308028  | -0.08473  | -0.645556  | 0.0465342  | -0.54165   | -0.715514 | -0.202146  | -0.620138 |         |
| CI0C    | -0.49692   | -0.662226 | -0.000574 | -0.062925  | -0.236655 | -0.86607  | -0.47257   | 0.1043419   | -0.33607   | -0.196932 | 0.5157766 | -0.395854  | 0.21591421 | -0.803293  | -0.518795 | -2.17199  | 0.678808  | -0.253383 | 0.3234803 | 1.1206734  | 0.0479466  | 0.7153264  | -0.429482 | 0.34505143 |           |         |
| PD04    | 0.1491053  | 2.4324873 | -0.700354 | 0.3327348  | 1.3974383 | 0.7362629 | 1.5944305  | -0.633901   | -0.427678  | -0.711377 | 1.177023  | -0.501463  | 1.9853196  | -0.812084  | -0.914565 | -0.730023 | -0.664238 | -0.16116  | -0.450237 | 0.5807263  | -0.015074  | 1.445164   | -0.256576 | 0.717651   |           |         |
| FDM3    | -0.494725  | -0.539681 | -0.69979  | -0.473706  | -0.435643 | -0.309639 | -0.525105  | 3.8181304   | -0.122219  | -0.310747 | 0.701794  | 0.5644802  | 2.2551075  | -0.19791   | -1.728108 | -0.793905 | 0.3559042 | -0.557984 | 0.5597913 | -0.681289  | -0.447117  | -1.097764  | 0.1475974 | -0.81464   |           |         |
| SI00A9  | -0.872479  | -0.687187 | -0.924317 | -0.824514  | -0.861613 | -0.795136 | -1.184639  | 2.206316    | -0.520329  | -0.319215 | -0.303214 | 1.0651007  | -0.449962  | -0.924298  | 0.0521519 | -0.191649 | -0.020199 | -0.554422 | -0.87097  | 0.8908468  | 2.2063164  | 1.7629233  | 0.8706773 | 0.4560143  |           |         |
| LM001   | -0.9565157 | -0.213268 | 0.4065563 | 3.8188707  | 0.4563931 | 0.4320834 | 1.1189721  | -0.726909   | -0.5195529 | -0.475234 | -0.486315 | -0.625212  | -0.213531  | 0.577814   | 0.8680699 | -0.65272  | -0.951972 | -0.590413 | -0.407426 | -0.202041  | -0.553132  | -1.942228  | 0.4853194 | -0.305742  |           |         |
| CRD1    | 0.6753546  | 1.877308  | 1.3172788 | -0.362313  | 0.927073  | 0.532386  | 1.818215   | -0.427986   | -0.659004  | -0.05691  | -0.703436 | -0.181079  | 0.6184308  | -0.545414  | -1.264794 | 0.1032672 | 1.2551337 | -0.26285  | -0.201948 | -0.65918   | -0.259277  | 0.0582199  | 1.015067  | -1.572221  |           |         |
| PCD1A   | -0.3382    | -0.86669  | -0.120707 | -0.632862  | -0.915131 | 0.552386  | -1.028355  | 0.4879825   | -0.659004  | -0.05691  | -0.703436 | -0.181079  | 0.6184308  | -0.545414  | -1.264794 | 0.1032672 | 1.2551337 | -0.26285  | -0.201948 | -0.65918   | -0.259277  | 0.0582199  | 1.015067  | -1.572221  |           |         |
| CITD2   | 0.1119603  | 0.3446394 | 0.6003427 | 1.9735755  | 0.3239906 | 1.7213617 | 1.51871    | -0.20357    | -1.11393   | 0.992004  | 0.8417016 | -0.106652  | 2.1818264  | -0.349377  | 0.822143  | -0.818125 | -0.333637 | -1.460085 | -0.30073  | -0.606238  | -0.5736    | -0.7936523 | 0.212775  | -1.451684  |           |         |
| REL12   | 0.0387666  | -1.054331 | -0.89108  | -0.831809  | -0.818235 | -1.556749 | -0.667445  | -0.52528    | -0.585306  | 0.2305015 | 0.035653  | 0.21218328 | 0.3281993  | -1.167451  | -1.127232 | -1.105152 | -0.659301 | 2.0268191 | 0.3119142 | 0.873991   | 0.0067498  | 0.7153264  | -0.429482 | 0.34505143 |           |         |
| VMA12   | -1.27762   | -0.748356 | -0.357891 | -0.464584  | -1.181487 | -1.526048 | -0.754654  | -0.545483   | -0.754654  | -0.545483 | -0.754654 | -0.545483  | -0.754654  | -0.545483  | -0.754654 | -0.545483 | -0.754654 | -0.545483 | -0.754654 | -0.545483  | -0.754654  | -0.545483  | -0.754654 | -0.545483  |           |         |
| TM165   | -2.079323  | -1.684315 | -0.76122  | 0.4157178  | 1.630736  | -0.768893 | -1.550533  | -0.193956   | -0.547834  | 0.6757161 | 0.3825085 | 1.424065   | -0.190904  | 0.0353702  | 2.067499  | 0.838763  | -0.2323   | 1.444609  | -0.325392 | 0.6049502  | 0.0245069  | 1.1375059  | -0.386659 | -0.20499   |           |         |
| FB1     | 0.3733233  | 0.1702236 | 0.1203949 | -0.073328  | 1.9576826 | 2.5159731 | 0.9344404  | -0.149193   | -0.422946  | 0.2103097 | -0.38958  | 2.5847561  | -0.995292  | -1.202348  | -1.470947 | 0.5839239 | -0.244482 | -0.665122 | -0.162575 | -0.477484  | -0.449619  | 0.964055   | -1.068633 | -0.04692   |           |         |
| WNR2    | 2.5850038  | 0.7417834 | -0.181122 | 0.8340406  | 0.292747  | 1.7234518 | 1.012268   | -0.849201   | -0.405851  | -0.921975 | -0.303214 | 1.0651007  | -0.449962  | -0.924298  | 0.0521519 | -0.191649 | -0.020199 | -0.554422 | -0.87097  | 0.8908468  | 2.2063164  | 1.7629233  | 0.8706773 | 0.4560143  |           |         |
| GMR2    | -0.806219  | -0.38065  | -0.6865   | -0.644092  | -0.274581 | -1.002159 | -0.941118  | 0.046001    | -0.678464  | -0.666236 | -0.007167 | 1.1141649  | -0.660367  | -0.333252  | -0.582387 | 0.343325  | -0.704731 | 0.242659  | -0.579627 | 0.6546873  | 2.8377057  | 0.614315   | 0.646402  | -0.56678   |           |         |
| STK32C  | -0.96674   | -0.949409 | 0.7750687 | -0.393495  | -0.870054 | -0.074668 | -0.433307  | -0.35353    | 0.2534959  | 0.0126378 | -0.050506 | -0.155549  | 0.186605   | -0.113091  | -2.064136 | 0.2844664 | -0.922165 | 0.1995121 | 0.0546892 | 0.607786   | 0.917888   | 0.1239897  | 3.6657167 | -0.11165   |           |         |
| ATB32   | -0.26874   | 1.316209  | 1.245066  | -0.30375   | 1.039705  | 1.4245018 | 2.021416   | -0.76135    | -0.4727107 | 0.5107978 | 0.1261529 | -0.39361   | 1.6492518  | -0.33401   | -1.52535  | -0.98709  | 0.821165  | -0.641389 | -0.38007  | -0.588894  | -0.971065  | -1.132153  | -0.924452 | -0.908827  |           |         |
| TP1112  | -0.14804   | 2.047476  | 0.316682  | 0.0748714  | -0.054721 | 0.7918184 | 1.0194129  | 0.556031    | 0.388167   | 0.0268984 | 0.0353585 | -0.056494  | -0.61601   | 2.2794269  | 0.080288  | -0.848117 | 0.2237819 | -1.3386   | 1.7933994 | -0.08861   | -1.580037  | -0.588894  | -0.971065 | -1.132153  |           |         |
| CR8     | 0.0152009  | 0.355561  | 1.0862106 | -0.202553  | 0.9079476 | 0.674065  | 2.209462   | -0.539689   | -0.345928  | -0.027579 | 0.1818564 | -0.795982  | -0.299918  | 1.5453152  | -2.55376  | -1.765254 | 0.0598595 | -0.2705   | -0.409312 | -0.207751  | -0.178784  | -0.217372  | -0.741391 | -2.19516   |           |         |
| TRM144  | -0.1786343 | -0.355661 | -0.096146 | 0.5070553  | -0.461295 | -1.88128  | -1.339848  | 1.126467    | 0.2399559  | -0.579703 | 0.2399559 | -1.282873  | -1.399122  | 0.8173152  | 0.5664092 | 2.440704  | 0.910464  | -1.004995 | 0.049454  | -0.158874  | -0.460739  | 0.465451   | 0.2311876 | 0.5171917  |           |         |
| USP4    | 3.0747466  | -0.933386 | 2.3609258 | 0.702555   | 0.832390  | -0.561939 | 0.0802494  | 0.017021    | -0.90301   | -0.107644 | -0.375504 | -0.422823  | -0.175927  | -0.596814  | 1.3115550 | -0.524641 | -0.195528 | -0.11375  | -0.667337 | -0.752359  | -1.17384   | -0.853864  | -0.513771 | -0.429305  |           |         |
| LMU1    | 1.132592   | 0.251419  | -0.35165  | -0.459179  | -0.510127 | 1.4803154 | 0.8485441  | -0.400194   | -0.7123868 | 0.8988356 | -0.477564 | -0.519985  | 0.3957714  | 2.195764   | -2.091394 | 0.9951639 | -0.554007 | -0.477117 | -0.226781 | -0.414907  | -0.5724018 | -0.383716  | -0.082018 |            |           |         |
| GPT     | -1.461654  | 0.5369204 | -0.52384  | 0.4729283  | 1.1746953 | 1.9000247 | 2.9063123  | 0.0602402   | -0.797362  | -0.261628 | -0.796668 | 0.1207943  | 0.8004134  | -0.363534  | -1.069775 | -1.112817 | -0.924655 | 0.3454316 | -0.445329 | -0.298531  | -0.383716  | -0.082018  | 0.0251929 | -1.089163  |           |         |
| WD081   | -0.108415  | -0.580872 | -1.373412 | -0.754514  | 0.0631503 | -0.946427 | -1.447419  | -0.595406</ |            |           |           |            |            |            |           |           |           |           |           |            |            |            |           |            |           |         |



|         |             |           |           |           |           |            |            |           |            |           |            |            |            |            |           |           |           |           |            |             |            |            |            |           |           |           |
|---------|-------------|-----------|-----------|-----------|-----------|------------|------------|-----------|------------|-----------|------------|------------|------------|------------|-----------|-----------|-----------|-----------|------------|-------------|------------|------------|------------|-----------|-----------|-----------|
| GATM    | 2.5013932   | 0.3239977 | 0.3174561 | 0.8879214 | 3.30E-05  | 1.1049556  | 0.8031157  | -0.93241  | 0.6496967  | 1.4522051 | 0.2675438  | -0.77753   | -0.20508   | 0.9812507  | -1.343551 | 0.3021387 | 0.6517776 | -1.378211 | -0.054555  | 0.077671    | -1.439326  | -0.874817  | -0.500206  | -1.624237 | -0.840090 | -0.322879 |
| IMDPTC  | -0.283897   | 0.178123  | 1.2015942 | 1.3318289 | -0.430566 | 2.8129526  | 1.6931537  | -0.58521  | -0.426259  | -0.298325 | -0.32686   | -0.305066  | -0.109406  | -0.323462  | -0.597045 | -0.130681 | -0.147072 | -0.565534 | -1.325297  | -0.61407    | 0.0274417  | -0.340205  | -1.108759  | -0.667310 | -0.424024 |           |
| AMNOC1  | 0.0550051   | 0.2912673 | 1.2414383 | 0.7823188 | 2.476246  | -0.712466  | 0.7676146  | -0.20541  | -0.729998  | -0.794105 | 1.1366627  | -0.672194  | -0.627942  | 0.4274653  | 2.2661493 | -0.555354 | -1.825192 | -0.824707 | -0.565354  | -1.825192   | -0.824707  | -0.565354  | -1.825192  | -0.824707 | -0.565354 |           |
| ONC1    | -0.557409   | -0.223291 | 1.4060909 | 0.830668  | -0.211088 | 1.7867392  | 1.6521871  | 1.491535  | -0.45864   | -0.427995 | 0.6672483  | -0.095186  | 0.7518209  | 0.553818   | -1.527035 | -1.326807 | 0.460931  | -1.419306 | 0.105040   | -0.397592   | -0.540689  | -0.093902  | 0.9595026  | -1.765897 | -0.753849 |           |
| LCAT1   | -1.952743   | -0.014414 | -1.36692  | -0.049238 | -0.217781 | -0.235488  | -1.282185  | -0.102715 | -0.154151  | -0.222097 | 0.0967808  | -0.522263  | 0.9859046  | -0.522263  | 0.9859046 | -0.522263 | 0.9859046 | -0.522263 | 0.9859046  | -0.522263   | 0.9859046  | -0.522263  | 0.9859046  | -0.522263 | 0.9859046 |           |
| BNCC    | 0.707491    | 2.6811731 | 1.9721059 | 1.0787281 | -0.026456 | -0.217761  | -0.235488  | -1.282185 | -0.102715  | -0.154151 | -0.222097  | 0.0967808  | -0.522263  | 0.9859046  | -0.522263 | 0.9859046 | -0.522263 | 0.9859046 | -0.522263  | 0.9859046   | -0.522263  | 0.9859046  | -0.522263  | 0.9859046 |           |           |
| BNZC    | -0.259088   | 0.2800008 | 1.3982243 | 0.8874442 | 2.6011718 | -0.659072  | 0.077742   | -0.3315   | -0.342133  | 0.8613007 | -0.13017   | -1.031454  | -0.714201  | 2.381871   | -0.092166 | 0.009657  | -0.269594 | -1.35933  | -0.149195  | -0.491236   | -0.889931  | -0.812497  | -0.241335  | 0.1579312 | -0.70604  |           |
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| TRN1    | -0.215972   | 2.511359  | 0.278977  | 0.313222  | 0.1559668 | 1.2970761  | 1.172625   | -0.55445  | 0.3567566  | -0.030365 | 0.6686814  | -0.786519  | 2.3441903  | 1.2945634  | -1.531404 | -0.982435 | 0.5070519 | 0.0612825 | -0.67088   | -0.175881   | 0.5187733  | -0.35635   | -0.3542078 | -0.669397 | -0.01371  |           |
| POC     | 1.4528523   | -0.454712 | 0.7454608 | 0.3737513 | 0.0200561 | 0.661945   | 2.0771698  | -0.202328 | 0.134498   | -0.090363 | 0.6686814  | -0.786519  | 2.3441903  | 1.2945634  | -1.531404 | -0.982435 | 0.5070519 | 0.0612825 | -0.67088   | -0.175881   | 0.5187733  | -0.35635   | -0.3542078 | -0.669397 | -0.01371  |           |
| SC669   | 0.4152061   | 1.5604318 | -0.636183 | 0.3295244 | -0.374271 | 1.11464752 | 1.0069947  | 0.7191091 | -0.07225   | 0.0673088 | 2.9562798  | -0.635889  | 0.1292022  | -0.830917  | -0.529385 | -0.927383 | 2.1170041 | -0.873072 | -0.946083  | 1.1463086   | -0.677931  | -0.831041  | -0.36609   | -0.993751 | -0.687635 |           |
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| RN1     | 0.0377464   | 0.1800239 | 0.4011978 | -0.248963 | -0.352723 | -0.03015   | -0.90117   | 0.06441   | -0.253558  | -0.348784 | -0.295793  | 0.4358414  | -0.898915  | -0.414353  | -2.229302 | 0.4498457 | -0.641206 | -0.645214 | -0.56403   | -0.180938   | 0.472516   | 0.1312421  | 0.3862636  | 3.3023804 | 1.025347  |           |
| LEP     | -0.953184   | 0.0057358 | -0.92056  | -0.356961 | -0.51507  | -0.546408  | -0.20784   | 3.1346358 | -0.621632  | -0.707473 | -0.470236  | 0.0163074  | -0.642292  | 0.0741969  | -1.33175  | -1.443445 | 0.6534484 | 0.2535464 | -0.174304  | 0.0661285   | -0.350132  | -0.424052  | -0.458307  | 0.23151   | 2.5497169 |           |
| SN      | -0.702933   | -0.155984 | -0.62335  | -1.146674 | -1.20114  | -0.387184  | 0.9099791  | -1.383533 | -0.356414  | -0.868692 | 0.1376207  | -1.147283  | 0.1064366  | -1.237978  | 2.105052  | -0.581829 | 0.8825294 | -0.346253 | 0.3228857  | -0.24363063 | -0.008165  | -0.041205  | -0.2658    | 1.2416217 | 2.105052  |           |
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| HS01182 | -0.727254   | 0.6127303 | -0.176201 | -0.131191 | 0.2745456 | 2.3835239  | 1.0432656  | 2.154741  | 0.4788101  | -0.549301 | -0.46902   | -0.9589534 | 0.9222001  | 0.3508235  | -2.353516 | 0.8962018 | -1.04393  | 0.1483085 | 0.2146628  | -0.808153   | -0.654431  | -0.152079  | -0.721185  | -0.944111 | -0.135894 |           |
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| PNN142  | -0.00145    | -0.109036 | 0.038528  | 0.0572192 | 0.2026217 | 1.9465967  | 2.9086007  | -0.320187 | -0.129449  | -0.085506 | 0.1863366  | -0.319194  | 1.532109   | -0.208892  | -2.729484 | -0.956878 | 0.327888  | -0.381001 | -0.379608  | -0.429464   | -0.658314  | -0.331434  | -0.884349  | -1.064711 | -0.97301  |           |
| EC6MA   | 0.2605344   | 0.3174431 | 0.0719846 | 0.4464314 | 0.6270743 | 2.5635363  | 0.798485   | -0.400248 | -0.146442  | -0.147008 | -0.470236  | 0.0163074  | -0.642292  | 0.0741969  | -1.33175  | -1.443445 | 0.6534484 | 0.2535464 | -0.174304  | 0.0661285   | -0.350132  | -0.424052  | -0.458307  | 0.23151   | 2.5497169 |           |
| PER1    | -0.187983   | -0.35778  | 0.8300957 | 0.4545261 | -0.227565 | 1.6539063  | 1.2735084  | 0.0772099 | 0.431738   | 0.008549  | 0.182134   | -0.280546  | 1.5457267  | 3.0397021  | -1.482059 | 0.2537755 | -1.151068 | -0.491036 | -0.315099  | -0.052829   | -0.090901  | -0.506862  | -1.055511  | -0.624952 | -1.066532 |           |
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| CNO142  | 1.4324322   | -0.575165 | -1.226209 | 2.3617077 | 0.091742  | 0.9610397  | 1.3464101  | -0.99849  | -1.2097    | -0.423283 | 0.599776   | 0.1380636  | 0.2143682  | -0.076391  | -0.798325 | -0.707944 | -0.804675 | 0.6199653 | -1.199439  | -0.069441   | 1.392079   | 0.00700823 | 0.968751   | 0.379151  | 1.0897379 |           |
| ZN7F46  | -0.732555   | 1.2671677 | -0.987868 | -0.127453 | -0.107573 | -0.310829  | 0.9180729  | -0.31593  | -0.736691  | -0.886329 | 0.8336467  | -0.363688  | -0.527346  | 1.2068542  | -0.164467 | -0.700885 | -1.303159 | -1.545909 | 0.5311654  | 1.6324434   | 1.1876461  | 0.0623727  | 0.1204126  | 0.2298845 | 1.6166873 |           |
| RNMA    | 0.7326587   | 0.5123152 | 1.8717505 | -0.182623 | 1.2539472 | 2.1467382  | 2.1212167  | -1.254942 | -0.501386  | -0.577869 | -0.304933  | -0.616501  | 0.5064058  | 0.610168   | -0.918447 | -0.669338 | -0.422236 | -0.2115   | -0.88525   | 0.239335    | -0.684529  | -0.444414  | 0.7545174  | -1.465362 | -0.398662 |           |
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| CDM1    | -0.68877    | -1.670955 | 0.0524425 | 0.5877093 | 0.8161236 | 2.3275263  | 0.07999317 | 0.776158  | -0.310921  | 2.0487428 | 1.201588   | 0.445627   | -0.208148  | -0.172637  | 1.1560363 | 0.5806742 | 0.7110283 | 1.2867025 | 0.247898   | -1.53171    | -1.891427  | 0.0277001  | -0.657321  | -1.525062 | -0.580754 |           |
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| CNTM4   | 0.1388892   | 1.986658  | 0.7480001 | 0.8017999 | 0.731687  | -0.384505  | -0.944993  | -1.421408 | -0.641751  | -0.63042  | 1.8732397  | -0.332544  | -0.702662  | -0.150158  | 1.9582188 | -0.452469 | 1.8121866 | -0.35487  | -0.888317  | -0.580922   | 0.0950638  | -1.1798    | -0.348171  | -0.152634 | 0.0288751 |           |
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| ULB2    | -0.239037   | -0.316194 | -0.729852 | -0.441237 | -0.502145 | -0.608874  | -1.205938  | -0.98035  | -0.500657  | -0.201535 | 0.4891633  | 1.3313809  | -0.005767  | -0.716488  | -1.678233 | -0.059402 | 0.8687248 | -0.981433 | -0.93987   | 0.5130614   | 2.805814   | 0.3986311  | 1.3979532  | 1.1404181 | 0.3393315 |           |
| PLZG6   | 0.5762044   | 1.2046259 | 1.2311509 | 0.087448  | 0.004575  | 1.1369958  | 1.543362   | -0.9243   | -0.331388  | -0.469195 | 1.2481923  | 0.8771287  | 0.8673571  | -1.155238  | -0.136059 | -0.868696 | 1.4361748 | -0.149054 | -0.584256  | -0.396316   | 1.6190361  | -0.271764  | -1.58734   | -0.58744  | -1.58734  |           |
| SOC3    | -0.88767    | 0.658977  | 1.832541  | 0.742313  | 1.742925  | 0.0380761  | 1.7855412  | -0.422031 | -0.781593  | -0.845319 | -0.55586   | -0.985349  | -1.3579495 | -0.5451319 | -0.951862 | -0.659592 | -0.759496 | -0.660674 | -0.679326  | -0.882217   | -0.560162  | -0.455737  | -0.426669  | -0.405399 | -0.205746 |           |
| PE4H    | -0.136469   | 1.0423027 | -0.362809 | 1.804701  | 0.0607807 | 0.868422   | 0.155009   | -0.71448  | -0.597133  | -1.06373  | 3.7160326  | -0.969391  | 1.2521892  | 0.307358   | 0.033369  | -0.660674 | -0.679326 | -0.882217 | -0.560162  | -0.455737   | -0.426669  | -0.405399  | -0.205746  | -0.405399 | -0.205746 |           |
| FM1748  | -0.326927</ |           |           |           |           |            |            |           |            |           |            |            |            |            |           |           |           |           |            |             |            |            |            |           |           |           |







ITGA1 -0.622411 -0.873889 -0.657454 -0.15268 0.6553509 -0.873418 -0.838498 -0.849543 -1.262263 -0.179654 -0.249516 0.8060084 -0.883251 0.1083494 1.4766204 -0.423834 -0.860287 -0.217823 -0.521815 1.9365498 1.9448685 1.5840277 -0.486381 -0.222487 1.9532168 -0.28979  
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|          |           |            |            |           |            |           |           |           |           |            |            |            |            |            |            |            |           |           |            |            |            |           |           |           |           |           |
|----------|-----------|------------|------------|-----------|------------|-----------|-----------|-----------|-----------|------------|------------|------------|------------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|-----------|-----------|-----------|
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| UCHC3    | -1.389187 | -0.776603  | -1.419653  | -0.318148 | -0.25676   | -0.558561 | -0.982708 | -1.225801 | -0.886665 | 0.7452434  | 1.6490937  | 1.3505349  | 1.4874081  | 0.0119702  | -0.1055534 | 0.8005697  | -0.122256 | 0.9833229 | 1.0871111  | 0.9029527  | 1.6549143  | -0.48516  | -0.217869 | -0.97464  | -0.127969 |           |
| CCRC92   | -0.867231 | -1.272623  | -0.156224  | -0.55668  | 0.171392   | -0.157652 | -0.376526 | -0.190552 | -1.301009 | -0.886665  | 0.7452434  | 1.6490937  | 1.3505349  | 0.056692   | -0.6673126 | 0.5950353  | -1.386767 | -0.728279 | -0.810545  | 1.527646   | -0.465555  | 0.805214  | 1.9406558 | -0.429577 | -0.163466 | 0.978656  |
| NRMA3    | -0.520357 | 0.3416294  | 3.6827725  | 0.487888  | 0.5845315  | -0.071564 | 0.8906208 | 0.2485489 | -0.543133 | -0.662768  | -0.636309  | -0.565341  | 0.121359   | 2.193193   | -0.42235   | -0.327353  | -0.375058 | -0.567386 | -0.566447  | -0.551444  | -0.623888  | -0.59217  | -0.48516  | -0.422718 | -0.280344 |           |
| PG       | -0.810934 | -0.0461802 | -0.1504971 | -0.106355 | -0.009471  | -0.106355 | -0.368597 | 0.1934585 | -0.427251 | -0.780861  | -0.165802  | -0.317174  | -0.435465  | -0.464262  | -2.392121  | 0.605097   | -0.926712 | 1.581035  | -0.22134   | 0.0555954  | 0.1795882  | 0.993136  | 0.1651626 | 2.865036  | 1.4772261 | 0.689445  |
| DUSP1    | -0.279022 | -0.261187  | 0.232324   | 0.3680993 | 0.1648961  | 0.6395289 | 1.877010  | 0.2880933 | -0.438475 | -0.362739  | -0.26052   | -0.3527998 | 0.8844066  | 3.765466   | 0.937916   | -0.659607  | -0.604870 | -0.504281 | -0.802116  | -0.198219  | -0.259771  | -0.738012 | -0.847831 | -0.817653 | -0.698494 |           |
| HPH1     | -0.592005 | 1.421178   | -0.349377  | -0.79207  | -0.535515  | -0.765338 | 1.4868662 | -0.182219 | 0.1220314 | -1.18555   | -0.991398  | -0.738681  | -0.57092   | -0.81522   | -0.934387  | -0.718554  | 0.5587031 | 2.0215019 | -0.038213  | -0.765854  | 2.8358883  | -0.424017 | 0.4243671 | 1.0762532 | -0.38116  | -0.694723 |
| DUSP4    | -0.619407 | 0.6797999  | 0.6522529  | 0.7115791 | 1.78153    | 0.6579231 | 1.2684368 | 0.3383957 | -0.925309 | -0.912355  | -0.241573  | -0.607651  | 2.436077   | 0.516014   | -0.938472  | -0.718554  | 0.5587031 | 2.0215019 | -0.038213  | -0.765854  | 2.8358883  | -0.424017 | 0.4243671 | 1.0762532 | -0.38116  | -0.694723 |
| G186     | -0.992939 | -0.781664  | -0.670018  | -0.713446 | -0.921446  | -0.673172 | -0.722425 | 0.0555114 | -0.867396 | -0.592923  | -0.507923  | -0.287822  | 0.8636995  | -0.658242  | -0.839788  | 1.2281584  | 0.2179933 | 0.2179933 | -0.346129  | 1.5377052  | 3.298891   | 1.0528291 | 0.6395921 | -0.663002 | 0.8195244 | 0.0241785 |
| TNFRSF10 | -0.138281 | -0.137688  | -0.694565  | -1.153162 | -0.80877   | -1.447131 | 1.1580301 | -0.973004 | -0.967304 | -0.7450187 | -0.2450187 | -0.287905  | 0.8066059  | -0.1329856 | 0.1198373  | -0.283468  | 0.4984593 | -0.563085 | -0.974397  | -0.330761  | -0.7162779 | -0.521034 | -0.602621 | -0.606021 | -0.574995 | 0.0453008 |
| CNFR     | 1.5104112 | 0.1319793  | -0.505634  | -0.586044 | -0.356904  | -0.186482 | 0.0994642 | -0.063847 | -0.725264 | -0.44846   | -0.290292  | -0.056694  | 0.345523   | -0.6614272 | -0.627209  | 0.4514927  | -2.478794 | 0.8344281 | -1.361261  | -0.390408  | -0.462128  | 0.1971471 | 2.9189841 | 0.5971311 | 1.0072784 | 1.2751646 |
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| RAE22A   | -1.156452 | -0.531326  | -0.951683  | -1.17283  | -0.961962  | -1.540775 | 0.2479323 | -0.16980  | 0.4121116 | 0.6468914  | 0.0203487  | 1.103727   | -1.136609  | -0.687538  | 0.615646   | 0.8741995  | -0.12088  | 2.4232545 | -1.121582  | -0.350559  | 2.1897792  | 0.3564863 | 0.5533408 | -0.178401 | 0.109305  | 0.3416438 |
| RIN2     | -0.286729 | 0.6779267  | -0.107399  | -0.508328 | 0.786746   | 0.672868  | -0.131913 | -1.226851 | -0.909592 | 0.7264903  | -0.7913    | -0.5139628 | -0.459602  | -1.448890  | -0.2065319 | -1.1959922 | 2.7001531 | 2.818415  | -0.0204895 | 0.5391344  | -0.856219  | 0.5068365 | 0.9528646 | 0.7399737 | -0.503082 |           |
| PANX2    | -1.137359 | -0.877461  | -0.69537   | -0.640245 | -0.830236  | -0.587067 | -0.338002 | 1.1943134 | -0.385254 | -1.01749   | -0.019128  | -0.812008  | -0.399686  | -0.182151  | 0.2982887  | 1.0747324  | -0.38492  | -0.772627 | -0.343136  | -0.151952  | -0.351286  | -0.276466 | -1.222818 | -0.342558 | -0.169536 | -0.196433 |
| MC2L1    | 0.5360015 | 2.4231703  | 0.593515   | 0.5454814 | 1.0559447  | 0.0393161 | 2.5955957 | -0.87856  | 0.1983134 | -0.105346  | 0.1878109  | -0.708935  | -0.420423  | 0.5054637  | -0.717394  | -0.599607  | 0.532796  | -0.853978 | -0.524254  | -1.276999  | -0.524254  | -1.276999 | -0.524254 | -1.276999 | -0.524254 | -1.276999 |
| MLL1B1   | -0.684204 | -0.35006   | -0.123007  | -0.747663 | -0.1899482 | -0.473833 | -0.644104 | -0.46145  | 0.691523  | -0.373252  | -0.037422  | -0.157154  | -0.027306  | 0.7338674  | -0.105923  | 2.3638245  | -0.19558  | -0.400211 | -0.573941  | -0.135499  | -0.1748074 | 3.2706674 | 0.5994784 | 0.0256581 | -0.319687 | 0.4442425 |
| RAB1B    | 0.2745607 | -0.636888  | 1.420903   | -0.588769 | -0.221675  | -0.386317 | 0.6031492 | -0.895963 | 0.1035204 | -1.805912  | -0.413254  | 0.4686343  | -1.068883  | 0.2415096  | 1.1589348  | -0.85453   | -1.174607 | 0.3282938 | -0.559816  | 0.2017402  | 1.764677   | 1.6099496 | -1.40867  | 0.0284622 | 1.2478253 | 0.6677125 |
| RAC2     | -0.354959 | -0.28242   | -0.749927  | -0.8023   | -0.710333  | -0.070292 | 0.6093132 | 0.5376146 | -0.389024 | -0.26064   | -0.443509  | 0.970518   | -0.586693  | -0.717372  | 2.1868758  | -1.28596   | -0.10073  | -0.309696 | -0.777033  | 0.0586     | 1.632917   | 0.3338872 | 6.07904   | 1.8297406 | 0.2189317 | 1.2525767 |
| CN1A     | 3.0296295 | 0.2051333  | 2.5738102  | 0.6396078 | 0.3394585  | 0.2943442 | 0.0444811 | -0.796083 | -0.807825 | -0.045919  | -0.125481  | -1.026563  | -0.33137   | 0.020525   | 1.113115   | -0.133584  | -0.147714 | -0.996607 | 0.4401943  | -0.765804  | -1.017076  | -1.124714 | -0.229964 | -0.452538 | -0.240247 | -0.4114   |
| CD101    | -0.624052 | -0.309409  | -0.023555  | 1.7525479 | 2.9182707  | 1.2761594 | 1.2761594 | -0.621607 | -0.637408 | -0.20364   | -0.1211715 | -0.446893  | 1.029285   | -0.282677  | 0.0816107  | -1.184125  | -0.33584  | -0.147714 | -0.996607  | 0.4401943  | -0.765804  | -1.017076 | -1.124714 | -0.229964 | -0.452538 | -0.240247 |
| MILTA    | 1.0539839 | 2.1233037  | 1.9888254  | 0.4297871 | -0.593725  | -0.400353 | -0.347523 | 0.8803915 | -0.242673 | -0.928354  | 0.5561191  | 1.097964   | -0.852774  | -0.346411  | 2.0071751  | -0.377619  | 0.343556  | 0.3010841 | -0.022266  | -1.324596  | -1.129892  | -1.337744 | -0.283066 | -0.701888 | -0.045306 | -0.267423 |
| AIIND    | -0.280251 | -0.017036  | 0.1440064  | 0.8177859 | 0.5322016  | 1.6492399 | 1.6875196 | -0.385229 | -0.346787 | -0.438391  | -0.234615  | -0.346405  | 2.5317537  | 1.618186   | -1.9222081 | -0.108154  | -0.772627 | -0.343136 | -0.151952  | -0.351286  | -0.276466  | -1.222818 | -0.342558 | -0.169536 | -0.196433 |           |
| AAAP12   | 3.2740771 | -0.279944  | 1.2579578  | 0.8363747 | 1.241622   | -0.206043 | 0.2311447 | -0.585254 | -1.01749  | -0.019128  | -0.812008  | -0.399686  | -0.182151  | 0.2982887  | 1.0747324  | -0.38492   | -0.772627 | -0.343136 | -0.151952  | -0.351286  | -0.276466  | -1.222818 | -0.342558 | -0.169536 | -0.196433 |           |
| CAP1     | -0.855905 | -0.845072  | -0.604246  | -0.500402 | -0.670711  | -0.998596 | -0.668247 | 0.0503272 | -0.50759  | -0.467083  | 0.027306   | 0.7338674  | -0.105923  | 2.3638245  | -0.19558   | -0.400211  | -0.573941 | -0.135499 | -0.1748074 | 3.2706674  | 0.5994784  | 0.0256581 | -0.319687 | 0.4442425 | -0.389254 |           |
| SAP185   | -0.092976 | 0.4070563  | 1.6911513  | 0.8895469 | 2.5862729  | 0.661625  | 2.3983461 | -0.284318 | -0.907382 | -0.61638   | -0.157154  | -0.027306  | 0.7338674  | -0.105923  | 2.3638245  | -0.19558   | -0.400211 | -0.573941 | -0.135499  | -0.1748074 | 3.2706674  | 0.5994784 | 0.0256581 | -0.319687 | 0.4442425 |           |
| GPPT2    | -0.459944 | 10.749093  | 0.3988972  | -0.430409 | 0.337241   | -0.774361 | 2.2159392 | 0.208943  | -0.973832 | -0.226857  | -0.19498   | -0.129132  | 0.4643674  | -1.068883  | 0.2415096  | 1.1589348  | -0.85453  | -1.174607 | 0.3282938  | -0.559816  | 0.2017402  | 1.764677  | 1.6099496 | -1.40867  | 0.0284622 | 1.2478253 |
| GC11     | -0.805208 | 0.0950503  | 0.3209248  | 0.311344  | 0.339476   | -0.222238 | 0.491055  | 0.9759932 | 0.337832  | -0.163096  | -0.377523  | -0.163607  | 0.853464   | 0.5830991  | -1.343297  | 0.1131303  | -0.954923 | -1.003777 | -1.177373  | 0.2259808  | -0.38373   | -0.195369 | -0.126535 | -1.150308 | -0.526766 | -0.006683 |
| BT03     | 0.2427681 | -1.756511  | -0.440768  | -0.147455 | -0.59346   | -1.43685  | -1.420267 | 0.2018689 | -0.683217 | -0.04605   | -0.128088  | 0.501614   | -1.37061   | 0.2417435  | 1.3028931  | 0.2926889  | 0.489841  | 1.103261  | -0.461571  | 0.6641677  | 0.6978629  | 1.555367  | -0.080287 | -0.72982  | -0.102595 | 0.7935758 |
| RIN3     | 0.0143137 | 0.202453   | 1.229336   | -0.2282   | 0.034801   | 1.359336  | -0.017412 | 0.340849  | 0.6039718 | 0.489351   | 0.8485397  | -0.447655  | 0.053166   | -0.006134  | -1.475763  | -0.363675  | -0.33137  | 0.103681  | -0.133681  | -0.133681  | -0.133681  | -0.133681 | -0.133681 | -0.133681 | -0.133681 | -0.133681 |
| LYE1     | 2.830564  | -0.35023   | 1.4375664  | 0.4440682 | 1.473386   | -0.262672 | 0.3184042 | -0.47363  | -0.847016 | 0.3032012  | -0.543448  | -0.384277  | -0.574689  | 2.6182007  | 0.3190794  | -0.315318  | -0.682177 | -0.877131 | -0.488655  | -0.538082  | -0.677036  | -0.130343 | -0.64192  | -0.961023 | 0.2020908 | -0.44788  |
| RIN122   | -0.484339 | -0.003209  | 0.361647   | 0.0370719 | 1.5717012  | 0.668018  | 3.1657636 | -0.12458  | -0.277547 | -0.146303  | -0.333338  | -0.793338  | 0.733736   | 1.012347   | -1.50264   | -0.1949208 | -0.10902  | -0.340932 | -0.443758  | -0.287876  | -0.502106  | -0.33842  | -0.83136  | -0.02427  | 0.5717134 | -0.677413 |
| MEIS2    | 1.9612894 | -0.308001  | 1.8950273  | 0.8929824 | -0.16504   | 0.735148  | -1.873641 | -1.017364 | -0.218333 | -0.360426  | -0.197891  | -0.793638  | 0.698083   | 0.3653856  | 0.582467   | -0.94668   | 0.2049679 | -0.942873 | -0.942873  | -0.942873  | -0.942873  | -0.942873 | -0.942873 | -0.942873 | -0.942873 | -0.942873 |
| NOTCH2   | 1.4207015 | 1.5188283  | 1.5095623  | 0.5050314 | -0.75205   | -0.760171 | 0.2017746 | -0.357354 | 0.550342  | -0.181785  | -0.181785  | -0.181785  | -0.181785  | -0.181785  | -0.181785  | -0.181785  | -0.181785 | -0.181785 | -0.181785  | -0.181785  | -0.181785  | -0.181785 | -0.181785 | -0.181785 | -0.181785 |           |
| FS1      | -0.404313 | 0.098536   | 2.2669235  | -0.083817 | 2.5782712  | -0.404695 | 1.404778  | -1.44835  | -0.762832 | 0.653212   | -0.73734   | -0.89854   | 0.5314759  | -0.295299  | -0.380163  | -1.89761   | 1.423106  | -0.97328  | -0.112191  | -0.91345   | -0.702495  | -0.222022 | -0.797014 | -0.851701 | 1.2287465 | 0.910335  |
| RNF138   | -1.05184  | -0.757504  | -0.440533  | -0.823923 |            |           |           |           |           |            |            |            |            |            |            |            |           |           |            |            |            |           |           |           |           |           |



|          |            |            |            |           |           |           |            |           |           |           |            |            |            |            |            |            |            |            |            |            |            |           |            |           |            |
|----------|------------|------------|------------|-----------|-----------|-----------|------------|-----------|-----------|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|-----------|------------|
| GRMA     | 1.4186245  | 0.5127312  | -0.0085361 | 1.2519969 | 1.6208528 | 0.942008  | 1.118392   | -0.33149  | -0.514964 | 0.1819299 | 1.730794   | -0.568222  | 0.6847072  | 1.956762   | -1.017018  | -1.048734  | 0.2960497  | -1.126948  | -0.755412  | -0.647976  | -1.360255  | -0.701868 | -0.500132  | -0.37481  | -0.997953  |
| PANK1    | 0.8060765  | 1.7420367  | -0.921729  | 1.037321  | 1.5127244 | 1.500139  | 0.553876   | -0.8004   | -0.703473 | -0.457823 | 0.0084236  | -0.994488  | 1.6415669  | -1.011021  | 0.721616   | -0.424935  | 1.5873661  | -1.283868  | -0.234332  | -0.19553   | -1.2031    | -0.543035 | 0.0960609  | -0.70464  | -0.900588  |
| ZICI     | -0.500511  | -0.742389  | -0.26774   | 1.4141023 | -0.554335 | -0.005137 | -0.469704  | -0.64615  | -0.784111 | -0.369287 | 0.0708436  | -0.470507  | 0.0011628  | 2.9547931  | -0.735392  | -0.543384  | -0.668947  | -0.402934  | -0.494367  | -0.383692  | -0.510427  | -0.403232 | -0.742417  | -0.734913 | -0.691284  |
| NRM42    | -0.480202  | -0.114681  | 2.0722294  | 1.2930777 | 0.8198924 | 0.4790154 | 1.8986651  | -0.3475   | -0.476652 | -0.509689 | -0.041296  | -0.47507   | 0.0011628  | 2.9547931  | -0.735392  | -0.543384  | -0.668947  | -0.402934  | -0.494367  | -0.383692  | -0.510427  | -0.403232 | -0.742417  | -0.734913 | -0.691284  |
| NNKH     | 0.0463607  | 0.9383071  | -0.046447  | 0.6767059 | 0.5231464 | 0.9578521 | 1.7985327  | -0.68549  | -0.126659 | 0.535091  | -0.264008  | -0.501248  | 0.7470396  | -0.222972  | -2.777663  | 0.907811   | 1.637466   | -0.740975  | -0.407845  | -0.805107  | -0.611071  | -1.025649 | -0.895734  | -0.393986 | -0.870135  |
| SOM82    | 1.0017536  | 0.5132879  | 1.5124462  | 3.0884479 | 1.8439626 | 0.4099468 | 0.4421439  | -0.98754  | -0.741951 | -0.791951 | -0.262092  | -0.106963  | -0.198618  | -0.198618  | -0.005187  | 0.7090797  | -0.159645  | 0.0002199  | -0.730945  | -0.805107  | -0.611071  | -1.025649 | -0.895734  | -0.393986 |            |
| SLC16A1  | -0.683396  | -1.388616  | -0.802665  | -0.673956 | -0.479316 | -0.933312 | -0.692396  | 0.3424992 | -0.361002 | -0.509484 | -0.55469   | 1.5833338  | -0.863513  | -0.775451  | 1.0395381  | -0.1499459 | 0.3194543  | 0.02457912 | -0.818957  | -0.454708  | 1.4885741  | -0.160086 | 0.097104   | 0.7593228 | 0.7852141  |
| SLC7A7   | -0.937494  | -1.125344  | 0.6265777  | -0.814986 | -0.923763 | 0.1603607 | -1.636729  | 1.1093919 | 1.6223504 | -0.891948 | -0.292919  | 0.6761487  | 0.2504523  | 0.314875   | 0.000337   | -1.4699459 | 0.3194543  | 0.02457912 | -0.818957  | -0.454708  | 1.4885741  | -0.160086 | 0.097104   | 0.7593228 | 0.7852141  |
| C14orf43 | 1.5258071  | -0.177848  | 2.9935213  | 0.410376  | -0.215858 | -0.403123 | 0.46676429 | 0.4775809 | 1.8885399 | 0.0140781 | -0.484431  | -1.227676  | -0.5016169 | 0.0810821  | 2.1075888  | -0.660599  | -0.402661  | -0.402661  | -0.402661  | -0.402661  | -0.402661  | -0.402661 | -0.402661  | -0.402661 | -0.402661  |
| SC4F4    | 0.1566295  | 2.2408014  | -1.112921  | -0.216354 | -0.14326  | 1.1630402 | -0.590826  | 1.7878316 | -1.378133 | -0.594635 | -1.411121  | -0.931846  | -0.424975  | 0.0780492  | -0.080421  | -0.03331   | 0.0322852  | 0.1021625  | 0.397312   | 0.5714075  | -0.678931  | -1.471823 | -1.40292   | -0.312994 | -0.057283  |
| PCPH1    | -0.405851  | 0.756094   | -0.948485  | 1.0878166 | 0.7424837 | -0.227361 | 0.5119304  | -0.112248 | -1.55246  | 1.5986862 | 2.2788202  | 0.0332291  | 0.1775258  | -0.364694  | 1.3299331  | -0.546734  | 0.087606   | -0.821651  | 2.531874   | 0.67923029 | 0.4100174  | -0.88558  | -0.793826  | -0.331565 | -1.786475  |
| PP2R2B   | 0.2914125  | -1.231931  | -0.762714  | -0.840865 | -0.974131 | -0.208347 | 0.4191934  | -0.17229  | -0.452129 | -0.062459 | -0.729236  | -0.666494  | -0.434133  | -0.247897  | -0.1444705 | -0.247897  | -0.1444705 | -0.247897  | -0.1444705 | -0.247897  | -0.1444705 | -0.247897 | -0.1444705 | -0.247897 | -0.1444705 |
| MMPL4    | -0.354355  | -0.683136  | -0.201708  | -0.381078 | -0.504022 | -1.011054 | -0.974178  | -0.888473 | -0.49327  | -0.174523 | -0.1656    | 0.2002588  | -1.108538  | 0.485052   | -0.609444  | 1.627777   | -1.571761  | -0.721987  | -0.335524  | 1.2383509  | 3.0220281  | 1.068645  | 0.188846   | -0.404595 | 1.4979562  |
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| SLC26A6  | -0.435656  | -0.089797  | -0.467611  | -0.257819 | -0.389898 | -1.306472 | -1.003373  | -0.20203  | 0.1917291 | -0.297947 | -0.161802  | -0.3483267 | 0.2917088  | 0.8079682  | -2.33071   | -0.219149  | -0.227165  | -0.358554  | 0.6699381  | -0.022682  | 0.0852848  | -0.341361 | 0.737354   | 3.615177  | 0.3216336  |
| LRP5     | 0.1307554  | -0.005847  | 0.0701964  | -0.053093 | -0.047621 | 1.6825796 | 2.1342927  | -0.65506  | 0.5436588 | -0.100128 | -0.131893  | -0.593112  | -0.081098  | -0.001028  | -0.131893  | -0.593112  | -0.081098  | -0.001028  | -0.131893  | -0.593112  | -0.081098  | -0.001028 | -0.131893  | -0.593112 | -0.081098  |
| NDR4A    | 1.9067099  | 0.1684477  | 1.390197   | 1.0428298 | 0.9852033 | -0.02501  | 0.5563472  | -1.38283  | 0.2092885 | -0.739787 | 1.1808352  | -0.1610707 | -0.930208  | -0.225372  | 1.8840046  | -0.425066  | -0.584977  | 0.8017005  | -0.101788  | 0.7808523  | 1.2091321  | -1.285784 | -0.904597  | -0.468653 | -0.571091  |
| PRKCE1   | 1.3009843  | 1.069891   | -0.251173  | 1.720407  | 1.6752554 | -0.53108  | -0.31395   | 1.370744  | -1.417565 | -0.793867 | 1.3803352  | -0.332595  | -0.654071  | -0.339074  | 2.1900358  | -0.232952  | -0.387631  | -1.276496  | -0.719402  | 0.7497549  | -0.030477  | -0.867324 | -0.555599  | -0.411728 | -0.098914  |
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| NPL3     | -0.98134   | 0.4839356  | 1.2165133  | 1.497618  | 1.9803129 | 1.1151048 | 1.6398263  | 0.1198276 | -0.785617 | -0.755215 | -0.737477  | -0.412169  | 0.2929132  | -1.802059  | -0.568739  | -0.075291  | -0.86421   | 1.034196   | -0.304342  | -0.627618  | -0.1937992 | -0.819278 | -0.82234   | -0.796788 | -0.612507  |
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| CEU2     | 2.593185   | 0.273652   | 2.173614   | 0.790296  | 0.349624  | -0.405527 | 0.4006485  | -1.789293 | -0.205651 | -0.301618 | -1.110894  | -0.585237  | 1.8294271  | 0.809318   | -0.96667   | 0.719167   | -0.706808  | 0.4100115  | -0.781654  | -0.589984  | -0.332906  | -0.50937  | -0.791417  | -0.20238  | -0.286572  |
| NDRG2    | 1.4979395  | 0.524019   | 0.8245601  | 1.0367054 | 0.7202721 | 1.3630978 | 2.2152357  | 1.0467662 | -0.418736 | -0.669305 | 0.7623831  | -0.7878738 | 0.4384242  | -0.244266  | 1.120249   | -0.34835   | 0.6646391  | -1.424011  | 0.119613   | -0.949424  | -1.346485  | -0.764924 | 0.178224   | -1.46036  | -0.936653  |
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| USP4     | 3.0747486  | -0.933386  | 2.3609258  | 0.702555  | 0.832906  | -0.561995 | 0.0802946  | 0.017021  | -0.930101 | -0.107644 | 0.181504   | -0.422833  | -0.175927  | 1.5843152  | -2.55316   | -0.524641  | -0.1959585 | -0.113705  | -0.669317  | -0.20751   | -0.187864  | -0.271332 | -0.741391  | -2.1935   | 0.0601804  |
| MCN7     | -0.98305   | -0.52153   | -0.495257  | -0.596265 | -0.898821 | -0.318174 | -0.634219  | 2.318363  | 0.7272504 | -0.078915 | -0.746142  | -0.173347  | -0.620533  | -0.510338  | -1.804550  | 0.0190725  | -0.05597   | 1.8572934  | 0.0017385  | -0.934907  | 0.142656   | -0.153886 | 0.793466   | 2.9425888 | -0.473748  |
| SCAL1    | -1.7014389 | -1.08557   | 0.2832325  | -1.291384 | -0.716652 | -0.407726 | -1.048817  | 0.202369  | -0.652031 | 0.8462387 | -0.85609   | -0.173347  | -0.620533  | -0.510338  | -1.804550  | 0.0190725  | -0.05597   | 1.8572934  | 0.0017385  | -0.934907  | 0.142656   | -0.153886 | 0.793466   | 2.9425888 | -0.473748  |
| TUBA1A   | -0.686704  | -0.974566  | -0.512567  | 0.4496663 | 0.105342  | 0.6012403 | -1.16102   | -1.371929 | -0.49187  | -0.096998 | 0.5867714  | 0.590295   | -0.370988  | 0.4538273  | -0.25988   | -1.425412  | 0.1716858  | -0.83759   | 1.4060474  | 1.7996615  | 1.975744   | -0.41887  | -1.346991  | 1.716085  | 1.372486   |
| NNX1     | -0.953363  | 0.0060623  | 1.4049071  |           |           |           |            |           |           |           |            |            |            |            |            |            |            |            |            |            |            |           |            |           |            |



SILT3 -0.8500158 -0.222386 1.9340015 -0.247371 0.1030932 -0.033651 0.3946639 -0.67815 -0.581805 1.7077779 -0.492067 -0.708541 -0.502602 3.460075 -0.445868 -0.209287 -0.779468 -0.314284 0.2853497 -0.455997 -0.795966 -0.718532 -0.607092 -0.843931 0.1762051 -0.274174

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SHR6R 0.8023405 0.4093887 2.9352586 0.0884288 1.872465 -0.344913 1.2061029 -0.92728 -0.448258 -0.005783 -1.004087 -0.403451 1.499704 -0.09038 0.6858559 0.0370288 0.014836 -0.591003 -0.059031 -0.68307 -1.184194 -1.223374 -0.506329 -0.905849 -0.44605 -0.728018

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| humanNeAT_04.01.2s |           |            |            |           |           |           |            |            |           |           |            |           |            |            |
|--------------------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|------------|-----------|------------|------------|
| Sample             | 2-NS      | 3-NS       | 4-NS       | 5-NS      | 6-NS      | 8-NS      | 10-NS      | 2-AK       | 3-AK      | 4-AK-1    | 5-AK       | 6-AK      | 8-AK       | 12-AK      |
| EV04               | -0.568682 | -0.271382  | 2.292197   | 1.386248  | 0.626029  | 0.157407  | 0.124709   | -0.44467   | -0.092123 | -0.695307 | 1.359397   | 1.827840  | -0.822219  | 0.017519   |
| EV11               | 1.8465259 | -1.587316  | 0.979828   | 0.466249  | 2.170301  | -0.945392 | -0.817594  | -0.6688    | -0.161919 | -0.465216 | -0.1882748 | -0.091604 | -0.729717  | 0.2454504  |
| BALP3              | 0.0334419 | -0.055112  | -0.19359   | 0.0706992 | 1.232420  | 0.257266  | 0.682829   | 0.142760   | -0.294412 | -0.583147 | -0.60878   | -0.009104 | -0.587887  | -0.507812  |
| TRAP2B             | -0.564906 | 0.0446381  | 1.608461   | 1.352001  | -0.21104  | 1.508424  | 0.6358028  | -0.00874   | 0.727542  | 0.0879784 | -0.659744  | -0.105661 | 0.108702   | -0.368107  |
| NFX                | 0.952016  | 0.4020388  | 1.608461   | 0.2451183 | -0.28618  | 1.333172  | 1.0824618  | -0.68721   | 0.300799  | 0.657924  | -0.5731    | -0.877661 | 0.1829406  | 0.2119516  |
| ABHD5              | -0.381477 | 1.425524   | -0.721498  | 0.954271  | 1.6571261 | 1.125131  | 0.7482367  | -0.827821  | 0.0755418 | -0.323252 | 1.0986842  | -0.59347  | 1.0315252  | -0.883629  |
| DCN                | 2.9102504 | -0.55655   | 2.9102504  | -0.313274 | 0.2949101 | 0.2234414 | 0.0824079  | -0.84326   | -0.773226 | 0.2949101 | -0.706615  | -0.509182 | -0.29905   | 1.158265   |
| ATP12A             | -0.373985 | -0.5576    | 2.2955823  | 0.930895  | 0.565431  | 1.955715  | -0.69504   | -0.773226  | -0.22705  | -0.60478  | -0.251038  | -0.487331 | 0.0045624  | 0.085591   |
| PHLH2              | 1.1973617 | 0.207618   | 1.4270521  | 0.4721557 | 0.289168  | 0.1007364 | 1.153502   | -1.25412   | -0.327681 | -0.391678 | -0.8147    | -0.477595 | -0.611133  | 2.255104   |
| NCN                | -0.339295 | -0.981684  | 0.3372692  | -0.737469 | -0.06093  | -1.411235 | -0.914119  | -1.00603   | 0.280331  | 1.628046  | -1.02012   | 0.2434371 | -0.34138   | -0.689799  |
| TMNP               | -0.448132 | -0.262778  | -0.5364825 | -0.39569  | -0.462093 | -1.220594 | -0.706731  | 0.1712945  | -0.138    | -0.473869 | -0.072849  | 0.1163664 | -0.326741  | 0.1590562  |
| SHD2A              | -0.70408  | -0.47895   | -0.64276   | -0.594987 | -0.264693 | -1.181894 | 0.03848    | 1.3945955  | -0.3904   | -0.72587  | -0.07764   | 0.062994  | -0.23274   | 0.156524   |
| MA2P3              | -0.64816  | 1.155437   | 0.032294   | -0.174448 | 0.0311156 | 0.505151  | 0.5726296  | -0.383778  | -0.104056 | 0.2306745 | -0.747019  | 0.8053869 | 0.603183   | 2.375392   |
| USP2               | -0.73682  | 0.3002317  | -0.143802  | 0.589771  | 0.4935236 | 2.5332397 | -0.66741   | -0.0303718 | 0.1936772 | 2.500251  | -0.657956  | 1.0453909 | -0.106911  | -0.200038  |
| NEODL              | 0.5575276 | 0.2305027  | 0.8328493  | -0.25204  | 1.065362  | 0.628172  | 1.1753105  | -0.34069   | -0.668646 | -0.521461 | -0.68856   | -0.130033 | -0.703914  | 0.420256   |
| USP6               | -0.148606 | 0.6528201  | 1.329883   | 1.0336782 | 0.4976901 | 0.621982  | 2.6716648  | 0.370768   | -0.98549  | 0.192351  | -0.796909  | -1.045719 | 1.3160021  | -0.1410064 |
| PRMT1              | 0.4458    | 1.4967595  | -0.701387  | -0.407591 | -0.594918 | -0.407525 | -0.041953  | 3.407469   | -0.56235  | -0.06618  | -0.180442  | -0.66193  | 0.0045624  | 0.096862   |
| GLT1B3             | 0.2170637 | -0.101683  | -0.056439  | -0.07714  | 0.4192944 | -1.000753 | -0.985191  | -1.41894   | -1.199742 | -0.270131 | -0.794233  | -0.160508 | -0.947889  | 0.1059605  |
| ERH3               | 0.6027918 | 0.1368232  | -0.80364   | 1.8267005 | 0.0994874 | -0.329824 | -0.26348   | -0.135214  | -0.291415 | 1.791694  | 2.5197524  | -0.150165 | -0.321653  | -0.254881  |
| CACN1              | -0.103381 | -0.231281  | -0.13118   | 2.6033413 | 0.3016485 | 1.1503987 | 2.641957   | -0.79622   | -0.589371 | -0.039585 | 0.8359076  | -0.3244   | 0.0639005  | -0.190693  |
| PRM1               | -0.403466 | -0.675663  | -0.352     | -1.065322 | -1.645193 | -1.132707 | -0.884878  | 0.3865906  | 1.526054  | 0.5503883 | -0.59934   | -0.261559 | -0.994604  | 0.480087   |
| PGB                | -0.772612 | -0.420703  | -1.982928  | -0.601004 | -0.977575 | -0.220843 | -0.760356  | 0.2597336  | -0.121931 | -0.868117 | -1.31077   | 1.930017  | -0.208889  | 1.209522   |
| RHD11              | 0.3105025 | 2.7738658  | -0.989399  | -0.051678 | 1.1150282 | 0.975848  | 0.2656509  | 0.665776   | 0.2150468 | -0.853392 | 1.38721    | -0.53012  | 0.9974795  | -0.842105  |
| SMARCE1            | -1.156123 | -0.216557  | -1.539785  | 0.246402  | -0.419385 | -0.028219 | -0.67105   | 2.2074225  | -0.246114 | -0.739169 | 0.0794023  | 0.1485003 | -0.1011384 | -0.199566  |
| SEMA5A             | 0.2667862 | 0.14221    | 1.457186   | 0.628112  | 3.8767532 | -0.346692 | -0.061389  | -0.95134   | -0.944134 | 0.0071424 | -0.525238  | -0.308945 | -0.026445  | -0.106631  |
| PHF17              | 2.7508997 | 0.237101   | 0.2255807  | 1.2674206 | -0.076504 | 0.2690194 | 0.2449723  | 0.017973   | 1.3034844 | -0.17653  | -0.374769  | -0.461928 | -0.474619  | 0.222346   |
| FTSG               | 0.4117649 | 0.1287869  | 0.147008   | 0.8641203 | 1.248478  | -1.480258 | -0.487709  | -0.23577   | -0.312418 | -0.175826 | 0.82604    | 0.6986603 | -0.56517   | 0.1658922  |
| FAP                | -0.833511 | -0.399398  | -0.009283  | -0.520028 | -0.2049   | -0.88666  | -0.88112   | -0.964729  | -0.664927 | -0.189905 | -0.01094   | 0.2274253 | -0.874233  | -0.132947  |
| ADCF2              | 3.1364923 | -0.176506  | 0.4634792  | 0.2824597 | 0.2907194 | 1.351372  | 0.9261722  | -0.29143   | -0.180305 | -0.542594 | -0.53896   | -1.07053  | -0.437808  | 0.898115   |
| TNS1               | 1.2364661 | 0.664933   | 2.3610071  | 1.5621379 | 0.766309  | 0.0186226 | 0.5259750  | -0.14976   | -0.141832 | 0.583793  | -0.138181  | -1.032346 | -0.758006  | 1.8862274  |
| SMARCA2            | 1.8677488 | 0.525804   | 1.4342968  | 1.48657   | 0.075343  | 0.6176159 | 0.02059348 | -0.10977   | 0.5523426 | 0.686397  | -0.09447   | 1.1308887 | 0.2321808  | 0.688704   |
| CNCR2              | -0.753442 | 0.4332944  | -1.84443   | -0.333661 | -0.023124 | -1.00392  | -1.03136   | -0.08989   | 0.471819  | 0.9882904 | 0.9885514  | -0.003744 | -0.157963  | 0.33634    |
| SRFB1              | -0.089016 | 0.1047963  | 0.0210203  | 0.929303  | -0.683695 | -1.0178   | -0.75732   | -0.60763   | 0.544499  | 2.6539798 | 1.305346   | -0.64335  | 0.217376   | 1.456785   |
| ARH1               | 1.1341417 | 0.007953   | 1.046505   | -0.77422  | -0.648339 | -0.15896  | -0.985362  | -0.321475  | -0.397955 | -0.79093  | 0.930363   | -0.827575 | 0.304866   | 0.561880   |
| DNAH2              | -0.37362  | 1.945424   | -0.984708  | 0.8641203 | 1.248478  | 1.7126547 | 0.732513   | -1.113254  | -0.75543  | -0.621881 | -0.054767  | -0.868814 | 0.178564   | -0.971527  |
| ADAMT1             | -0.790267 | -0.015591  | -0.215448  | 0.265513  | -0.424278 | -1.480258 | -0.127302  | -0.05763   | -0.621881 | -0.054767 | -0.868814  | 0.178564  | -0.971527  | -0.971527  |
| PPP1R13B           | 1.4796808 | 1.692473   | -0.04485   | -0.094947 | 1.3312267 | 0.129318  | -1.38765   | 0.6846182  | -0.520009 | -0.069501 | 0.8912451  | 0.78761   | -0.58603   | 2.072618   |
| TRAP4              | -0.431256 | -1.288875  | -0.71281   | -0.333381 | -0.518448 | -0.410833 | -0.302493  | -1.38362   | -0.29166  | -0.480689 | 2.6783227  | -0.246325 | -0.540827  | -0.720737  |
| CCDC80             | 2.4068085 | -0.1281807 | -0.739245  | 0.7323163 | 0.472238  | 0.2661168 | 0.8109085  | -0.940149  | -0.682659 | -0.288986 | -0.250007  | -0.281936 | 0.990673   | 0.990673   |
| SEMA6A             | -0.405055 | 0.9748061  | 0.9676065  | 1.4874705 | 1.385239  | -0.394356 | 0.8634637  | -1.44339   | -1.078418 | 0.5447184 | 2.2161457  | -1.0825   | -0.6385    | 0.046704   |
| GNAT               | 0.1598841 | 1.2932017  | 0.477743   | 0.8356823 | -0.40931  | -0.901853 | -0.801773  | 1.0927451  | -0.18302  | 1.742608  | 0.6365559  | -0.3354   | -0.944315  | -0.005124  |
| CRM                | -0.679151 | 0.114453   | 0.2264366  | -0.019106 | 0.347905  | 0.276869  | 2.7198795  | -0.3142    | -0.12036  | -0.77077  | -0.28206   | 0.3638202 | 0.626944   | 0.7915971  |
| ABL1               | 0.3002142 | -0.543225  | 1.975335   | -0.121623 | 0.1088307 | 0.2529191 | 2.6087496  | -0.3138    | -0.386533 | 0.330086  | -1.122239  | -0.043422 | -0.463278  | 1.0057534  |
| GDAD58             | -0.640505 | 0.1477313  | 1.6117769  | 1.222254  | 0.0881133 | 0.2862628 | 1.532394   | -0.12646   | -0.83318  | -0.561335 | -0.255683  | -0.34158  | 0.7508031  | 1.3178233  |
| SOX10              | -0.160657 | -0.222292  | 0.5914008  | 0.9380965 | 0.5514236 | 0.3884084 | 4.195721   | -0.438693  | -0.144423 | 0.145314  | -0.1578    | -0.12111  | -0.318123  | -0.70392   |
| GTPBP1             | -0.684119 | -0.497197  | 1.6586801  | 1.8957411 | 0.7862988 | 0.3450377 | 2.2887708  | 0.574242   | -0.49457  | -1.143983 | -1.019384  | 0.3420998 | 0.1239386  | 1.6209284  |
| PODIF              | 1.4586215 | 0.7542296  | 0.3459395  | 0.1957586 | -0.856478 | -0.574853 | -0.879479  | -0.755429  | -1.110077 | -0.882316 | -0.617965  | -0.906413 | -0.64760   | 0.5312926  |
| PRMT5              | -1.718924 | -0.569426  | -0.83991   | -1.05827  | -0.58297  | -0.965074 | -0.744339  | 1.103410   | 1.2834067 | 0.086231  | -0.283361  | -0.167153 | -0.981078  | 1.102676   |
| TNMF5              | -0.39272  | 0.1484681  | -1.388752  | 0.0086054 | 2.393495  | -1.248023 | 0.9311665  | -0.90705   | -0.852806 | -0.479122 | -0.78793   | -0.26232  | 0.8119493  | -1.33616   |
| DAMM1              | 1.7151027 | 0.4929297  | 0.477743   | 0.8356823 | -0.40931  | -0.901853 | -0.801773  | 1.0927451  | -0.18302  | 1.742608  | 0.6365559  | -0.3354   | -0.944315  | -0.005124  |
| NFIB1A             | -0.592349 | -0.472111  | 0.7208668  | 0.709411  | 0.171044  | 0.0987048 | 3.2540877  | -0.101292  | -0.15677  | -0.415971 | -0.454553  | -0.107747 | 0.8955609  | 2.4817154  |
| JAG1               | -0.172921 | -0.768437  | 0.2767848  | -0.31025  | -0.191343 | -1.203521 | -1.185302  | -0.48194   | -0.126769 | -0.25562  | -0.043422  | -0.463278 | 1.0057534  | 0.1005466  |
| CDC013             | 0.3358378 | 0.9214578  | -0.83519   | 1.0709222 | 0.671665  | 0.954673  | 0.91753    | -0.336932  | -0.651959 | -0.77159  | -0.66245   | -0.565307 | -0.785548  | -0.881394  |
| CAB39L             | 1.840329  | -0.185378  | 2.6074618  | 0.964284  | 0.492355  | 0.443635  | 0.7398481  | -0.99973   | -1.251787 | 1.407716  | -0.49706   | -0.665006 | -0.290127  | 0.222706   |
| MAF3               | 1.531836  | 0.2421176  | 1.5615355  | -0.333636 | 0.669381  | -0.47076  | -0.485483  | 0.2080434  | 0.487641  | 1.1967653 | -0.040177  | -1.520967 | -0.484432  | -0.424794  |
| COL1               | -0.780362 | -0.892912  | -1.083622  | -0.477874 | -0.74226  | -0.250441 | -0.818322  | -0.11261   | -0.348456 | -0.129647 | -0.089384  | 1.7662862 | 2.4014047  | 0.7157901  |
| GDAP1              | -0.801361 | -0.734353  | -0.932574  | -0.524847 | -0.794196 | -0.728763 | -0.666327  | 0.3361067  | -0.634471 | -0.742489 | -0.506023  | 0.4248689 | -0.489139  | -0.135305  |
| SLC12A1            | -0.533399 | -0.391013  | -0.19249   | 0.1406262 | -0.497838 | -0.767539 | -0.635765  | -0.405916  | -0.284116 | -0.020746 | -0.293843  | -1.12165  | -0.747912  | -0.478193  |
| ICMTA              | 0.2539192 | -0.740369  | -0.12591   | -0.483939 | 0.8102489 | 1.8718184 | 1.575402   | -0.860218  | -0.619497 | 0.1561082 | -0.179216  | -0.323462 | 0.1282037  | -0.235356  |
| GERM1              | 0.1439967 | 0.320767   | 0.551388   | 0.4380568 | -0.47012  | -1.272537 | 0.233617   | -0.42582   | -0.081089 | 0.906504  | 0.631071   | -0.934547 | -0.353708  | 0.0015663  |
| CEP41              | 0.3817023 | -0.8232178 | -1.525314  | -0.996981 | -1.45013  | -0.915689 | -0.578658  | 2.02556    | 0.564675  | 0.9324271 | 0.313187   | 0.1352417 | -1.733404  | 0.015663   |
| EIF4H              | -1.593231 | 0.4293458  | -0.888807  | -0.125248 | 0.3518257 | -0.92136  | -0.681829  | 0.42458    | 0.1175905 | 0.470536  | -0.79771   | -0.392304 | -0.19256   | -1.38      |



|         |            |           |           |           |           |           |            |           |            |           |           |            |           |           |            |            |           |           |            |           |           |            |            |           |             |            |
|---------|------------|-----------|-----------|-----------|-----------|-----------|------------|-----------|------------|-----------|-----------|------------|-----------|-----------|------------|------------|-----------|-----------|------------|-----------|-----------|------------|------------|-----------|-------------|------------|
| CDK2AP1 | 0.71711783 | -1.905144 | 0.9028998 | -0.327898 | -0.673557 | -0.078955 | -0.96757   | -1.12239  | -1.113312  | -0.581918 | 0.290445  | -0.346627  | -0.484537 | 0.1284615 | -0.956452  | 0.3346713  | -1.308836 | 1.953072  | 0.02939203 | 0.3353845 | 1.4878647 | -0.279218  | -0.361581  | 2.2080978 | 0.622038    | 0.9426713  |
| TPH1    | -1.521348  | -0.367655 | -1.044926 | -0.38564  | 0.347428  | -1.095508 | -0.04393   | 0.3115154 | -0.195889  | -0.200601 | -0.309065 | 0.657332   | -1.015584 | 0.3707722 | -0.004087  | 0.7566892  | -0.880005 | 0.1164697 | -0.285665  | 1.4605398 | -0.279792 | 0.26652972 | -0.423315  | 0.0230328 | -0.550608   | -0.450802  |
| CNG2    | -0.782974  | -0.565092 | 0.0318168 | 2.080481  | 3.474728  | -0.311105 | -0.18197   | -0.006059 | -1.263738  | 0.5102414 | -0.394197 | -0.16116   | -0.308706 | 0.4047984 | 1.227077   | -0.004087  | 0.7566892 | -0.880005 | 0.1164697  | -0.285665 | 1.4605398 | -0.279792  | 0.26652972 | -0.423315 | 0.0230328   |            |
| PTC7    | -0.61935   | -0.222222 | 0.2897194 | -0.701979 | -0.684441 | -0.760936 | -0.63043   | -1.626995 | -0.08074   | -0.413863 | 0.626333  | 0.536684   | -1.027209 | -0.594132 | -1.438424  | 0.6607744  | -0.816338 | 0.196849  | 0.433365   | 0.5666723 | 2.8838191 | 1.5650941  | 0.4848831  | -0.06945  | 1.7704569   | 0.6021402  |
| VEFA    | -0.474064  | 0.6973651 | 0.0194245 | -1.15571  | 1.848353  | 0.0316196 | 2.5117747  | 0.2178338 | -0.503932  | -1.741306 | -0.692368 | -0.442401  | 0.6528294 | -0.257689 | -0.170751  | -0.519361  | -0.343801 | 0.665957  | -0.507486  | -0.50944  | -0.518697 | -0.771564  | -0.224841  | -0.185147 | -0.73849    |            |
| HMGFR   | 0.413295   | 3.4105181 | 0.3118958 | 1.2065544 | -0.75893  | 0.994319  | 0.7138767  | 0.634697  | -0.321316  | -0.564121 | 0.410082  | -0.892101  | 0.6528294 | -0.257689 | -0.170751  | -0.519361  | -0.343801 | 0.665957  | -0.507486  | -0.50944  | -0.518697 | -0.771564  | -0.224841  | -0.185147 | -0.73849    |            |
| PDE4D   | 0.583322   | 1.1779276 | 3.3405831 | 0.043295  | 1.6255457 | -0.428281 | -0.301394  | -1.122794 | -0.685101  | -0.676522 | -0.100119 | -0.104966  | -0.330058 | 0.1000871 | 2.1168592  | -0.237658  | -0.251845 | 0.535048  | 0.840192   | -0.427347 | -1.095095 | -0.150021  | -0.46132   | -0.280193 | -0.620148   | -0.2674874 |
| CFEB4   | -0.044322  | 2.8464971 | -0.421433 | 1.0432925 | 0.7791175 | -0.732289 | -0.675636  | 0.2340075 | -0.465431  | -0.378209 | 1.1883492 | -0.427343  | -0.43936  | -0.381346 | 2.2405108  | -0.143141  | 1.1242987 | -0.50404  | -0.757532  | -0.427343 | -1.246058 | -1.436385  | -0.428064  | -0.601942 | -0.607487   |            |
| BC16    | 1.6618036  | 0.9048469 | 0.656465  | 1.3010755 | 1.683019  | 0.428709  | 1.1363122  | 0.8446397 | -0.85241   | -0.513966 | -0.332788 | -0.427343  | -0.43936  | -0.381346 | 2.2405108  | -0.143141  | 1.1242987 | -0.50404  | -0.757532  | -0.427343 | -1.246058 | -1.436385  | -0.428064  | -0.601942 | -0.607487   |            |
| WNT5A   | -1.03006   | 0.297525  | -0.951619 | -0.763215 | -1.01348  | -0.839454 | -0.996635  | -0.596787 | -0.79278   | -0.039109 | -0.584432 | 0.6922904  | 0.3442592 | 0.7283917 | 0.618426   | -0.556544  | -1.126394 | -0.629499 | -0.759423  | -0.954885 | -0.331312 | -1.071182  | -0.438733  | -0.607296 | -0.573657   |            |
| SLC3A5  | -0.25606   | 0.434333  | 0.328342  | -0.875623 | 0.2849414 | 0.676315  | 1.219166   | 0.1877384 | -0.493738  | -0.8654   | -0.33348  | -0.465266  | -0.744851 | -0.615229 | -2.009179  | -0.883851  | 0.959333  | 0.3715569 | 0.240009   | 0.0166181 | 1.5775026 | -0.660532  | 1.8545566  | 1.667366  | -0.281481   |            |
| RTKN    | 0.0078244  | 0.143634  | -0.990005 | 0.4565763 | 0.131469  | 0.2862521 | 0.4444214  | -1.50146  | -0.637389  | -0.69573  | 0.4377662 | -1.191939  | 0.874706  | -1.20017  | -1.887129  | -0.707651  | 0.019564  | 0.328473  | 0.346028   | 0.291659  | 0.219197  | 0.4115218  | 0.2489666  | 2.657347  | -0.11847283 |            |
| SRPN1   | 1.6506601  | 0.2720012 | 1.6607811 | 1.66029   | 1.939633  | 0.188269  | 0.1796505  | -1.127458 | -0.97306   | -0.072215 | 0.2053227 | -0.444512  | 0.0833003 | -0.13935  | 2.8671     | -0.501556  | -0.516226 | -0.784572 | -0.337368  | -0.835389 | -0.407764 | -1.00047   | -0.511331  | -0.585101 | -0.453241   |            |
| PNMT6A  | -0.660818  | -0.318057 | 0.6893956 | -0.777218 | 0.4903405 | -0.928407 | -0.652165  | -0.946192 | -0.628355  | -0.713585 | -0.129857 | -0.702689  | -0.603984 | -0.701443 | -1.968612  | -0.5366548 | -0.473154 | 0.0065789 | 0.0176053  | 1.5173863 | -0.046803 | 0.7057529  | -0.580871  | -0.018074 | -0.57824    |            |
| FH1     | -0.529096  | -0.613354 | -0.122727 | -0.199547 | -0.121268 | -0.902143 | -0.874666  | -0.7232   | -0.697328  | 0.8761424 | 0.1213709 | -0.133921  | -1.000616 | -0.082743 | -0.481387  | 1.6657171  | -1.228474 | -0.75756  | -0.166001  | 3.2181991 | 0.0492341 | 0.2826097  | 0.9172653  | 1.5173863 | -0.046803   |            |
| EHF1    | 0.249489   | 0.1007059 | 0.3190121 | 0.060689  | 0.0811862 | 0.3523193 | 1.786994   | -0.498868 | -0.460404  | -0.493138 | -0.497555 | -0.555635  | 0.6836517 | -0.034294 | -1.182415  | -0.866649  | -0.904499 | -0.306423 | -0.1007729 | -0.423691 | -1.445077 | -1.552329  | -0.469074  | -0.292716 | -0.386303   |            |
| EHF1P   | 1.5413393  | 1.1774862 | 0.954669  | 0.668501  | -0.28325  | -0.389379 | -0.281579  | 1.860059  | 0.4443338  | -0.603336 | -0.088669 | -0.4584338 | -0.049858 | -0.565008 | -0.757168  | -0.896148  | -0.558087 | -0.142273 | 0.3657532  | 1.17044   | 1.7058108 | -0.138     | 0.9876868  | 1.1564895 | -0.882394   |            |
| ANAPC11 | 0.7975517  | 0.3776899 | 2.2087512 | 0.1114577 | 2.197796  | 0.60367   | 0.5963784  | -1.398818 | 0.1969607  | 0.971468  | -0.896148 | -0.558087  | -0.142273 | 0.3657532 | 1.17044    | 1.7058108  | -0.138    | 0.9876868 | 1.1564895  | -0.882394 | -0.882394 | -0.882394  | -0.882394  | -0.882394 | -0.882394   |            |
| RSG2    | -0.389677  | -0.188319 | -0.099277 | 0.6653871 | 0.0860329 | 0.5496522 | 0.2985374  | -0.04001  | -0.49642   | -0.331873 | 0.7274312 | 0.057942   | 0.8248925 | 0.3765336 | -1.120446  | -0.65845   | -0.861273 | -0.338014 | -0.320011  | 0.196004  | -0.320551 | -0.075471  | -0.983465  | -1.756481 | -0.922247   |            |
| HSO11A2 | 0.7249295  | 1.9650627 | -0.737384 | 0.6553962 | 1.1853431 | 1.900267  | 0.2774205  | -0.81455  | -1.24888   | -0.81469  | 1.395579  | -0.761493  | 0.820714  | -0.81813  | -0.758128  | -0.761088  | 0.0003327 | -0.595408 | -0.602016  | -0.66457  | -0.786124 | -0.803509  | 0.284075   | -0.823386 | -0.808947   |            |
| CTGF    | -0.228317  | 0.1952811 | 1.787788  | 0.1499943 | 0.3520159 | 0.059664  | 1.1446302  | -0.38052  | -0.396732  | -0.038591 | -0.313918 | -0.412316  | -0.157912 | 0.4057496 | -0.885493  | -0.215072  | -0.85391  | -0.241562 | -0.363387  | -0.022309 | -0.323228 | -0.398154  | -0.814221  | -0.862691 | -0.25747    |            |
| ZNF48   | 0.038636   | 3.4006947 | -0.98479  | -0.114206 | 0.012129  | 0.279669  | 0.4853327  | 0.091616  | 1.7118776  | -0.172066 | -0.172066 | -0.366718  | 1.2367182 | 0.0196112 | 0.949382   | -2.205408  | 0.538467  | -0.431922 | -1.027017  | -1.057396 | -0.265829 | -0.456765  | -0.946485  | -0.876382 | -0.517868   |            |
| NRE2B   | -1.082535  | 0.3404967 | 0.9594474 | 1.1549031 | 0.260591  | 0.6361636 | 2.8914481  | -0.154564 | -0.065716  | -0.127066 | -0.366718 | 1.2367182  | 0.0196112 | 0.949382  | -2.205408  | 0.538467   | -0.431922 | -1.027017 | -1.057396  | -0.265829 | -0.456765 | -0.946485  | -0.876382  | -0.517868 | -0.517868   |            |
| NRA3    | -0.520357  | 0.3416294 | 3.6827254 | 0.4878888 | 0.8545315 | -0.071564 | 0.8906708  | 0.2485489 | -0.543133  | -0.662768 | -0.636048 | -0.565434  | -0.42935  | -0.56006  | -0.565434  | -0.42935   | -0.56006  | -0.565434 | -0.42935   | -0.56006  | -0.565434 | -0.42935   | -0.56006   | -0.565434 | -0.42935    |            |
| KNIP2   | -0.081062  | -0.32088  | -0.137467 | 1.5824757 | 0.3079957 | 1.8579263 | 3.0273931  | -0.311195 | 1.0115451  | -0.440235 | -0.24935  | -0.56006   | -0.565434 | -0.42935  | -0.56006   | -0.565434  | -0.42935  | -0.56006  | -0.565434  | -0.42935  | -0.56006  | -0.565434  | -0.42935   | -0.56006  | -0.565434   |            |
| ARAP3   | -0.564202  | -0.247793 | 1.9645486 | 0.256933  | 0.0849523 | -0.773233 | -0.130545  | -0.780153 | -0.400135  | -0.233814 | 0.1418457 | -0.056367  | 0.263545  | 2.02265   | -0.280211  | -0.991472  | 0.5228315 | 0.2887733 | -0.151887  | -0.115394 | 0.1050275 | -0.270955  | 3.4363981  | 1.0311048 | -0.460809   |            |
| HPH1    | -0.599205  | 1.421178  | -0.349377 | -0.75027  | -0.535515 | -0.765338 | 1.486662   | -0.122219 | 0.1220314  | -1.18555  | -0.991398 | -0.736861  | -0.57092  | -0.15152  | -0.394283  | -0.173504  | -0.368321 | 2.021509  | -0.038213  | -0.763854 | 2.8358883 | -0.424017  | 0.4243367  | 0.1625392 | -0.559501   |            |
| SOCS2   | -0.250572  | 0.505052  | 0.596011  | 0.603835  | 0.8001492 | 0.1981356 | 2.938612   | -1.760319 | -0.3714434 | -0.920705 | -0.920705 | -0.920705  | -0.920705 | -0.920705 | -0.920705  | -0.920705  | -0.920705 | -0.920705 | -0.920705  | -0.920705 | -0.920705 | -0.920705  | -0.920705  | -0.920705 | -0.920705   |            |
| TKR2    | -0.772948  | -0.802935 | 0.0358875 | 0.117398  | 0.150938  | -0.605782 | -1.159552  | -0.15031  | -0.8845    | -0.70739  | 0.327219  | 1.3147981  | -0.39517  | 1.5205904 | -1.367597  | 0.3904698  | -1.38307  | -0.60509  | -0.470523  | 0.6202553 | 1.0683025 | 1.357572   | 0.2657109  | -0.111182 | 6.672677    |            |
| TNFSF10 | 0.9334585  | -0.318281 | -1.37688  | -0.694563 | -1.153162 | -0.88077  | -1.447211  | 1.5188301 | -0.504772  | 0.2450187 | 0.2827056 | 0.8062057  | -1.323886 | 0.188973  | 0.232658   | 0.4884595  | -0.563085 | -0.974337 | -1.30188   | 1.5887905 | 1.4939271 | 1.1062829  | 0.624218   | 0.8800032 | 0.7936245   |            |
| NHBA    | -0.913297  | -1.273966 | 2.4226038 | -0.066278 | 0.1937151 | -0.729246 | -0.1717681 | -0.87388  | -1.438484  | -0.581807 | 0.2437337 | -0.29367   | -0.747636 | -0.17461  | -0.24807   | 0.5507064  | -0.80952  | 1.1973223 | -0.77669   | 1.226037  | 2.032386  | 0.4425576  | -0.462392  | 0.0554384 | -0.693264   |            |
| AC01    | -0.119238  | 1.9462739 | -0.722761 | 1.2863064 | 1.988995  | 1.7451659 | 0.2380382  | -0.99711  | -0.28758   | -0.198439 | 0.4653112 | -0.984507  | 0.663131  | -0.758261 | -0.3109405 | -0.115333  | -0.109749 | -0.15333  | -0.169127  | 1.4696133 | 2.9323076 | 0.1935059  | -0.401313  | -0.337501 | 1.4868408   |            |
| NRA1    | -0.2077324 | 1.4063483 | -0.559586 | 2.8390143 | 0.916181  | 0.9581197 | 1.2000566  | -0.37895  | -0.513765  | -0.629543 | -0.151678 | -0.62948   | 0.8760194 | 0.883832  | -1.012352  | -0.97381   | -0.78704  | -0.760338 | -0.323147  | -0.199744 | -0.69085  | -0.88309   | 0.0614709  | -0.708425 | -0.923072   |            |
| EMG1    | -0.173714  | 1.4063483 | -0.559586 | 2.8390143 | 0.916181  | 0.9581197 | 1.2000566  | -0.37895  | -0.513765  | -0.629543 | -0.151678 | -0.62948   | 0.8760194 | 0.883832  | -1.012352  | -0.97381   | -0.78704  | -0.760338 | -0.323147  | -0.199744 | -0.69085  | -0.88309   | 0.0614709  | -0.708425 | -0.923072   |            |
| PD18    | -0.497177  | 0.1051117 | 2.7340005 | 0.1042921 | 0.2669381 | 0.4985796 | 2.2790079  | 0.2904362 | -0.763878  | -0.367618 | -0.116917 | -0.182224  | 1.8733456 | 0.0305063 | -1.591184  | -0.455448  | -0.30047  | -0.65305  | -0.20858   | -0.606021 | -0.537038 | -0.457596  | 0.0973558  | -0.691626 | -0.691626   |            |
| SD4     | 0.0867691  | 1.1805181 | 1.0905014 | 0.6312819 | 1.2166388 | 0.459353  | 3.258844   | -0.82857  | -0.758371  | -0.243101 | -0.252371 | -1.912524  | 0.591604  | 0.0305063 | -1.052707  | -0.250432  | -0.30467  | -0.481383 | -0.79735   | -0.88599  | 0.6623568 | -0.911734  | -1.054465  | 0.2176647 | -0.869504   |            |
| CDKN1A  | -0.429518  | 0.6452236 | 0.4404    |           |           |           |            |           |            |           |           |            |           |           |            |            |           |           |            |           |           |            |            |           |             |            |



|         |           |           |           |            |            |            |            |            |           |           |           |            |            |            |            |           |            |            |           |           |           |            |            |           |            |           |
|---------|-----------|-----------|-----------|------------|------------|------------|------------|------------|-----------|-----------|-----------|------------|------------|------------|------------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|------------|-----------|
| TIME117 | -1.530675 | -0.72263  | -0.256896 | -0.188207  | -1.114743  | -0.950379  | -0.865471  | -0.793518  | 0.2353076 | 1.966672  | 0.052257  | 0.9077129  | -0.919345  | 0.084589   | 2.98647361 | 0.0558711 | -0.254648  | -0.446412  | -0.178504 | 0.6589368 | 1.4007964 | 0.7324198  | -0.163332  | -0.724558 | 0.3421491  | -0.312479 |
| VP378   | -1.020988 | 0.1335564 | 2.1328982 | 0.4242807  | -0.8074506 | -0.7024169 | 0.2008812  | -0.12403   | -0.956854 | -0.826969 | -0.657006 | -0.865852  | -0.664909  | -0.657006  | -0.826969  | -0.657006 | -0.865852  | -0.664909  | -0.657006 | -0.826969 | -0.657006 | -0.865852  | -0.664909  | -0.657006 | -0.826969  |           |
| TPM1    | 1.5651598 | 0.2302539 | 2.9157639 | -0.257102  | -0.7073312 | -0.0674803 | 1.4639862  | -0.88584   | -0.649698 | -0.657006 | -0.865852 | -0.664909  | -0.657006  | -0.826969  | -0.657006  | -0.865852 | -0.664909  | -0.657006  | -0.826969 | -0.657006 | -0.865852 | -0.664909  | -0.657006  | -0.826969 |            |           |
| ADMN157 | 0.5467505 | 0.7925591 | 1.1364767 | 0.68066    | -0.65032   | -0.111532  | -0.118304  | -0.004391  | -0.673837 | 2.8261768 | -0.266544 | -0.447671  | -0.297944  | 0.0830571  | 1.3352322  | 0.3092573 | -0.47633   | 0.0629806  | -0.185827 | -1.020799 | -0.693168 | -0.921259  | -0.679561  | -0.88238  | 0.0456872  |           |
| ADAM157 | -0.308628 | -0.005101 | 0.642198  | -0.555697  | -0.211704  | -0.075264  | 0.339756   | -0.421353  | 0.8727724 | -0.69447  | -0.512821 | 0.31924    | 0.522649   | -0.810382  | -2.95054   | -0.729764 | -0.327319  | -0.265168  | -0.340805 | -0.586803 | 0.0083906 | -0.828336  | -0.909168  | -0.921259 | -0.679561  |           |
| STAC2   | 2.031313  | -0.103973 | 1.6458051 | 0.3413987  | 1.1893097  | 1.4383019  | 0.2376074  | -0.996657  | -0.583141 | -0.178545 | -0.748254 | -0.5638197 | 0.5171517  | 0.2192387  | -0.799705  | -0.454845 | -0.799705  | -0.454845  | -0.799705 | -0.454845 | -0.799705 | -0.454845  | -0.799705  | -0.454845 | -0.799705  |           |
| RE      | 0.6459394 | -0.066317 | 0.4992065 | 1.357887   | -0.889285  | -0.2326    | 0.0705156  | 0.2023635  | 1.6823855 | 0.302318  | 0.776792  | -0.110012  | -0.389108  | 1.80272369 | 0.743629   | -0.944559 | -0.219147  | -0.193765  | -0.389108 | -0.891968 | -1.549712 | -0.104394  | -0.873798  | -1.198379 | 0.793954   |           |
| IL22M1  | 0.6967533 | 0.5312553 | 0.04609   | -0.015671  | -0.558194  | 1.346681   | 1.008458   | 1.8452737  | -0.334825 | 0.6535389 | 0.1277126 | 0.1424808  | 0.3430685  | -1.10057   | -1.754584  | -0.124565 | 1.5970559  | -0.195765  | -0.389108 | -0.891968 | -1.549712 | -0.104394  | -0.873798  | -1.198379 | 0.793954   |           |
| CR61    | -0.165745 | 0.0079512 | 0.5887995 | 0.1655228  | -0.00305   | 0.3634524  | 0.8888513  | -0.163718  | -0.196959 | -0.144888 | -0.173871 | -0.193315  | 0.2938682  | 4.438595   | -0.879566  | -0.614741 | -0.808336  | -0.146361  | -0.389108 | -0.891968 | -1.549712 | -0.104394  | -0.873798  | -1.198379 | 0.793954   |           |
| TNMG11  | 0.253209  | 0.0341639 | 0.6357803 | 0.4592328  | 1.248505   | -0.188325  | 1.04000165 | -0.197154  | -0.870546 | -0.227023 | 0.8527673 | -0.602037  | 0.9689822  | 0.845828   | -2.58179   | -0.098411 | -0.453206  | -0.676052  | -0.53848  | 0.0592251 | 0.9962745 | -0.341845  | -0.216922  | 2.5905492 | 0.9165569  |           |
| MECE    | -0.64725  | 0.2047851 | 0.5516382 | 0.5741711  | 1.0975018  | 1.66323078 | 1.9310025  | -0.432975  | -0.576134 | -0.86856  | -0.75639  | -0.407329  | 0.9323469  | -0.79787   | 0.815188   | -0.765126 | 1.381564   | -0.28508   | -0.170066 | -0.161887 | -1.035394 | -0.20875   | -0.20875   | -0.20875  | -0.20875   |           |
| ATP181  | 0.8341021 | -0.088804 | 0.0307555 | 0.9362926  | 1.2975822  | 0.4472575  | 1.016028   | 2.417115   | -0.459102 | -0.86856  | -0.75639  | -0.407329  | 0.9323469  | -0.79787   | 0.815188   | -0.765126 | 1.381564   | -0.28508   | -0.170066 | -0.161887 | -1.035394 | -0.20875   | -0.20875   | -0.20875  | -0.20875   |           |
| ROIC    | -0.084371 | 1.1735749 | -0.180631 | 1.0395505  | 1.2040151  | 2.1053872  | 2.414658   | 0.808392   | -0.551262 | -0.03965  | 0.5138689 | -0.77825   | 1.4634099  | -0.023785  | -1.424857  | -0.386292 | 0.2446374  | -0.757712  | -0.532352 | -0.543383 | -0.792162 | -0.760923  | -0.109192  | -1.180301 | -0.62151   |           |
| SMVD2   | -1.525466 | -0.542791 | -0.732891 | -0.2984688 | -0.297262  | -0.467178  | -0.97553   | 0.46561932 | -0.179587 | -0.760697 | 1.0314056 | 1.2807657  | -0.107442  | -1.141536  | 0.020014   | 0.0601863 | 0.2380741  | -0.792081  | -0.29839  | -0.190265 | 1.1977673 | 0.7306297  | -0.286291  | 1.1840672 | 0.823854   |           |
| SI00A8  | -0.179904 | -0.537716 | -0.802382 | -0.694638  | -0.671011  | -0.954232  | -1.163818  | 0.2065913  | -0.179587 | -0.760697 | 1.0314056 | 1.2807657  | -0.107442  | -1.141536  | 0.020014   | 0.0601863 | 0.2380741  | -0.792081  | -0.29839  | -0.190265 | 1.1977673 | 0.7306297  | -0.286291  | 1.1840672 | 0.823854   |           |
| AFR3    | 0.6635919 | -0.085636 | -0.789173 | 1.464051   | -0.390466  | -0.467534  | -0.47725   | 1.6620774  | -0.274652 | 0.0963464 | 0.213746  | -0.563736  | 0.333792   | 2.2467403  | -0.3161    | -0.348224 | -0.188696  | -0.348224  | -0.188696 | -0.348224 | -0.188696 | -0.348224  | -0.188696  | -0.348224 | -0.188696  |           |
| SR2     | -0.895209 | -0.537193 | -0.519143 | -0.733294  | -1.438095  | -0.572734  | -1.484118  | -0.028972  | 0.953154  | 0.9063122 | 0.947656  | 0.0306454  | -0.462414  | -0.776712  | 0.48849308 | 1.6249588 | -0.283201  | 0.2952066  | -0.267858 | -0.75649  | -0.134303 | -1.41737   | -0.683624  | -0.398169 | -0.75788   |           |
| MUP     | 0.8007563 | -0.132364 | 0.1766062 | 0.7142978  | -0.2589122 | -0.46407   | 0.0830095  | 0.044157   | 1.5593613 | 2.0117127 | -0.200886 | 0.5607427  | 0.315051   | -0.405703  | -0.154748  | -0.300469 | -0.3523789 | -0.850288  | -1.264025 | -0.553237 | -1.120157 | -1.43234   | -0.747074  | -0.290458 | -0.409694  |           |
| CRFB5   | -0.5606   | 0.5957154 | 3.9534785 | 0.1832536  | 0.6702461  | -0.289422  | 1.5529118  | -0.50057   | -0.057729 | -0.766891 | 0.381742  | -0.197546  | -0.068523  | 0.2966551  | 0.9197194  | -0.551766 | -0.31066   | -0.469394  | -0.459301 | -0.221175 | -0.368011 | -0.520163  | -0.747074  | -0.290458 | -0.409694  |           |
| MECE    | -0.182349 | 0.4966425 | 0.1534814 | 0.3344166  | 0.630049   | -0.574402  | 1.3647408  | -0.152788  | -1.536621 | -0.007014 | -0.793687 | -0.387903  | -0.456393  | -0.411033  | -0.321878  | -0.256153 | 0.1197914  | 1.6647458  | -0.305851 | -0.039289 | -0.42591  | -0.555811  | 3.3532262  | -0.991845 | -0.001816  |           |
| SI06A7  | 2.910305  | -0.419171 | -0.667407 | 2.9212328  | 1.1962001  | 0.3142184  | 0.0863455  | -1.16726   | -0.22162  | -0.508959 | 0.1332402 | -1.002495  | 0.5121407  | -0.287802  | 0.0456051  | -0.422755 | -0.37683   | -0.6197183 | 0.1294476 | -0.944072 | -0.878843 | -0.661479  | -0.112877  | -0.073308 | -0.94716   |           |
| NHR     | 2.0289331 | 1.683035  | 2.5430478 | 0.2660654  | 0.2453016  | -0.23639   | -0.028922  | -0.179405  | 0.7728788 | -0.30034  | -0.503935 | -1.13765   | -0.240364  | -0.137584  | 1.7113157  | -0.22433  | 0.073037   | 0.831392   | 0.1575772 | -1.036211 | -1.261135 | -1.077713  | -0.319808  | -0.39978  | -0.23643   |           |
| CH07T2  | 0.7715366 | 0.502404  | 1.5271504 | -0.207096  | 2.2009646  | -0.2699303 | 0.2997035  | -0.387718  | -0.271316 | -0.894932 | 0.5413359 | 0.0448932  | -0.643015  | 0.5547831  | 1.9951539  | -0.41591  | -0.270935  | -0.206974  | 0.5279713 | -1.237902 | -1.36857  | 0.0470644  | -0.7934783 | -1.037663 | -0.350915  |           |
| GSN     | 2.647474  | -0.310962 | 0.3623504 | 0.3087976  | 0.3329414  | 1.6143003  | 2.338152   | -0.54638   | -0.681277 | 1.7080922 | -0.35339  | -0.5630762 | 0.3228096  | 0.0972839  | -1.2324827 | -0.38918  | -0.550057  | -0.753115  | -0.10079  | -0.738244 | -0.760964 | -0.628798  | -0.499329  | -0.931693 | -0.560915  |           |
| AD03    | 2.3834831 | -0.254703 | 2.2295173 | 0.3614602  | -0.45186   | -0.415737  | -0.758924  | -0.127865  | -0.357934 | 0.449766  | 0.0306454 | -0.462414  | -0.776712  | 0.48849308 | 1.6249588  | -0.283201 | 0.2952066  | -0.267858  | -0.75649  | -0.134303 | -1.41737  | -0.683624  | -0.398169  | -0.75788  | -0.409694  |           |
| PAW1    | 2.4431308 | 0.1719871 | 1.5411896 | -0.303366  | 0.4841686  | 0.7362151  | 1.5444163  | -1.108203  | -0.337373 | 2.313392  | -0.639013 | -0.16192   | -0.604579  | 0.3037385  | -0.02748   | -0.297978 | -0.386797  | -1.000483  | 0.6421377 | -0.755036 | -0.931611 | -0.895293  | -0.5239    | -0.752686 | -0.44427   |           |
| HMG42   | -0.556833 | -0.468183 | -0.511941 | -0.52781   | -0.559446  | -1.042178  | -0.975164  | -0.55645   | -0.559748 | 0.1339592 | 0.1449494 | -0.554408  | -0.1041278 | 1.9342467  | -0.011126  | 0.2947178 | -0.495322  | -0.53775   | 0.214151  | 1.5506629 | 2.8062471 | 0.1855814  | 0.9904355  | -0.412491 | 1.5913939  |           |
| MM93    | -0.588378 | -0.40688  | -0.58323  | -0.561369  | -0.457122  | -0.585382  | -0.484325  | -0.350383  | -0.583738 | -0.546396 | 1.0438901 | -0.378448  | -0.283049  | -0.538389  | 0.2083871  | -0.567344 | -0.537362  | -0.53775   | 0.214151  | 1.5506629 | 2.8062471 | 0.1855814  | 0.9904355  | -0.412491 | 1.5913939  |           |
| PD04    | 1.2905051 | -0.371769 | 1.3689546 | 1.8001072  | 1.1769641  | 0.48705304 | 0.831764   | -0.519693  | 0.1332575 | 0.5118395 | 0.734365  | -0.734365  | -0.339338  | 2.2220993  | 0.1159821  | -0.849591 | -1.06658   | -0.44664   | -0.47906  | -1.769896 | 0.4657599 | -0.240805  | -1.118214  | -0.193256 | 1.800678   |           |
| VEFC    | -0.852461 | 0.8737664 | 2.246038  | 0.1606014  | 1.508445   | -0.363245  | 1.8932839  | -0.02907   | -1.15258  | -0.99626  | -0.161605 | -0.161605  | -0.2978    | 0.039485   | -1.085497  | 0.819027  | -0.483351  | -1.04658   | -0.57894  | -0.159539 | 0.870504  | 0.4657599  | -0.240805  | -1.118214 | -0.193256  |           |
| DIG2    | 2.5472288 | -0.650537 | 1.395666  | 0.8739317  | 0.2924788  | -0.06256   | -0.073688  | -0.701418  | 1.3702438 | 1.2280012 | -0.666536 | 1.330432   | -0.496976  | 1.149317   | 1.1868286  | -0.204233 | -0.526932  | -1.46894   | -0.15838  | -0.25376  | -1.54446  | -0.123467  | -0.561684  | -0.86831  | -0.346033  |           |
| DH37    | -1.160631 | -0.640492 | -0.792355 | -0.521786  | -0.071289  | -0.582595  | -0.440409  | -0.86647   | 1.8941668 | 0.3294391 | -0.700104 | -0.565245  | -0.265457  | -0.854868  | -0.2078827 | -0.193691 | -0.297036  | 0.6698381  | -0.907328 | 0.0476182 | 0.7156542 | -0.0217495 | 1.1532962  | 2.2451707 | 0.6174916  |           |
| TPM1    | 2.8585661 | 0.513508  | 0.6433968 | -0.121297  | 1.717315   | -0.47373   | 0.0928464  | 1.4597200  | -0.991401 | -0.965447 | -0.611867 | -0.927637  | -0.555865  | -0.098727  | 2.2019572  | -0.156361 | -0.37604   | 0.7407008  | -0.608567 | -0.90305  | -1.41506  | -0.464819  | -0.355508  | -0.301318 | -0.7967639 |           |
| CCD3    | 1.7902801 | 1.048901  | 1.3851736 | -0.034023  | -0.664275  | -0.595902  | 0.8056014  | -0.71781   | 0.8581612 | 0.024288  | -0.593065 | -0.104594  | -0.754122  | 1.814632   | -0.80331   | 0.3698612 | 0.2081658  | 1.651939   | 0.5024078 | -0.262908 | -1.2442   | -0.182556  | -0.637362  | -1.870211 | -0.513751  |           |
| SI05M4  | -0.661815 | -0.072021 | -0.155197 | 0.5606062  | 2.9899676  | 1.6527745  | -0.270842  | -0.17394   | 0.4655333 | -0.392584 | -0.259085 | -0.134448  | -0.554329  | -0.380339  | -0.443429  | -0.383147 | 0.0298627  | 0.8757809  | -0.680331 | -0.87795  | -0.293667 | -0.755292  | -0.667335  | -0.991146 | -0.905877  |           |
| CC128   | 0.2668333 | -0.315075 | 1.4959527 | -0.219706  | 0.6819934  | 1.5911564  | 1.8282848  | 2.2701485  | -0.362481 | -0.362481 | -0.205575 | -0.109452  | -0.232949  | -0.330669  | -0.731232  | -0.31393  | -0.194565  | -0.70651   | 1.3258693 | -0.355729 | -0.747549 | -1.138167  | -0.904391  | -0.38887  | -0.20255   |           |
| ZIC1    | -0.500511 | -0.742389 | -0.246774 | 1.4141203  |            |            |            |            |           |           |           |            |            |            |            |           |            |            |           |           |           |            |            |           |            |           |



|          |           |            |            |           |           |            |           |           |            |           |           |            |            |            |            |            |            |           |            |            |            |           |           |           |            |            |           |
|----------|-----------|------------|------------|-----------|-----------|------------|-----------|-----------|------------|-----------|-----------|------------|------------|------------|------------|------------|------------|-----------|------------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|
| MTSS1    | -0.309988 | -1.357491  | -0.075218  | -0.230711 | -0.95069  | -1.030662  | -0.895621 | 0.8584561 | 0.613033   | 0.5410994 | -0.581553 | -0.683048  | -1.240194  | 1.0750281  | 0.0660095  | -0.691088  | -0.373141  | 3.0960621 | 0.0519745  | -0.596138  | 0.01001652 | 0.4327061 | -0.163302 | 2.1125442 | -0.135716  | 0.3152418  |           |
| CHS1T1   | -0.288362 | -0.615122  | -0.528205  | -0.743201 | -0.544518 | -0.742802  | -0.441516 | -0.312151 | -0.862068  | -0.288395 | 0.1250542 | 1.225758   | 0.5890229  | 1.5506949  | -1.588794  | -0.934337  | 0.25257429 | -0.203567 | 2.4967416  | -0.190903  | 0.501807   | 1.3141388 | 0.1229072 | 1.7415921 | -0.420404  | -0.245021  |           |
| ANPMT17  | -0.371823 | 2.8015942  | 1.3318289  | -0.430566 | 2.8129536 | 1.8913217  | -0.58321  | -0.298325 | -0.488899  | 0.298325  | -0.32688  | -0.343566  | -0.109060  | -0.323462  | -0.597045  | -0.91066   | -0.332297  | 1.282037  | -0.391204  | -0.299588  | -0.331181  | -0.597005 | -0.597045 | -0.597045 | -0.597045  | -0.597045  |           |
| IMD1C    | 0.5650591 | 0.2912673  | 1.2141383  | 0.7823818 | 2.762466  | -0.712466  | 0.7676146 | 0.20546   | -0.729988  | -0.794105 | 1.1366627 | -0.6272194 | -0.629742  | 0.4274653  | 2.2661427  | -0.134072  | -0.565354  | -1.821592 | -0.614047  | 0.0374417  | -0.340205  | -1.108759 | -0.687731 | -0.612012 | -0.127074  | -0.612863  |           |
| ID4      | 0.465358  | -0.624904  | 0.7154457  | 0.146788  | 0.4684661 | 1.071164   | 1.1579768 | -0.100809 | -0.956049  | -0.75979  | 0.707821  | -0.824614  | -0.585163  | -0.393191  | 1.2709133  | 0.113372   | 0.0502112  | -0.658761 | -0.945621  | -0.340556  | 0.0730531  | 0.0717668 | -0.88789  | -0.753499 | -0.159715  | -0.386619  |           |
| RNCAN2   | 2.4343379 | -0.247904  | 0.1714547  | 0.2685348 | 0.4684661 | 1.071164   | 1.1579768 | -0.100809 | -0.956049  | -0.75979  | 0.707821  | -0.824614  | -0.585163  | -0.393191  | 1.2709133  | 0.113372   | 0.0502112  | -0.658761 | -0.945621  | -0.340556  | 0.0730531  | 0.0717668 | -0.88789  | -0.753499 | -0.159715  | -0.386619  |           |
| OVL1     | -0.557409 | -0.232911  | 1.4069493  | 0.820668  | 0.211088  | 1.786792   | 1.6512187 | 1.4911535 | -0.459644  | -0.479955 | 0.6672483 | -0.059186  | 0.7518209  | 0.553818   | -1.527404  | -1.328607  | 0.460391   | -1.419306 | 0.0150449  | -0.359792  | -0.40369   | 0.093902  | 0.9595392 | -0.093902 | -0.9595392 | -0.792133  |           |
| BNOC2    | 0.7074912 | 2.6811131  | 1.2912059  | 1.0787281 | -0.024564 | -0.217371  | -0.235488 | -1.287185 | -0.154151  | -0.222097 | -0.060788 | -0.8261    | 0.3577889  | 1.6101486  | 0.3080411  | -0.7466    | -0.431731  | 1.1205024 | -0.3562908 | -0.871037  | -0.715183  | -1.213175 | 0.6898641 | -0.010182 | -0.707914  | -0.010182  |           |
| HN87     | -0.160686 | -0.526082  | 2.1736215  | 0.4557948 | 0.8593775 | 0.287734   | 0.3166613 | -0.612439 | -0.5557    | -0.305447 | -0.453969 | -0.821439  | 0.6509143  | 0.1797312  | -1.87973   | -0.493449  | -0.951049  | -0.615432 | -0.669028  | -0.597563  | -0.756793  | -0.664565 | -0.492423 | -0.337914 | -0.664565  |            |           |
| POON     | 1.4528523 | -0.454712  | 0.7454608  | 0.3737513 | 0.6200561 | 0.661945   | 2.0771698 | -0.702238 | -0.438338  | -0.109093 | 0.134498  | -0.807045  | 0.1234771  | 2.9746531  | -1.87973   | -0.493449  | -0.951049  | -0.615432 | -0.669028  | -0.597563  | -0.756793  | -0.664565 | -0.492423 | -0.337914 | -0.664565  |            |           |
| C12ofH5  | -1.120877 | -0.057635  | -0.970187  | -0.640565 | -0.938174 | -0.492703  | -0.471231 | 1.9731579 | 0.3825226  | -0.69386  | -0.429758 | 1.9436162  | -0.356056  | -0.296662  | 3.0244027  | -0.437928  | -0.346369  | 0.0752151 | 0.5504488  | 0.686304   | -1.056159  | 0.8338867 | -0.444506 | -0.215408 | -0.214173  | -0.285302  |           |
| RNI1     | 0.0173484 | 0.1800239  | 0.6011978  | -0.349693 | -0.352723 | -0.60165   | -0.901137 | -0.06441  | -0.255598  | -0.348784 | -0.295793 | 0.4358414  | -0.898915  | -0.414353  | -2.239022  | 0.4498457  | -0.641206  | -0.665471 | 0.5054008  | -0.180938  | 0.4725146  | 0.1332421 | 0.5862366 | 3.3023801 | 0.0253437  | 1.7295365  |           |
| DES      | 3.3262638 | 0.737355   | -0.351617  | 0.63774   | -0.149351 | 0.8248464  | 2.2500187 | -0.591345 | -0.591345  | -0.349488 | -0.118999 | -0.365996  | 0.1597426  | -0.216304  | -0.426878  | -0.1019387 | -0.084203  | -0.286535 | -0.554163  | -0.21474   | -0.4427316 | -0.585312 | -0.086796 | -1.060387 | -0.254536  | 1.3747005  |           |
| LP       | -0.609637 | -0.34556   | 1.1625316  | 2.943598  | 2.4604788 | -0.2871689 | 0.5020215 | -0.582911 | -0.869709  | -0.316583 | -0.303502 | 0.013982   | -0.0504234 | -0.204712  | 1.0789937  | -0.8271172 | -0.37184   | -0.960699 | -0.885361  | 0.394705   | -0.201548  | -0.287201 | 0.1044005 | -0.71941  | -0.261623  | -0.4857704 |           |
| RM152    | 0.9057436 | -0.3722318 | 1.1311296  | 1.2967476 | 0.5897489 | 0.5020215  | -0.582911 | -0.869709 | -0.316583  | -0.303502 | 0.013982  | -0.0504234 | -0.204712  | 1.0789937  | -0.8271172 | -0.37184   | -0.960699  | -0.885361 | 0.394705   | -0.201548  | -0.287201  | 0.1044005 | -0.71941  | -0.261623 | -0.4857704 |            |           |
| TG6T1    | -0.603637 | 0.0434445  | 1.0786293  | 2.3254443 | 0.6680307 | 0.593705   | 0.2738049 | -0.800311 | -0.346708  | -0.353347 | -0.303502 | -0.747107  | 0.8544288  | 2.1637907  | -0.983151  | -0.430281  | -0.983151  | -1.039582 | 0.0659572  | 0.7051497  | -0.393577  | -0.408541 | -0.663893 | -0.299922 | -0.458319  |            |           |
| APD1D1   | -0.602095 | 0.6041785  | 2.2420807  | 1.9065645 | 1.2187656 | 0.4161937  | 1.2271346 | -0.102225 | -0.62673   | -0.79836  | -0.813652 | -0.836568  | 0.507941   | 1.877949   | -0.412827  | -0.319405  | -0.757568  | -0.475763 | -0.66944   | -0.829272  | -0.73355   | -0.678041 | -0.539405 | -0.219320 | -0.421467  |            |           |
| RCC2     | -0.658951 | -0.138973  | -1.583116  | -0.38034  | -0.38034  | -0.365209  | -1.027201 | 1.2194167 | 0.524783   | -0.128002 | 0.2570702 | -0.38034   | -0.365209  | -0.530924  | -1.720194  | 0.4378813  | 0.6248743  | 1.8489603 | -0.550435  | 0.3428745  | 1.7786233  | -0.068271 | 1.8034163 | 1.285214  | 0.9241503  | 0.4736968  |           |
| TIME125  | -0.451632 | 2.5444105  | -0.466535  | 0.0787769 | 1.4154201 | 0.2389459  | 1.0981851 | -0.448316 | -0.4700018 | -0.470026 | 0.0163074 | -0.62292   | 0.0741969  | -1.33175   | -1.443445  | 0.6344484  | 0.2554364  | -0.174304 | 0.66861285 | -0.350132  | -0.424062  | -0.458507 | 0.231751  | 2.5497169 | -1.076591  | -1.174511  |           |
| KR2B28   | -0.283226 | -0.384042  | 0.0293484  | -0.730683 | -1.618375 | 0.656375   | -0.598721 | 1.9802472 | -0.131606  | -0.973887 | -1.214615 | -0.404834  | -0.31334   | 0.0297176  | 1.9717742  | -0.062061  | -1.027871  | 2.2991426 | -0.294632  | 0.7532431  | 1.6131263  | 0.5668474 | 0.0616342 | -0.309923 | 0.0020407  | 0.38658    |           |
| RTAP11.1 | -0.243506 | -0.243506  | 1.3090195  | 1.4181485 | -0.243506 | 4.3154349  | 0.1710027 | -0.243506 | -0.243506  | -0.243506 | -0.243506 | -0.243506  | -0.243506  | -0.243506  | -0.243506  | -0.243506  | -0.243506  | -0.243506 | -0.243506  | -0.243506  | -0.243506  | -0.243506 | -0.243506 | -0.243506 | -0.243506  | -0.243506  |           |
| CADMI    | -0.68877  | -1.67095   | 0.0524425  | 0.5877093 | 0.8161236 | 0.237263   | 0.0799917 | 0.7761583 | 1.130921   | 2.0487428 | -1.201588 | 0.448567   | -0.208148  | -0.172637  | 1.1560634  | 0.5808742  | 0.7110283  | 1.2867025 | 0.247398   | -1.53171   | -1.891427  | 0.0277001 | 0.657724  | 1.325062  | 0.580754   | -0.513355  |           |
| HLI3     | -0.49144  | 0.1154693  | -0.593113  | -0.414408 | -0.08726  | -0.291616  | -0.439308 | 1.1842712 | -0.701211  | -0.116496 | -0.535355 | 0.21207    | -0.967476  | -0.60529   | -2.425005  | 0.7723259  | -1.325158  | -0.354121 | 0.4327459  | 0.1617293  | 0.0828513  | 0.8276063 | 2.7573182 | 0.5781606 | 1.756338   |            |           |
| ICGAP3   | -0.548237 | -0.825431  | -0.453824  | -0.577273 | -0.734672 | -0.783397  | -0.350268 | 2.1641457 | 0.1529534  | -0.423997 | -0.436576 | -0.767456  | -1.313642  | -0.204716  | -1.139832  | 0.5994425  | 1.1448688  | 2.5039891 | -0.207603  | -0.643668  | 1.0139353  | -0.448928 | -0.194138 | 1.7769817 | -0.095939  | 0.7961235  |           |
| TOB2     | -0.465966 | 0.2854847  | 3.17166967 | -0.287381 | 0.8642312 | 0.7863015  | 0.57053   | -0.761758 | -0.071547  | -0.53894  | -0.525458 | 0.1355119  | 0.8602559  | 2.3859628  | -0.406537  | -0.821876  | -0.524881  | -0.389401 | -0.995562  | 0.04051175 | -1.133352  | -0.859876 | -0.7491   | -0.181718 | -0.793793  |            |           |
| TMFRSS2  | 2.0844766 | -0.715288  | 2.4555221  | 0.6594905 | 1.3047098 | 0.9684397  | 1.921515  | -0.37327  | -0.720378  | -0.254475 | -0.720378 | -1.183457  | 0.201665   | 0.5901551  | -0.343794  | -0.466357  | -0.722117  | -0.722117 | -0.722117  | -0.722117  | -0.722117  | -0.722117 | -0.722117 | -0.722117 | -0.722117  | -0.722117  |           |
| HLI2H2AC | -1.202303 | -1.076659  | -0.958132  | -0.410687 | 0.2004598 | -0.375557  | -0.454055 | -1.502148 | -0.254475  | -0.20685  | 1.3519046 | -0.291919  | -0.375557  | 2.9692347  | -0.375557  | -0.375557  | -0.375557  | -0.375557 | -0.375557  | -0.375557  | -0.375557  | -0.375557 | -0.375557 | -0.375557 | -0.375557  | -0.375557  |           |
| SLI73    | 0.8500158 | -0.222386  | 19340015   | -0.247371 | 0.1030932 | -0.033651  | 0.3946639 | -0.67815  | -0.588105  | 1.2077779 | -0.492067 | 0.0163074  | -0.62292   | 0.0741969  | -1.33175   | -1.443445  | 0.6344484  | 0.2554364 | -0.174304  | 0.66861285 | -0.350132  | -0.424062 | -0.458507 | 0.231751  | 2.5497169  | -1.076591  | -1.174511 |
| PD4F     | -0.187617 | -0.369497  | 1.0423027  | -0.365809 | 1.802401  | 0.0607872  | 0.0686422 | 0.155009  | -0.71448   | -0.529823 | -1.06373  | 3.7169326  | -0.062591  | 1.2521892  | 0.3073858  | 0.0337609  | -0.454165  | -0.660614 | -0.670731  | -0.679326  | -0.882217  | -0.560162 | -0.365472 | -0.426669 | -0.405399  | -0.50746   | -0.70015  |
| MAIF     | -0.367781 | 0.139726   | 1.509639   | 0.0843276 | 0.424056  | 0.2982148  | 2.803408  | 0.286727  | -0.16703   | -0.529823 | -1.06373  | 3.7169326  | -0.062591  | 1.2521892  | 0.3073858  | 0.0337609  | -0.454165  | -0.660614 | -0.670731  | -0.679326  | -0.882217  | -0.560162 | -0.365472 | -0.426669 | -0.405399  | -0.50746   | -0.70015  |
| ZFP5611  | 0.1914642 | 0.2000036  | 2.362368   | 1.3060248 | -0.344267 | 0.2453473  | 0.6817095 | 0.1749576 | -0.215619  | -0.471979 | -1.017669 | 0.891197   | -0.22976   | 3.3234519  | -0.647316  | -0.216225  | -0.79139   | 0.0854661 | 0.3004573  | -0.755874  | -0.490645  | -0.937434 | -0.43284  | -0.795165 | -0.270194  | -0.338864  |           |
| LVG2     | -0.36671  | -0.256805  | 1.5838091  | 1.0806846 | -0.347669 | 3.7518126  | 1.6384099 | -0.372581 | -0.420088  | -0.372581 | -0.073893 | -0.145546  | -0.202686  | -0.3441501 | -0.762737  | -0.815341  | -0.339346  | -0.182565 | -0.151192  | -0.580309  | -0.365971  | -0.316937 | -0.683028 | -0.796307 | -0.456791  | -0.67091   |           |
| PTCH1    | 2.8665511 | 0.3850707  | 0.4901304  | 1.8214105 | 0.7112616 | -0.144771  | 0.0473433 | -1.66361  | 0.3484458  | -0.729909 | -0.277302 | -1.650681  | -0.410895  | -0.490676  | 1.1861469  | -0.458612  | -0.360185  | 0.8981236 | 0.337191   | -1.080299  | -0.365971  | -0.316937 | -0.683028 | -0.796307 | -0.456791  | -0.67091   |           |
| RSC2     | -0.738952 | 1.337244   | 3.322865   | 0.4813793 | 0.9691218 | 0.8508583  | 0.1833816 | 0.9368576 | -0.782051  | -0.252915 | -0.489719 | -1.183457  | 0.201665   | 0.5901551  | -0.343794  | -0.466357  | -0.722117  | -0.722117 | -0.722117  | -0.722117  | -0.722117  | -0.722117 | -0.722117 | -0.722117 | -0.722117  | -0.722117  |           |
| C12ofH4  | -2.093615 | 0.4773853  | -1.544877  | 0.1726253 | -0.957241 | -0.730254  | -0.827147 | 0.079177  | -1.380545  | 0.7112827 | -0.723405 | 1.466058   | -1.813542  | 0.0774339  | 1.2281963  | 0.9218053  | -0.583135  | 0.2513355 | 0.9279536  | 1.509714   | 0.61453    |           |           |           |            |            |           |



## Appendix 6.

### Linear mixed effects model results



[illegible]



|      |      |      |      |      |      |      |      |      |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        | 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|------|------|------|------|------|------|------|------|------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|----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| AMN1 | AMN2 | AMN3 | AMN4 | AMN5 | AMN6 | AMN7 | AMN8 | AMN9 | AMN10 | AMN11 | AMN12 | AMN13 | AMN14 | AMN15 | AMN16 | AMN17 | AMN18 | AMN19 | AMN20 | AMN21 | AMN22 | AMN23 | AMN24 | AMN25 | AMN26 | AMN27 | AMN28 | AMN29 | AMN30 | AMN31 | AMN32 | AMN33 | AMN34 | AMN35 | AMN36 | AMN37 | AMN38 | AMN39 | AMN40 | AMN41 | AMN42 | AMN43 | AMN44 | AMN45 | AMN46 | AMN47 | AMN48 | AMN49 | AMN50 | AMN51 | AMN52 | AMN53 | AMN54 | AMN55 | AMN56 | AMN57 | AMN58 | AMN59 | AMN60 | AMN61 | AMN62 | AMN63 | AMN64 | AMN65 | AMN66 | AMN67 | AMN68 | AMN69 | AMN70 | AMN71 | AMN72 | AMN73 | AMN74 | AMN75 | AMN76 | AMN77 | AMN78 | AMN79 | AMN80 | AMN81 | AMN82 | AMN83 | AMN84 | AMN85 | AMN86 | AMN87 | AMN88 | AMN89 | AMN90 | AMN91 | AMN92 | AMN93 | AMN94 | AMN95 | AMN96 | AMN97 | AMN98 | AMN99 | AMN100 | AMN101 | AMN102 | AMN103 | AMN104 | AMN105 | AMN106 | AMN107 | AMN108 | AMN109 | AMN110 | AMN111 | AMN112 | AMN113 | AMN114 | AMN115 | AMN116 | AMN117 | AMN118 | AMN119 | AMN120 | AMN121 | AMN122 | AMN123 | 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|------|------|------|------|------|------|------|------|------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|----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|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-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| 0001 | 0002 | 0003 | 0004 | 0005 | 0006 | 0007 | 0008 | 0009 | 0010 | 0011 | 0012 | 0013 | 0014 | 0015 | 0016 | 0017 | 0018 | 0019 | 0020 | 0021 | 0022 | 0023 | 0024 | 0025 | 0026 | 0027 | 0028 | 0029 | 0030 | 0031 | 0032 | 0033 | 0034 | 0035 | 0036 | 0037 | 0038 | 0039 | 0040 | 0041 | 0042 | 0043 | 0044 | 0045 | 0046 | 0047 | 0048 | 0049 | 0050 | 0051 | 0052 | 0053 | 0054 | 0055 | 0056 | 0057 | 0058 | 0059 | 0060 | 0061 | 0062 | 0063 | 0064 | 0065 | 0066 | 0067 | 0068 | 0069 | 0070 | 0071 | 0072 | 0073 | 0074 | 0075 | 0076 | 0077 | 0078 | 0079 | 0080 | 0081 | 0082 | 0083 | 0084 | 0085 | 0086 | 0087 | 0088 | 0089 | 0090 | 0091 | 0092 | 0093 | 0094 | 0095 | 0096 | 0097 | 0098 | 0099 | 0100 | 0101 | 0102 | 0103 | 0104 | 0105 | 0106 | 0107 | 0108 | 0109 | 0110 | 0111 | 0112 | 0113 | 0114 | 0115 | 0116 | 0117 | 0118 | 0119 | 0120 | 0121 | 0122 | 0123 | 0124 | 0125 | 0126 | 0127 | 0128 | 0129 | 0130 | 0131 | 0132 | 0133 | 0134 | 0135 | 0136 | 0137 | 0138 | 0139 | 0140 | 0141 | 0142 | 0143 | 0144 | 0145 | 0146 | 0147 | 0148 | 0149 | 0150 | 0151 | 0152 | 0153 | 0154 | 0155 | 0156 | 0157 | 0158 | 0159 | 0160 | 0161 | 0162 | 0163 | 0164 | 0165 | 0166 | 0167 | 0168 | 0169 | 0170 | 0171 | 0172 | 0173 | 0174 | 0175 | 0176 | 0177 | 0178 | 0179 | 0180 | 0181 | 0182 | 0183 | 0184 | 0185 | 0186 | 0187 | 0188 | 0189 | 0190 | 0191 | 0192 | 0193 | 0194 | 0195 | 0196 | 0197 | 0198 | 0199 | 0200 | 0201 | 0202 | 0203 | 0204 | 0205 | 0206 | 0207 | 0208 | 0209 | 0210 | 0211 | 0212 | 0213 | 0214 | 0215 | 0216 | 0217 | 0218 | 0219 | 0220 | 0221 | 0222 | 0223 | 0224 | 0225 | 0226 | 0227 | 0228 | 0229 | 0230 | 0231 | 0232 | 0233 | 0234 | 0235 | 0236 | 0237 | 0238 | 0239 | 0240 | 0241 | 0242 | 0243 | 0244 | 0245 | 0246 | 0247 | 0248 | 0249 | 0250 | 0251 | 0252 | 0253 | 0254 | 0255 | 0256 | 0257 | 0258 | 0259 | 0260 | 0261 | 0262 | 0263 | 0264 | 0265 | 0266 | 0267 | 0268 | 0269 | 0270 | 0271 | 0272 | 0273 | 0274 | 0275 | 0276 | 0277 | 0278 | 0279 | 0280 | 0281 | 0282 | 0283 | 0284 | 0285 | 0286 | 0287 | 0288 | 0289 | 0290 | 0291 | 0292 | 0293 | 0294 | 0295 | 0296 | 0297 | 0298 | 0299 | 0300 | 0301 | 0302 | 0303 | 0304 | 0305 | 0306 | 0307 | 0308 | 0309 | 0310 | 0311 | 0312 | 0313 | 0314 | 0315 | 0316 | 0317 | 0318 | 0319 | 0320 | 0321 | 0322 | 0323 | 0324 | 0325 | 0326 | 0327 | 0328 | 0329 | 0330 | 0331 | 0332 | 0333 | 0334 | 0335 | 0336 | 0337 | 0338 | 0339 | 0340 | 0341 | 0342 | 0343 | 0344 | 0345 | 0346 | 0347 | 0348 | 0349 | 0350 | 0351 | 0352 | 0353 | 0354 | 0355 | 0356 | 0357 | 0358 | 0359 | 0360 | 0361 | 0362 | 0363 | 0364 | 0365 | 0366 | 0367 | 0368 | 0369 | 0370 | 0371 | 0372 | 0373 | 0374 | 0375 | 0376 | 0377 | 0378 | 0379 | 0380 | 0381 | 0382 | 0383 | 0384 | 0385 | 0386 | 0387 | 0388 | 0389 | 0390 | 0391 | 0392 | 0393 | 0394 | 0395 | 0396 | 0397 | 0398 | 0399 | 0400 | 0401 | 0402 | 0403 | 0404 | 0405 | 0406 | 0407 | 0408 | 0409 | 0410 | 0411 | 0412 | 0413 | 0414 | 0415 | 0416 | 0417 | 0418 | 0419 | 0420 | 0421 | 0422 | 0423 | 0424 | 0425 | 0426 | 0427 | 0428 | 0429 | 0430 | 0431 | 0432 | 0433 | 0434 | 0435 | 0436 | 0437 | 0438 | 0439 | 0440 | 0441 | 0442 | 0443 | 0444 | 0445 | 0446 | 0447 | 0448 | 0449 | 0450 | 0451 | 0452 | 0453 | 0454 | 0455 | 0456 | 0457 | 0458 | 0459 | 0460 | 0461 | 0462 | 0463 | 0464 | 0465 | 0466 | 0467 | 0468 | 0469 | 0470 | 0471 | 0472 | 0473 | 0474 | 0475 | 0476 | 0477 | 0478 | 0479 | 0480 | 0481 | 0482 | 0483 | 0484 | 0485 | 0486 | 0487 | 0488 | 0489 | 0490 | 0491 | 0492 | 0493 | 0494 | 0495 | 0496 | 0497 | 0498 | 0499 | 0500 | 0501 | 0502 | 0503 | 0504 | 0505 | 0506 | 0507 | 0508 | 0509 | 0510 | 0511 | 0512 | 0513 | 0514 | 0515 | 0516 | 0517 | 0518 | 0519 | 0520 | 0521 | 0522 | 0523 | 0524 | 0525 | 0526 | 0527 | 0528 | 0529 | 0530 | 0531 | 0532 | 0533 | 0534 | 0535 | 0536 | 0537 | 0538 | 0539 | 0540 | 0541 | 0542 | 0543 | 0544 | 0545 | 0546 | 0547 | 0548 | 0549 | 0550 | 0551 | 0552 | 0553 | 0554 | 0555 | 0556 | 0557 | 0558 | 0559 | 0560 | 0561 | 0562 | 0563 | 0564 | 0565 | 0566 | 0567 | 0568 | 0569 | 0570 | 0571 | 0572 | 0573 | 0574 | 0575 | 0576 | 0577 | 0578 | 0579 | 0580 | 0581 | 0582 | 0583 | 0584 | 0585 | 0586 | 0587 | 0588 | 0589 | 0590 | 0591 | 0592 | 0593 | 0594 | 0595 | 0596 | 0597 | 0598 | 0599 | 0600 | 0601 | 0602 | 0603 | 0604 | 0605 | 0606 | 0607 | 0608 | 0609 | 0610 | 0611 | 0612 | 0613 | 0614 | 0615 | 0616 | 0617 | 0618 | 0619 | 0620 | 0621 | 0622 | 0623 | 0624 | 0625 | 0626 | 0627 | 0628 | 0629 | 0630 | 0631 | 0632 | 0633 | 0634 | 0635 | 0636 | 0637 | 0638 | 0639 | 0640 | 0641 | 0642 | 0643 | 0644 | 0645 | 0646 | 0647 | 0648 | 0649 | 0650 | 0651 | 0652 | 0653 | 0654 | 0655 | 0656 | 0657 | 0658 | 0659 | 0660 | 0661 | 0662 | 0663 | 0664 | 0665 | 0666 | 0667 | 0668 | 0669 | 0670 | 0671 | 0672 | 0673 | 0674 | 0675 | 0676 | 0677 | 0678 | 0679 | 0680 | 0681 | 0682 | 0683 | 0684 | 0685 | 0686 | 0687 | 0688 | 0689 | 0690 | 0691 | 0692 | 0693 | 0694 | 0695 | 0696 | 0697 | 0698 | 0699 | 0700 | 0701 | 0702 | 0703 | 0704 | 0705 | 0706 | 0707 | 0708 | 0709 | 0710 | 0711 | 0712 | 0713 | 0714 | 0715 | 0716 | 0717 | 0718 | 0719 | 0720 | 0721 | 0722 | 0723 | 0724 | 0725 | 0726 | 0727 | 0728 | 0729 | 0730 | 0731 | 0732 | 0733 | 0734 | 0735 | 0736 | 0737 | 0738 | 0739 | 0740 | 0741 | 0742 | 0743 | 0744 | 0745 | 0746 | 0747 | 0748 | 0749 | 0750 | 0751 | 0752 | 0753 | 0754 | 0755 | 0756 | 0757 | 0758 | 0759 | 0760 | 0761 | 0762 | 0763 | 0764 | 0765 | 0766 | 0767 | 0768 | 0769 | 0770 | 0771 | 0772 | 0773 | 0774 | 0775 | 0776 | 0777 | 0778 | 0779 | 0780 | 0781 | 0782 | 0783 | 0784 | 0785 | 0786 | 0787 | 0788 | 0789 | 0790 | 0791 | 0792 | 0793 | 0794 | 0795 | 0796 | 0797 | 0798 | 0799 | 0800 | 0801 | 0802 | 0803 | 0804 | 0805 | 0806 | 0807 | 0808 | 0809 | 0810 | 0811 | 0812 | 0813 | 0814 | 0815 | 0816 | 0817 | 0818 | 0819 | 0820 | 0821 | 0822 | 0823 | 0824 | 0825 | 0826 | 0827 | 0828 | 0829 | 0830 | 0831 | 0832 | 0833 | 0834 | 0835 | 0836 | 0837 | 0838 | 0839 | 0840 | 0841 | 0842 | 0843 | 0844 | 0845 | 0846 | 0847 | 0848 | 0849 | 0850 | 0851 | 0852 | 0853 | 0854 | 0855 | 0856 | 0857 | 0858 | 0859 | 0860 | 0861 | 0862 | 0863 | 0864 | 0865 | 0866 | 0867 | 0868 | 0869 | 0870 | 0871 | 0872 | 0873 | 0874 | 0875 | 0876 | 0877 | 0878 | 0879 | 0880 | 0881 | 0882 | 0883 | 0884 | 0885 | 0886 | 0887 | 0888 | 0889 | 0890 | 0891 | 0892 | 0893 | 0894 | 0895 | 0896 | 0897 | 0898 | 0899 | 0900 | 0901 | 0902 | 0903 | 0904 | 0905 | 0906 | 0907 | 0908 | 0909 | 0910 | 0911 | 0912 | 0913 | 0914 | 0915 | 0916 | 0917 | 0918 | 0919 | 0920 | 0921 | 0922 | 0923 | 0924 | 0925 | 0926 | 0927 | 0928 | 0929 | 0930 | 0931 | 0932 | 0933 | 0934 | 0935 | 0936 | 0937 | 0938 | 0939 | 0940 | 0941 | 0942 | 0943 | 0944 | 0945 | 0946 | 0947 | 0948 | 0949 | 0950 | 0951 | 0952 | 0953 | 0954 | 0955 | 0956 | 0957 | 0958 | 0959 | 0960 | 0961 | 0962 | 0963 | 0964 | 0965 | 0966 | 0967 | 0968 | 0969 | 0970 | 0971 | 0972 | 0973 | 0974 | 0975 | 0976 | 0977 | 0978 | 0979 | 0980 | 0981 | 0982 | 0983 | 0984 | 0985 | 0986 | 0987 | 0988 | 0989 | 0990 | 0991 | 0992 | 0993 | 0994 | 0995 | 0996 | 0997 | 0998 | 0999 | 1000 |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-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| CMR00 | CMR01 | CMR02 | CMR03 | CMR04 | CMR05 | CMR06 | CMR07 | CMR08 | CMR09 | CMR10 | CMR11 | CMR12 | CMR13 | CMR14 | CMR15 | CMR16 | CMR17 | CMR18 | CMR19 | CMR20 | CMR21 | CMR22 | CMR23 | CMR24 | CMR25 | CMR26 | CMR27 | CMR28 | CMR29 | CMR30 | CMR31 | CMR32 | CMR33 | CMR34 | CMR35 | CMR36 | CMR37 | CMR38 | CMR39 | CMR40 | CMR41 | CMR42 | CMR43 | CMR44 | CMR45 | CMR46 | CMR47 | CMR48 | CMR49 | CMR50 | CMR51 | CMR52 | CMR53 | CMR54 | CMR55 | CMR56 | CMR57 | CMR58 | CMR59 | CMR60 | CMR61 | CMR62 | CMR63 | CMR64 | CMR65 | CMR66 | CMR67 | CMR68 | CMR69 | CMR70 | CMR71 | CMR72 | CMR73 | CMR74 | CMR75 | CMR76 | CMR77 | CMR78 | CMR79 | CMR80 | CMR81 | CMR82 | CMR83 | CMR84 | CMR85 | CMR86 | CMR87 | CMR88 | CMR89 | CMR90 | CMR91 | CMR92 | CMR93 | CMR94 | CMR95 | CMR96 | CMR97 | CMR98 | CMR99 | CMR100 | CMR101 | CMR102 | CMR103 | CMR104 | CMR105 | CMR106 | CMR107 | CMR108 | CMR109 | CMR110 | CMR111 | CMR112 | CMR113 | CMR114 | CMR115 | CMR116 | CMR117 | CMR118 | CMR119 | CMR120 | CMR121 | 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|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|-----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185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 524 | 525 | 526 | 527 | 528 | 529 | 530 | 531 | 532 | 533 | 534 | 535 | 536 | 537 | 538 | 539 | 540 | 541 | 542 | 543 | 544 | 545 | 546 | 547 | 548 | 549 | 550 | 551 | 552 | 553 | 554 | 555 | 556 | 557 | 558 | 559 | 560 | 561 | 562 | 563 | 564 | 565 | 566 | 567 | 568 | 569 | 570 | 571 | 572 | 573 | 574 | 575 | 576 | 577 | 578 | 579 | 580 | 581 | 582 | 583 | 584 | 585 | 586 | 587 | 588 | 589 | 590 | 591 | 592 | 593 | 594 | 595 | 596 | 597 | 598 | 599 | 600 | 601 | 602 | 603 | 604 | 605 | 606 | 607 | 608 | 609 | 610 | 611 | 612 | 613 | 614 | 615 | 616 | 617 | 618 | 619 | 620 | 621 | 622 | 623 | 624 | 625 | 626 | 627 | 628 | 629 | 630 | 631 | 632 | 633 | 634 | 635 | 636 | 637 | 638 | 639 | 640 | 641 | 642 | 643 | 644 | 645 | 646 | 647 | 648 | 649 | 650 | 651 | 652 | 653 | 654 | 655 | 656 | 657 | 658 | 659 | 660 | 661 | 662 | 663 | 664 | 665 | 666 | 667 | 668 | 669 | 670 | 671 | 672 | 673 | 674 | 675 | 676 | 677 | 678 | 679 | 680 | 681 | 682 | 683 | 684 | 685 | 686 | 687 | 688 | 689 | 690 | 691 | 692 | 693 | 694 | 695 | 696 | 697 | 698 | 699 | 700 | 701 | 702 | 703 | 704 | 705 | 706 | 707 | 708 | 709 | 710 | 711 | 712 | 713 | 714 | 715 | 716 | 717 | 718 | 719 | 720 | 721 | 722 | 723 | 724 | 725 | 726 | 727 | 728 | 729 | 730 | 731 | 732 | 733 | 734 | 735 | 736 | 737 | 738 | 739 | 740 | 741 | 742 | 743 | 744 | 745 | 746 | 747 | 748 | 749 | 750 | 751 | 752 | 753 | 754 | 755 | 756 | 757 | 758 | 759 | 760 | 761 | 762 | 763 | 764 | 765 | 766 | 767 | 768 | 769 | 770 | 771 | 772 | 773 | 774 | 775 | 776 | 777 | 778 | 779 | 780 | 781 | 782 | 783 | 784 | 785 | 786 | 787 | 788 | 789 | 790 | 791 | 792 | 793 | 794 | 795 | 796 | 797 | 798 | 799 | 800 | 801 | 802 | 803 | 804 | 805 | 806 | 807 | 808 | 809 | 810 | 811 | 812 | 813 | 814 | 815 | 816 | 817 | 818 | 819 | 820 | 821 | 822 | 823 | 824 | 825 | 826 | 827 | 828 | 829 | 830 | 831 | 832 | 833 | 834 | 835 | 836 | 837 | 838 | 839 | 840 | 841 | 842 | 843 | 844 | 845 | 846 | 847 | 848 | 849 | 850 | 851 | 852 | 853 | 854 | 855 | 856 | 857 | 858 | 859 | 860 | 861 | 862 | 863 | 864 | 865 | 866 | 867 | 868 | 869 | 870 | 871 | 872 | 873 | 874 | 875 | 876 | 877 | 878 | 879 | 880 | 881 | 882 | 883 | 884 | 885 | 886 | 887 | 888 | 889 | 890 | 891 | 892 | 893 | 894 | 895 | 896 | 897 | 898 | 899 | 900 | 901 | 902 | 903 | 904 | 905 | 906 | 907 | 908 | 909 | 910 | 911 | 912 | 913 | 914 | 915 | 916 | 917 | 918 | 919 | 920 | 921 | 922 | 923 | 924 | 925 | 926 | 927 | 928 | 929 | 930 | 931 | 932 | 933 | 934 | 935 | 936 | 937 | 938 | 939 | 940 | 941 | 942 | 943 | 944 | 945 | 946 | 947 | 948 | 949 | 950 | 951 | 952 | 953 | 954 | 955 | 956 | 957 | 958 | 959 | 960 | 961 | 962 | 963 | 964 | 965 | 966 | 967 | 968 | 969 | 970 | 971 | 972 | 973 | 974 | 975 | 976 | 977 | 978 | 979 | 980 | 981 | 982 | 983 | 984 | 985 | 986 | 987 | 988 | 989 | 990 | 991 | 992 | 993 | 994 | 995 | 996 | 997 | 998 | 999 | 1000 |
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185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 524 | 525 | 526 | 527 | 528 | 529 | 530 | 531 | 532 | 533 | 534 | 535 | 536 | 537 | 538 | 539 | 540 | 541 | 542 | 543 | 544 | 545 | 546 | 547 | 548 | 549 | 550 | 551 | 552 | 553 | 554 | 555 | 556 | 557 | 558 | 559 | 560 | 561 | 562 | 563 | 564 | 565 | 566 | 567 | 568 | 569 | 570 | 571 | 572 | 573 | 574 | 575 | 576 | 577 | 578 | 579 | 580 | 581 | 582 | 583 | 584 | 585 | 586 | 587 | 588 | 589 | 590 | 591 | 592 | 593 | 594 | 595 | 596 | 597 | 598 | 599 | 600 | 601 | 602 | 603 | 604 | 605 | 606 | 607 | 608 | 609 | 610 | 611 | 612 | 613 | 614 | 615 | 616 | 617 | 618 | 619 | 620 | 621 | 622 | 623 | 624 | 625 | 626 | 627 | 628 | 629 | 630 | 631 | 632 | 633 | 634 | 635 | 636 | 637 | 638 | 639 | 640 | 641 | 642 | 643 | 644 | 645 | 646 | 647 | 648 | 649 | 650 | 651 | 652 | 653 | 654 | 655 | 656 | 657 | 658 | 659 | 660 | 661 | 662 | 663 | 664 | 665 | 666 | 667 | 668 | 669 | 670 | 671 | 672 | 673 | 674 | 675 | 676 | 677 | 678 | 679 | 680 | 681 | 682 | 683 | 684 | 685 | 686 | 687 | 688 | 689 | 690 | 691 | 692 | 693 | 694 | 695 | 696 | 697 | 698 | 699 | 700 | 701 | 702 | 703 | 704 | 705 | 706 | 707 | 708 | 709 | 710 | 711 | 712 | 713 | 714 | 715 | 716 | 717 | 718 | 719 | 720 | 721 | 722 | 723 | 724 | 725 | 726 | 727 | 728 | 729 | 730 | 731 | 732 | 733 | 734 | 735 | 736 | 737 | 738 | 739 | 740 | 741 | 742 | 743 | 744 | 745 | 746 | 747 | 748 | 749 | 750 | 751 | 752 | 753 | 754 | 755 | 756 | 757 | 758 | 759 | 760 | 761 | 762 | 763 | 764 | 765 | 766 | 767 | 768 | 769 | 770 | 771 | 772 | 773 | 774 | 775 | 776 | 777 | 778 | 779 | 780 | 781 | 782 | 783 | 784 | 785 | 786 | 787 | 788 | 789 | 790 | 791 | 792 | 793 | 794 | 795 | 796 | 797 | 798 | 799 | 800 | 801 | 802 | 803 | 804 | 805 | 806 | 807 | 808 | 809 | 810 | 811 | 812 | 813 | 814 | 815 | 816 | 817 | 818 | 819 | 820 | 821 | 822 | 823 | 824 | 825 | 826 | 827 | 828 | 829 | 830 | 831 | 832 | 833 | 834 | 835 | 836 | 837 | 838 | 839 | 840 | 841 | 842 | 843 | 844 | 845 | 846 | 847 | 848 | 849 | 850 | 851 | 852 | 853 | 854 | 855 | 856 | 857 | 858 | 859 | 860 | 861 | 862 | 863 | 864 | 865 | 866 | 867 | 868 | 869 | 870 | 871 | 872 | 873 | 874 | 875 | 876 | 877 | 878 | 879 | 880 | 881 | 882 | 883 | 884 | 885 | 886 | 887 | 888 | 889 | 890 | 891 | 892 | 893 | 894 | 895 | 896 | 897 | 898 | 899 | 900 | 901 | 902 | 903 | 904 | 905 | 906 | 907 | 908 | 909 | 910 | 911 | 912 | 913 | 914 | 915 | 916 | 917 | 918 | 919 | 920 | 921 | 922 | 923 | 924 | 925 | 926 | 927 | 928 | 929 | 930 | 931 | 932 | 933 | 934 | 935 | 936 | 937 | 938 | 939 | 940 | 941 | 942 | 943 | 944 | 945 | 946 | 947 | 948 | 949 | 950 | 951 | 952 | 953 | 954 | 955 | 956 | 957 | 958 | 959 | 960 | 961 | 962 | 963 | 964 | 965 | 966 | 967 | 968 | 969 | 970 | 971 | 972 | 973 | 974 | 975 | 976 | 977 | 978 | 979 | 980 | 981 | 982 | 983 | 984 | 985 | 986 | 987 | 988 | 989 | 990 | 991 | 992 | 993 | 994 | 995 | 996 | 997 | 998 | 999 | 1000 |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-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| 2024 | 2023 | 2022 | 2021 | 2020 | 2019 | 2018 | 2017 | 2016 | 2015 | 2014 | 2013 | 2012 | 2011 | 2010 | 2009 | 2008 | 2007 | 2006 | 2005 | 2004 | 2003 | 2002 | 2001 | 2000 | 1999 | 1998 | 1997 | 1996 | 1995 | 1994 | 1993 | 1992 | 1991 | 1990 | 1989 | 1988 | 1987 | 1986 | 1985 | 1984 | 1983 | 1982 | 1981 | 1980 | 1979 | 1978 | 1977 | 1976 | 1975 | 1974 | 1973 | 1972 | 1971 | 1970 | 1969 | 1968 | 1967 | 1966 | 1965 | 1964 | 1963 | 1962 | 1961 | 1960 | 1959 | 1958 | 1957 | 1956 | 1955 | 1954 | 1953 | 1952 | 1951 | 1950 | 1949 | 1948 | 1947 | 1946 | 1945 | 1944 | 1943 | 1942 | 1941 | 1940 | 1939 | 1938 | 1937 | 1936 | 1935 | 1934 | 1933 | 1932 | 1931 | 1930 | 1929 | 1928 | 1927 | 1926 | 1925 | 1924 | 1923 | 1922 | 1921 | 1920 | 1919 | 1918 | 1917 | 1916 | 1915 | 1914 | 1913 | 1912 | 1911 | 1910 | 1909 | 1908 | 1907 | 1906 | 1905 | 1904 | 1903 | 1902 | 1901 | 1900 | 1899 | 1898 | 1897 | 1896 | 1895 | 1894 | 1893 | 1892 | 1891 | 1890 | 1889 | 1888 | 1887 | 1886 | 1885 | 1884 | 1883 | 1882 | 1881 | 1880 | 1879 | 1878 | 1877 | 1876 | 1875 | 1874 | 1873 | 1872 | 1871 | 1870 | 1869 | 1868 | 1867 | 1866 | 1865 | 1864 | 1863 | 1862 | 1861 | 1860 | 1859 | 1858 | 1857 | 1856 | 1855 | 1854 | 1853 | 1852 | 1851 | 1850 | 1849 | 1848 | 1847 | 1846 | 1845 | 1844 | 1843 | 1842 | 1841 | 1840 | 1839 | 1838 | 1837 | 1836 | 1835 | 1834 | 1833 | 1832 | 1831 | 1830 | 1829 | 1828 | 1827 | 1826 | 1825 | 1824 | 1823 | 1822 | 1821 | 1820 | 1819 | 1818 | 1817 | 1816 | 1815 | 1814 | 1813 | 1812 | 1811 | 1810 | 1809 | 1808 | 1807 | 1806 | 1805 | 1804 | 1803 | 1802 | 1801 | 1800 | 1799 | 1798 | 1797 | 1796 | 1795 | 1794 | 1793 | 1792 | 1791 | 1790 | 1789 | 1788 | 1787 | 1786 | 1785 | 1784 | 1783 | 1782 | 1781 | 1780 | 1779 | 1778 | 1777 | 1776 | 1775 | 1774 | 1773 | 1772 | 1771 | 1770 | 1769 | 1768 | 1767 | 1766 | 1765 | 1764 | 1763 | 1762 | 1761 | 1760 | 1759 | 1758 | 1757 | 1756 | 1755 | 1754 | 1753 | 1752 | 1751 | 1750 | 1749 | 1748 | 1747 | 1746 | 1745 | 1744 | 1743 | 1742 | 1741 | 1740 | 1739 | 1738 | 1737 | 1736 | 1735 | 1734 | 1733 | 1732 | 1731 | 1730 | 1729 | 1728 | 1727 | 1726 | 1725 | 1724 | 1723 | 1722 | 1721 | 1720 | 1719 | 1718 | 1717 | 1716 | 1715 | 1714 | 1713 | 1712 | 1711 | 1710 | 1709 | 1708 | 1707 | 1706 | 1705 | 1704 | 1703 | 1702 | 1701 | 1700 | 1699 | 1698 | 1697 | 1696 | 1695 | 1694 | 1693 | 1692 | 1691 | 1690 | 1689 | 1688 | 1687 | 1686 | 1685 | 1684 | 1683 | 1682 | 1681 | 1680 | 1679 | 1678 | 1677 | 1676 | 1675 | 1674 | 1673 | 1672 | 1671 | 1670 | 1669 | 1668 | 1667 | 1666 | 1665 | 1664 | 1663 | 1662 | 1661 | 1660 | 1659 | 1658 | 1657 | 1656 | 1655 | 1654 | 1653 | 1652 | 1651 | 1650 | 1649 | 1648 | 1647 | 1646 | 1645 | 1644 | 1643 | 1642 | 1641 | 1640 | 1639 | 1638 | 1637 | 1636 | 1635 | 1634 | 1633 | 1632 | 1631 | 1630 | 1629 | 1628 | 1627 | 1626 | 1625 | 1624 | 1623 | 1622 | 1621 | 1620 | 1619 | 1618 | 1617 | 1616 | 1615 | 1614 | 1613 | 1612 | 1611 | 1610 | 1609 | 1608 | 1607 | 1606 | 1605 | 1604 | 1603 | 1602 | 1601 | 1600 | 1599 | 1598 | 1597 | 1596 | 1595 | 1594 | 1593 | 1592 | 1591 | 1590 | 1589 | 1588 | 1587 | 1586 | 1585 | 1584 | 1583 | 1582 | 1581 | 1580 | 1579 | 1578 | 1577 | 1576 | 1575 | 1574 | 1573 | 1572 | 1571 | 1570 | 1569 | 1568 | 1567 | 1566 | 1565 | 1564 | 1563 | 1562 | 1561 | 1560 | 1559 | 1558 | 1557 | 1556 | 1555 | 1554 | 1553 | 1552 | 1551 | 1550 | 1549 | 1548 | 1547 | 1546 | 1545 | 1544 | 1543 | 1542 | 1541 | 1540 | 1539 | 1538 | 1537 | 1536 | 1535 | 1534 | 1533 | 1532 | 1531 | 1530 | 1529 | 1528 | 1527 | 1526 | 1525 | 1524 | 1523 | 1522 | 1521 | 1520 | 1519 | 1518 | 1517 | 1516 | 1515 | 1514 | 1513 | 1512 | 1511 | 1510 | 1509 | 1508 | 1507 | 1506 | 1505 | 1504 | 1503 | 1502 | 1501 | 1500 | 1499 | 1498 | 1497 | 1496 | 1495 | 1494 | 1493 | 1492 | 1491 | 1490 | 1489 | 1488 | 1487 | 1486 | 1485 | 1484 | 1483 | 1482 | 1481 | 1480 | 1479 | 1478 | 1477 | 1476 | 1475 | 1474 | 1473 | 1472 | 1471 | 1470 | 1469 | 1468 | 1467 | 1466 | 1465 | 1464 | 1463 | 1462 | 1461 | 1460 | 1459 | 1458 | 1457 | 1456 | 1455 | 1454 | 1453 | 1452 | 1451 | 1450 | 1449 | 1448 | 1447 | 1446 | 1445 | 1444 | 1443 | 1442 | 1441 | 1440 | 1439 | 1438 | 1437 | 1436 | 1435 | 1434 | 1433 | 1432 | 1431 | 1430 | 1429 | 1428 | 1427 | 1426 | 1425 | 1424 | 1423 | 1422 | 1421 | 1420 | 1419 | 1418 | 1417 | 1416 | 1415 | 1414 | 1413 | 1412 | 1411 | 1410 | 1409 | 1408 | 1407 | 1406 | 1405 | 1404 | 1403 | 1402 | 1401 | 1400 | 1399 | 1398 | 1397 | 1396 | 1395 | 1394 | 1393 | 1392 | 1391 | 1390 | 1389 | 1388 | 1387 | 1386 | 1385 | 1384 | 1383 | 1382 | 1381 | 1380 | 1379 | 1378 | 1377 | 1376 | 1375 | 1374 | 1373 | 1372 | 1371 | 1370 | 1369 | 1368 | 1367 | 1366 | 1365 | 1364 | 1363 | 1362 | 1361 | 1360 | 1359 | 1358 | 1357 | 1356 | 1355 | 1354 | 1353 | 1352 | 1351 | 1350 | 1349 | 1348 | 1347 | 1346 | 1345 | 1344 | 1343 | 1342 | 1341 | 1340 | 1339 | 1338 | 1337 | 1336 | 1335 | 1334 | 1333 | 1332 | 1331 | 1330 | 1329 | 1328 | 1327 | 1326 | 1325 | 1324 | 1323 | 1322 | 1321 | 1320 | 1319 | 1318 | 1317 | 1316 | 1315 | 1314 | 1313 | 1312 | 1311 | 1310 | 1309 | 1308 | 1307 | 1306 | 1305 | 1304 | 1303 | 1302 | 1301 | 1300 | 1299 | 1298 | 1297 | 1296 | 1295 | 1294 | 1293 | 1292 | 1291 | 1290 | 1289 | 1288 | 1287 | 1286 | 1285 | 1284 | 1283 | 1282 | 1281 | 1280 | 1279 | 1278 | 1277 | 1276 | 1275 | 1274 | 1273 | 1272 | 1271 | 1270 | 1269 | 1268 | 1267 | 1266 | 1265 | 1264 | 1263 | 1262 | 1261 | 1260 | 1259 | 1258 | 1257 | 1256 | 1255 | 1254 | 1253 | 1252 | 1251 | 1250 | 1249 | 1248 | 1247 | 1246 | 1245 | 1244 | 1243 | 1242 | 1241 | 1240 | 1239 | 1238 | 1237 | 1236 | 1235 | 1234 | 1233 | 1232 | 1231 | 1230 | 1229 | 1228 | 1227 | 1226 | 1225 | 1224 | 1223 | 1222 | 1221 | 1220 | 1219 | 1218 | 1217 | 1216 | 1215 | 1214 | 1213 | 1212 | 1211 | 1210 | 1209 | 1208 | 1207 | 1206 | 1205 | 1204 | 1203 | 1202 | 1201 | 1200 | 1199 | 1198 | 1197 | 1196 | 1195 | 1194 | 1193 | 1192 | 1191 | 1190 | 1189 | 1188 | 1187 | 1186 | 1185 | 1184 | 1183 | 1182 | 1181 | 1180 | 1179 | 1178 | 1177 | 1176 | 1175 | 1174 | 1173 | 1172 | 1171 | 1170 | 1169 | 1168 | 1167 | 1166 | 1165 | 1164 | 1163 | 1162 | 1161 | 1160 | 1159 | 1158 | 1157 | 1156 | 1155 | 1154 | 1153 | 1152 | 1151 | 1150 | 1149 | 1148 | 1147 | 1146 | 1145 | 1144 | 1143 | 1142 | 1141 | 1140 | 1139 | 1138 | 1137 | 1136 | 1135 | 1134 | 1133 | 1132 | 1131 | 1130 | 1129 | 1128 | 1127 | 1126 | 1125 | 1124 | 1123 | 1122 | 1121 | 1120 | 1119 | 1118 | 1117 | 1116 | 1115 | 1114 | 1113 | 1112 | 1111 | 1110 | 1109 | 1108 | 1107 | 1106 | 1105 | 1104 | 1103 | 1102 | 1101 | 1100 | 1099 | 1098 | 1097 | 1096 | 1095 | 1094 | 1093 | 1092 | 1091 | 1090 | 1089 | 1088 | 1087 | 1086 | 1085 | 1084 | 1083 | 1082 | 1081 | 1080 | 1079 | 1078 | 1077 | 1076 | 1075 | 1074 | 1073 | 1072 | 1071 | 1070 | 1069 | 1068 | 1067 | 1066 | 1065 | 1064 | 1063 | 1062 | 1061 | 1060 | 1059 | 1058 | 1057 | 1056 | 1055 | 1054 | 1053 | 1052 | 1051 | 1050 | 1049 | 1048 | 1047 | 1046 | 1045 | 1044 | 1043 | 1042 | 1041 | 1040 | 1039 | 1038 | 1037 | 1036 | 1035 | 1034 | 1033 | 1032 | 1031 | 1030 | 1029 | 1028 | 1027 | 1026 | 1025 | 1024 | 1023 | 1022 | 1021 | 1020 | 1019 | 1018 | 1017 | 1016 | 1015 | 1014 | 1013 | 1012 | 1011 | 1010 | 1009 | 1008 | 1007 | 1006 | 1005 | 1004 | 1003 | 1002 | 1001 | 1000 | 999 | 998 | 997 | 996 | 995 | 994 | 993 | 992 | 991 | 990 | 989 | 988 | 987 | 986 | 985 | 984 | 983 | 982 | 981 | 980 | 979 | 978 | 977 | 976 | 975 | 974 | 973 | 972 | 971 | 970 | 969 | 968 | 967 | 966 | 965 | 964 | 963 | 962 | 961 | 960 | 959 | 958 | 957 | 956 | 955 | 954 | 953 | 952 | 951 | 950 | 949 | 948 | 947 | 946 | 945 | 944 | 943 | 942 | 941 | 940 | 939 | 938 | 937 | 936 | 935 | 934 | 933 | 932 | 931 | 930 | 929 | 928 | 927 | 926 | 925 | 924 | 923 | 922 | 921 | 920 | 919 | 918 | 917 | 916 | 915 | 914 | 913 | 912 | 911 | 910 | 909 | 908 | 907 | 906 | 905 | 904 | 903 | 902 | 901 | 900 | 899 | 898 | 897 | 896 | 895 | 894 | 893 | 892 | 891 | 890 | 889 | 888 | 887 | 886 | 885 | 884 | 883 | 882 | 881 | 880 | 879 | 878 | 877 | 876 | 875 | 874 | 873 | 872 | 871 | 870 | 869 | 868 | 867 | 866 | 865 | 864 | 863 | 862 | 861 | 860 | 859 | 858 | 857 | 856 | 855 | 854 | 853 | 852 | 851 | 850 | 849 | 848 | 847 | 846 | 845 | 844 | 843 | 842 | 841 | 840 | 839 | 838 | 837 | 836 | 835 | 834 | 833 | 832 | 831 | 830 | 829 | 828 | 827 | 826 | 825 | 824 | 823 | 822 | 821 | 820 | 819 | 818 | 817 | 816 | 815 | 814 | 813 | 812 | 811 | 810 | 809 | 808 | 807 | 806 | 805 | 804 | 803 | 802 | 801 | 800 | 799 | 798 | 797 | 796 | 795 | 794 | 793 | 792 | 791 | 790 | 789 | 788 | 787 | 786 | 785 | 784 | 783 | 782 | 781 | 780 | 779 | 778 | 777 | 776 | 775 | 774 | 773 | 772 | 771 | 770 | 769 | 768 | 767 | 766 | 765 | 764 | 763 | 762 | 761 | 760 | 759 | 758 | 757 | 756 | 755 | 754 | 753 | 752 | 751 | 750 | 749 | 748 | 747 | 746 | 745 | 744 | 743 | 742 | 741 | 740 | 739 | 738 | 737 | 736 | 735 | 734 | 733 | 732 | 731 | 730 | 729 | 728 | 727 | 726 | 725 | 724 | 723 | 722 | 721 | 720 | 719 | 718 | 717 | 716 | 715 | 714 | 713 | 712 | 711 | 710 | 709 | 708 | 707 | 706 | 705 | 704 | 703 | 702 | 701 | 700 | 699 | 698 | 697 | 696 | 695 | 694 | 693 | 692 | 691 | 690 | 689 | 688 | 687 | 686 | 685 | 684 | 683 | 682 | 681 | 680 | 679 | 678 | 677 | 676 | 675 | 674 | 673 | 672 | 671 | 670 | 669 | 668 | 667 | 666 | 665 | 664 | 663 | 662 | 661 | 660 | 659 | 658 | 657 | 656 | 655 | 654 | 653 | 652 | 651 | 650 | 649 | 648 | 647 | 646 | 645 | 644 | 643 | 642 | 641 | 640 | 639 | 638 | 637 | 636 | 635 | 634 | 633 | 632 | 631 | 630 | 629 | 628 | 627 | 626 | 625 | 624 | 623 | 622 | 621 | 620 | 619 | 618 | 617 | 616 | 615 | 614 | 613 | 612 | 611 | 610 | 609 | 608 | 607 | 606 | 6 |
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| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
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| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
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| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
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| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
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185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 524 | 525 | 526 | 527 | 528 | 529 | 530 | 531 | 532 | 533 | 534 | 535 | 536 | 537 | 538 | 539 | 540 | 541 | 542 | 543 | 544 | 545 | 546 | 547 | 548 | 549 | 550 | 551 | 552 | 553 | 554 | 555 | 556 | 557 | 558 | 559 | 560 | 561 | 562 | 563 | 564 | 565 | 566 | 567 | 568 | 569 | 570 | 571 | 572 | 573 | 574 | 575 | 576 | 577 | 578 | 579 | 580 | 581 | 582 | 583 | 584 | 585 | 586 | 587 | 588 | 589 | 590 | 591 | 592 | 593 | 594 | 595 | 596 | 597 | 598 | 599 | 600 | 601 | 602 | 603 | 604 | 605 | 606 | 607 | 608 | 609 | 610 | 611 | 612 | 613 | 614 | 615 | 616 | 617 | 618 | 619 | 620 | 621 | 622 | 623 | 624 | 625 | 626 | 627 | 628 | 629 | 630 | 631 | 632 | 633 | 634 | 635 | 636 | 637 | 638 | 639 | 640 | 641 | 642 | 643 | 644 | 645 | 646 | 647 | 648 | 649 | 650 | 651 | 652 | 653 | 654 | 655 | 656 | 657 | 658 | 659 | 660 | 661 | 662 | 663 | 664 | 665 | 666 | 667 | 668 | 669 | 670 | 671 | 672 | 673 | 674 | 675 | 676 | 677 | 678 | 679 | 680 | 681 | 682 | 683 | 684 | 685 | 686 | 687 | 688 | 689 | 690 | 691 | 692 | 693 | 694 | 695 | 696 | 697 | 698 | 699 | 700 | 701 | 702 | 703 | 704 | 705 | 706 | 707 | 708 | 709 | 710 | 711 | 712 | 713 | 714 | 715 | 716 | 717 | 718 | 719 | 720 | 721 | 722 | 723 | 724 | 725 | 726 | 727 | 728 | 729 | 730 | 731 | 732 | 733 | 734 | 735 | 736 | 737 | 738 | 739 | 740 | 741 | 742 | 743 | 744 | 745 | 746 | 747 | 748 | 749 | 750 | 751 | 752 | 753 | 754 | 755 | 756 | 757 | 758 | 759 | 760 | 761 | 762 | 763 | 764 | 765 | 766 | 767 | 768 | 769 | 770 | 771 | 772 | 773 | 774 | 775 | 776 | 777 | 778 | 779 | 780 | 781 | 782 | 783 | 784 | 785 | 786 | 787 | 788 | 789 | 790 | 791 | 792 | 793 | 794 | 795 | 796 | 797 | 798 | 799 | 800 | 801 | 802 | 803 | 804 | 805 | 806 | 807 | 808 | 809 | 810 | 811 | 812 | 813 | 814 | 815 | 816 | 817 | 818 | 819 | 820 | 821 | 822 | 823 | 824 | 825 | 826 | 827 | 828 | 829 | 830 | 831 | 832 | 833 | 834 | 835 | 836 | 837 | 838 | 839 | 840 | 841 | 842 | 843 | 844 | 845 | 846 | 847 | 848 | 849 | 850 | 851 | 852 | 853 | 854 | 855 | 856 | 857 | 858 | 859 | 860 | 861 | 862 | 863 | 864 | 865 | 866 | 867 | 868 | 869 | 870 | 871 | 872 | 873 | 874 | 875 | 876 | 877 | 878 | 879 | 880 | 881 | 882 | 883 | 884 | 885 | 886 | 887 | 888 | 889 | 890 | 891 | 892 | 893 | 894 | 895 | 896 | 897 | 898 | 899 | 900 | 901 | 902 | 903 | 904 | 905 | 906 | 907 | 908 | 909 | 910 | 911 | 912 | 913 | 914 | 915 | 916 | 917 | 918 | 919 | 920 | 921 | 922 | 923 | 924 | 925 | 926 | 927 | 928 | 929 | 930 | 931 | 932 | 933 | 934 | 935 | 936 | 937 | 938 | 939 | 940 | 941 | 942 | 943 | 944 | 945 | 946 | 947 | 948 | 949 | 950 | 951 | 952 | 953 | 954 | 955 | 956 | 957 | 958 | 959 | 960 | 961 | 962 | 963 | 964 | 965 | 966 | 967 | 968 | 969 | 970 | 971 | 972 | 973 | 974 | 975 | 976 | 977 | 978 | 979 | 980 | 981 | 982 | 983 | 984 | 985 | 986 | 987 | 988 | 989 | 990 | 991 | 992 | 993 | 994 | 995 | 996 | 997 | 998 | 999 | 1000 |
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|------------------------|----------------|--------|---------|-------|---------------|-----------|-------|-----------|------|-------|
| Country                | City           | Lat    | Long    | Alt   | Pop           | Area      | Dist  | Time      | Code | Notes |
| Albania                | Tirana         | 41.33  | 19.82   | 350   | 615,000       | 28,748    | 1,000 | UTC+1     | AL   |       |
| Algeria                | Algiers        | 36.77  | 3.06    | 1,050 | 3,400,000     | 238,174   | 1,000 | UTC+1     | DZ   |       |
| Angola                 | Luanda         | -8.86  | -13.24  | 1,000 | 17,000,000    | 1,246,700 | 1,000 | UTC+1     | AO   |       |
| Argentina              | Buenos Aires   | -34.61 | -58.38  | 30    | 45,000,000    | 2,367,000 | 1,000 | UTC-3     | AR   |       |
| Australia              | Sydney         | -33.87 | 151.21  | 10    | 22,000,000    | 7,682,300 | 1,000 | UTC+10    | AU   |       |
| Austria                | Vienna         | 48.21  | 16.37   | 170   | 8,900,000     | 83,858    | 1,000 | UTC+1     | AT   |       |
| Azerbaijan             | Baku           | 40.41  | 49.84   | 860   | 10,000,000    | 86,600    | 1,000 | UTC+4     | AZ   |       |
| Bahrain                | Manama         | 26.24  | 50.63   | 10    | 1,500,000     | 660       | 1,000 | UTC+3     | BH   |       |
| Bangladesh             | Dhaka          | 23.81  | 90.41   | 25    | 160,000,000   | 147,570   | 1,000 | UTC+6     | BD   |       |
| Barbados               | Bridgetown     | 13.11  | -59.61  | 100   | 280,000       | 166       | 1,000 | UTC-4     | BB   |       |
| Belarus                | Minsk          | 53.90  | 27.56   | 250   | 9,500,000     | 203,610   | 1,000 | UTC+3     | BY   |       |
| Belgium                | Brussels       | 50.85  | 4.34    | 100   | 11,000,000    | 30,528    | 1,000 | UTC+1     | BE   |       |
| Belize                 | Belize City    | 17.14  | -88.16  | 10    | 400,000       | 22,965    | 1,000 | UTC-6     | BZ   |       |
| Benin                  | Cotonou        | 6.36   | 1.87    | 10    | 10,000,000    | 112,621   | 1,000 | UTC+1     | BJ   |       |
| Bhutan                 | Thimphu        | 27.46  | 89.61   | 3,500 | 750,000       | 38,394    | 1,000 | UTC+6     | BT   |       |
| Bolivia                | Sucre          | -19.05 | -65.11  | 2,700 | 11,000,000    | 1,098,581 | 1,000 | UTC-4     | BO   |       |
| Bosnia and Herzegovina | Sarajevo       | 45.76  | 18.45   | 510   | 3,500,000     | 51,129    | 1,000 | UTC+1     | BA   |       |
| Botswana               | Gaborone       | -24.31 | 25.90   | 1,000 | 2,300,000     | 360,000   | 1,000 | UTC+2     | BS   |       |
| Brazil                 | Brazilia       | -15.78 | -47.92  | 1,100 | 210,000,000   | 8,511,910 | 1,000 | UTC-3     | BR   |       |
| Bulgaria               | Sofia          | 42.71  | 23.32   | 550   | 7,500,000     | 110,910   | 1,000 | UTC+2     | BG   |       |
| Burkina Faso           | Ouagadougou    | 12.37  | -1.51   | 100   | 19,000,000    | 274,000   | 1,000 | UTC+0     | BF   |       |
| Burundi                | Bujumbura      | -3.38  | 29.37   | 1,000 | 10,000,000    | 27,834    | 1,000 | UTC+2     | BI   |       |
| Cambodia               | Phnom Penh     | 11.56  | 104.91  | 10    | 16,000,000    | 181,035   | 1,000 | UTC+7     | KH   |       |
| Cameroon               | Yaounde        | 3.86   | 11.50   | 100   | 22,000,000    | 475,339   | 1,000 | UTC+1     | CM   |       |
| Canada                 | Ottawa         | 45.42  | -75.69  | 40    | 38,000,000    | 9,970,671 | 1,000 | UTC-5     | CA   |       |
| Chad                   | Ndjamena       | 12.17  | 15.00   | 100   | 12,000,000    | 1,284,000 | 1,000 | UTC+1     | TD   |       |
| Chile                  | Santiago       | -33.45 | -70.66  | 360   | 19,000,000    | 756,099   | 1,000 | UTC-4     | CL   |       |
| China                  | Beijing        | 39.90  | 116.40  | 40    | 1,400,000,000 | 9,596,961 | 1,000 | UTC+8     | CN   |       |
| Colombia               | Bogota         | 4.61   | -76.62  | 2,600 | 48,000,000    | 1,104,746 | 1,000 | UTC-5     | CO   |       |
| Costa Rica             | San Jose       | 9.93   | -84.09  | 1,000 | 5,000,000     | 52,061    | 1,000 | UTC-6     | CR   |       |
| Croatia                | Zagreb         | 45.76  | 15.98   | 100   | 4,500,000     | 56,538    | 1,000 | UTC+1     | HR   |       |
| Cuba                   | Havana         | 23.11  | -82.36  | 100   | 11,500,000    | 110,820   | 1,000 | UTC-5     | CU   |       |
| Cyprus                 | Nicosia        | 35.29  | 33.43   | 100   | 1,200,000     | 9,251     | 1,000 | UTC+2     | CY   |       |
| Czechia                | Prague         | 50.08  | 14.43   | 200   | 4,700,000     | 78,866    | 1,000 | UTC+1     | CZ   |       |
| Denmark                | Copenhagen     | 59.41  | 12.57   | 10    | 5,600,000     | 4,308     | 1,000 | UTC+1     | DK   |       |
| Dominican Republic     | Santiago       | 18.47  | -70.16  | 100   | 7,500,000     | 76,615    | 1,000 | UTC-4     | DO   |       |
| Dominica               | Roseau         | 15.86  | -61.38  | 100   | 70,000        | 750       | 1,000 | UTC-4     | DM   |       |
| DRC                    | Kinshasa       | -4.34  | 15.31   | 1,000 | 75,000,000    | 2,267,000 | 1,000 | UTC+1     | CD   |       |
| Ecuador                | Quito          | -0.18  | -78.48  | 2,800 | 16,000,000    | 283,560   | 1,000 | UTC-5     | EC   |       |
| Egypt                  | Cairo          | 30.06  | 31.23   | 100   | 95,000,000    | 1,001,450 | 1,000 | UTC+2     | EG   |       |
| El Salvador            | San Salvador   | 13.69  | -88.93  | 1,000 | 6,000,000     | 21,369    | 1,000 | UTC-6     | SV   |       |
| Equatorial Guinea      | Malabo         | 1.65   | 10.34   | 1,000 | 1,300,000     | 28,011    | 1,000 | UTC+1     | GQ   |       |
| Estonia                | Tallinn        | 59.44  | 24.50   | 10    | 1,300,000     | 45,226    | 1,000 | UTC+2     | EE   |       |
| Ethiopia               | Addis Ababa    | 9.03   | 38.74   | 2,500 | 100,000,000   | 1,104,300 | 1,000 | UTC+3     | ET   |       |
| Fiji                   | Suva           | -17.72 | 178.07  | 10    | 850,000       | 183,346   | 1,000 | UTC+12    | FJ   |       |
| Finland                | Helsinki       | 60.17  | 24.93   | 100   | 5,500,000     | 143,300   | 1,000 | UTC+2     | FI   |       |
| France                 | Paris          | 48.86  | 2.33    | 100   | 67,000,000    | 643,801   | 1,000 | UTC+1     | FR   |       |
| Gabon                  | Libreville     | 0.39   | 10.17   | 100   | 2,000,000     | 267,667   | 1,000 | UTC+1     | GA   |       |
| Gambia                 | Banjul         | 13.47  | -16.68  | 100   | 2,000,000     | 11,300    | 1,000 | UTC+0     | GM   |       |
| Germany                | Berlin         | 52.52  | 13.40   | 30    | 83,000,000    | 357,021   | 1,000 | UTC+1     | DE   |       |
| Ghana                  | Accra          | 5.60   | -0.18   | 100   | 24,000,000    | 579,300   | 1,000 | UTC+0     | GH   |       |
| Greece                 | Athens         | 37.98  | 23.73   | 100   | 11,500,000    | 113,500   | 1,000 | UTC+2     | GR   |       |
| Greenland              | Narsarsuaq     | 69.21  | -51.10  | 100   | 56,000        | 2,166,000 | 1,000 | UTC-3     | GL   |       |
| Guatemala              | Guatemala City | 14.62  | -90.52  | 1,000 | 16,000,000    | 33,600    | 1,000 | UTC-6     | GT   |       |
| Haiti                  | Port-au-Prince | 18.54  | -72.28  | 100   | 11,000,000    | 77,816    | 1,000 | UTC-5     | HT   |       |
| Honduras               | Tegucigalpa    | 14.06  | -88.55  | 1,000 | 7,500,000     | 31,360    | 1,000 | UTC-6     | HN   |       |
| Hungary                | Budapest       | 47.50  | 19.04   | 100   | 10,500,000    | 93,030    | 1,000 | UTC+1     | HU   |       |
| Iceland                | Reykjavik      | 64.15  | -21.94  | 100   | 340,000       | 109,251   | 1,000 | UTC+0     | IS   |       |
| India                  | New Delhi      | 28.64  | 77.10   | 200   | 1,200,000,000 | 3,287,263 | 1,000 | UTC+5:30  | IN   |       |
| Indonesia              | Jakarta        | -6.18  | 106.82  | 10    | 250,000,000   | 1,919,348 | 1,000 | UTC+7     | ID   |       |
| Iran                   | Tehran         | 35.68  | 51.37   | 1,000 | 80,000,000    | 1,648,195 | 1,000 | UTC+3:30  | IR   |       |
| Ireland                | Dublin         | 53.35  | -8.07   | 100   | 4,500,000     | 70,276    | 1,000 | UTC+0     | IE   |       |
| Israel                 | Tel Aviv       | 32.04  | 34.84   | 100   | 7,500,000     | 20,386    | 1,000 | UTC+2     | IL   |       |
| Italy                  | Rome           | 41.90  | 12.51   | 200   | 60,000,000    | 301,330   | 1,000 | UTC+1     | IT   |       |
| Jamaica                | Kingston       | 18.01  | -76.82  | 100   | 2,800,000     | 10,991    | 1,000 | UTC-5     | JM   |       |
| Japan                  | Tokyo          | 35.68  | 139.76  | 40    | 125,000,000   | 377,930   | 1,000 | UTC+9     | JP   |       |
| Jordan                 | Amman          | 31.95  | 35.86   | 1,000 | 6,000,000     | 92,222    | 1,000 | UTC+2     | JO   |       |
| Kazakhstan             | Nur-Sultan     | 51.73  | 71.48   | 350   | 18,000,000    | 2,003,400 | 1,000 | UTC+6     | KZ   |       |
| Kenya                  | Nairobi        | -1.28  | 36.82   | 1,000 | 45,000,000    | 225,167   | 1,000 | UTC+3     | KE   |       |
| Kiribati               | Tarawa         | 3.37   | 15.75   | 10    | 120,000       | 811       | 1,000 | UTC+12    | KI   |       |
| Korea                  | Seoul          | 37.57  | 127.11  | 40    | 51,000,000    | 100,032   | 1,000 | UTC+9     | KR   |       |
| Kosovo                 | Pristina       | 42.66  | 20.91   | 1,000 | 2,000,000     | 10,908    | 1,000 | UTC+1     | XK   |       |
| Kuwait                 | Kuwait City    | 29.38  | 47.98   | 10    | 4,000,000     | 17,818    | 1,000 | UTC+3     | KW   |       |
| Kyrgyzstan             | Bishkek        | 42.88  | 74.57   | 3,500 | 6,000,000     | 199,500   | 1,000 | UTC+6     | KG   |       |
| Laos                   | Vientiane      | 17.97  | 102.60  | 100   | 7,000,000     | 236,800   | 1,000 | UTC+7     | LA   |       |
| Latvia                 | Riga           | 56.94  | 24.01   | 10    | 1,300,000     | 64,589    | 1,000 | UTC+2     | LV   |       |
| Lebanon                | Beirut         | 33.89  | 15.50   | 100   | 6,000,000     | 10,450    | 1,000 | UTC+2     | LB   |       |
| Lesotho                | Maseru         | -29.31 | 27.08   | 1,000 | 2,500,000     | 30,354    | 1,000 | UTC+2     | LS   |       |
| Lithuania              | Vilnius        | 54.65  | 25.27   | 100   | 3,400,000     | 65,300    | 1,000 | UTC+2     | LT   |       |
| Luxembourg             | Luxembourg     | 49.81  | 6.13    | 100   | 600,000       | 1,782     | 1,000 | UTC+1     | LU   |       |
| Macao                  | Macao          | 22.19  | 113.54  | 10    | 650,000       | 30,000    | 1,000 | UTC+8     | MO   |       |
| Macedonia              | Skopje         | 41.99  | 21.72   | 100   | 2,100,000     | 25,713    | 1,000 | UTC+1     | MK   |       |
| Madagascar             | Antananarivo   | -18.76 | 37.50   | 1,000 | 27,000,000    | 587,800   | 1,000 | UTC+3     | MG   |       |
| Malawi                 | Lilongwe       | -13.12 | 33.78   | 1,000 | 20,000,000    | 118,480   | 1,000 | UTC+2     | MW   |       |
| Malaysia               | Kuala Lumpur   | 3.14   | 101.68  | 10    | 200,000,000   | 330,846   | 1,000 | UTC+8     | MY   |       |
| Maldives               | Male           | 4.17   | 73.53   | 10    | 500,000       | 298       | 1,000 | UTC+5     | MD   |       |
| Mali                   | Bamako         | 12.67  | -8.00   | 100   | 20,000,000    | 1,240,000 | 1,000 | UTC+0     | ML   |       |
| Malta                  | Valletta       | 35.89  | 14.51   | 100   | 450,000       | 316       | 1,000 | UTC+1     | MT   |       |
| Marshall Islands       | Majuro         | 7.08   | 171.38  | 10    | 60,000        | 181       | 1,000 | UTC+12    | MH   |       |
| Martinique             | Fort-de-France | 14.59  | -61.08  | 100   | 370,000       | 361       | 1,000 | UTC-4     | MQ   |       |
| Mauritania             | Nouakchott     | 18.10  | -15.90  | 100   | 3,500,000     | 106,600   | 1,000 | UTC+0     | MR   |       |
| Mauritius              | Port Louis     | -20.17 | 57.50   | 100   | 1,200,000     | 443       | 1,000 | UTC+4     | MU   |       |
| Mexico                 | Mexico City    | 19.43  | -99.13  | 2,200 | 130,000,000   | 2,237,600 | 1,000 | UTC-6     | MX   |       |
| Moldova                | Chisinau       | 47.02  | 27.04   | 100   | 4,000,000     | 33,850    | 1,000 | UTC+2     | MD   |       |
| Monaco                 | Monaco         | 43.74  | 7.42    | 100   | 35,000        | 2.02      | 1,000 | UTC+1     | MC   |       |
| Mongolia               | Ulaanbaatar    | 47.91  | 106.88  | 1,000 | 3,000,000     | 236,400   | 1,000 | UTC+8     | MN   |       |
| Montenegro             | Podgorica      | 42.71  | 19.25   | 100   | 620,000       | 13,910    | 1,000 | UTC+1     | ME   |       |
| Morocco                | Rabat          | 34.03  | -5.10   | 100   | 35,000,000    | 446,560   | 1,000 | UTC+1     | MA   |       |
| Mozambique             | Maputo         | -17.02 | 28.32   | 1,000 | 28,000,000    | 309,000   | 1,000 | UTC+2     | MZ   |       |
| Myanmar                | Nay Pyi Taw    | 19.75  | 96.10   | 100   | 55,000,000    | 676,580   | 1,000 | UTC+6:30  | MM   |       |
| Namibia                | Windhoek       | -17.92 | 16.60   | 1,000 | 2,500,000     | 824,290   | 1,000 | UTC+1     | NA   |       |
| Nauru                  | Yaren          | -0.54  | 167.05  | 10    | 10,000        | 21        | 1,000 | UTC+12    | NR   |       |
| Nepal                  | Kathmandu      | 27.72  | 85.31   | 1,000 | 28,000,000    | 147,181   | 1,000 | UTC+5:45  | NP   |       |
| Netherlands            | Amsterdam      | 52.37  | 4.83    | 10    | 17,000,000    | 51,921    | 1,000 | UTC+1     | NL   |       |
| New Zealand            | Auckland       | -36.85 | 174.76  | 10    | 5,000,000     | 264,537   | 1,000 | UTC+12    | NZ   |       |
| New Caledonia          | Noumea         | -22.27 | 166.43  | 100   | 280,000       | 18,500    | 1,000 | UTC+11:30 | NC   |       |
| Nicaragua              | Managua        | 12.12  | -86.25  | 1,000 | 6,000,000     | 136,600   | 1,000 | UTC-6     | NI   |       |
| Niger                  | Niamey         | 13.52  | 7.69    | 100   | 20,000,000    | 1,266,700 | 1,000 | UTC+0     | NE   |       |
| Nigeria                | Lagos          | 6.45   | 3.38    | 100   | 200,000,000   | 923,768   | 1,000 | UTC+1     | NG   |       |
| North Macedonia        | Skopje         | 41.99  | 21.72   | 100   | 2,100,000     | 25,713    | 1,000 | UTC+1     | MK   |       |
| North Korea            | Pyongyang      | 39.01  | 125.76  | 40    | 25,000,000    | 120,540   | 1,000 | UTC+9     | KP   |       |
| Norway                 | Oslo           | 59.91  | 18.06   | 100   | 5,500,000     | 385,203   | 1,000 | UTC+1     | NO   |       |
| Oman                   | Muscat         | 23.59  | 58.40   | 100   | 4,000,000     | 309,500   | 1,000 | UTC+3     | OM   |       |
| Pakistan               | Islamabad      | 33.69  | 73.06   | 1,000 | 230,000,000   | 796,095   | 1,000 | UTC+5     | PK   |       |
| Palestine              | Ramallah       | 31.90  | 34.81   | 100   | 5,000,000     | 17,540    | 1,000 | UTC+2     | PS   |       |
| Panama                 | Panama City    | 9.10   | -79.51  | 100   | 4,000,000     | 781       | 1,000 | UTC-5     | PA   |       |
| Papua New Guinea       | Port Moresby   | -9.46  | 155.14  | 100   | 8,000,000     | 462,540   | 1,000 | UTC+10    | PG   |       |
| Paraguay               | Asuncion       | -23.55 | -58.44  | 1,000 | 7,000,000     | 406,750   | 1,000 | UTC-4     | PY   |       |
| Peru                   | Lima           | -12.04 | -77.04  | 1,000 | 33,000,000    | 1,285,170 | 1,000 | UTC-5     | PE   |       |
| Philippines            | Manila         | 14.59  | 120.98  | 10    | 100,000,000   | 300,000   | 1,000 | UTC+8     | PH   |       |
| Pitcairn Islands       | Nassau         | -24.70 | -127.00 | 10    | 50            | 47        | 1,000 | UTC-8     | PN   |       |
| Poland                 | Warsaw         | 52.23  | 21.01   | 100   | 38,000,000    | 312,686   | 1,000 | UTC+1     | PL   |       |
| Portugal               | Lisbon         | 38.72  | -9.13   | 100   | 11,000,000    |           |       |           |      |       |















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|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
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| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
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| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
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    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      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185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 524 | 525 | 526 | 527 | 528 | 529 | 530 | 531 | 532 | 533 | 534 | 535 | 536 | 537 | 538 | 539 | 540 | 541 | 542 | 543 | 544 | 545 | 546 | 547 | 548 | 549 | 550 | 551 | 552 | 553 | 554 | 555 | 556 | 557 | 558 | 559 | 560 | 561 | 562 | 563 | 564 | 565 | 566 | 567 | 568 | 569 | 570 | 571 | 572 | 573 | 574 | 575 | 576 | 577 | 578 | 579 | 580 | 581 | 582 | 583 | 584 | 585 | 586 | 587 | 588 | 589 | 590 | 591 | 592 | 593 | 594 | 595 | 596 | 597 | 598 | 599 | 600 | 601 | 602 | 603 | 604 | 605 | 606 | 607 | 608 | 609 | 610 | 611 | 612 | 613 | 614 | 615 | 616 | 617 | 618 | 619 | 620 | 621 | 622 | 623 | 624 | 625 | 626 | 627 | 628 | 629 | 630 | 631 | 632 | 633 | 634 | 635 | 636 | 637 | 638 | 639 | 640 | 641 | 642 | 643 | 644 | 645 | 646 | 647 | 648 | 649 | 650 | 651 | 652 | 653 | 654 | 655 | 656 | 657 | 658 | 659 | 660 | 661 | 662 | 663 | 664 | 665 | 666 | 667 | 668 | 669 | 670 | 671 | 672 | 673 | 674 | 675 | 676 | 677 | 678 | 679 | 680 | 681 | 682 | 683 | 684 | 685 | 686 | 687 | 688 | 689 | 690 | 691 | 692 | 693 | 694 | 695 | 696 | 697 | 698 | 699 | 700 | 701 | 702 | 703 | 704 | 705 | 706 | 707 | 708 | 709 | 710 | 711 | 712 | 713 | 714 | 715 | 716 | 717 | 718 | 719 | 720 | 721 | 722 | 723 | 724 | 725 | 726 | 727 | 728 | 729 | 730 | 731 | 732 | 733 | 734 | 735 | 736 | 737 | 738 | 739 | 740 | 741 | 742 | 743 | 744 | 745 | 746 | 747 | 748 | 749 | 750 | 751 | 752 | 753 | 754 | 755 | 756 | 757 | 758 | 759 | 760 | 761 | 762 | 763 | 764 | 765 | 766 | 767 | 768 | 769 | 770 | 771 | 772 | 773 | 774 | 775 | 776 | 777 | 778 | 779 | 780 | 781 | 782 | 783 | 784 | 785 | 786 | 787 | 788 | 789 | 790 | 791 | 792 | 793 | 794 | 795 | 796 | 797 | 798 | 799 | 800 | 801 | 802 | 803 | 804 | 805 | 806 | 807 | 808 | 809 | 810 | 811 | 812 | 813 | 814 | 815 | 816 | 817 | 818 | 819 | 820 | 821 | 822 | 823 | 824 | 825 | 826 | 827 | 828 | 829 | 830 | 831 | 832 | 833 | 834 | 835 | 836 | 837 | 838 | 839 | 840 | 841 | 842 | 843 | 844 | 845 | 846 | 847 | 848 | 849 | 850 | 851 | 852 | 853 | 854 | 855 | 856 | 857 | 858 | 859 | 860 | 861 | 862 | 863 | 864 | 865 | 866 | 867 | 868 | 869 | 870 | 871 | 872 | 873 | 874 | 875 | 876 | 877 | 878 | 879 | 880 | 881 | 882 | 883 | 884 | 885 | 886 | 887 | 888 | 889 | 890 | 891 | 892 | 893 | 894 | 895 | 896 | 897 | 898 | 899 | 900 | 901 | 902 | 903 | 904 | 905 | 906 | 907 | 908 | 909 | 910 | 911 | 912 | 913 | 914 | 915 | 916 | 917 | 918 | 919 | 920 | 921 | 922 | 923 | 924 | 925 | 926 | 927 | 928 | 929 | 930 | 931 | 932 | 933 | 934 | 935 | 936 | 937 | 938 | 939 | 940 | 941 | 942 | 943 | 944 | 945 | 946 | 947 | 948 | 949 | 950 | 951 | 952 | 953 | 954 | 955 | 956 | 957 | 958 | 959 | 960 | 961 | 962 | 963 | 964 | 965 | 966 | 967 | 968 | 969 | 970 | 971 | 972 | 973 | 974 | 975 | 976 | 977 | 978 | 979 | 980 | 981 | 982 | 983 | 984 | 985 | 986 | 987 | 988 | 989 | 990 | 991 | 992 | 993 | 994 | 995 | 996 | 997 | 998 | 999 | 1000 | 1001 | 1002 | 1003 | 1004 | 1005 | 1006 | 1007 | 1008 | 1009 | 1010 | 1011 | 1012 | 1013 | 1014 | 1015 | 1016 | 1017 | 1018 | 1019 | 1020 | 1021 | 1022 | 1023 | 1024 | 1025 | 1026 | 1027 | 1028 | 1029 | 1030 | 1031 | 1032 | 1033 | 1034 | 1035 | 1036 | 1037 | 1038 | 1039 | 1040 | 1041 | 1042 | 1043 | 1044 | 1045 | 1046 | 1047 | 1048 | 1049 | 1050 | 1051 | 1052 | 1053 | 1054 | 1055 | 1056 | 1057 | 1058 | 1059 | 1060 | 1061 | 1062 | 1063 | 1064 | 1065 | 1066 | 1067 | 1068 | 1069 | 1070 | 1071 | 1072 | 1073 | 1074 | 1075 | 1076 | 1077 | 1078 | 1079 | 1080 | 1081 | 1082 | 1083 | 1084 | 1085 | 1086 | 1087 | 1088 | 1089 | 1090 | 1091 | 1092 | 1093 | 1094 | 1095 | 1096 | 1097 | 1098 | 1099 | 1100 | 1101 | 1102 | 1103 | 1104 | 1105 | 1106 | 1107 | 1108 | 1109 | 1110 | 1111 | 1112 | 1113 | 1114 | 1115 | 1116 | 1117 | 1118 | 1119 | 1120 | 1121 | 1122 | 1123 | 1124 | 1125 | 1126 | 1127 | 1128 | 1129 | 1130 | 1131 | 1132 | 1133 | 1134 | 1135 | 1136 | 1137 | 1138 | 1139 | 1140 | 1141 | 1142 | 1143 | 1144 | 1145 | 1146 | 1147 | 1148 | 1149 | 1150 | 1151 | 1152 | 1153 | 1154 | 1155 | 1156 | 1157 | 1158 | 1159 | 1160 | 1161 | 1162 | 1163 | 1164 | 1165 | 1166 | 1167 | 1168 | 1169 | 1170 | 1171 | 1172 | 1173 | 1174 | 1175 | 1176 | 1177 | 1178 | 1179 | 1180 | 1181 | 1182 | 1183 | 1184 | 1185 | 1186 | 1187 | 1188 | 1189 | 1190 | 1191 | 1192 | 1193 | 1194 | 1195 | 1196 | 1197 | 1198 | 1199 | 1200 | 1201 | 1202 | 1203 | 1204 | 1205 | 1206 | 1207 | 1208 | 1209 | 1210 | 1211 | 1212 | 1213 | 1214 | 1215 | 1216 | 1217 | 1218 | 1219 | 1220 | 1221 | 1222 | 1223 | 1224 | 1225 | 1226 | 1227 | 1228 | 1229 | 1230 | 1231 | 1232 | 1233 | 1234 | 1235 | 1236 | 1237 | 1238 | 1239 | 1240 | 1241 | 1242 | 1243 | 1244 | 1245 | 1246 | 1247 | 1248 | 1249 | 1250 | 1251 | 1252 | 1253 | 1254 | 1255 | 1256 | 1257 | 1258 | 1259 | 1260 | 1261 | 1262 | 1263 | 1264 | 1265 | 1266 | 1267 | 1268 | 1269 | 1270 | 1271 | 1272 | 1273 | 1274 | 1275 | 1276 | 1277 | 1278 | 1279 | 1280 | 1281 | 1282 | 1283 | 1284 | 1285 | 1286 | 1287 | 1288 | 1289 | 1290 | 1291 | 1292 | 1293 | 1294 | 1295 | 1296 | 1297 | 1298 | 1299 | 1300 | 1301 | 1302 | 1303 | 1304 | 1305 | 1306 | 1307 | 1308 | 1309 | 1310 | 1311 | 1312 | 1313 | 1314 | 1315 | 1316 | 1317 | 1318 | 1319 | 1320 | 1321 | 1322 | 1323 | 1324 | 1325 | 1326 | 1327 | 1328 | 1329 | 1330 | 1331 | 1332 | 1333 | 1334 | 1335 | 1336 | 1337 | 1338 | 1339 | 1340 | 1341 | 1342 | 1343 | 1344 | 1345 | 1346 | 1347 | 1348 | 1349 | 1350 | 1351 | 1352 | 1353 | 1354 | 1355 | 1356 | 1357 | 1358 | 1359 | 1360 | 1361 | 1362 | 1363 | 1364 | 1365 | 1366 | 1367 | 1368 | 1369 | 1370 | 1371 | 1372 | 1373 | 1374 | 1375 | 1376 | 1377 | 1378 | 1379 | 1380 | 1381 | 1382 | 1383 | 1384 | 1385 | 1386 | 1387 | 1388 | 1389 | 1390 | 1391 | 1392 | 1393 | 1394 | 1395 | 1396 | 1397 | 1398 | 1399 | 1400 | 1401 | 1402 | 1403 | 1404 | 1405 | 1406 | 1407 | 1408 | 1409 | 1410 | 1411 | 1412 | 1413 | 1414 | 1415 | 1416 | 1417 | 1418 | 1419 | 1420 | 1421 | 1422 | 1423 | 1424 | 1425 | 1426 | 1427 | 1428 | 1429 | 1430 | 1431 | 1432 | 1433 | 1434 | 1435 | 1436 | 1437 | 1438 | 1439 | 1440 | 1441 | 1442 | 1443 | 1444 | 1445 | 1446 | 1447 | 1448 | 1449 | 1450 | 1451 | 1452 | 1453 | 1454 | 1455 | 1456 | 1457 | 1458 | 1459 | 1460 | 1461 | 1462 | 1463 | 1464 | 1465 | 1466 | 1467 | 1468 | 1469 | 1470 | 1471 | 1472 | 1473 | 1474 | 1475 | 1476 | 1477 | 1478 | 1479 | 1480 | 1481 | 1482 | 1483 | 1484 | 1485 | 1486 | 1487 | 1488 | 1489 | 1490 | 1491 | 1492 | 1493 | 1494 | 1495 | 1496 | 1497 | 1498 | 149 |
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185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 524 | 525 | 526 | 527 | 528 | 529 | 530 | 531 | 532 | 533 | 534 | 535 | 536 | 537 | 538 | 539 | 540 | 541 | 542 | 543 | 544 | 545 | 546 | 547 | 548 | 549 | 550 | 551 | 552 | 553 | 554 | 555 | 556 | 557 | 558 | 559 | 560 | 561 | 562 | 563 | 564 | 565 | 566 | 567 | 568 | 569 | 570 | 571 | 572 | 573 | 574 | 575 | 576 | 577 | 578 | 579 | 580 | 581 | 582 | 583 | 584 | 585 | 586 | 587 | 588 | 589 | 590 | 591 | 592 | 593 | 594 | 595 | 596 | 597 | 598 | 599 | 600 | 601 | 602 | 603 | 604 | 605 | 606 | 607 | 608 | 609 | 610 | 611 | 612 | 613 | 614 | 615 | 616 | 617 | 618 | 619 | 620 | 621 | 622 | 623 | 624 | 625 | 626 | 627 | 628 | 629 | 630 | 631 | 632 | 633 | 634 | 635 | 636 | 637 | 638 | 639 | 640 | 641 | 642 | 643 | 644 | 645 | 646 | 647 | 648 | 649 | 650 | 651 | 652 | 653 | 654 | 655 | 656 | 657 | 658 | 659 | 660 | 661 | 662 | 663 | 664 | 665 | 666 | 667 | 668 | 669 | 670 | 671 | 672 | 673 | 674 | 675 | 676 | 677 | 678 | 679 | 680 | 681 | 682 | 683 | 684 | 685 | 686 | 687 | 688 | 689 | 690 | 691 | 692 | 693 | 694 | 695 | 696 | 697 | 698 | 699 | 700 | 701 | 702 | 703 | 704 | 705 | 706 | 707 | 708 | 709 | 710 | 711 | 712 | 713 | 714 | 715 | 716 | 717 | 718 | 719 | 720 | 721 | 722 | 723 | 724 | 725 | 726 | 727 | 728 | 729 | 730 | 731 | 732 | 733 | 734 | 735 | 736 | 737 | 738 | 739 | 740 | 741 | 742 | 743 | 744 | 745 | 746 | 747 | 748 | 749 | 750 | 751 | 752 | 753 | 754 | 755 | 756 | 757 | 758 | 759 | 760 | 761 | 762 | 763 | 764 | 765 | 766 | 767 | 768 | 769 | 770 | 771 | 772 | 773 | 774 | 775 | 776 | 777 | 778 | 779 | 780 | 781 | 782 | 783 | 784 | 785 | 786 | 787 | 788 | 789 | 790 | 791 | 792 | 793 | 794 | 795 | 796 | 797 | 798 | 799 | 800 | 801 | 802 | 803 | 804 | 805 | 806 | 807 | 808 | 809 | 810 | 811 | 812 | 813 | 814 | 815 | 816 | 817 | 818 | 819 | 820 | 821 | 822 | 823 | 824 | 825 | 826 | 827 | 828 | 829 | 830 | 831 | 832 | 833 | 834 | 835 | 836 | 837 | 838 | 839 | 840 | 841 | 842 | 843 | 844 | 845 | 846 | 847 | 848 | 849 | 850 | 851 | 852 | 853 | 854 | 855 | 856 | 857 | 858 | 859 | 860 | 861 | 862 | 863 | 864 | 865 | 866 | 867 | 868 | 869 | 870 | 871 | 872 | 873 | 874 | 875 | 876 | 877 | 878 | 879 | 880 | 881 | 882 | 883 | 884 | 885 | 886 | 887 | 888 | 889 | 890 | 891 | 892 | 893 | 894 | 895 | 896 | 897 | 898 | 899 | 900 | 901 | 902 | 903 | 904 | 905 | 906 | 907 | 908 | 909 | 910 | 911 | 912 | 913 | 914 | 915 | 916 | 917 | 918 | 919 | 920 | 921 | 922 | 923 | 924 | 925 | 926 | 927 | 928 | 929 | 930 | 931 | 932 | 933 | 934 | 935 | 936 | 937 | 938 | 939 | 940 | 941 | 942 | 943 | 944 | 945 | 946 | 947 | 948 | 949 | 950 | 951 | 952 | 953 | 954 | 955 | 956 | 957 | 958 | 959 | 960 | 961 | 962 | 963 | 964 | 965 | 966 | 967 | 968 | 969 | 970 | 971 | 972 | 973 | 974 | 975 | 976 | 977 | 978 | 979 | 980 | 981 | 982 | 983 | 984 | 985 | 986 | 987 | 988 | 989 | 990 | 991 | 992 | 993 | 994 | 995 | 996 | 997 | 998 | 999 | 1000 |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-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[illegible]







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| 1   | 2   | 3   | 4   | 5   | 6   | 7   | 8   | 9   | 10  | 11  | 12  | 13  | 14  | 15  | 16  | 17  | 18  | 19  | 20  | 21  | 22  | 23  | 24  | 25  | 26  | 27  | 28  | 29  | 30  | 31  | 32  | 33  | 34  | 35  | 36  | 37  | 38  | 39  | 40  | 41  | 42  | 43  | 44  | 45  | 46  | 47  | 48  | 49  | 50  | 51  | 52  | 53  | 54  | 55  | 56  | 57  | 58  | 59  | 60  | 61  | 62  | 63  | 64  | 65  | 66  | 67  | 68  | 69  | 70  | 71  | 72  | 73  | 74  | 75  | 76  | 77  | 78  | 79  | 80  | 81  | 82  | 83  | 84  | 85  | 86  | 87  | 88  | 89  | 90  | 91  | 92  | 93  | 94  | 95  | 96  | 97  | 98  | 99  | 100  |
| 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200  |
| 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300  |
| 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400  |
| 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500  |
| 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 524 | 525 | 526 | 527 | 528 | 529 | 530 | 531 | 532 | 533 | 534 | 535 | 536 | 537 | 538 | 539 | 540 | 541 | 542 | 543 | 544 | 545 | 546 | 547 | 548 | 549 | 550 | 551 | 552 | 553 | 554 | 555 | 556 | 557 | 558 | 559 | 560 | 561 | 562 | 563 | 564 | 565 | 566 | 567 | 568 | 569 | 570 | 571 | 572 | 573 | 574 | 575 | 576 | 577 | 578 | 579 | 580 | 581 | 582 | 583 | 584 | 585 | 586 | 587 | 588 | 589 | 590 | 591 | 592 | 593 | 594 | 595 | 596 | 597 | 598 | 599 | 600  |
| 601 | 602 | 603 | 604 | 605 | 606 | 607 | 608 | 609 | 610 | 611 | 612 | 613 | 614 | 615 | 616 | 617 | 618 | 619 | 620 | 621 | 622 | 623 | 624 | 625 | 626 | 627 | 628 | 629 | 630 | 631 | 632 | 633 | 634 | 635 | 636 | 637 | 638 | 639 | 640 | 641 | 642 | 643 | 644 | 645 | 646 | 647 | 648 | 649 | 650 | 651 | 652 | 653 | 654 | 655 | 656 | 657 | 658 | 659 | 660 | 661 | 662 | 663 | 664 | 665 | 666 | 667 | 668 | 669 | 670 | 671 | 672 | 673 | 674 | 675 | 676 | 677 | 678 | 679 | 680 | 681 | 682 | 683 | 684 | 685 | 686 | 687 | 688 | 689 | 690 | 691 | 692 | 693 | 694 | 695 | 696 | 697 | 698 | 699 | 700  |
| 701 | 702 | 703 | 704 | 705 | 706 | 707 | 708 | 709 | 710 | 711 | 712 | 713 | 714 | 715 | 716 | 717 | 718 | 719 | 720 | 721 | 722 | 723 | 724 | 725 | 726 | 727 | 728 | 729 | 730 | 731 | 732 | 733 | 734 | 735 | 736 | 737 | 738 | 739 | 740 | 741 | 742 | 743 | 744 | 745 | 746 | 747 | 748 | 749 | 750 | 751 | 752 | 753 | 754 | 755 | 756 | 757 | 758 | 759 | 760 | 761 | 762 | 763 | 764 | 765 | 766 | 767 | 768 | 769 | 770 | 771 | 772 | 773 | 774 | 775 | 776 | 777 | 778 | 779 | 780 | 781 | 782 | 783 | 784 | 785 | 786 | 787 | 788 | 789 | 790 | 791 | 792 | 793 | 794 | 795 | 796 | 797 | 798 | 799 | 800  |
| 801 | 802 | 803 | 804 | 805 | 806 | 807 | 808 | 809 | 810 | 811 | 812 | 813 | 814 | 815 | 816 | 817 | 818 | 819 | 820 | 821 | 822 | 823 | 824 | 825 | 826 | 827 | 828 | 829 | 830 | 831 | 832 | 833 | 834 | 835 | 836 | 837 | 838 | 839 | 840 | 841 | 842 | 843 | 844 | 845 | 846 | 847 | 848 | 849 | 850 | 851 | 852 | 853 | 854 | 855 | 856 | 857 | 858 | 859 | 860 | 861 | 862 | 863 | 864 | 865 | 866 | 867 | 868 | 869 | 870 | 871 | 872 | 873 | 874 | 875 | 876 | 877 | 878 | 879 | 880 | 881 | 882 | 883 | 884 | 885 | 886 | 887 | 888 | 889 | 890 | 891 | 892 | 893 | 894 | 895 | 896 | 897 | 898 | 899 | 900  |
| 901 | 902 | 903 | 904 | 905 | 906 | 907 | 908 | 909 | 910 | 911 | 912 | 913 | 914 | 915 | 916 | 917 | 918 | 919 | 920 | 921 | 922 | 923 | 924 | 925 | 926 | 927 | 928 | 929 | 930 | 931 | 932 | 933 | 934 | 935 | 936 | 937 | 938 | 939 | 940 | 941 | 942 | 943 | 944 | 945 | 946 | 947 | 948 | 949 | 950 | 951 | 952 | 953 | 954 | 955 | 956 | 957 | 958 | 959 | 960 | 961 | 962 | 963 | 964 | 965 | 966 | 967 | 968 | 969 | 970 | 971 | 972 | 973 | 974 | 975 | 976 | 977 | 978 | 979 | 980 | 981 | 982 | 983 | 984 | 985 | 986 | 987 | 988 | 989 | 990 | 991 | 992 | 993 | 994 | 995 | 996 | 997 | 998 | 999 | 1000 |







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| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
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185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 | 467 | 468 | 469 | 470 | 471 | 472 | 473 | 474 | 475 | 476 | 477 | 478 | 479 | 480 | 481 | 482 | 483 | 484 | 485 | 486 | 487 | 488 | 489 | 490 | 491 | 492 | 493 | 494 | 495 | 496 | 497 | 498 | 499 | 500 | 501 | 502 | 503 | 504 | 505 | 506 | 507 | 508 | 509 | 510 | 511 | 512 | 513 | 514 | 515 | 516 | 517 | 518 | 519 | 520 | 521 | 522 | 523 | 524 | 525 | 526 | 527 | 528 | 529 | 530 | 531 | 532 | 533 | 534 | 535 | 536 | 537 | 538 | 539 | 540 | 541 | 542 | 543 | 544 | 545 | 546 | 547 | 548 | 549 | 550 | 551 | 552 | 553 | 554 | 555 | 556 | 557 | 558 | 559 | 560 | 561 | 562 | 563 | 564 | 565 | 566 | 567 | 568 | 569 | 570 | 571 | 572 | 573 | 574 | 575 | 576 | 577 | 578 | 579 | 580 | 581 | 582 | 583 | 584 | 585 | 586 | 587 | 588 | 589 | 590 | 591 | 592 | 593 | 594 | 595 | 596 | 597 | 598 | 599 | 600 | 601 | 602 | 603 | 604 | 605 | 606 | 607 | 608 | 609 | 610 | 611 | 612 | 613 | 614 | 615 | 616 | 617 | 618 | 619 | 620 | 621 | 622 | 623 | 624 | 625 | 626 | 627 | 628 | 629 | 630 | 631 | 632 | 633 | 634 | 635 | 636 | 637 | 638 | 639 | 640 | 641 | 642 | 643 | 644 | 645 | 646 | 647 | 648 | 649 | 650 | 651 | 652 | 653 | 654 | 655 | 656 | 657 | 658 | 659 | 660 | 661 | 662 | 663 | 664 | 665 | 666 | 667 | 668 | 669 | 670 | 671 | 672 | 673 | 674 | 675 | 676 | 677 | 678 | 679 | 680 | 681 | 682 | 683 | 684 | 685 | 686 | 687 | 688 | 689 | 690 | 691 | 692 | 693 | 694 | 695 | 696 | 697 | 698 | 699 | 700 | 701 | 702 | 703 | 704 | 705 | 706 | 707 | 708 | 709 | 710 | 711 | 712 | 713 | 714 | 715 | 716 | 717 | 718 | 719 | 720 | 721 | 722 | 723 | 724 | 725 | 726 | 727 | 728 | 729 | 730 | 731 | 732 | 733 | 734 | 735 | 736 | 737 | 738 | 739 | 740 | 741 | 742 | 743 | 744 | 745 | 746 | 747 | 748 | 749 | 750 | 751 | 752 | 753 | 754 | 755 | 756 | 757 | 758 | 759 | 760 | 761 | 762 | 763 | 764 | 765 | 766 | 767 | 768 | 769 | 770 | 771 | 772 | 773 | 774 | 775 | 776 | 777 | 778 | 779 | 780 | 781 | 782 | 783 | 784 | 785 | 786 | 787 | 788 | 789 | 790 | 791 | 792 | 793 | 794 | 795 | 796 | 797 | 798 | 799 | 800 | 801 | 802 | 803 | 804 | 805 | 806 | 807 | 808 | 809 | 810 | 811 | 812 | 813 | 814 | 815 | 816 | 817 | 818 | 819 | 820 | 821 | 822 | 823 | 824 | 825 | 826 | 827 | 828 | 829 | 830 | 831 | 832 | 833 | 834 | 835 | 836 | 837 | 838 | 839 | 840 | 841 | 842 | 843 | 844 | 845 | 846 | 847 | 848 | 849 | 850 | 851 | 852 | 853 | 854 | 855 | 856 | 857 | 858 | 859 | 860 | 861 | 862 | 863 | 864 | 865 | 866 | 867 | 868 | 869 | 870 | 871 | 872 | 873 | 874 | 875 | 876 | 877 | 878 | 879 | 880 | 881 | 882 | 883 | 884 | 885 | 886 | 887 | 888 | 889 | 890 | 891 | 892 | 893 | 894 | 895 | 896 | 897 | 898 | 899 | 900 | 901 | 902 | 903 | 904 | 905 | 906 | 907 | 908 | 909 | 910 | 911 | 912 | 913 | 914 | 915 | 916 | 917 | 918 | 919 | 920 | 921 | 922 | 923 | 924 | 925 | 926 | 927 | 928 | 929 | 930 | 931 | 932 | 933 | 934 | 935 | 936 | 937 | 938 | 939 | 940 | 941 | 942 | 943 | 944 | 945 | 946 | 947 | 948 | 949 | 950 | 951 | 952 | 953 | 954 | 955 | 956 | 957 | 958 | 959 | 960 | 961 | 962 | 963 | 964 | 965 | 966 | 967 | 968 | 969 | 970 | 971 | 972 | 973 | 974 | 975 | 976 | 977 | 978 | 979 | 980 | 981 | 982 | 983 | 984 | 985 | 986 | 987 | 988 | 989 | 990 | 991 | 992 | 993 | 994 | 995 | 996 | 997 | 998 | 999 | 1000 |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-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[illegible]























## Appendix 7.

### GATHER-based analysis of TF motifs in linear mixed effects model











|   |       |          |       |     |          |       |     |
|---|-------|----------|-------|-----|----------|-------|-----|
| V\$E2F1_Q4_01   |       | 3.31E-06 | 37.61 | 191 | 6.59E-06 | 46.73 | 141 |
| V\$E2F1_Q6  | E2F-1 | 3.31E-06 | 25.81 | 316 | 6.59E-06 | 58.6  | 250 |
| <p>ACT16A AF15014 ALG8 ANKRD26 APRT ARHGAP11A ARPC4 ASK<br/> ATA2J ATIC ATP13A1 BLM BMO39 BUB1B BUB3 C13orf3<br/> C14orf106 C18orf24 C20orf172 C22orf18 Gcorf157 C7orf19 CAD<br/> CCNA2 CNE1 CCTL5 CDC2 CDC25A CDC25C CDC45L DCCA4<br/> CDC45 CDC48 CENPH CHEK1 CKAP2 CKS2 CLSPN CNAAP1<br/> COMMD8 CP5F3 CSTF1 DAP3 DCC1 DCK DKFZP434B168<br/> DKFZP434G1415 DKFZP564K2062 DKFZP761A078 DMTE1<br/> DNAJC9 DRB1 DUT E2F7 EIF2B1 EIF2S1 ERH EXO1 EXOSC8 FBXO5<br/> FIGL1 FKSJ14 FLJ10706 FLJ2716 FLJ20105 FLJ20364 FLJ20516<br/> FLJ21816 FLJ2624 FLJ40869 FOXM1 GIB2 GMMN GSG2 GTF3C2<br/> HCAP-G HDCA18P HELB HIST1H2AG HIST1H2AI HIST1H2AK<br/> HIST1H3D HIST1H3F HIST1H41 HMMR HSPA8 HSPC138 IARS<br/> KIAA0101 KIAA1333 KIF11 KIF18A KIF4A KNS17 KNTC1 KNTC2<br/> KRT16 KUB3 LMBN1 LOC116143 LOC201725 LOC84661 MAD2L1<br/> MBD4 MCM10 MCM2 MCM3 MCM4 MCM5 MCM7 MELK<br/> MGCC3371 MGCS352 MRPS16 MRPS24 MSJ13.1 MTRF1L MYBL2<br/> NEK2 NEUGRIN NIF3L1 NUDCD2 NUP107 NUP155 NUP205<br/> NUSAP1 OIP5 ORC1L ORC6L PBK PCNA PGM2 PAK2B PI3W PIN1<br/> PKNX PLK4 PLRG1 POLE2 POLR2B POLR3F PP1H PPP1B8 PRM1<br/> PRKDC PYGO2 QRSL1 RAB9P40 RAE1 RAMP RBL1 RFC3 RFC5<br/> RFP2 RGM1TD2 RRM2 RUVBL2 SF3A3 SF3B1 SRS1 SHD1 SHFM1<br/> SIL SIP1 SMC2L1 SMC4L1 SMC6L1 SNRPF STG6 TACC3 TDP1<br/> THAP1 TIMELESS TMPO TOPBP1 TPB6 TRAM1 TRIM59 TROAP<br/> TTK TXNDC USP1 USP39 VBP1 VHL WBSCH16 WNT17A ZC3HD8</p> <p>191 ZMYND19 ZNNT4 DB83A.3</p> <p>ASNDPPT ACT16A AF15014 ALG10 ALG5 ALG8 ANAPC1<br/> ANAPC4 ANAPC7 ANKRD26 APRT ARHGAP11A ARNTL2 ARPC4<br/> ASF1B ASK ASPM ATAD2 ATIC ATP13A1 BLM BMO39 BRCA2<br/> BRN1 BUB1 BUB1B BUB3 C10orf3 C13orf3 C14orf104<br/> C14orf106 C14orf142 C18orf24 C1orf33 C20orf172 C22orf18<br/> C6orf157 C6orf167 C7orf19 C9orf85 CAD CDC5 CEN2 CNE1<br/> CCTL5 CDC2 CDC25A CDC25C CDC45L CDC7 DCCA1 CDC42 CDC44<br/> CDC45 CDC48 CENPA CENPH CHEK1 CKAP2 CKS2 CLSPN CNAAP1<br/> COMMD3 COMMD8 COR56 COTL1 CP5F3 CSE1L CSTF1 CTF3<br/> DAP3 DAP3 DCC1 DCK DEPDCL1B DHFR DKFZP434B168<br/> DKFZP434G1415 DKFZP564K2062 DKFZP564O1664<br/> DKFZP434K2435 DKFZP761A078 DLG7 DMTE1 DNAC9 DRB1<br/> DUT E2F7 E2IG5 EIF2B1 EIF2S1 EPRS ERH EXO1 EXOSC1 EXOSC8<br/> FAM49B FANCD2 FANSLB FBXO5 FGFRIOP FIGL1 FKBP3<br/> FKSG14 FLJ10036 FLJ10156 FLJ10706 FLJ11184 FLJ12436<br/> FLJ2716 FLJ13912 FLJ14803 FLJ20105 FLJ20211 FLJ20331<br/> FLJ20364 FLJ20516 FLJ20641 FLJ21816 FLJ22624 FLJ25416<br/> FLJ39660 FLJ40869 FOXM1 FSPRHL GIB2 GLE1L GMMN GSG2<br/> GTF3C2 GTF3C3 HCAP-G HDCA18P HELB HIST1H2AG<br/> HIST1H2AI HIST1H2AK HIST1H3D HIST1H3F HIST1H41 HMB5<br/> HMMR HPR8BP HSPA8 HSPBP1 HSPC138 HSPC150 IARS IL19<br/> JTV1 KIAA0101 KIAA1229 KIAA1333 KIAA1524 KIF11 KIF18A<br/> KIF20A KIF23 KIF2C KIF4A KNS17 KNTC1 KNTC2 KRT1E KUB3<br/> LENG5 LMBN1 LMBN2 LOC116143 LOC201725 LOC494143 LSM4<br/> LSM6 W11S1 MAD2L1 MBD4 MCM10 MCM2 MCM3 MCM4<br/> MCM5 MCM7 MELK MGCI0911 MGCI4151 MGCI6943<br/> MGCC32020 MGCC3371 MGCS297 MGCS352 MKI67 MPHOSPH1<br/> MRPL47 MRPL52 MRPS10 MRPS16 MRPS24 MSJ13.1 MTRP<br/> MTRF1L MYBL2 NEK2 NEUGRIN NIFB NIF3L1 NOL8 NUDCD2</p>   |       |          |       |     |          |       |     |
| <p>061009C03R1K 2310031118R1K 2310066N05R1K 26100040E16R1K<br/> 2610300B10R1K 2700084L22R1K 2700085W18R1K 2810037C03R1K<br/> 2810047I02R1K 2810418N01R1K 2810453112R1K 5930412E3R1K<br/> 9530020D24R1K Act16a Alg5 Alg8 Anapc1 Anapc7 Aprt Arhgap11a Atic<br/> BC005624 BC025462 Barf1 Bim Brn1 Bubb1 Ccnel Cdc25a Cdc2a<br/> Cdc45 Cdkn3 Chek1 Cispn Commd3 Commhd Gpsr2 Gcstf Gcst3<br/> D3Ert250e Dap3 Dck Depdcl1b Dhfr Dig7 Dnajc9 Drbp1 E2F7 Ec2 Ec2<br/> Efrs Efrs Exo1 Exosc1 Exosc8 Fbpb5 Fancd2 Fbxo5 Figl1 Fhbp3 Foxm1 Gmmn<br/> Gtf3c2 Hist1h2ac Hist1h2af Hist1h2ah Hist1h2an Hist1h2bb Hist1h3i<br/> Hist1h4h Hmnr Jvt1 Kif11 Kif14 Kif18a Kns17 Lmbn2 Lsm4 Mcm10<br/> Mcm2 Mcm3 Mcm5 Mcm7 Melk Metap1 Mki67 Mrps24 Mtpb Wylb2<br/> Nek2 Nl8 Nudcd2 Oip5 Orc1l Orc5l Orc6l Pbk Pgm1 Plk4z2 Plgw Pln2<br/> Plk4 Pole2 Pph1 Ppil1 Ppils Pppl18 Prm1 Pygo2 Ragaap1 Rad51ap1 Rael<br/> Rl1 Rfc3 Rgm1td2 Rntf34 Rps3 Sfrs1 Sfrs9 Sgo1 Shtdg1 Sipl1 Smarcd1<br/> Smecl1 Smecl1 Srp1 Sumoz Suw39h1 Tacc3 Tfdp1 Tpin Tmpo Topbp1<br/> Tpm1 Tramt1 Trnms9 Trp13 Usp1 Wnt7a Zc3hd8 Zmpste24 Zmynd19</p> <p>141 Tgbe Tramt1 Trnms9 Trp13 Usp1 Wnt7a Zc3hd8 Zmpste24 Zmynd19<br/> 061009C03R1K 1200009B18R1K 221040ZC18R1K 2310031118R1K<br/> 2310043D08R1K 2310066N05R1K 2410004C24R1K 2410011603R1K<br/> 2410012H02R1K 2510040D07R1K 2600001117R1K 2610002176R1K<br/> 2610040E16R1K 2610300B10R1K 2610528A17R1K 2700084L22R1K<br/> 2700085W18R1K 2810037C03R1K 2810047I02R1K 2810418N01R1K<br/> 2810453112R1K 4933424N09R1K 57305905R1K 5930412E3R1K<br/> 9530020D24R1K A467484 AWS52001 Aasdhpp Act16a Alg5 Alg8 Anapc1<br/> Anapc4 Anapc7 Aprt Arhgap11a Arpc4 Asf1b Atic Aurka Aurkb<br/> BC005624 BC025462 BC066140 Barf1 Birc5 Bim Brn1 Bubb1<br/> C730036B14R1K Cad Calmbp1 Cdc45 Ccnel Ccts Cdc25a Cdc25c Cdc2a<br/> Cdc7 Cdc4l Cdc4a Cdc4s Cdc48 Cdkn3 Cenpe Cenp1 Cenph Chek1<br/> Capln1 Kap2 Cispn Commd3 Commhd Cotl1 Cpsf2 Cpsf3 Cstf1 Cstf3<br/> D11Wsu68e D3Ert250e Dap3 Dck Dcps Depdcl2 Depdclb Dhfr Dig7<br/> Dnajc9 Drbp1 Dsc2 E2F7 Ec2c Efr2b1 Efr2s1 Efrs Efrs Exo1 Exosc1 Exosc8<br/> Fbpb5 Fancd2 Fbxo5 Fgftr1p Figl1 Fhbp3 Fhbp3 Foxm1 Gie1l<br/> Gmmn Gpiap1 Gsg2 Gtf3c2 Hebl Hist1h2ac Hist1h2af Hist1h2ah<br/> Hist1h2an Hist1h2bb Hist1h3a Hist1h3i Hist1h4h Hmbs Hmnr Hspa8<br/> Jvt1 Kif11 Kif14 Kif18a Kif20a Kif23 Kns17 Kntc2 Leng5 Lmbn2 Lsm4<br/> Mbd4 Mcm10 Mcm2 Mcm3 Mcm5 Mcm7 Melk Metap1 Mki67 Mrps147<br/> Mrps52 Mrps10 Mrps24 Msj13 Mtpb Mtrf1l Wylb2 Nek2 Nif31 Nl8<br/> Nudcd2 Nup107 Nup155 Nup205 Nupap1 Oip5l Oip5s Orc1l Orc5l Orc6l<br/> Pbk Pema Pcdcl2 Pgm1 Plk4z2 Plgw Ppl1 Pp1z Pp1z Pp1z Pp1z Pp1z<br/> Pole2 Polr2b Polr3f Pp1e Pp1h Pp1l Pp1l Pp1l Pp1l Pp1l Pp1l Pp1l<br/> Pygo2 Qrs1l Ragaap1 Rad51ap1 Rael Rbl1 Rfc3 Rfc5 Rfwd3 Rgm1td2<br/> Rntf34 Rntf34 Rps3 Ruvbl2 S100A8 S100B1 Sfrs1 Sfrs9 Sgo1 Shtdg1 Sipl1<br/> Skb1 Smarcd1 Smecl1 Smecl1 Solt Ssrp1 Sumoz Suw39h1 Tacc3 Tafs<br/> Taktpr Tfdp1 Thap1 Tpin Tpin Topo1 Topo2 Topo3 Tpm2 Tramt1<br/> Trnms9 Trp13 Tropa Ttk Trn1 Tnacd1 Tnacd9 Ube2c Usp1 Usp39<br/> Wbnd1 Wnt7a Xpmc2h Zc3hd8 Zfp482 Zfp526 Zmpste24 Zmynd19</p> |       |          |       |     |          |       |     |







|              |     |          |       |     |   |          |       |     |   |
|--------------|-----|----------|-------|-----|---|----------|-------|-----|---|
| V\$EZF_Q3    | EZF | 3.31E-06 | 26.65 | 46  | ACT16A AR15014 ALG8 ANKR26 ARHGAP11A ARPC4 ASK<br>ATAD2 ATP13A1 BLM BUB3 C13orf3 C14orf106 C20orf172<br>C6orf157 C7orf19 CCNA2 CDC2 CDC25A CDC45L CDC45 CHEK1<br>CKAP2 CPSF3 CSTF1 DCC1 DCK DKFZP434B168 DKFZP564A2062<br>DKFZP761A078 DMTF1 DNAC9 DUT ERH EXO1 FSG14<br>FLJ10706 FLJ12716 FLJ20105 FLJ20516 FLJ21816 FLJ22624<br>FLJ40869 FOXM1 HIST1H2AG HIST1H2AN HIST1H2AK HIST1H3F<br>HIST1H4I IARS KIAA0101 KIAA1333 KIT11 KIT18A KNSL7 KNTC2<br>LOC116143 MCM10 MCM2 MCM3 MCM4 MCM5 MCM7<br>MGC33371 MGC5352 MRPS16 MRPS24 NUP107 NUP155<br>NUP205 NUSAP1 OIP5 ORC1L ORC6L PRK PGM2 PIK4ZB PIGW<br>PINK1 PLK4 PLRG1 PPM1 PRKDC PYGO2 ORSL1 RAB9P40<br>RAMP RBL1 RFC5 RFEP2 RRM2 RUVBL2 SF3B1 SFRS1 SFRS9 SHD1<br>SMC6L1 SNRPF STK6 TACC3 TDP1 TOPBP1 TPBG TRAM1<br>113 TRIM59 TROAP TXNDC USP1 USP39 VHL ZMYND19 ZWINT   | 6.59E-06 | 35.75 | 86  | 2310031118RK 2310066N05RK 2610040E16RK 2610300B10RK<br>2700084L22RK 2700085M14RK 2810037C03RK 2810047L02RK<br>2810418N01RK 2810453L12RK 5930412E22RK 5930020D24RK Act16a<br>Alg8 Anapc7 Arhgap11a Atc BC025462 Brn11 Ccn1 Cdc25a Cdc2a<br>Cdc45 Chek1 Cispn Commnd8 Cpsr2 Dap3 Dck Dhfr E2f7 Ect2<br>Eh1 Exol Fapb5 Fboxs Fozm1 GfR3C2 Hist1h2ac Hist1h2ah<br>Hist1h2an Hist1h2bb Hist1h3i Hmnr1 Kit11 Kit18a Knsf7 Lmbd2 Lsm4<br>Mcm10 Mcm2 Mcm3 Mcm5 Mcm7 Meik Mki67 No18 Oip5 Orc1l Orc5l<br>Orc6l PIK4ZB Plegw Plk4 Pole2 Ppil1 Pppl18 Raggap1 Rbl1 Rfc3 Rps3 Sfrs1<br>Sgpl1 Shldg1 Tac3 Ttdp1 Tipin Topbp1 Trami Trim59 Usp1 Zc3hdc8<br>Zmpste24 Zmynd19   |
| V\$EZF_Q3    | EZF | 3.31E-06 | 26.65 | 46  | ACT16A AR15014 ALG8 ANKR26 ARHGAP11A ARPC4 ASK<br>ATAD2 ATP13A1 BLM BUB3 C13orf3 C14orf106 C20orf172<br>C6orf157 C7orf19 CCNA2 CDC2 CDC25A CDC45L CDC45 CHEK1<br>CKAP2 CPSF3 CSTF1 DCC1 DCK DKFZP434B168 DKFZP564A2062<br>DKFZP761A078 DMTF1 DNAC9 DUT ERH EXO1 FSG14<br>FLJ10706 FLJ12716 FLJ20105 FLJ20516 FLJ21816 FLJ22624<br>FLJ40869 FOXM1 HIST1H2AG HIST1H2AN HIST1H2AK HIST1H3F<br>HIST1H4I IARS KIAA0101 KIAA1333 KIT11 KIT18A KNSL7 KNTC2<br>LOC116143 MCM10 MCM2 MCM3 MCM4 MCM5 MCM7<br>MGC33371 MGC5352 MRPS16 MRPS24 NUP107 NUP155<br>NUP205 NUSAP1 OIP5 ORC1L ORC6L PRK PGM2 PIK4ZB PIGW<br>PINK1 PLK4 PLRG1 PPM1 PRKDC PYGO2 ORSL1 RAB9P40<br>RAMP RBL1 RFC5 RFEP2 RRM2 RUVBL2 SF3B1 SFRS1 SFRS9 SHD1<br>SMC6L1 SNRPF STK6 TACC3 TDP1 TOPBP1 TPBG TRAM1<br>113 TRIM59 TROAP TXNDC USP1 USP39 VHL ZMYND19 ZWINT   | 6.59E-06 | 28.67 | 36  | 2610300B10RK 2810047L02RK 2810418N01RK 2810453L12RK<br>5930412E22RK 5930020D24RK Arhgap11a Cdc25a Cdc2a Cispn Dck<br>Dhfr Eh1 Exol GfR3C2 Hist1h2af Hist1h2ah Hist1h2an Hist1h3i Kit18a<br>Knsf7 Mcm2 Mcm3 Mcm5 Mcm7 Orc1l Pole2 Ppil1 Pppl18 Rbl1 Rfc3<br>Ttdp1 Tipin Topbp1 Trami Usp1  |
| V\$EZF_Q3_01 |     | 3.31E-06 | 39.56 | 264 | RC3 RFC5 RFP2 RGM1D2 RIKO2 RNIF34 RRM2 RUVBL2 S100A8<br>ACT16A AR15014 ALG8 ANKR26 ARHGAP11A ARPC4 ASK<br>ATAD2 ATP13A1 BLM BUB3 C13orf3 C14orf106 C20orf172<br>C6orf157 C7orf19 CCNA2 CDC2 CDC25A CDC45L CDC45 CHEK1<br>CKAP2 CPSF3 CSTF1 DCC1 DCK DKFZP434B168 DKFZP564A2062<br>DKFZP761A078 DMTF1 DNAC9 DUT ERH EXO1 FSG14<br>FLJ10706 FLJ12716 FLJ20105 FLJ20516 FLJ21816 FLJ22624<br>FLJ40869 FOXM1 GIB2 GLE1L GNMN GSG2 GTF3C2<br>GTF3C3 HCAP G HDCA18P HELB HIST1H2AG HIST1H2AI<br>HIST1H2AK HIST1H3D HIST1H3F HIST1H4I HMNR HSP48<br>HSPC138 IARS JTV1 KIAA0101 KIAA1333 KIAA1524 KIT11 KIT18A<br>KIT20A KIF23 KIF2C KIF4A KNSL7 KNTC1 KNTC2 KRT16 KUB3<br>LMB1 LOC116143 LOC201725 LOC4661 LSW6 M11S1<br>MAD2L1 MBD4 MCM10 MCM2 MCM3 MCM4 MCM5 MCM7<br>MEIK MGC10911 MGC16943 MGC33371 MGC5352 MKI67<br>MRPL47 MRPL52 MRPS10 MRPS16 MRPS24 MSL3L1 MTRF1L<br>MYBL2 NEK2 NEUGRIN NIF3L1 NUDCD2 NUP107 NUP155<br>NUP205 NUSAP1 OIP5 ORC1L ORC5L ORC6L PRK PCG6 PCNA<br>POLR2B POLR3F PPIH PPI15 PPR18 PRM1 PRKDC PSM014 PTX1<br>PYGO2 ORSL1 RAB9P40 RACGAP1 RAD51AP1 RAEL1 RAMP RBL1<br>RFC3 RFC5 RFP2 RGM1D2 RIKO2 RNIF34 RRM2 RUVBL2 S100A8 | 6.59E-06 | 63.78 | 203 | 0610009C03RK 1200009B18RK 2210402C18RK 2310031118RK<br>2310066N05RK 2410004C24RK 2610040E16RK 2610300B10RK<br>2700084L22RK 2700085M14RK 2810037C03RK 2810047L02RK<br>2810418N01RK 2810453L12RK 5930412E22RK 5930020D24RK<br>A467484 AWS52001 Act16a Ar108 Alg5 Alg8 Anapc1 Anapc7 Aprt<br>Arhgap11a Asf1b Atc Aurbo BC005624 BC025462 BC066140 Banf1 Bir5<br>Bim Brn1 Bub1b Calmbp1 Ccd5 Cnrd2 Cnrd1 Cc5 Cdc25a Cdc2a Cdc7<br>Cdc4 Cdc45 Cdc48 Cdkn3 Chek1 Clapn1 Cispn Commnd8 Commnd8 Cpsr2<br>Cstf1 Cstf3 D3Efrd250e Dap3 Dck Dcps Depc1a Depc1b Dhfr Dig7<br>Dna1g9 Dtpb1 E2f7 E2f2 E2f21 Efrs Efr1 Exol Exoc1 Exoc8 Fapb5<br>Fancd2 Fbox5 Fignl1 Fndp3 Foxm1 GfR2 Gmn1 Gp1ap1 Gsg2 GfR3C2 Heib<br>Hist1h2ac Hist1h2af Hist1h2an Hist1h2bb Hist1h3i Hist1h3l<br>Hist1h4i Hmnr Hsp48 Iars Jtv1 Kit11 Kit14 Kit18a Knsf7 Kntc2 Lmbd2<br>Lsm4 MGC5590 Mad2L1 Mcm10 Mcm2 Mcm3 Mcm5 Mcm7 Meik<br>Metap1 Mki67 Mrpl47 Mrps10 Mrps24 Mtbp Mtrf1l Mybl2 Nek2 No18<br>Nudcd2 Nup107 Nup155 Nup205 Nusap1 Obf1 Oip5 Orc1l Orc5l Orc6l<br>Pik Pna Pcd2 Pgm1 PIK4ZB Plegw Ppil1 Pppl18 Pppl1 Pppl14 Pppl1 Pppl1<br>Pole2 Polr2b Polr3f Ppil1 Ppi1 Ppi5 Pppl18 Prm1 Psm014 Psg02<br>Raggap1 Rad51ap1 Rael1 Rbl1 Rfc3 Rfc5 Rfw03 Rgntm2 Rikoz2 Rnt134<br>Rps3 Ruvbl2 S100a9 Sfrs1 Sfrs9 Skn1 Sgpl1 Shldg1 Sp1 Smarcd1<br>Smc2L1 Smc4L1 Solt Ssrp1 Sumo2 Suv39h1 Tac3 Ttdp1 Tipin Tmpo<br>Tnp01 Top2a Topbp1 Tpbg Trami Trim59 Trim13 Txn1 Usp1 Usp39<br>Wdrh1 Wnt7a Zc3hdc Zfp482 Zfp526 Zmpste24 Zmynd19 |



|              |     |          |       |     |          |       |   |          |       |     |
|--------------|-----|----------|-------|-----|----------|-------|---|----------|-------|-----|
| V\$EZF_Q4_01 |     |          |       |     |          |       | <p>AS5DHPPT ACT16A AF15Q14 AUG10 AUG5 AUG8 ANAPCA</p> <p>ANAPC7 ANKRD26 ARHGAP11A ARNT12 ARPC4 ASFB1 ASK</p> <p>ATAD2 ATIC ATP13A1 BANF1 BLM BRCA2 BUB1B BUB3 C13orf3</p> <p>C14orf106 C14orf142 C18orf24 C20orf172 C22orf18 C6orf157</p> <p>C7orf19 C9orf73 CCNA2 CCNE1 CDC2 CDC25A CDC25C CDC45L</p> <p>CDC7 CDCA1 CDCA4 CDCA5 CDC48 CCNPA CENPE CENPH CHEK1</p> <p>CKAP2 CKS2 CLSPN CNAP1 COMMD3 COMMD8 GPSF3 CSTF1</p> <p>CST3 DAP3 DCC1 DCK DKFZP434B168 DKFZP434G1415</p> <p>DKFZP564K2062 DKFZP434K2435 DKFZP761A078 DLG7 DNMT1</p> <p>DNACF9 DRB1 DUT EZF7 EIF2S1 ERH EXO1 EXOSC1 EXOSC8</p> <p>FAM33A FAM49B FANCD2 FBXO5 FGFRI1OP FIGL1 FKBP3</p> <p>FKSG14 FLJ10036 FLJ10706 FLJ11184 FLJ12436 FLJ12716</p> <p>FLJ13912 FLJ14803 FLJ20105 FLJ20211 FLJ20364 FLJ20516</p> <p>FLJ21816 FLJ22624 FLJ25416 FLJ39660 FLJ40869 FOXM1 GJB2</p> <p>GLE1L GNMN GTF3C2 HDCCMA18P HELB HIST1H2AG HIST1H2AI</p> <p>HIST1H2AK HIST1H3D HIST1H3F HIST1H4I HMMR HPRR8BP</p> <p>HSP48 HSPBP1 HSPC150 IANS IL19 ITY1 KIAA0101 KIAA1333</p> <p>KIAA1524 KIF11 KIF18A KIF20A KIF23 KIF2C KNSL7 KNTC2 KRT16</p> <p>LMNB1 LOC116143 M1151 MAD2L1 MBD4 MCM10 MCM2</p> <p>MCM3 MCM4 MCM5 MCM7 MGC14151 MGC16943 MGC33371</p> <p>MGC5352 MRPS10 MRPS16 MRPS24 MSL3L1 MTBP MYBL2</p> <p>NEUGRN NFYB NFE3L1 NUDCD2 NUP107 NUP155 NUP205</p> <p>NUSAP1 OIP5 ORC1L ORC5L ORC6L PRK PGCF6 PCNA PDCD2</p> <p>PGM2 PI4K2B PI6W PIN1 PKN2 PLK1 PLK4 PLRG1 POLD1 POLE2</p> <p>POLR2B PP1L5 PPP1R8 PRKDC PSMD14 PTTG1 PYGO2 PIZ2 QRS1L</p> <p>RAB9P40 RACGAP1 RAD51AP1 RAE1 RAMP RBL1 RFC3 RFC5</p> <p>REF2 RGNMTD2 ROK2 RPF1 RRM2 RUVBL2 S100A8 SF3B1 SFBS1</p> <p>SFRS9 SHD1 SIL SMO1 SLDS SMC4L1 SMC6L1 SNRPF SRRP1 STK6</p> <p>239 TACG3 TFDPI THAPI TIMELESS TMPO TOPBP1 TPBG TPX2</p> <p>ACTB2A AF15Q14 AFOS RANNOZ20 ANNOA17L1A ANCA1 ASK</p> <p>ATAD2 ATP13A1 BLM BM039 BUB3 C13orf3 C14orf106 C18orf24</p> <p>C20orf172 C22orf18 C6orf157 C7orf19 CAD CCNA2 CCNE1 CCT5</p> <p>CDC2 CDC25A CDC25C CDC45L CDCA4 CDCA5 CDC48 CENPH</p> <p>CHEK1 CKAP2 CKS2 CLSPN CNAP1 GPSF3 CSTF1 DAP3 DCC1 DCK</p> <p>DKFZP434B168 DKFZP434G1415 DKFZP564K2062</p> <p>DKFZP761A078 DNMT1 DNACF9 DRB1 DUT EZF7 EPNS ERH EXO1</p> <p>EXOSC8 FBXO5 FIGL1 FKSG14 FLJ10706 FLJ12716 FLJ20105</p> <p>FLJ20364 FLJ20516 FLJ21816 FLJ22624 FLJ40869 FOXM1 GJB2</p> <p>GNMN GSG2 GTF3C2 HCAP G-HDCCMA18P HELB HIST1H2AG</p> <p>HIST1H2AI HIST1H2AK HIST1H3D HIST1H3F HIST1H4I HMMR</p> <p>IARS KIAA0101 KIAA1333 KIF11 KIF18A KNSL7 KNTC1 KNTC2</p> <p>KUB3 LMNB1 LOC116143 LOC201725 MAD2L1 MCM10 MCM2</p> <p>MCM3 MCM4 MCM5 MCM7 MELK MGC33371 MGC5352</p> <p>MRPS16 MRPS24 MTRE1L MYBL2 NEUGRN NUDCD2 NUP107</p> <p>NUP155 NUP205 NUSAP1 OIP5 ORC1L ORC6L PRK PCNA PGM2</p> <p>PI4K2B PI6W PIN1 PLK4 PLRG1 POLE2 POLR2B PP1H PPP1R8</p> <p>PRIM1 PRKDC PYGO2 QRS1L RAB9P40 RAMP RBL1 RFC3 RFC5</p> <p>REF2 RGNMTD2 RRM2 RUVBL2 SF3A3 SF3B1 SFBS1 SHD1 SIL</p> <p>SMC2L1 SMC6L1 SNRPF STK6 TACG3 TFDPI THAPI TMPO</p> <p>TOPBP1 TPBG TRAM1 TRIM59 TIOAP TTK TXNDC USP1 USP39</p> <p>VBP1 VHL WBSCR16 WNT7A ZC3HDC8 ZMYND19 ZWINT</p> <p>170 d138314.3</p>   | 6.59E-06 | 45.34 | 132 |
| V\$EZF_Q4    | EZF | 3.31E-06 | 24.89 | 239 | 6.59E-06 | 36.01 | <p>179 Zfp482 Zimpste24 Zmynd19</p> <p>0610009C03RK 23100311L18RK 2310066N05RK 2610040E16RK</p> <p>2610300B10RK 2700084L22RK 2700085M18RK 2810037C03RK</p> <p>2810047I02RK 2810418N01RK 2810453L12RK 4933424N09RK</p> <p>5930412E23RK 9530020D24RK AW552001 Aasdtpot Act16a Alg5 Alg8</p> <p>Anapc1 Anapc7 Appt Arhgap11a Atc Atp13a1 Aurka Aurkb BC005624</p> <p>BC025462 Barf1 Birc5 Brn1 C730036B14RK Cad Calmbp1 Cdc65 Ccne1</p> <p>Cdc25a Cdc2a Cdc7 Cdc45 Cdc48 Cdkn3 Cenpe Cenpf Cenph Chek1 Cks2</p> <p>Clsn Commn3 Commh8 Cpsp6 Cpsf2 Cpsf3 Cstf1 Cstf3 D3Efrnd250e</p> <p>Dap3 Dck Dcps Dhtf Dlg7 Dnaif9 Drbp1 EZF7 Ec2 Efr2s1 Ern Exo1 Exosc1</p> <p>Exosc8 Fapb5 Fancd2 Fbox5 Figl1 Fhbp3 Foxm1 Gnmn GTF3C2 Helb</p> <p>HIST1H2Ac HIST1H2af HIST1H2an HIST1H2an HIST1H2b HIST1H3 HIST1H4</p> <p>Hmmr Hsp48 Ity1 Kif11 Kif14 Kif28a Kif4 Kns7 Leng5 Lmbd2 Lsm4</p> <p>MGC65590 Mcm10 Mcm2 Mcm3 Mcm5 Mcm7 Melk Mki67 Mphosph1</p> <p>Mrp52 Mrps24 Mtpb Nn18 Nudcd2 Obfc1 Oip5 Orc1l Orc5l Orc6l Pcdcd2</p> <p>Pgm1 Pk42b Plgw Pin1 Pkn2 Plk1 Plk4 Plrg1 Pp1t1 Pold1 Pole2 Polr2b</p> <p>Pp1l1 Pp1l5 Pp1l8 Prim1 Pks9 Pygo2 Raccap1 Rad51ap1 Rae1 Rbl1 Rfc3</p> <p>Rgmdm2 Rntf134 Rntf34 Rps3 Rps6kad Ruvbl2 Sfrs1 Sfrs9 Sgo1 Shtdg1</p> <p>Sip1 Skb1 Smc2l1 Srrp1 Sumo2 Suw39h1 Tacc3 Taf5 Tfdp1 Tgpn Top2a</p> <p>Topbp1 Tpbp Tpx2 Tramt1 Trim59 Txn1 Txndc1 Txndc9 Usp1 Zc3hdc8</p> <p>0610009C03RK 23100311L18RK 2310066N05RK 2610040E16RK</p> <p>2610300B10RK 2700084L22RK 2700085M18RK 2810037C03RK</p> <p>2810047I02RK 2810418N01RK 2810453L12RK 4933424N09RK</p> <p>5930412E23RK 9530020D24RK AW552001 Aasdtpot Act16a Alg5 Alg8</p> <p>Anapc1 Anapc7 Appt Arhgap11a Atc Atp13a1 Aurka Aurkb BC005624</p> <p>BC025462 Barf1 Birc5 Brn1 C730036B14RK Cad Calmbp1 Cdc65 Ccne1</p> <p>Cdc25a Cdc2a Cdc7 Cdc45 Cdc48 Cdkn3 Cenpe Cenpf Cenph Chek1 Cks2</p> <p>Clsn Commn3 Commh8 Cpsp6 Cpsf2 Cpsf3 Cstf1 Cstf3 D3Efrnd250e</p> <p>Dap3 Dck Dcps Dhtf Dlg7 Dnaif9 Drbp1 EZF7 Ec2 Efr2s1 Ern Exo1 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Pp1l5 Pp1l8 Prim1 Pks9 Pygo2 Raccap1 Rad51ap1 Rae1 Rbl1 Rfc3</p> <p>Rgmdm2 Rntf134 Rntf34 Rps3 Rps6kad Ruvbl2 Sfrs1 Sfrs9 Sgo1 Shtdg1</p> <p>Sip1 Skb1 Smc2l1 Srrp1 Sumo2 Suw39h1 Tacc3 Taf5 Tfdp1 Tgpn Top2a</p> <p>Topbp1 Tpbp Tpx2 Tramt1 Trim59 Txn1 Txndc1 Txndc9 Usp1 Zc3hdc8</p> <p>0610009C03RK 23100311L18RK 2310066N05RK 2610040E16RK</p> <p>2610300B10RK 2700084L22RK 2700085M18RK 2810037C03RK</p> <p>2810047I02RK 2810418N01RK 2810453L12RK 4933424N09RK</p> <p>5930412E23RK 9530020D24RK AW552001 Aasdtpot Act16a Alg5 Alg8</p> <p>Anapc1 Anapc7 Appt Arhgap11a Atc Atp13a1 Aurka Aurkb BC005624</p> <p>BC025462 Barf1 Birc5 Brn1 C730036B14RK Cad Calmbp1 Cdc65 Ccne1</p> <p>Cdc25a Cdc2a Cdc7 Cdc45 Cdc48 Cdkn3 Cenpe Cenpf Cenph Chek1 Cks2</p> <p>Clsn Commn3 Commh8 Cpsp6 Cpsf2 Cpsf3 Cstf1 Cstf3 D3Efrnd250e</p> <p>Dap3 Dck Dcps Dhtf Dlg7 Dnaif9 Drbp1 EZF7 Ec2 Efr2s1 Ern Exo1 Exosc1</p> <p>Exosc8 Fapb5 Fancd2 Fbox5 Figl1 Fhbp3 Foxm1 Gnmn GTF3C2 Helb</p> <p>HIST1H2Ac HIST1H2af HIST1H2an HIST1H2an HIST1H2b HIST1H3 HIST1H4</p> <p>Hmmr Hsp48 Ity1 Kif11 Kif14 Kif28a Kif4 Kns7 Leng5 Lmbd2 Lsm4</p> <p>MGC65590 Mcm10 Mcm2 Mcm3 Mcm5 Mcm7 Melk Mki67 Mphosph1</p> <p>Mrp52 Mrps24 Mtpb Nn18 Nudcd2 Obfc1 Oip5 Orc1l Orc5l Orc6l Pcdcd2</p> <p>Pgm1 Pk42b Plgw Pin1 Pkn2 Plk1 Plk4 Plrg1 Pp1t1 Pold1 Pole2 Polr2b</p> <p>Pp1l1 Pp1l5 Pp1l8 Prim1 Pks9 Pygo2 Raccap1 Rad51ap1 Rae1 Rbl1 Rfc3</p> <p>Rgmdm2 Rntf134 Rntf34 Rps3 Rps6kad Ruvbl2 Sfrs1 Sfrs9 Sgo1 Shtdg1</p> <p>Sip1 Skb1 Smc2l1 Srrp1 Sumo2 Suw39h1 Tacc3 Taf5 Tfdp1 Tgpn Top2a</p> <p>Topbp1 Tpbp Tpx2 Tramt1 Trim59 Txn1 Txndc1 Txndc9 Usp1 Zc3hdc8</p> <p>0610009C03RK 23100311L18RK 2310066N05RK 2610040E16RK</p> <p>2610300B10RK 2700084L22RK 2700085M18RK 2810037C03RK</p> <p>2810047I02RK 2810418N01RK 2810453L12RK 4933424N09RK</p> <p>5930412E23RK 9530020D24RK AW552001 Aasdtpot Act16a Alg5 Alg8</p> <p>Anapc1 Anapc7 Appt Arhgap11a Atc Atp13a1 Aurka Aurkb BC005624</p> <p>BC025462 Barf1 Birc5 Brn1 C730036B14RK Cad Calmbp1 Cdc65 Ccne1</p> <p>Cdc25a Cdc2a Cdc7 Cdc45 Cdc48 Cdkn3 Cenpe Cenpf Cenph Chek1 Cks2</p> <p>Clsn Commn3 Commh8 Cpsp6 Cpsf2 Cpsf3 Cstf1 Cstf3 D3Efrnd250e</p> <p>Dap3 Dck Dcps Dhtf Dlg7 Dnaif9 Drbp1 EZF7 Ec2 Efr2s1 Ern Exo1 Exosc1</p> <p>Exosc8 Fapb5 Fancd2 Fbox5 Figl1 Fhbp3 Foxm1 Gnmn GTF3C2 Helb</p> <p>HIST1H2Ac HIST1H2af HIST1H2an HIST1H2an HIST1H2b HIST1H3 HIST1H4</p> <p>Hmmr Hsp48 Ity1 Kif11 Kif14 Kif28a Kif4 Kns7 Leng5 Lmbd2 Lsm4</p> <p>MGC65590 Mcm10 Mcm2 Mcm3 Mcm5 Mcm7 Melk Mki67 Mphosph1</p> <p>Mrp52 Mrps24 Mtpb Nn18 Nudcd2 Obfc1 Oip5 Orc1l Orc5l Orc6l Pcdcd2</p> <p>Pgm1 Pk42b Plgw Pin1 Pkn2 Plk1 Plk4 Plrg1 Pp1t1 Pold1 Pole2 Polr2b</p> <p>Pp1l1 Pp1l5 Pp1l8 Prim1 Pks9 Pygo2 Raccap1 Rad51ap1 Rae1 Rbl1 Rfc3</p> <p>Rgmdm2 Rntf134 Rntf34 Rps3 Rps6kad Ruvbl2 Sfrs1 Sfrs9 Sgo1 Shtdg1</p> <p>Sip1 Skb1 Smc2l1 Srrp1 Sumo2 Suw39h1 Tacc3 Taf5 Tfdp1 Tgpn Top2a</p> <p>Topbp1 Tpbp Tpx2 Tramt1 Trim59 Txn1 Txndc1 Txndc9 Usp1 Zc3hdc8</p> <p>0610009C03RK 23100311L18RK 2310066N05RK 2610040E16RK</p> <p>2610300B10RK 2700084L22RK 2700085M18RK 2810037C03RK</p> <p>2810047I02RK 2810418N01RK 2810453L12RK 4933424N09RK</p> <p>5930412E23RK 9530020D24RK AW552001 Aasdtpot Act16a Alg5 Alg8</p> <p>Anapc1 Anapc7 Appt Arhgap11a Atc Atp13a1 Aurka Aurkb BC005624</p> <p>BC025462 Barf1 Birc5 Brn1 C730036B14RK Cad Calmbp1 Cdc65 Ccne1</p> <p>Cdc25a Cdc2a Cdc7 Cdc45 Cdc48 Cdkn3 Cenpe Cenpf Cenph Chek1 Cks2</p> <p>Clsn Commn3 Commh8 Cpsp6 Cpsf2 Cpsf3 Cstf1 Cstf3 D3Efrnd250e</p> <p>Dap3 Dck Dcps Dhtf Dlg7 Dnaif9 Drbp1 EZF7 Ec2 Efr2s1 Ern Exo1 Exosc1</p> <p>Exosc8 Fapb5 Fancd2 Fbox5 Figl1 Fhbp3 Foxm1 Gnmn GTF3C2 Helb</p> <p>HIST1H2Ac HIST1H2af HIST1H2an HIST1H2an HIST1H2b HIST1H3 HIST1H4</p> <p>Hmmr Hsp48 Ity1 Kif11 Kif14 Kif28a Kif4 Kns7 Leng5 Lmbd2 Lsm4</p> <p>MGC65590 Mcm10 Mcm2 Mcm3 Mcm5 Mcm7 Melk Mki67 Mphosph1</p> <p>Mrp52 Mrps24 Mtpb Nn18 Nudcd2 Obfc1 Oip5 Orc1l Orc5l Orc6l Pcdcd2</p> <p>Pgm1 Pk42b Plgw Pin1 Pkn2 Plk1 Plk4 Plrg1 Pp1t1 Pold1 Pole2 Polr2b</p> <p>Pp1l1 Pp1l5 Pp1l8 Prim1 Pks9 Pygo2 Raccap1 Rad51ap1 Rae1 Rbl1 Rfc3</p> <p>Rgmdm2 Rntf134 Rntf34 Rps3 Rps6kad Ruvbl2 Sfrs1 Sfrs9 Sgo1 Shtdg1</p> <p>Sip1 Skb1 Smc2l1 Srrp1 Sumo2 Suw39h1 Tacc3 Taf5 Tfdp1 Tgpn Top2a</p> <p>Topbp1 Tpbp Tpx2 Tramt1 Trim59 Txn1 Txndc1 Txndc9 Usp1 Zc3hdc8</p> <p>0610009C03RK 23100311L18RK 2310066N05RK 2610040E16RK</p> <p>2610300B10RK 2700084L22RK 2700085M18RK 2810037C03RK</p> <p>2810047I02RK 2810418N01RK 2810453L12RK 4933424N09RK</p> <p>5930412E23RK 9530020D24RK AW552001 Aasdtpot Act16a Alg5 Alg8</p> <p>Anapc1 Anapc7 Appt Arhgap11a Atc Atp13a1 Aurka Aurkb BC005624</p> <p>BC025462 Barf1 Birc5 Brn1 C730036B14RK Cad Calmbp1 Cdc65 Ccne1</p> <p>Cdc25a Cdc2a Cdc7 Cdc45 Cdc48 Cdkn3 Cenpe Cenpf Cenph Chek1 Cks2</p> <p>Clsn Commn3 Commh8 Cpsp6 Cpsf2 Cpsf3 Cstf1 Cstf3 D3Efrnd250e</p> <p>Dap3 Dck Dcps Dhtf Dlg7 Dnaif9 Drbp1 EZF7 Ec2 Efr2s1 Ern Exo1 Exosc1</p> <p>Exosc8 Fapb5 Fancd2 Fbox5 Figl1 Fhbp3 Foxm1 Gnmn GTF3C2 Helb</p> <p>HIST1H2Ac HIST1H2af HIST1H2an HIST1H2an HIST1H2b HIST1H3 HIST1H4</p> <p>Hmmr Hsp48 Ity1 Kif11 Kif14 Kif28a Kif4 Kns7 Leng5 Lmbd2 Lsm4</p> <p>MGC65590 Mcm10 Mcm2 Mcm3 Mcm5 Mcm7 Melk Mki67 Mphosph1</p> <p>Mrp52 Mrps24 Mtpb Nn18 Nudcd2 Obfc1 Oip5 Orc1l Orc5l Orc6l Pcdcd2</p> <p>Pgm1 Pk42b Plgw Pin1 Pkn2 Plk1 Plk4 Plrg1 Pp1t1 Pold1 Pole2 Polr2b</p> <p>Pp1l1 Pp1l5 Pp1l8 Prim1 Pks9 Pygo2 Raccap1 Rad51ap1 Rae1 Rbl1 Rfc3</p> <p>Rgmdm2 Rntf134 Rntf34 Rps3 Rps6kad Ruvbl2 Sfrs1 Sfrs9 Sgo1 Shtdg1</p> <p>Sip1 Skb1 Smc2l1 Srrp1 Sumo2 Suw39h1 Tacc3 Taf5 Tfdp1 Tgpn Top2a</p> <p>Topbp1 Tpbp Tpx2 Tramt1 Trim59 Txn1 Txndc1 Txndc9 Usp1 Zc3hdc8</p> <p>0610009C03RK 23100311L18RK 2310066N05RK 2610040E16RK</p> <p>2610300B10RK 2700084L22RK 2700085M18RK 2810037C03RK</p> <p>2810047I02RK 2810418N01RK 2810453L12RK 4933424N09RK</p> <p>5930412E23RK 9530020D24RK AW552001 Aasdtpot Act16a Alg5 Alg8</p> <p>Anapc1 Anapc7 Appt Arhgap11a Atc Atp13a1 Aurka Aurkb BC005624</p> <p>BC025462 Barf1 Birc5 Brn1 C730036B14RK Cad Calmbp1 Cdc65 Ccne1</p> <p>Cdc25a Cdc2a Cdc7 Cdc45 Cdc48 Cdkn3 Cenpe Cenpf Cenph Chek1 Cks2</p> <p>Clsn Commn3 Commh8 Cpsp6 Cpsf2 Cpsf3 Cstf1 Cstf3 D3Efrnd250e</p> <p>Dap3 Dck Dcps Dhtf Dlg7 Dnaif9 Drbp1 EZF7 Ec2 Efr2s1 Ern Exo1 Exosc1</p> <p>Exosc8 Fapb5 Fancd2 Fbox5 Figl1 Fhbp3 Foxm1 Gnmn GTF3C2 Helb</p> <p>HIST1H2Ac HIST1H2af HIST1H2an HIST1H2an HIST1H2b HIST1H3 HIST1H4</p> <p>Hmmr Hsp48 Ity1 Kif11 Kif14 Kif28a Kif4 Kns7 Leng5 Lmbd2 Lsm4</p> <p>MGC65590 Mcm10 Mcm2 Mcm3 Mcm5 Mcm7 Melk Mki67 Mphosph1</p> <p>Mrp52 Mrps24 Mtpb Nn18 Nudcd2 Obfc1 Oip5 Orc1l Orc5l Orc6l Pcdcd2</p> <p>Pgm1 Pk42b Plgw Pin1 Pkn2 Plk1 Plk4 Plrg1 Pp1t1 Pold1 Pole2 Polr2b</p> <p>Pp1l1 Pp1l5 Pp1l8 Prim1 Pks9 Pygo2 Raccap1 Rad51ap1 Rae1 Rbl1 Rfc3</p> <p>Rgmdm2 Rntf134 Rntf34 Rps3 Rps6kad Ruvbl2 Sfrs1 Sfrs9 Sgo1 Shtdg1</p> <p>Sip1 Skb1 Smc2l1 Srrp1 Sumo2 Suw39h1 Tacc3 Taf5 Tfdp1 Tgpn Top2a</p> <p>Topbp1 Tpbp Tpx2 Tramt1 Trim59 Txn1 Txndc1 Txndc9 Usp1 Zc3hdc8</p> <p>0610009C03RK 23100311L18RK 2310066N05RK 2610040E16RK</p> <p>2610300B10RK 2700084L22RK 2700085M18RK 2810037C03RK</p> <p>2810047I02RK 2810418N01RK 2810453L12RK 4933424N09RK</p> <p></p> |          |       |     |







|              |     |          |       |     |  |          |       |     |  |
|--------------|-----|----------|-------|-----|--|----------|-------|-----|--|
| V\$ENF_Q6    | EZF | 6.59E-06 | 8.1   | 337 | MGC35297 MGC35352 MKI67 MPHOSPH1 MRPL47 MRPS510  | 6.59E-06 | 31.75 | 281 | Smardcrt1 Smc211 Smc411 Smc611 Solt Ssrp1 Sumo2 Suw391l Tacc3 Trf15  |
| V\$NFY_Q6_01 |     | 3.31E-06 | 12.23 | 203 | ZMWNID19 ZNF482 ZNF526 ZNFIN1<br>ASDHPP1 ACT16A ADAMDECT1 AT15Q14 ALG10 ALG5 ALG8<br>ANAPC1 ANAPC4 ANAPC7 ANKRD26 APRT ARHGAP11A ARNT12<br>ARRCA ASFB1B ASK ASPM AT1A2 ATIC ATP13A1 AURKB BANF1<br>BLM BMO39 BRCA2 BRRN1 BUB1 BUB1B BUB3 C10orf3 C13orf3<br>C14orf10A C14orf106 C14orf142 C18orf2A C1orf3 C20orf172<br>C22orf18 C6orf157 C6orf167 C7orf19 C9orf78 C9orf85 CAD<br>CCDC5 CCNA2 CNE1 CTT5 CDC2 CDC23A CDC25C CDC45L CDC7<br>CDOA1 CDCA2 CDCA4 CDCAS CDCAS CDKN3 CENPA CENPF<br>CENPH CHEK1 KAP2 CKS2 CLSPN CMAS CNAP1 COMMB3<br>COMMID8 COTL1 CPSF2 CPSF3 CSE1L CSTF1 CSTF3 DAP13 DAP3<br>DCC1 DCK DCP5 DEPD1C1 DEPD1C1B DHFR DKFZP4348168<br>DKFZP434G1415 DKFZP564K2062 DKFZP564O1664<br>DKFZP434K2435 DKFZP761A078 DLG7 DMTEL1 DNAC9 DRB1<br>DSG3 DUT EZF7 EZIG5 EIF2B1 EIF2S1 EPNS ENH ESP1L EXO1<br>EXOSC1 EXOSC8 FAM133A FAM49B FANCD2 FANSLB FBXO5<br>FGR1OP FIGNL1 FKBP3 FKSG14 FLJ10036 FLJ10156 FLJ10706<br>FLJ1184 FLJ11752 FLJ12436 FLJ12716 FLJ13912 FLJ14803<br>FLJ20105 FLJ20211 FLJ20331 FLJ20364 FLJ20516 FLJ20641<br>FLJ21816 FLJ2624 FLJ25416 FLJ39660 FLJ40869 FOXM1<br>FSHRPH1 GJB2 GLE1L GMNN GSG2 GTF3C2 GTF3G HCAP-G<br>HDCMA18P HELB HIST1H2AG HIST1H2AI HIST1H2AK HIST1H3D<br>HIST1H3F HIST1H4I HMB5 HMMR HRR88P HSPA8 HSPBP1<br>HSPC138 HSPC150 IARS IL19 JTV1 KIAA0101 KIAA1229 KIAA1333<br>KIAA1524 KIF11 KIF18A KIF20A KIF23 KIF2C KIF4A KNL2 KNTC1<br>KNTC2 KRT16 KUB3 LENG5 LMNB1 LOC116143 LOC201725<br>LOC494143 LOC84661 LSM4 LSM6 M1JST MAD2L1 MB04<br>MCM10 MCM2 MCM3 MCM4 MCM5 MCM7 MELK MGC10540<br>MGC10911 MGC14151 MGC16943 MGC33371 MGC35274 | 3.64E-05 | 6.15  | 168 | 061009C03R1K 1200008012R1K 2210402C18R1K 2510040D007R1K<br>2600001117R1K 2610002117R1K 2610300810R1K 2610528A17R1K<br>2700084122R1K 2810037030R1K 2810047102R1K 2810418N01R1K<br>5930412E23R1K A167484 Aasdhpp1 Act16a Adamdelect1 Alg5 Arhgap11a<br>Arnt12 Asfb1b Aurkb B930062P21R1K BC004701 BC025462<br>BC066140 Bim Bub1b Cad Cnna2 Cnna2 Cdc25a Cdc25c Cdc2a Cdc42<br>Cdc4a Cdc4s Cdc48 Cdkn3 Cnna2 Chap2 Cks2 Clspn Comm3 Comm48<br>Cops6 Corti Cpsf2 Cse1l Cstf1 Cstf3 D3Ertd250c Depdc1a Depdc1b Dhfr<br>Dmrt1 Dsg3 Dut EZ17 Ec12 Eif2b1 Eps1 Etn Exo1 Exosc1 Exosc8 Fabp5<br>Foxo5 Fgr10p Fkbp3 Fmbp3 Foxm1 Fshphr11 Gmn Gsg2 Hs1b12ac<br>Hist1h2af Hist1h2ah Hist1h2an Hist1h2b1 Hist1h3a Hist1h3i Hmnr<br>Hsp48 Iars IL19 Jtv1 Kif11 Kif18a Kif20a Kif23 Lsm4 Mcm10 Mcm2 Mcm3<br>Mcm5 Mcm7 Metap1 Mki67 Mrps16 Nek2 Nfyb Nudcd4 Nup155 Nup37<br>Nusap1 Oips Orc1 Orc6l Pona Pcdcd2 Pgm1 Pgw Pmt Pk1 Ppmt1 Polr13f<br>Pp1l1 Prmt1 Pxy9 Ptgt1 Qrst Raccap1 Rad51ap1 Rael Rfc3 Rfw3<br>Rgmtd4 Rnf34 Rpa3 Ruvb2 S100a8 S1a3a Sfrs1 Sfrn1 Sgol1 Sipt1 Sko1<br>Smc211 Solt Sumo2 Suw391l Tacc3 Takrp Tarst1 Thap1 Tmpo Trmpss11a<br>Tnpol1 Top2a Topbp1 Tpx2 Trm113 Trm159 Troap Ttk Txndc9 Ube2c Usp1<br>Usp39 Vbp1 Wnt7a Zfp482 Zfp526 Znyvnt1 Znwnt |
|              |     |          |       |     | ARRHGAP11A ASFB1B ASPM AT1A2 ATP13A1 AURKB BLM BUB1<br>BUB3 C10orf3 C14orf106 C14orf142 C1orf3 C20orf129<br>C6orf167 C9orf85 CCNA2 CCNB2 CDC2 CDC25A CDC25C CDC45L<br>CDC7 CDCA2 CDCA4 CDCAS CDKN3 CENPA CENPF CKAP2 CKS2<br>CLSPN CNAP1 COTL1 CPSF2 CSE1L CSTF1 CSTF3 DAP13 DCC1<br>DCK DCP5 DEPD1C1 DKFZP434B168 DKFZP564K2062<br>DKFZP564O1664 DKFZD434K2435 DLG7 DNAC9 EZF7 EZIG5 ENH<br>ESP1L ETAA16 EXOSC1 FANB5 FAM133A FAM49B FKBP3 FKSG14<br>FLJ10156 FLJ11752 FLJ12436 FLJ12716 FLJ13912 FLJ20105<br>FLJ20211 FLJ20331 FLJ20364 FLJ20516 FLJ20641 FLJ21816<br>FLJ21908 FLJ22624 FLJ25416 FOXM1 GJB2 GLE1L HELB<br>HIST1H2AG HIST1H2AI HIST1H2AK HIST1H3D HIST1H3F HMMNR<br>HRR88P HSPA8 HSPC138 HSPC150 IARS JTV1 KIAA0101<br>KIAA1229 KIF11 KIF18A KIF20A KIF23 KNS17 KNTC2 KUB3<br>LMNB1 LMNB2 LOC201725 LOC494143 LOC84661 LSM4 LSM6<br>MBD4 MCM10 MCM3 MCM4 MCM5 MCM7 MELK METAP1<br>MGC10540 MGC10911 MGC14151 MGC16943 MGC32020<br>MGC33371 MGC35274 MGC5297 MKI67 MPHOSPH1 MRPL47<br>MRPS10 MRPS16 MS131 MTRFEL1 NEK2 NEUGRIN NFB<br>NUDCD2 NUP37 NUSAP1 OIPS ORC1L ORC6L PCNA PIK4CB PIN1<br>PLK1 PNPT1 POLD1 POLR3B POLR3F PPLA PRKDC PTTG1 Pfs2<br>QBS11 RACGAP1 RADS4B RAMP RBL1 RFC4 ROK2 RNIF3A RPA3<br>RRM2 RUVBL2 S100A8 SGOL1 SIL SKB1 SUD5 SMC4L1 STKG<br>SUMO2 SUW39H1 TA-KRP TACC3 TARSL1 THAP1 TIMELESS<br>TTP120A TNPOT TNPOT1 TOP2A TPX2 TRIM59 TROAP TTK TXNDG9<br>UBE2C UZF1 USP39 VBP1 WDS51A XRC2 ZCCH9 ZNFINTE24  |          |       |     |  |



|             |                            |          |      |   |          |       |          |  |
|-------------|----------------------------|----------|------|---|----------|-------|----------|--|
| V\$NMNR2_02 | V-MNyb                     | 0.000018 | 4.76 | 108.0138314.3   | 6.59E-06 | 20.44 | 97.17a15 | Topop1 T1ms9 Tr1p13 Txn1 Usp1 Vh1h Zc3h1dc2 Zfp482               |
| V\$NMNR2_01 | nuclear respiratory factor | 7.87E-05 | 5.61 | 112.XPMcH2 ZC4G3 ZM5TE24 ZNF482                         | 6.59E-06 | 28.97 | 108      | T1mcd1 Usp1 Vbp1 Vh1h Wdh1d1 XpmcH2 Zfp482                       |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  | EK-1                       | 6.59E-06 | 7.44 | 336.MPHOSPH1.MRPL47.MRPL52.MRPS10.MRPS16.MRPS24.MSL3.L1 | 6.59E-06 | 17.65 | 278      | Smc211 Smc411 Solt Serp1 Sumo2 Suv39h1 Tacc3 Ta15 Takrp Tarst1   |
| V\$EKL1_01  | EZF                        | 1.65E-05 | 6.92 | 15.MCMA2.MCMA3.MCMA4.MCMA5.PKRCQ.PK3.RIOX2.TEDP1        | 0.000254 | 4.39  | 10       | Thap1 Timeless Tlpm1 Tlpmo Tlpmss1a1 Topo1 Top2a Topk1 Tpbg Tpx2 |
| V\$EKL1_02  |                            |          |      |   |          |       |          |  |



|               |                          |          |      |  |          |      |     |  |
|---------------|--------------------------|----------|------|--|----------|------|-----|--|
|               |                          |          |      | AASDHPT AF15Q14 AKR1B10 ANKRD26 ASPM AUKR8 BANF1 BRCA2 BRRN1 C10orf13 C14orf106 C18orf24 C20orf172 C6orf167 C7orf19 C9orf78 CCNA2 CDC2 CDC25C CDC41L CDC41 CDC42 CDC4A CDC4S CDKN3 CENPA CENPE CHEK1 CKS2 CNAP1 CPSF2 CPSF3 CSTF1 CSTF3 DAP3 DCK DCP5 DEPDCL DEPDCLB DKFZP44B168 DKFZP434G1415 DLG7 DMTEL DNAC9 E2IG5 EIF2B1 ESPL1 EXO1 FANCD2 FBXO5 FIGL1 FKBP3 FKS614 FLJ10036 FLJ10719 FLJ11184 FLJ12436 FLJ20331 FLJ21908 FLJ22624 FOXM1 GNMN GTF3C2 HIST1H2AG HIST1H2AI HIST1H2AK HMBS HMNMR HPRRP8BP HSPC138 HSPC150 IL19 ITY1 KIAA1229 KIAA1333 KIAA1524 KIF20A KIF23 KIF2C KNS17 KNTC2 LENG5 LOC116143 LOC201725 LSM4 MAD2L1 MBDA MCM10 MCM2 MCM3 MCM5 MELK MGCL10911 MGCA1451 MGCG2020 MGCG3371 MGCG5274 MGCG5297 MRPL47 MRPL52 MRPS24 MS13L1 MTBP MTRF1L MYBL2 NIF3L1 NOL8 NUDDC2 NUP205 OBFCL ORCL1 ORCSL ORCL6 PRK PCGF6 PCNA PRN2 PLK1 PLK4 PNPT1 POLR3F PPL1S PRIM1 PSMD14 PTX1 RACGAP1 RAD51AP1 RAMP RFC3 RFC5 RFP2 RGNMTD2 RPL1 RUVBL2 SF3A3 SFRS1 SFRS9 SGOL1 SHFM1 SILSP1 SUD5 SMARCAO1 SMC4L1 SMC6L1 STK6 TACC3 TFDP1 TTP120A TNP01 TOP2A TOPBP1 TTK TXNDC TXNDC9 USP1 USP39 WBSR16 WDR1 WNT7A XNRC2 ZC3HDC8 ZCCH9 ZMRPTE24 ZMYND19 ZNF482 ZNF526 |          |      |     |  |
| V\$CREBATE_06 |                          | 0.00022  | 4.52 | 167  | 0.00093  | 3.14 | 116 |  |
|               |                          |          |      | AASDHPT ALG5 ANAPC1 ANAPC7 ANKRD26 APRT ASF1B ASPM ATAD2 BANF1 BIRC5 BLM BMD039 C14orf106 C22orf18 C6orf167 C9orf85 CCNA2 CCNB2 CCT5 CDCA2 CDC41L CDC41 CDC42 CDC44 CDKN3 CENPH CKAP2 CMAS CNAP1 CPSF2 DCC1 DCK DEPDCL DHFR DKFZP434B168 DKFZP434G1415 DKFZP56A01664 DKFZP434K2435 DMRT1 DNAC9 DRB1 DSG3 E2IG5 EIF2B1 EPRS ERH EXOSC8 FABP5 FANSLB FBXO5 FGR1OP FIGL1 FKBP3 FKS614 FLJ10036 FLJ10706 FLJ11184 FLJ12716 FLJ20331 FLJ20364 FLJ21816 FLJ21908 FLJ22624 FLJ25416 FLJ29660 GSG2 GTF3C2 GTF3C3 HELB HIST1H2AI HMBS HMNR HSPA48 IL19 KIAA0101 KIAA1229 KIAA1524 KIF11 KIF18A KIF23 KIF2C KNS17 KNTC2 LENG5 LMANB1 LSM4 M11S1 MAD2L1 MBDA MCM2 MELK METAP1 MGCL1451 MGCG3020 MGCG3371 MGCG5352 MKI67 MRPL47 MRPL52 MTBP MTRF1L NFB NIF3L1 NUDDC2 NUP155 NUP205 OIP5 ORCL6 PCGF6 PCGM2 PAK42B PIGW PIN1 PLK1 PNPT1 POLD1 POLE2 POLR2B POLR3B POLR3F PPIE PPL1L PPL1S PRIMA1 PTTG1 Pfs2 ORSL1 RAB9P40 RFC3 RFC4 RFC5 RNF34 RPL1 RPS6K4A RUVBL2 SF3A3 SUD5 SSRPL SUMO2 TACC3 TNP01 TOP2A TOPBP1 TPBG TPX2 TRIM59 TXNDC9 UBE2C USP1 VHL ZCCH9 ZMRPTE24 ZWINT   | 9.61E-05 | 5.32 | 105 |  |
| SWHN_B        | winged-helix factor nude | 0.000414 | 3.93 | 155  |          |      |     |  |



|               |                     |          |      |     |          |       |     |  |
|---------------|---------------------|----------|------|-----|----------|-------|-----|--|
| V\$PAX3_B     | Pax-3 binding sites | 0.000801 | 3.32 | 289 | 6.59E-06 | 15.76 | 235 | <p>AS5DHPPT ADAMDECI AF15Q14 AKR1B1U ALG10 ALG5 ALG8<br/>ANAPC1 ANAPC7 ANKRD26 ARHGAP11A ARPC4 ASY1B ASK<br/>ASPM ATIC ATP13A1 AURKB BAFN1 BIRC5 BMO39 BRCA2 BRRN1<br/>BUB1 BUB1B C10orf3 C14orf104 C14orf106 C18orf24 C1orf73<br/>C20orf129 C20orf172 C22orf18 C6orf157 C7orf19 C9orf85 CAD<br/>CCDC5 CCNA2 CCNB2 CCNE1 CCT5 CCDC2 CDC25A CDC45L CDS7<br/>CDC41 CDC42 CDC44 CDC48 CCKN3 CENPA CENPE CHEK1 CKC2<br/>CLSPN CNA1 COMMD3 COMMD8 COP56 COTL1 CPSF2 CPSF3<br/>CSE1L CSTF1 CSTF3 DAP3 DCC1 DCK DCP5 DEPD1<br/>DKFZP434B168 DKFZP34G1415 DKFZP564K2062<br/>DKFZP564O1664 DKFZP434K2435 DLG7 DMTF1 DNALG9 DNRI<br/>DSC2 DSG3 EIF2B1 ESR1L EXO1 EXOSC1 EXOSC8 FAFB5 FAM33A<br/>FAM49B FANCD2 FANSLB FBXOS FGFRLDP HGNL1 FKBP3<br/>FKSG14 FUJ10036 FUJ10156 FUJ10706 FUJ11752 FUJ12436<br/>FUJ12716 FUJ13912 FUJ14803 FUJ20105 FUJ20211 FUJ20331<br/>FUJ20364 FUJ20516 FUJ20641 FUJ21816 FUJ21908 FUJ22624<br/>FUJ25416 FLK0869 FOXM1 GJB2 GLE1L GNMN GSG2 GTF3C2<br/>GTF3C3 HCAP G HIST1H2AG HIST1H2AJ HIST1H2AK HIST1H3D<br/>HIST1H41 HMNR HPRR8BP HSP48 HSPBP1 HSPC150 IARS IL19<br/>JTV1 KIAA1229 KIAA1333 KIAA1524 KIF11 KIF18A KIF20A KIF23<br/>KIF2C KNSL7 KNTC1 KNTC2 KRT16 KUB3 LENG5 LMNB1<br/>LOC116143 LOC201725 LOC84661 LSM4 LSM6 M151L MAD2L1<br/>MBD4 MCM10 MCM2 MCM3 MCM4 MCM7 MGCI0911<br/>MGCS2020 MGCS3371 MGCS297 MGCS352 MIK67 MRPL47<br/>MRPL52 MRPS16 MRPS24 MS13L1 MTBP MTRF1L MYBL2 NERX<br/>NEUGRIN NFYB NFE3L1 NOL8 NUDCD2 NUP107 NUP205 NUP37<br/>NUSAP1 OIP5 ORC5L ORC6L PRK PCG6 PCNA PDCC2 PGM2<br/>PIK4Z8 PI3W PIN1 PKNZ PLK4 PLK6 PLRG1 POLD1 POLE2 POLQ<br/>POLR2B POLR3B PPIE PPIH PPL1L PPL1S PPR18 PRIM1 PRKDC<br/>PSSDPTT PTCT24 RAKT102 RANAPC1 RANND20 RSK ASPM<br/>ATAD2 AURKB BAFN1 BRCA2 BRRN1 C10orf3 C14orf106<br/>C18orf24 C20orf172 C22orf18 C6orf167 C7orf19 C9orf78 CCNA2<br/>CCDC2 CDC45L CDC41 CDC42 CDC44 CDC45 CENPA CENPE<br/>CHEK1 CKS2 CNA1 CPSF2 CPSF3 CSTF1 CSTF3 DAP3 DCK DCP5<br/>DEPD1 DEPD1B DKFZP434B168 DKFZP434G1415 DLG7 DMTF1<br/>DNALG9 E2F3G EIF2S1 ESR1L EXO1 FANCD2 FBXOS FGFRLDP<br/>FIGNL1 FKBP3 FKSG14 FUJ10036 FUJ10706 FUJ10719 FUJ11184<br/>FUJ12436 FUJ20331 FOXM1 GLE1L GNMN GTF3C2 HIST1H2AG<br/>HIST1H2AJ HIST1H2AK HMBS HMNR HPRR8BP HSPC138<br/>HSPC150 IL19 JTV1 KIAA1229 KIAA1333 KIAA1524 KIF20A KIF23<br/>KIF2C KNSL7 KNTC2 LENG5 LOC116143 LOC201725 LSM4 MBD4<br/>MCM10 MCM2 MCM3 MCM5 MELK MGCI0911 MGCI4151<br/>MGCS2020 MGCS3371 MGCS5274 MGCS297 MRPL47 MRPL52<br/>MRPS24 MS13L1 MTBP MTRF1L MYBL2 NFE3L1 NOL8 NUDCD2<br/>NUP155 NUSAP1 OBF1 OIP5 ORC1L ORC5L PRK PCG6 PCNA<br/>PDCC2 PKNZ PLK4 PNP1 PPIE PPL1S PRIM1 PSSMD14 PTX1<br/>RACGAP1 RAD51AP1 RAMP RFC3 RFC5 RFP2 RGSMTD2 RUVBL2<br/>SF3A3 SFRS1 SFRS9 SGO1L SHFM1 SIL SIP1 SLDS SNARCAD1<br/>SMC4L SMC6L STK6 TACC3 TDFP1 TIP120A TNP01 TOP2A<br/>TOPBP1 TPB6 TXNDC USP1 USP39 VBP1 WBSOR16 WHHD1<br/>WN17A XRCC2 ZC3HDC8 ZCCH9C ZMPSTE24 ZMYND19 ZNF482<br/>ZNF526</p> |
| V\$CREB_Q2_Q1 |                     | 0.001136 | 3.04 | 169 | 6.59E-06 | 12.37 | 139 | <p>0610009C03RK 1200008012RK 1200009B18RK 23100311L18RK<br/>24100116G03RK 2410012H02RK 251004007RK 2600001117RK<br/>2610000217RK 2610040616RK 2610528A17RK 2700084L2RK<br/>28100037C03RK 2810047102RK 2810418V01RK 2810453L12RK<br/>3000003F02RK 4933424N09RK 5730568A12RK 573059905RK<br/>5930412E23RK 953002D024RK A4A545217 A1A67484 A4ADHP1 Act1a<br/>Act1b8 Algs Algs Anapc1 Anapc4 Anapc7 Ap1r Antgap11a Arnt12 As11b<br/>Atad2 Atic Atp13a1 Aurka Aurth BC004701 BC005624 BC066140 Bant1<br/>Birc5 Blm Brn1 Bub1b C730036B14RK Ccd5 Cna2 Cne1 Cc5 Cdc25a<br/>Cdc25C Cdc7 Cdc41 Cdc4 Cdc45 Cdkn3 Cempa Cempa Cemp1 Cenph<br/>Chek1 Clapn1 Cks2 Clspn Cnas Commn3 Comm8 Cop56 Ccot1 Cpsf2<br/>Cpsf3 Cse1l Cstf1 Cstf3 Dap3 Dck Depdc1b Dfif Dig7 Dmtf1 Dna1c9<br/>Drbp1 Dsc2 Durt Eif2b1 Eif2s1 Eprs Etn Exosc1 Exosc8 Fafb5 Fancd2<br/>Fbxos Fgf1r1op Fignl1 Fkbp3 Fkbp3 Foxm1 Gjb2 Glei1 Gnmn Gsg2 Gtf3c2<br/>Heb1 Hist1h2ac Hist1h2ah Hist1h2an Hist1h2b Hist1h3a Hist1h3l<br/>Hist1h4h Hmb5 Hmnr Hsp48 Iars il19 Jtv1 Kif11 Kif14 Kif18a Kif20a Kif23<br/>Kif4 Kns17 Kntc1 Krt1-16 Leng5 Lmnb1 Lmnb2 Lsm4 Lsm6 Mad2L1 Mbd4<br/>Mcm10 Mcm2 Mcm3 Mcm5 Mcm7 Metap1 MME67 Mmp147 Mmp152<br/>Mmp310 Mmp516 Mmp24 Mtrf1l Myb2 Nfyb NF33L NOL8 Nudcd2 Nup107<br/>Nup155 Nup37 Nusap1 Obf1 Oip5 Orc1l Pdk Pkna Pcdcd2 P4k2b Pgw<br/>Pint Pkn2 Plk1 Plka Prg1 Prg1 Pold1 Polr2b Polr3b Polr3f Ppie Pp1l<br/>Pp1l5 Pp1r18 Psm14 Ptk6 Pygo2 Raedap1 Rad51ap1 Rbl1 Rfc3 Rfw3<br/>Rgmd12 Rlk2 Rnf3A Rps3 Rps6ka4 S100b8 S100b9 SF3A3 Sfrs1 Sgo1l<br/>Shtdg1 Sip1 Sbk1 Smc21 Sotl Sumo2 Tacc3 Taf5 Tafp Taraf1 Tfdp1<br/>Thap1 Timeless Trpo Top2a Topbp1 Topg Tpx2 Trami Trm13 Trp13<br/>Ttn1 Ubez2c Usp1 Usp39 Vbp1 Wdrtd1 Wnt7a xpmc2h Zcch9c Zfp482<br/>Zfp526 Zmpste24 Zmynd19 Zwiint</p>  |







| early, human up, mouse down |                                   |                  | Human    |              |         |  |   | Mouse        |         |   |
|-----------------------------|-----------------------------------|------------------|----------|--------------|---------|--|---|--------------|---------|---|
|                             |                                   |                  |          |              |         |  |   |              |         |   |
| TRANSFAC ID                 | Description                       | Max Bayes Factor | p        | Bayes Factor | # Genes | Gene symbols   | p | Bayes Factor | # Genes | Gene symbols  |
| V\$KROX_Q6                  |                                   | 6.88             | 1.65E-05 | 6.88         | 42      | C14orf175 C6orf62 CARD11 CD47<br>CORO1A CYBA DCIRE1C DERL3<br>DKFZP434B0335 FAM31B FAM40B<br>FAM155C FLJ14213 FLJ25067 GGH GYG                   | 1 | -1.74        | 32      | Ap3m2 Armc7 Arp13a2 BC005537<br>BC022150 BC025872 BC042698 Card12<br>Cd47 Cc4-2se2 Cyba Ggh Gyg1 Igf2bp3<br>32 Itga4 Mdfic Mulik Parp11 Pex13 Pou2f2  |
| V\$DEAF1_Q1                 |                                   | 6.83             | 1.65E-05 | 6.83         | 15      | CD22 CD47 CYBA DKFZP434B0335<br>FAM40B GTF2A1 MGC19764 MYO1G<br>PPT1 RAB711 SNX11 SYK TFE1C TTC16<br>ZAP70                                       | 1 | -2.27        | 17      | Ap3m2 Arp13a2 BC025872 BC042698<br>Covak Igf2bp3 Mulik Parp11 Pou2f2<br>Rab11fip2 Sit Snx11 Tfecf TTC16 Unc13d<br>Zap70 Zfp366                        |
| V\$IRE_Q6_Q1                |                                   | 6.73             | 1.65E-05 | 6.73         | 77      | G6orf62 CARD12 CD2 CD22 CD244 CD3E<br>CD3G CDC42SE2 CLEC12A CLEC4C CTSW<br>CXCR3 CXorf21 CYBA CYBB DCIRE1C<br>DERL3 DKFZP434B0335 EPST11 FAM155C | 1 | -1.63        | 38      | Cd244 Cd3e Cd3g Clec4b Clnk Covak<br>Cxcl13 Cybb Dclre1c Eps11 Ggh Gpr1<br>Gtf2a1 Igf2bp3 Impda1 Itga4 Lpxn<br>38 Marck1 Mdfic Mulik Myo1g Nkg7 Pex13 |
| V\$ATF3_Q6                  | activating transcription factor 3 | 6.38             | 3.30E-05 | 6.38         | 1       | TTC16  | 1 | -2.34        | 11      | Gpr1 Gtf2a1 Itgae Mdfic Pex13 Ppt1<br>Prkcd Rac2 Rnasel TTC16 Zap70   |
| V\$IRE_Q6                   |                                   | 4.78             | 0.00018  | 4.78         | 48      | CARD12 CD2 CD244 CD3G CDC42SE2<br>CLEC12A CXCR3 CXorf21 CYBB DCIRE1C<br>DERL3 EPST11 FLJ14213 FLJ14397<br>FLJ30990 FLJ90709 GYG IMP-3 INPP4A     | 1 | -1.74        | 19      | Ap3m2 Armc7 BC005537 BC022150<br>BC025872 C1qg Card11 Cd226 Cd244<br>Cd3e Clec12a Clec4b Clnk Cxcl13 Cybb<br>19 Slamf6 Slamf7                         |
| V\$IRE7_Q1                  | interferon regulatory factor 7    | 3.73             | 0.000542 | 3.73         | 81      | ARMC7 ATP13A2 C1orf22 C6orf62<br>CARD12 CD2 CD22 CD226 CD244 CD3G<br>CDC42SE2 CLEC12A CLEC4C COVA1<br>CXCR3 CXorf21 CYBA CYBB DCIRE1C            | 1 | -1.99        | 50      | Dclre1c Eps11 Ggh Gtf2a1 Gyg1 Igf2bp3   |







## Appendix 8.

### Differentially-expressed microRNAs in human samples



| Human microRNA | Groups |      | correlation |    | Sample |    | 1-NS |    | 2-NS |    | 3-NS |    | 4-NS |    | 5-NS |    | 6-NS |    | 10-NS |    | 8-NS |    | 1-AK |    | 2-AK |    | 3-AK |    | 4-AK |    | 5-AK |    | 6-AK |    | 10-AK |    | 12-AK |    | 4-AK2 |    | 8-AK |    | 2.5CC |    | 3.5CC |    | 4.5CC1 |    | 5.5CC |    | 6.5CC |    | 10.5CC |    | 12.5CC |    | 4.5CC2 |    | 8.5CC |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |   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|----------------|--------|------|-------------|----|--------|----|------|----|------|----|------|----|------|----|------|----|------|----|-------|----|------|----|------|----|------|----|------|----|------|----|------|----|------|----|-------|----|-------|----|-------|----|------|----|-------|----|-------|----|--------|----|-------|----|-------|----|--------|----|--------|----|--------|----|-------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|--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|                | 1-NS   | 2-NS | NS          | NS | NS     | NS | NS   | NS | NS   | NS | NS   | NS | NS   | NS | NS   | NS | NS   | NS | NS    | NS | NS   | NS | AK   | AK | AK   | AK | AK   | AK | AK   | AK | AK   | AK | AK   | AK | AK    | AK | AK    | AK | AK    | AK | AK   | AK | AK    | AK | AK    | AK | AK     | AK | AK    | AK | AK    | AK | AK     | AK | AK     | AK | AK     | AK | AK    | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK | AK |



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AK-NS

| <b>microRNAs</b> | <b>p-value</b> | <b>AK/NS fold change</b> |
|------------------|----------------|--------------------------|
| hsa-mir-31-5p    | 9.793E-03      | 3.48                     |
| hsa-mir-452-5p   | 6.936E-03      | 3.33                     |
| hsa-mir-155-5p   | 1.371E-02      | 3.12                     |
| hsa-mir-629-5p   | 1.658E-02      | 3.01                     |
| hsa-mir-95       | 1.603E-02      | 2.97                     |
| hsa-mir-150-3p   | 3.922E-02      | 2.75                     |
| hsa-mir-4443     | 2.027E-02      | 2.70                     |
| hsa-mir-27b-5p   | 3.685E-02      | 2.64                     |
| hsa-mir-181a-3p  | 2.443E-02      | 2.55                     |
| hsa-mir-3676-5p  | 1.798E-02      | 2.50                     |
| hsa-mir-6724-5p  | 3.155E-02      | 2.48                     |
| hsa-mir-21-3p    | 3.650E-02      | 2.45                     |
| hsa-mir-4521     | 1.579E-02      | 2.41                     |
| hsa-mir-4784     | 1.905E-02      | 2.13                     |
| hsa-mir-4730     | 4.259E-02      | 2.11                     |
| hsa-mir-224-5p   | 4.964E-04      | 1.98                     |
| hsa-mir-21-5p    | 4.879E-02      | 1.96                     |
| hsa-mir-17-5p    | 8.025E-03      | 1.70                     |
| hsa-mir-27b-3p   | 1.169E-03      | 1.69                     |
| hsa-mir-203a     | 1.976E-02      | 1.66                     |
| hsa-mir-25-3p    | 4.161E-02      | 1.64                     |
| hsa-let-7g-5p    | 1.285E-02      | 1.55                     |
| hsa-mir-589-5p   | 3.416E-02      | 1.52                     |
| hsa-mir-103a-3p  | 2.201E-02      | 1.50                     |
| hsa-let-7d-3p    | 1.351E-02      | 0.67                     |
| hsa-mir-874      | 5.809E-03      | 0.65                     |
| hsa-mir-664a-3p  | 1.558E-02      | 0.65                     |
| hsa-mir-574-5p   | 1.137E-02      | 0.64                     |
| hsa-mir-195-5p   | 2.763E-02      | 0.62                     |
| hsa-mir-143-3p   | 3.998E-02      | 0.61                     |
| hsa-mir-125a-5p  | 6.229E-03      | 0.60                     |
| hsa-mir-675-3p   | 1.984E-02      | 0.58                     |
| hsa-mir-497-5p   | 1.517E-02      | 0.57                     |
| hsa-mir-4524a-3p | 2.047E-03      | 0.55                     |
| hsa-mir-30a-3p   | 1.163E-02      | 0.55                     |
| hsa-mir-100-5p   | 7.152E-03      | 0.53                     |
| hsa-mir-139-5p   | 2.119E-03      | 0.52                     |
| hsa-mir-30a-5p   | 9.301E-04      | 0.50                     |
| hsa-mir-99a-3p   | 7.810E-03      | 0.49                     |
| hsa-mir-6511b-3p | 4.701E-02      | 0.45                     |
| hsa-mir-574-3p   | 1.901E-03      | 0.45                     |
| hsa-mir-218-1-3p | 3.460E-02      | 0.45                     |
| hsa-mir-99b-3p   | 3.284E-02      | 0.45                     |
| hsa-mir-296-5p   | 3.134E-02      | 0.40                     |
| hsa-mir-328      | 1.923E-03      | 0.40                     |
| hsa-mir-4655-3p  | 3.307E-02      | 0.39                     |
| hsa-mir-30c-2-3p | 7.128E-03      | 0.38                     |



|                 |           |      |
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| hsa-mir-143-5p  | 7.250E-03 | 0.38 |
| hsa-mir-145-3p  | 1.651E-03 | 0.37 |
| hsa-let-7e-3p   | 3.879E-03 | 0.35 |
| hsa-mir-6510-3p | 7.491E-03 | 0.35 |
| hsa-mir-383     | 3.750E-02 | 0.33 |
| hsa-mir-451a    | 3.637E-02 | 0.31 |
| hsa-mir-885-5p  | 3.482E-03 | 0.31 |
| hsa-mir-504     | 7.266E-03 | 0.30 |
| hsa-mir-145-5p  | 6.146E-05 | 0.28 |
| hsa-mir-486-5p  | 4.505E-03 | 0.25 |
| hsa-mir-133a    | 1.223E-03 | 0.22 |



SCC-NS

| <b>microRNAs</b> | <b>p-value</b> | <b>NS/SCC fold change</b> |
|------------------|----------------|---------------------------|
| hsa-mir-21-3p    | 8.980E-04      | 6.71                      |
| hsa-mir-31-5p    | 1.477E-05      | 6.05                      |
| hsa-mir-452-5p   | 6.371E-04      | 5.91                      |
| hsa-mir-21-5p    | 5.670E-05      | 5.91                      |
| hsa-mir-142-5p   | 2.627E-03      | 4.66                      |
| hsa-mir-31-3p    | 3.288E-04      | 4.58                      |
| hsa-mir-196a-5p  | 8.115E-03      | 4.35                      |
| hsa-mir-3676-5p  | 2.751E-04      | 4.29                      |
| hsa-mir-24-2-5p  | 4.946E-03      | 4.20                      |
| hsa-mir-629-5p   | 9.979E-04      | 4.19                      |
| hsa-mir-22-5p    | 3.110E-03      | 3.85                      |
| hsa-mir-424-3p   | 6.249E-03      | 3.77                      |
| hsa-mir-155-5p   | 6.882E-04      | 3.72                      |
| hsa-mir-421      | 3.481E-04      | 3.64                      |
| hsa-mir-340-5p   | 2.885E-03      | 3.59                      |
| hsa-mir-192-5p   | 1.111E-02      | 3.45                      |
| hsa-mir-181a-3p  | 6.690E-03      | 3.43                      |
| hsa-mir-95       | 2.267E-03      | 3.37                      |
| hsa-mir-27b-5p   | 3.245E-03      | 3.32                      |
| hsa-mir-455-5p   | 5.710E-04      | 3.20                      |
| hsa-mir-431-5p   | 1.207E-03      | 3.17                      |
| hsa-let-7a-3p    | 2.840E-03      | 3.16                      |
| hsa-mir-424-5p   | 1.943E-03      | 3.12                      |
| hsa-mir-323b-3p  | 9.244E-03      | 3.10                      |
| hsa-mir-34c-5p   | 4.777E-03      | 3.09                      |
| hsa-mir-146b-5p  | 2.848E-03      | 3.01                      |
| hsa-mir-130b-3p  | 2.316E-04      | 2.97                      |
| hsa-mir-493-5p   | 5.890E-03      | 2.91                      |
| hsa-mir-331-5p   | 6.434E-03      | 2.87                      |
| hsa-mir-16-2-3p  | 1.972E-02      | 2.85                      |
| hsa-mir-15a-5p   | 1.931E-03      | 2.82                      |
| hsa-mir-493-3p   | 1.109E-03      | 2.82                      |
| hsa-mir-181d     | 3.571E-03      | 2.78                      |
| hsa-mir-4443     | 4.334E-02      | 2.77                      |
| hsa-mir-374b-5p  | 3.762E-02      | 2.59                      |
| hsa-mir-450a-5p  | 1.993E-02      | 2.55                      |
| hsa-mir-1303     | 2.309E-02      | 2.55                      |
| hsa-mir-132-5p   | 1.174E-02      | 2.49                      |
| hsa-mir-503-5p   | 1.410E-02      | 2.47                      |
| hsa-mir-193a-3p  | 1.961E-02      | 2.44                      |
| hsa-mir-340-3p   | 1.607E-02      | 2.43                      |
| hsa-mir-329      | 5.250E-03      | 2.43                      |
| hsa-mir-181c-3p  | 1.207E-03      | 2.37                      |
| hsa-mir-582-5p   | 1.175E-03      | 2.36                      |
| hsa-mir-758-3p   | 4.613E-02      | 2.32                      |
| hsa-mir-224-5p   | 1.289E-04      | 2.30                      |
| hsa-mir-660-5p   | 4.570E-02      | 2.28                      |



|                  |           |      |
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| hsa-mir-1301     | 2.361E-02 | 2.28 |
| hsa-mir-30c-1-3p | 6.333E-03 | 2.27 |
| hsa-mir-210      | 2.933E-04 | 2.27 |
| hsa-mir-15b-3p   | 3.492E-03 | 2.25 |
| hsa-mir-17-5p    | 4.957E-03 | 2.21 |
| hsa-mir-187-3p   | 3.707E-02 | 2.19 |
| hsa-mir-500a-5p  | 3.061E-02 | 2.18 |
| hsa-mir-654-5p   | 2.033E-02 | 2.17 |
| hsa-mir-22-3p    | 3.479E-04 | 2.14 |
| hsa-mir-20a-5p   | 1.128E-02 | 2.14 |
| hsa-mir-200a-5p  | 3.171E-02 | 2.12 |
| hsa-mir-16-5p    | 8.229E-04 | 2.11 |
| hsa-mir-151a-3p  | 4.855E-04 | 2.08 |
| hsa-mir-429      | 3.194E-02 | 2.05 |
| hsa-mir-141-5p   | 1.938E-02 | 2.02 |
| hsa-mir-17-3p    | 8.126E-03 | 2.00 |
| hsa-mir-106b-5p  | 1.541E-02 | 1.97 |
| hsa-mir-203a     | 1.965E-02 | 1.95 |
| hsa-mir-130b-5p  | 1.332E-02 | 1.95 |
| hsa-mir-1285-3p  | 1.743E-02 | 1.94 |
| hsa-mir-146a-5p  | 1.452E-02 | 1.94 |
| hsa-mir-200c-5p  | 1.160E-02 | 1.93 |
| hsa-mir-10b-3p   | 3.575E-02 | 1.92 |
| hsa-mir-411-5p   | 1.798E-02 | 1.89 |
| hsa-mir-708-5p   | 1.527E-02 | 1.87 |
| hsa-mir-27a-3p   | 9.799E-03 | 1.82 |
| hsa-mir-27b-3p   | 3.926E-04 | 1.81 |
| hsa-mir-24-3p    | 3.084E-03 | 1.80 |
| hsa-let-7f-5p    | 1.427E-02 | 1.78 |
| hsa-let-7i-5p    | 1.219E-03 | 1.76 |
| hsa-mir-10b-5p   | 8.663E-03 | 1.75 |
| hsa-mir-28-5p    | 9.828E-04 | 1.72 |
| hsa-mir-548o-3p  | 1.333E-02 | 1.71 |
| hsa-mir-548av-3p | 1.358E-02 | 1.71 |
| hsa-mir-532-5p   | 1.003E-03 | 1.66 |
| hsa-mir-103a-3p  | 2.025E-03 | 1.66 |
| hsa-mir-598      | 3.420E-02 | 1.66 |
| hsa-mir-495-3p   | 3.701E-02 | 1.65 |
| hsa-mir-2277-5p  | 3.751E-02 | 1.64 |
| hsa-mir-944      | 2.945E-02 | 1.61 |
| hsa-mir-454-5p   | 4.966E-03 | 1.58 |
| hsa-mir-93-5p    | 1.636E-02 | 1.58 |
| hsa-let-7g-5p    | 5.943E-03 | 1.57 |
| hsa-mir-769-5p   | 2.886E-02 | 1.56 |
| hsa-mir-23a-3p   | 3.553E-02 | 1.56 |
| hsa-mir-25-3p    | 8.693E-03 | 1.56 |
| hsa-mir-181b-5p  | 2.004E-04 | 1.52 |
| hsa-mir-221-3p   | 1.360E-03 | 1.52 |
| hsa-let-7a-5p    | 9.831E-03 | 1.52 |



|                  |           |      |
|------------------|-----------|------|
| hsa-mir-889      | 1.811E-02 | 1.51 |
| hsa-mir-140-3p   | 1.037E-02 | 0.66 |
| hsa-mir-744-5p   | 3.708E-02 | 0.65 |
| hsa-mir-1226-3p  | 3.731E-02 | 0.63 |
| hsa-mir-491-5p   | 9.673E-03 | 0.63 |
| hsa-mir-193b-3p  | 2.245E-02 | 0.63 |
| hsa-mir-4524a-3p | 1.432E-02 | 0.61 |
| hsa-let-7b-3p    | 8.303E-03 | 0.59 |
| hsa-mir-574-5p   | 5.109E-04 | 0.58 |
| hsa-let-7c       | 4.368E-02 | 0.58 |
| hsa-let-7e-3p    | 8.191E-03 | 0.57 |
| hsa-mir-146b-3p  | 1.213E-02 | 0.56 |
| hsa-mir-497-5p   | 8.185E-03 | 0.56 |
| hsa-mir-664a-3p  | 5.706E-03 | 0.55 |
| hsa-mir-423-5p   | 3.206E-03 | 0.53 |
| hsa-mir-3158-3p  | 1.231E-02 | 0.53 |
| hsa-mir-423-3p   | 7.194E-03 | 0.53 |
| hsa-mir-30c-2-3p | 4.104E-02 | 0.52 |
| hsa-mir-4330     | 1.490E-02 | 0.51 |
| hsa-mir-125a-5p  | 1.649E-03 | 0.50 |
| hsa-mir-193a-5p  | 1.158E-03 | 0.50 |
| hsa-mir-320a     | 4.986E-04 | 0.49 |
| hsa-mir-532-3p   | 7.008E-03 | 0.48 |
| hsa-mir-365a-5p  | 3.322E-02 | 0.47 |
| hsa-mir-320b     | 2.714E-02 | 0.45 |
| hsa-mir-433      | 1.470E-02 | 0.44 |
| hsa-mir-30a-3p   | 2.022E-03 | 0.44 |
| hsa-let-7d-3p    | 4.258E-04 | 0.44 |
| hsa-mir-338-5p   | 1.367E-02 | 0.43 |
| hsa-mir-125b-5p  | 1.152E-03 | 0.43 |
| hsa-mir-100-5p   | 1.757E-03 | 0.41 |
| hsa-mir-378a-5p  | 7.316E-03 | 0.41 |
| hsa-mir-664b-3p  | 2.339E-03 | 0.40 |
| hsa-mir-2110     | 9.962E-04 | 0.40 |
| hsa-mir-5787     | 2.482E-02 | 0.39 |
| hsa-mir-4497     | 2.504E-03 | 0.39 |
| hsa-mir-149-5p   | 8.314E-04 | 0.39 |
| hsa-mir-197-3p   | 3.804E-04 | 0.38 |
| hsa-mir-3605-3p  | 7.492E-04 | 0.37 |
| hsa-mir-4739     | 9.632E-03 | 0.37 |
| hsa-mir-4732-3p  | 1.413E-02 | 0.37 |
| hsa-mir-139-5p   | 6.045E-05 | 0.37 |
| hsa-mir-3665     | 4.435E-02 | 0.36 |
| hsa-mir-1538     | 1.496E-02 | 0.36 |
| hsa-mir-4655-3p  | 1.525E-02 | 0.36 |
| hsa-mir-574-3p   | 6.520E-05 | 0.36 |
| hsa-mir-1908     | 9.407E-03 | 0.33 |
| hsa-mir-139-3p   | 3.122E-03 | 0.33 |
| hsa-mir-296-5p   | 9.221E-04 | 0.32 |



|                  |           |      |
|------------------|-----------|------|
| hsa-mir-4634     | 1.731E-02 | 0.32 |
| hsa-mir-133a     | 1.496E-02 | 0.31 |
| hsa-mir-214-3p   | 3.428E-03 | 0.31 |
| hsa-mir-375      | 9.973E-03 | 0.31 |
| hsa-mir-718      | 4.854E-03 | 0.30 |
| hsa-mir-762      | 1.284E-03 | 0.30 |
| hsa-mir-6511b-3p | 6.868E-04 | 0.30 |
| hsa-mir-652-3p   | 1.472E-04 | 0.29 |
| hsa-mir-218-1-3p | 4.708E-03 | 0.27 |
| hsa-mir-885-5p   | 4.670E-04 | 0.26 |
| hsa-mir-3196     | 4.202E-03 | 0.26 |
| hsa-mir-145-5p   | 1.792E-06 | 0.25 |
| hsa-mir-3663-3p  | 9.161E-04 | 0.23 |
| hsa-mir-1247-5p  | 9.438E-03 | 0.22 |
| hsa-mir-6087     | 1.184E-03 | 0.22 |
| hsa-mir-504      | 1.399E-03 | 0.21 |
| hsa-mir-383      | 1.403E-03 | 0.19 |
| hsa-mir-451a     | 6.713E-04 | 0.19 |
| hsa-mir-3178     | 1.842E-04 | 0.19 |
| hsa-mir-486-3p   | 6.381E-03 | 0.19 |
| hsa-mir-3656     | 5.193E-03 | 0.18 |
| hsa-mir-6511a-3p | 4.454E-03 | 0.18 |
| hsa-mir-4508     | 1.529E-03 | 0.18 |
| hsa-mir-3195     | 2.494E-04 | 0.17 |
| hsa-mir-3621     | 5.084E-04 | 0.16 |
| hsa-mir-6089     | 5.547E-04 | 0.16 |
| hsa-mir-6510-3p  | 4.576E-05 | 0.15 |
| hsa-mir-328      | 7.045E-05 | 0.14 |
| hsa-mir-4532     | 2.774E-04 | 0.14 |
| hsa-mir-486-5p   | 1.199E-06 | 0.06 |



SCC-AK

| <b>microRNAs</b> | <b>p-value</b> | <b>SCC/AK fold change</b> |
|------------------|----------------|---------------------------|
| hsa-mir-34c-5p   | 2.604E-03      | 3.10                      |
| hsa-mir-22-5p    | 3.102E-03      | 3.03                      |
| hsa-mir-21-5p    | 6.196E-03      | 3.01                      |
| hsa-let-7a-3p    | 3.959E-04      | 3.00                      |
| hsa-mir-31-3p    | 1.524E-02      | 2.97                      |
| hsa-mir-374b-5p  | 7.191E-03      | 2.96                      |
| hsa-mir-455-5p   | 8.256E-04      | 2.78                      |
| hsa-mir-21-3p    | 3.938E-03      | 2.73                      |
| hsa-mir-424-5p   | 6.614E-03      | 2.63                      |
| hsa-mir-340-5p   | 1.109E-02      | 2.56                      |
| hsa-mir-381-3p   | 3.164E-02      | 2.49                      |
| hsa-mir-181c-3p  | 1.256E-04      | 2.48                      |
| hsa-mir-24-2-5p  | 4.130E-02      | 2.47                      |
| hsa-mir-10a-5p   | 1.885E-02      | 2.43                      |
| hsa-mir-493-3p   | 4.265E-03      | 2.43                      |
| hsa-mir-450a-5p  | 1.764E-02      | 2.41                      |
| hsa-mir-424-3p   | 4.967E-02      | 2.34                      |
| hsa-mir-503-5p   | 1.002E-02      | 2.33                      |
| hsa-mir-675-3p   | 4.363E-02      | 2.32                      |
| hsa-mir-369-5p   | 1.070E-02      | 2.28                      |
| hsa-mir-10b-5p   | 4.918E-03      | 2.25                      |
| hsa-mir-181d     | 4.129E-03      | 2.24                      |
| hsa-mir-665      | 2.731E-02      | 2.18                      |
| hsa-mir-34c-3p   | 4.076E-03      | 2.12                      |
| hsa-mir-130b-3p  | 2.719E-03      | 2.12                      |
| hsa-mir-143-3p   | 2.272E-02      | 2.11                      |
| hsa-mir-141-5p   | 8.039E-03      | 2.10                      |
| hsa-mir-99b-3p   | 2.829E-02      | 2.08                      |
| hsa-mir-582-5p   | 1.560E-02      | 2.06                      |
| hsa-mir-331-5p   | 4.994E-02      | 1.96                      |
| hsa-mir-454-3p   | 1.192E-02      | 1.92                      |
| hsa-mir-421      | 2.687E-02      | 1.90                      |
| hsa-mir-744-3p   | 2.553E-04      | 1.87                      |
| hsa-mir-181c-5p  | 3.576E-02      | 1.86                      |
| hsa-mir-3182     | 4.985E-02      | 1.82                      |
| hsa-mir-22-3p    | 2.734E-03      | 1.81                      |
| hsa-mir-126-3p   | 2.534E-02      | 1.81                      |
| hsa-mir-411-3p   | 4.493E-02      | 1.79                      |
| hsa-mir-6499-5p  | 1.567E-02      | 1.79                      |
| hsa-mir-136-3p   | 1.151E-02      | 1.75                      |
| hsa-mir-20a-5p   | 4.713E-02      | 1.73                      |
| hsa-mir-18a-5p   | 4.524E-02      | 1.73                      |
| hsa-mir-15b-3p   | 3.455E-02      | 1.70                      |
| hsa-mir-944      | 9.193E-03      | 1.69                      |
| hsa-mir-218-5p   | 2.442E-02      | 1.68                      |
| hsa-mir-151a-3p  | 6.568E-03      | 1.67                      |
| hsa-mir-411-5p   | 4.169E-02      | 1.66                      |



|                 |           |      |
|-----------------|-----------|------|
| hsa-mir-152     | 1.979E-02 | 1.63 |
| hsa-mir-7-1-3p  | 5.696E-03 | 1.61 |
| hsa-mir-30a-5p  | 2.788E-02 | 1.60 |
| hsa-mir-30e-5p  | 3.046E-02 | 1.60 |
| hsa-mir-379-5p  | 3.493E-02 | 1.55 |
| hsa-mir-548o-3p | 2.028E-02 | 1.51 |
| hsa-mir-135b-5p | 2.657E-02 | 1.50 |
| hsa-mir-193a-5p | 4.676E-02 | 0.66 |
| hsa-mir-330-3p  | 4.672E-02 | 0.66 |
| hsa-let-7d-3p   | 8.802E-03 | 0.65 |
| hsa-mir-320a    | 1.037E-02 | 0.65 |
| hsa-mir-193b-3p | 4.563E-02 | 0.64 |
| hsa-mir-4258    | 1.705E-02 | 0.64 |
| hsa-mir-125b-5p | 3.552E-02 | 0.62 |
| hsa-mir-197-3p  | 1.120E-02 | 0.56 |
| hsa-mir-532-3p  | 2.043E-02 | 0.54 |
| hsa-mir-1538    | 4.635E-02 | 0.53 |
| hsa-mir-423-5p  | 6.951E-03 | 0.52 |
| hsa-mir-423-3p  | 1.035E-02 | 0.51 |
| hsa-mir-664b-3p | 5.465E-03 | 0.50 |
| hsa-mir-3665    | 2.813E-02 | 0.49 |
| hsa-mir-3196    | 1.503E-02 | 0.49 |
| hsa-mir-2110    | 5.939E-03 | 0.48 |
| hsa-mir-139-3p  | 2.442E-02 | 0.45 |
| hsa-mir-3656    | 4.843E-02 | 0.45 |
| hsa-mir-1915-3p | 3.577E-02 | 0.42 |
| hsa-mir-6510-3p | 1.854E-02 | 0.41 |
| hsa-mir-4492    | 4.721E-02 | 0.41 |
| hsa-mir-375     | 4.172E-02 | 0.41 |
| hsa-mir-762     | 4.574E-02 | 0.41 |
| hsa-mir-652-3p  | 2.816E-03 | 0.40 |
| hsa-mir-6089    | 1.875E-02 | 0.39 |
| hsa-mir-6087    | 4.979E-02 | 0.38 |
| hsa-mir-211-5p  | 2.096E-02 | 0.38 |
| hsa-mir-3178    | 4.084E-02 | 0.37 |
| hsa-mir-486-3p  | 3.055E-02 | 0.36 |
| hsa-mir-328     | 6.802E-03 | 0.36 |
| hsa-mir-4508    | 1.419E-02 | 0.35 |
| hsa-mir-3663-3p | 8.322E-03 | 0.35 |
| hsa-mir-3195    | 7.322E-03 | 0.34 |
| hsa-mir-4634    | 5.818E-03 | 0.34 |
| hsa-mir-3621    | 3.620E-02 | 0.32 |
| hsa-mir-486-5p  | 2.044E-03 | 0.23 |



## Appendix 9.

### Differentially-expressed microRNAs in mouse samples



| Mouse microRNA correlation |          |           |           |           |           |           |           |           |           |           |           |           |           |           |            |            |           |           |     |     |     |
|----------------------------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----|-----|-----|
| Groups                     | CHR      | CHR       | CHR       | CHR       | CHR       | CHR       | CHR       | PAP       | PAP       | PAP       | PAP       | PAP       | PAP       | PAP       | PAP        | PAP        | PAP       | SCC       | SCC | SCC | SCC |
| Sample                     | HR10_CHR | HR2_CHR   | HR9_CHR   | HR3_CHR   | HR7_CHR   | HR8_CHR   | HR7_PAP   | HR10_PAP  | HR2_PAP   | HR3_PAP   | HR8_PAP   | HR9_PAP   | HR8_SCC   | HR3_SCC   | HR7_SCC    | HR2_SCC    | HR9_SCC   | HR10_SCC  |     |     |     |
| HR10_CHR                   | 1        | 0.4807997 | 0.5129811 | 0.5052758 | 0.5293939 | 0.511163  | -0.325758 | -0.45242  | -0.325852 | -0.334687 | 0.0317878 | -0.268221 | -0.204318 | -0.356543 | -0.121577  | -0.215138  | -0.253432 | -0.550236 |     |     |     |
| HR2_CHR                    |          | 1         | 0.4551531 | 0.7069139 | 0.6011912 | 0.7338695 | -0.256613 | -0.486118 | -0.193605 | -0.133502 | 0.2607079 | -0.10467  | -0.504847 | -0.534633 | -0.387735  | -0.480074  | -0.356056 | -0.599283 |     |     |     |
| HR9_CHR                    |          |           | 1         | 0.5627597 | 0.5473848 | 0.6343135 | -0.46867  | -0.627762 | -0.423457 | -0.531147 | -0.274831 | -0.419817 | 0.0804298 | -0.031381 | -0.1388523 | -0.03561   | -0.243363 | -0.599283 |     |     |     |
| HR3_CHR                    |          |           |           | 1         | 0.6840277 | 0.7445844 | -0.350285 | -0.525575 | -0.319196 | -0.266671 | 0.0587675 | -0.210817 | -0.335611 | -0.466826 | -0.195744  | -0.4456    | -0.277738 | -0.638086 |     |     |     |
| HR7_CHR                    |          |           |           |           | 1         | 0.6959966 | -0.337567 | -0.538633 | -0.394889 | -0.332247 | 0.0222547 | -0.140216 | -0.297732 | -0.42352  | -0.115463  | -0.377639  | -0.289167 | -0.661904 |     |     |     |
| HR8_CHR                    |          |           |           |           |           | 1         | -0.413473 | -0.595077 | -0.394829 | -0.394468 | 0.0101933 | -0.202408 | -0.256723 | -0.380292 | -0.084161  | -0.317349  | -0.026286 | -0.638426 |     |     |     |
| HR7_PAP                    |          |           |           |           |           |           | 1         | 0.3229686 | 0.2336162 | 0.4042176 | 0.3085753 | 0.3010723 | -0.168803 | -0.150642 | -0.187096  | -0.025743  | -0.026286 | -0.638426 |     |     |     |
| HR10_PAP                   |          |           |           |           |           |           |           | 1         | 0.2549459 | 0.384514  | 0.123497  | 0.217483  | -0.119931 | -0.013362 | -0.187096  | -0.025743  | -0.026286 | -0.638426 |     |     |     |
| HR2_PAP                    |          |           |           |           |           |           |           |           | 1         | 0.443741  | 0.1208746 | 0.1907612 | -0.131084 | -0.034666 | -0.226465  | -0.090666  | -0.025743 | -0.026286 |     |     |     |
| HR3_PAP                    |          |           |           |           |           |           |           |           |           | 1         | 0.4241975 | 0.2981075 | -0.36399  | -0.305822 | -0.425661  | -0.287075  | -0.056967 | -0.025743 |     |     |     |
| HR8_PAP                    |          |           |           |           |           |           |           |           |           |           | 1         | 0.2878628 | -0.61731  | -0.587804 | -0.505759  | -0.041629  | -0.056967 | -0.025743 |     |     |     |
| HR9_PAP                    |          |           |           |           |           |           |           |           |           |           |           | 1         | -0.286485 | -0.253636 | -0.250859  | -0.2617807 | -0.041629 | -0.056967 |     |     |     |
| HR8_SCC                    |          |           |           |           |           |           |           |           |           |           |           |           | 1         | 0.721135  | 0.5062211  | 0.6169215  | 0.2617807 | 0.0695303 |     |     |     |
| HR3_SCC                    |          |           |           |           |           |           |           |           |           |           |           |           |           | 1         | 0.5498377  | 0.731151   | 0.1721452 | 0.2422264 |     |     |     |
| HR7_SCC                    |          |           |           |           |           |           |           |           |           |           |           |           |           |           | 1          | 0.5072446  | 0.3064958 | -0.087604 |     |     |     |
| HR2_SCC                    |          |           |           |           |           |           |           |           |           |           |           |           |           |           |            | 1          | 0.1599865 | 0.1244661 |     |     |     |
| HR9_SCC                    |          |           |           |           |           |           |           |           |           |           |           |           |           |           |            |            | 1         | 0.0792956 |     |     |     |
| HR10_SCC                   |          |           |           |           |           |           |           |           |           |           |           |           |           |           |            |            |           | 1         |     |     |     |



| Mouse microRNA |            |           |           |           |           |           |           |            |           |           |           |           |           |            |           |           |           |           |         |         |          |         |         |          |         |
|----------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|---------|---------|----------|---------|---------|----------|---------|
| Groups         | CHR        | CHR       | CHR       | CHR       | CHR       | CHR       | PAP       | PAP        | PAP       | PAP       | PAP       | PAP       | PAP       | PAP        | PAP       | PAP       | PAP       | PAP       | PAP     | PAP     | PAP      | PAP     | PAP     | PAP      | PAP     |
| Experiment     | HR10_CHR   | HR2_CHR   | HR9_CHR   | HR3_CHR   | HR7_CHR   | HR8_CHR   | HR7_PAP   | HR10_PAP   | HR2_PAP   | HR3_PAP   | HR8_PAP   | HR9_PAP   | HR8_SCC   | HR3_SCC    | HR7_SCC   | HR2_SCC   | HR9_SCC   | HR10_SCC  | HR2_SCC | HR9_SCC | HR10_SCC | HR2_SCC | HR9_SCC | HR10_SCC | HR2_SCC |
| mmu-miR-1      | 0.0321057  | -1.290409 | -1.139994 | -1.716482 | -0.681284 | -0.749451 | 0.900392  | 1.4949715  | -0.167395 | 0.337746  | 0.337746  | -0.472554 | 0.0631303 | 1.4060373  | -0.486717 | 1.2237728 | -0.643295 | 1.5516789 |         |         |          |         |         |          |         |
| mmu-miR-1      | 0.709046   | -0.027649 | 0.6990921 | -0.709046 | -0.709046 | -0.114507 | -0.709046 | -0.709046  | -0.709046 | -0.709046 | -0.709046 | -0.709046 | -0.709046 | -0.709046  | -0.709046 | -0.709046 | -0.709046 | -0.709046 |         |         |          |         |         |          |         |
| mmu-miR-1      | 1.5548233  | 0.9964858 | 0.9426841 | 1.1055454 | 1.4084486 | 0.782954  | -0.352187 | -2.375108  | -0.403808 | -0.482951 | 0.538426  | -0.252926 | -0.429166 | -0.955189  | -0.492106 | -0.59914  | -0.228393 | -0.82145  |         |         |          |         |         |          |         |
| mmu-miR-1      | 0.4559638  | 0.085244  | -0.877691 | 0.4559638 | 0.9380292 | 0.6201736 | 1.1963168 | 0.041161   | -0.710543 | 0.8098624 | 1.9705092 | 0.6201736 | -0.745166 | -1.445306  | -0.675921 | -1.445306 | -0.556231 | 0.2627866 |         |         |          |         |         |          |         |
| mmu-miR-1      | 2.0668119  | 0.7280238 | 0.7280238 | 0.9761585 | 1.211265  | 0.7280238 | -1.0056   | -0.653528  | 0.4592807 | -0.888899 | 0.7280238 | -0.888899 | -1.0056   | -0.653528  | -0.888899 | -0.653528 | 0.4592807 | -1.446411 |         |         |          |         |         |          |         |
| mmu-miR-1      | 0.879456   | -1.136483 | -0.924396 | -1.884558 | -0.634818 | 0.63796   | 1.6207417 | 0.1463259  | 0.8182103 | 0.2967086 | 0.4004734 | 0.2416306 | 0.1249175 | 0.4085984  | 0.9431348 | 0.7624335 | 0.9431348 |           |         |         |          |         |         |          |         |
| mmu-let-7f     | 2.1425445  | 0.5894693 | -0.310631 | 1.3059613 | 1.5703582 | 0.1165568 | -0.790173 | -0.790173  | -0.790173 | -0.790173 | -0.790173 | 1.5703582 | -0.790173 | -0.730202  | -0.18462  | 0.0708822 | -0.609466 | -0.790173 |         |         |          |         |         |          |         |
| mmu-miR-1      | 1.3545812  | 1.1162418 | 0.5922763 | 1.2560282 | 1.21595   | 1.21595   | -0.156271 | -1.909122  | -1.028699 | -0.082635 | -0.340454 | -0.656897 | -0.300443 | -1.329809  | 0.2592037 | -1.164435 | 0.3944655 | -0.642332 |         |         |          |         |         |          |         |
| mmu-miR-2      | -0.867051  | -1.103759 | -0.795018 | -1.103759 | -1.103759 | -1.103759 | -1.103759 | 1.2102981  | -1.103759 | 0.4090949 | 0.9168411 | 0.6633548 | 0.7200244 | 1.2102981  | 0.065304  | 0.6430833 | 1.2102981 | 1.2360238 |         |         |          |         |         |          |         |
| mmu-miR-2      | -0.503383  | -0.601077 | -0.601077 | -0.601077 | -0.601077 | -0.601077 | -0.601077 | -0.601077  | -0.601077 | -0.601077 | -0.601077 | -0.601077 | -0.601077 | -0.601077  | -0.601077 | -0.601077 | -0.601077 | -0.601077 |         |         |          |         |         |          |         |
| mmu-miR-2      | 1.293862   | -0.555936 | -0.877218 | -0.797483 | -1.951299 | -0.920166 | 0.8539128 | 1.3941116  | 0.2888044 | -0.492406 | 0.1126281 | 0.6530052 | 0.8173254 | 0.6095612  | -0.534172 | -0.169746 | 1.6511174 | 1.2478225 |         |         |          |         |         |          |         |
| mmu-miR-2      | 1.2486896  | 1.1303266 | 1.1045914 | 1.2722409 | 1.1970283 | 1.2965446 | -1.111458 | -1.111458  | -0.00221  | -1.11458  | -0.577017 | -1.111458 | 0.7438117 | -0.212302  | -0.468546 | -0.278237 | -0.897595 | 1.1247825 |         |         |          |         |         |          |         |
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| mmu-miR-3      | -1.022646  | -1.098412 | -1.098412 | -1.098412 | -1.098412 | -1.098412 | 1.3999074 | 0.2936264  | 0.9919975 | -0.622419 | 0.5201852 | 0.572092  | 1.3449457 | 1.1465615  | 0.3485574 | 0.5382293 | 1.0794332 |           |         |         |          |         |         |          |         |
| mmu-miR-4      | -0.964804  | -0.316545 | -2.302552 | -0.722397 | -0.883122 | 0.9202701 | 1.5677918 | 0.3092202  | 1.6279336 | -0.014299 | 0.1825277 | -0.672026 | 0.6832488 | -0.287249  | 0.6832488 | -0.287249 | 0.6832488 | -0.287249 |         |         |          |         |         |          |         |
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| mmu-miR-1      | 0.937801   | -0.722427 | -0.937801 | -0.937801 | -0.937801 | -0.937801 | -0.937801 | -0.937801  | -0.937801 | -0.937801 | -0.937801 | -0.937801 | -0.937801 | -0.937801  | -0.937801 | -0.937801 | -0.937801 | -0.937801 |         |         |          |         |         |          |         |
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| mmu-miR-1      | 0.9729381  | 0.9134475 | 0.6437253 | 1.0256449 | 0.1502887 | 0.6941287 | -0.116008 | -3.306929  | 0.0525555 | 0.0404029 | -0.361631 | -1.089496 | 0.0196685 | 0.2199167  | 0.3137592 | 0.1156988 | -0.77674  | 0.444829  |         |         |          |         |         |          |         |
| mmu-miR-3      | 1.3702588  | 0.5261319 | 0.9396359 | 1.1658229 | 1.1658229 | 0.4985859 | -0.933678 | -3.020682  | -0.068942 | 0.1133454 | 0.1133454 | -0.081282 | 0.013046  | -0.515881  | 0.013046  | -0.560214 | -0.135133 | -0.60323  |         |         |          |         |         |          |         |
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| mmu-miR-5      | 0.8080406  | 0.4463929 | 0.7245251 | 1.0166244 | 1.4275885 | 0.7072417 | -2.018218 | 0.3087236  | -2.018218 | -0.18428  | 0.5291192 | -0.489989 | 0.320653  | -1.397859  | 0.3887145 | -0.195719 | 0.4987064 | -0.872046 |         |         |          |         |         |          |         |
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| mmu-miR-1      | 0.0327303  | -1.44087  | -0.04982  | -0.334029 | -0.314698 | -0.587429 | -1.319521 | -0.1212286 | -0.604578 | -1.645625 | -0.008629 | 1.6422236 | 1.8319897 | 1.3942046  | 0.739469  | 0.0853957 | 0.9616713 |           |         |         |          |         |         |          |         |
| mmu-miR-4      | -0.037831  | 1.729469  | 0.3572118 | 0.4994084 | -0.18864  | 0.4994084 | 0.1240456 | -0.941742  | 0.920673  | 1.0787705 | 0.4994084 | -1.75839  | -0.501179 | -1.355372  | -1.860046 | 0.3572118 | -0.501179 |           |         |         |          |         |         |          |         |
| mmu-miR-1      | 0.4792257  | 0.6244444 | 0.5920159 | 0.8714991 | 0.9255085 | 0.7462415 | -2.010661 | -2.010661  | 0.8111149 | 0.1216712 | 0.4309787 | -2.010661 | 0.1004242 | -0.280066  | 0.7462415 | -0.329316 | 0.3173262 | -0.123527 |         |         |          |         |         |          |         |
| mmu-miR-5      | 0.8222563  | 0.6024457 | 0.83681   | 0.7851932 | 1.3296523 | 0.2476069 | 0.5961113 | -1.484785  | 0.272406  | -1.484785 | 0.7654969 | -1.484785 | 0.2650034 | -1.159604  | 0.6624058 | -0.792844 | 0.706199  | -1.484785 |         |         |          |         |         |          |         |
| mmu-miR-4      | 1.8499836  | 1.3396555 | 0.4349599 | 1.1507252 | 0.0420569 | 0.1902436 | 0.267743  | -0.437318  | -0.250267 | -0.267743 | 1.3396555 | -0.437318 | -1.560289 | -1.457032  | -1.36563  | -0.770568 | -0.872087 | 0.267743  |         |         |          |         |         |          |         |
| mmu-miR-4      | 1.379733   | -1.142438 | -1.272395 | -0.854684 | -1.694604 | -1.206939 | 1.0380594 | 1.4287808  | 0.2495306 | 0.8234772 | 0.7727154 | 1.0380594 | -0.075256 | -0.2971977 | 0.0862296 | 0.412856  | 0.412856  | 1.0662871 |         |         |          |         |         |          |         |
| mmu-miR-5      | 1.3973286  | 1.120118  | 0.1939291 | 1.2431956 | 1.310382  | 0.5186128 | 0.0438656 | -0.178355  | -0.55284  | -0.361925 | 0.7419806 | 0.262215  | -0.651935 | -1.970216  | 0.2989102 | -1.682957 | -0.41613  | -1.316179 |         |         |          |         |         |          |         |
| mmu-miR-1      | 0.7374368  | -1.402714 | 0.4814135 | -0.660099 | 0.0436571 | -0.016316 | -0.968655 | -0.6783    | -0.213829 | -1.18437  | -1.601203 | -0.90869  | 1.5544602 | 1.3464216  | 1.2933974 | 0.9841186 | 0.5966355 | 0.5966355 |         |         |          |         |         |          |         |
| mmu-miR-1      | 0.824033   | -0.923285 | 0.7025273 | 0.2364176 | -0.923285 | -0.353068 | -0.923285 | -0.923285  | -0.923285 | -0.923285 | -0.923285 | -0.923285 | -0.923285 | -0.923285  | -0.923285 | -0.923285 | -0.923285 | -0.923285 |         |         |          |         |         |          |         |
| mmu-miR-1      | 0.0198711  | 0.9143343 | 0.1058711 | 0.2914967 | -0.170971 | 0.2914967 | -0.170971 | 0.9143343  | 1.2757718 | 1.2757718 | 1.2757718 | 1.2757718 | 1.2757718 | 1.2757718  | 1.2757718 | 1.2757718 | 1.2757718 | 1.2757718 |         |         |          |         |         |          |         |
| mmu-let-7c     | -0.4963    | 1.1348575 | 0.3237493 | 1.2904069 | 0.5808617 | -0.679571 | -0.961744 | -0.116052  | 1.2904069 | 1.2904069 | 0.3237493 | -1.80292  | -1.131363 | -0.584798  | -1.443747 | -0.204176 | -0.204176 | -0.204176 |         |         |          |         |         |          |         |
| mmu-miR-1      | 0.57544569 | -0.673646 | 0.2359389 | -0.886153 | 0.3780783 | -0.44189  | -2.283274 | 0.0952196  | -0.782773 | -0.960234 | -0.886153 | -0.202046 | 1.2962763 | 1.9527505  | 0.8188033 | 0.9314957 | 0.3204979 | 0.5326532 |         |         |          |         |         |          |         |
| mmu-miR-2      | -1.3414649 | -1.329524 | -0.766125 | -1.4274   | -1.746072 | -0.330509 | 1.3645498 | 0.5740407  | 0.058869  | 0.607402  | 0.2132945 | 0.3380834 | 1.18505   | 0.2657862  | 0.1848822 |           |           |           |         |         |          |         |         |          |         |



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mmu-mir-2 -1.401008 -0.661409 -1.178196 -0.485521 -1.365692 -0.730037 1.1940999 0.4955255 -0.170886 1.8877537 1.8033988 0.0806142 0.2186935 -0.1858743 -0.426948 -0.661409 0.0533311 1.1618166  
mmu-mir-1 1.2371321 1.5047818 -0.290232 1.0110112 1.4883695 0.2737344 -1.011877 -1.011877 0.3347325 -1.011877 1.3244412 -1.011877 -1.011877 -0.609394 -0.427484 -0.668878 0.8930439 -1.011877  
mmu-mir-1 1.3420337 1.1973119 0.6640223 1.3050086 0.8403976 0.2593474 -1.287611 -1.287611 0.9918597 0.7020153 0.6856215 -1.287611 -1.287611 -0.053813 -1.000338 -0.048602 -1.287611  
mmu-mir-5 0.2384258 1.5242738 -0.377405 1.172537 0.9652341 0.7517868 0.8460297 0.2384258 -0.459045 -0.112197 1.5242738 -0.286183 -1.578142 -1.737103 -1.373073 -0.459045 -0.112197 -0.766597  
mmu-mir-5 0.5027691 1.7794135 0.8442535 1.5293668 1.3580261 1.492893 -0.964008 -0.964008 -0.964008 -0.964008 -0.964008 -0.964008 -0.964008 -0.964008 -0.964008 -0.964008 -0.964008  
mmu-mir-2 -1.368314 -0.87331 -0.87331 -0.87331 -0.87331 -0.87331 1.6853405 0.1994534 1.0966029 0.7691903 -0.219175 -0.030376 0.4548231 0.7691903 -0.586556 1.0966029 -1.185572 1.6853405  
mmu-mir-1 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804 -1.060804  
mmu-mir-5 -0.524513 -0.532377 -0.428829 -2.934309 -0.878726 0.1366597 1.6346987 -0.09726 0.455652 -0.412156 -0.013879 0.8936521 0.510147 0.1857575 0.510147 0.510147 1.4140026  
mmu-mir-2 0.4474947 -0.438951 -0.193792 -1.678902 -2.728071 -1.118819 1.0682263 0.4474947 0.1616831 1.0682263 0.2534569 0.2534569 -0.357442 0.2534569 0.3496876 1.2832893 0.5798165  
mmu-mir-2 -0.379515 -1.048797 -0.914599 -1.39045 -1.942939 -0.992808 -0.035561 1.5436877 0.9603 1.2877843 -0.25754 0.7305674 0.0606546 0.227265 0.1900981 0.649986 -0.145994 1.4578594  
mmu-mir-5 -0.125153 1.0501305 0.2344999 1.1705083 -0.592286 0.3211516 0.7353875 -1.689072 0.93704 1.7256246 0.8277798 0.4781872 -1.636383 -0.952986 -0.028485 -1.019196 -0.417752 -1.019196  
mmu-mir-2 -0.720163 -1.272494 -0.404706 -0.207366 -1.913369 -1.679111 1.4186288 0.6360769 0.3323848 1.013065 -0.279878 -0.690387 0.9716671 1.4186288 -0.139484 0.7980089 0.2096663 0.5846304  
mmu-mir-2 0.255805 -2.51138 -0.004271 -0.51035 -0.258496 -0.51035 0.9241807 -0.905361 -0.004271 -1.587243 -0.004271 1.3572307 0.5724017 0.9241807 0.9241807 0.9241807 0.9241807  
mmu-mir-5 1.5021934 0.8263659 -0.270261 0.5574484 0.8263659 0.1166112 0.1166112 0.315426 0.315426 -0.077732 1.8205364 -0.270261 -1.546166 -1.546166 -0.721949 -0.721949 0.5574484 -1.799949  
mmu-mir-5 -0.052657 -0.89956 0.8714712 -1.133722 -1.133722 -0.471372 -1.133722 -1.133722 0.28093 0.7210188 -0.655747 -1.133722 1.4217176 1.9029807 1.062634 0.8663521 0.176505 0.4443658  
mmu-mir-1 -0.722555 -1.946847 -0.146204 -1.126505 -0.40759 -1.107074 0.4722665 0.557872 0.7951753 -0.94034 -1.181967 -0.30943 1.0542112 1.4737709 0.725496 0.8777548 0.8777548 1.0542112  
mmu-mir-5 0.4068998 1.1237586 1.2465882 1.3650233 0.9478469 0.4719864 -1.701931 -1.701931 1.3438811 1.050104 -0.23055 -1.701931 -0.448108 -0.718494 0.8895576 -0.448108 -0.263797 -0.104596  
mmu-mir-2 -1.398891 -0.261198 -1.714242 -1.02299 -1.604941 -1.604941 -1.100124 0.3308015 1.4238587 1.4246924 1.5560579 -0.453327 0.6316857 -0.453327 -0.071852 -0.071852 0.3419745 1.4246924  
mmu-mir-1 1.9829246 0.8013301 0.9987949 0.9635101 0.5780947 -1.392131 -1.3285824 -0.562291 -1.458057 -0.26316 -0.179565 0.2962816 -0.179565 0.2962816 -0.040599 0.4342486 -1.698274  
mmu-mir-1 -0.640429 -0.334939 -0.65587 -1.910965 -0.619379 1.5979827 0.9871139 0.1804561 0.5319156 0.2406402 0.4583182 -0.532529 -0.298139 -0.024568 0.6481523 0.6481523 1.6854102  
mmu-mir-1 -0.070553 -1.00763 -0.577671 -0.499616 -2.668343 -0.123428 0.3296286 0.6188937 -0.006317 -0.077565 -0.96542 -0.509437 0.9938378 1.2674307 0.7820521 1.2674307 -0.077565 1.3242717  
mmu-mir-2 1.2484595 1.2484595 1.061601 1.528406 0.6253407 -0.774558 -1.705337 -0.1119636 -1.125628 -0.365454 -0.1119636 -0.250587 -0.774558 0.1262978 -1.354277 0.4215284 -0.91834



PAP-vs-CHR

| <b>microRNA</b>   | <b>p-value PAP vs CHR</b> | <b>fold change PAP-over-CHR</b> |
|-------------------|---------------------------|---------------------------------|
| mmu-mir-6240      | 1.299E-04                 | 176.17                          |
| mmu-mir-5109      | 7.683E-04                 | 77.27                           |
| mmu-mir-451a      | 5.305E-04                 | 27.47                           |
| mmu-mir-6243      | 2.152E-03                 | 15.50                           |
| mmu-mir-138-5p    | 1.166E-04                 | 14.92                           |
| mmu-mir-31-5p     | 1.081E-05                 | 9.24                            |
| mmu-mir-210-3p    | 6.604E-07                 | 8.97                            |
| mmu-mir-31-3p     | 3.041E-03                 | 6.28                            |
| mmu-mir-200a-5p   | 3.619E-04                 | 5.71                            |
| mmu-mir-5617-3p   | 8.897E-03                 | 5.64                            |
| mmu-mir-6538      | 2.031E-02                 | 5.30                            |
| mmu-mir-335-3p    | 6.435E-03                 | 5.08                            |
| mmu-mir-17-5p     | 7.731E-05                 | 4.98                            |
| mmu-mir-3096a-5p  | 4.355E-02                 | 4.94                            |
| mmu-mir-205-3p    | 1.373E-04                 | 4.57                            |
| mmu-mir-1983      | 1.409E-02                 | 4.24                            |
| mmu-mir-210-5p    | 1.172E-04                 | 3.94                            |
| mmu-mir-183-3p    | 1.743E-02                 | 3.80                            |
| mmu-mir-98-5p     | 3.211E-02                 | 3.75                            |
| mmu-mir-20a-5p    | 1.859E-02                 | 3.73                            |
| mmu-mir-429-3p    | 1.767E-03                 | 3.66                            |
| mmu-mir-182-5p    | 1.323E-05                 | 3.38                            |
| mmu-mir-92a-1-5p  | 9.892E-04                 | 3.26                            |
| mmu-mir-141-5p    | 3.887E-02                 | 3.15                            |
| mmu-mir-141-3p    | 5.822E-03                 | 3.00                            |
| mmu-mir-125b-1-3p | 9.828E-04                 | 2.92                            |
| mmu-mir-93-5p     | 6.780E-05                 | 2.92                            |
| mmu-mir-28a-3p    | 8.242E-04                 | 2.80                            |
| mmu-mir-18a-3p    | 7.529E-03                 | 2.76                            |
| mmu-mir-25-3p     | 6.889E-04                 | 2.65                            |
| mmu-mir-106b-3p   | 2.425E-04                 | 2.64                            |
| mmu-mir-200b-5p   | 5.743E-03                 | 2.36                            |
| mmu-mir-200c-3p   | 5.101E-04                 | 2.36                            |
| mmu-mir-582-3p    | 1.691E-02                 | 2.31                            |
| mmu-mir-21a-5p    | 4.118E-02                 | 2.23                            |
| mmu-mir-92a-3p    | 1.009E-03                 | 2.19                            |
| mmu-mir-183-5p    | 1.632E-02                 | 2.11                            |
| mmu-mir-27b-3p    | 5.665E-04                 | 2.08                            |
| mmu-mir-27a-5p    | 3.236E-02                 | 2.07                            |
| mmu-mir-331-3p    | 1.351E-02                 | 2.04                            |
| mmu-mir-200b-3p   | 1.308E-02                 | 1.95                            |
| mmu-mir-27a-3p    | 6.186E-03                 | 1.93                            |
| mmu-mir-186-5p    | 4.178E-03                 | 1.88                            |
| mmu-mir-24-3p     | 1.277E-02                 | 1.78                            |
| mmu-mir-30e-5p    | 1.450E-02                 | 1.77                            |
| mmu-mir-28c       | 6.763E-03                 | 1.77                            |



|                   |           |      |
|-------------------|-----------|------|
| mmu-mir-28a-5p    | 6.763E-03 | 1.77 |
| mmu-mir-26b-5p    | 4.295E-02 | 1.60 |
| mmu-mir-15b-5p    | 9.242E-04 | 1.57 |
| mmu-mir-29a-3p    | 1.668E-02 | 0.66 |
| mmu-mir-146b-3p   | 4.609E-02 | 0.61 |
| mmu-mir-219-1-3p  | 3.706E-02 | 0.61 |
| mmu-mir-667-3p    | 2.558E-02 | 0.58 |
| mmu-mir-378c      | 1.207E-02 | 0.55 |
| mmu-mir-532-3p    | 5.580E-03 | 0.54 |
| mmu-mir-146b-5p   | 1.464E-02 | 0.52 |
| mmu-mir-664-3p    | 1.516E-02 | 0.50 |
| mmu-mir-221-5p    | 1.371E-02 | 0.49 |
| mmu-mir-338-3p    | 1.208E-02 | 0.47 |
| mmu-mir-874-3p    | 3.104E-02 | 0.46 |
| mmu-mir-328-3p    | 1.416E-02 | 0.44 |
| mmu-mir-125a-5p   | 3.322E-03 | 0.43 |
| mmu-mir-184-3p    | 4.302E-02 | 0.42 |
| mmu-mir-351-5p    | 1.202E-02 | 0.42 |
| mmu-mir-196b-5p   | 4.067E-02 | 0.40 |
| mmu-let-7i-3p     | 3.895E-02 | 0.39 |
| mmu-mir-1306-5p   | 3.079E-02 | 0.39 |
| mmu-mir-181b-5p   | 1.098E-02 | 0.39 |
| mmu-mir-199b-3p   | 1.086E-02 | 0.36 |
| mmu-mir-199a-3p   | 1.086E-02 | 0.36 |
| mmu-mir-143-3p    | 3.427E-03 | 0.35 |
| mmu-mir-146a-5p   | 4.710E-03 | 0.31 |
| mmu-mir-222-3p    | 6.630E-05 | 0.31 |
| mmu-mir-214-5p    | 1.352E-02 | 0.31 |
| mmu-mir-10b-5p    | 2.881E-03 | 0.31 |
| mmu-mir-350-5p    | 1.788E-02 | 0.30 |
| mmu-mir-34c-3p    | 1.520E-03 | 0.30 |
| mmu-mir-181a-1-3p | 1.382E-02 | 0.29 |
| mmu-mir-125b-2-3p | 4.494E-02 | 0.29 |
| mmu-mir-1943-5p   | 2.599E-02 | 0.27 |
| mmu-mir-339-3p    | 1.078E-02 | 0.27 |
| mmu-mir-128-3p    | 1.825E-02 | 0.25 |
| mmu-mir-181a-5p   | 7.543E-03 | 0.25 |
| mmu-mir-700-5p    | 2.731E-02 | 0.25 |
| mmu-mir-326-3p    | 1.381E-02 | 0.22 |
| mmu-mir-199a-5p   | 4.857E-02 | 0.21 |
| mmu-mir-195a-5p   | 3.982E-03 | 0.21 |
| mmu-mir-511-5p    | 6.112E-05 | 0.20 |
| mmu-mir-339-5p    | 1.054E-02 | 0.19 |
| mmu-mir-497-5p    | 1.322E-02 | 0.18 |
| mmu-mir-1843b-5p  | 5.369E-05 | 0.18 |
| mmu-mir-150-5p    | 1.940E-04 | 0.16 |
| mmu-mir-1843b-3p  | 1.268E-06 | 0.16 |
| mmu-mir-195a-3p   | 1.025E-05 | 0.15 |



|                   |           |      |
|-------------------|-----------|------|
| mmu-mir-145a-5p   | 1.307E-04 | 0.14 |
| mmu-mir-196a-5p   | 2.145E-04 | 0.14 |
| mmu-mir-5107-5p   | 1.627E-04 | 0.13 |
| mmu-mir-133b-3p   | 1.906E-07 | 0.13 |
| mmu-mir-218-1-3p  | 8.199E-09 | 0.13 |
| mmu-mir-5107-3p   | 2.265E-06 | 0.13 |
| mmu-mir-669o-3p   | 3.441E-06 | 0.12 |
| mmu-mir-669a-3p   | 3.441E-06 | 0.12 |
| mmu-mir-92b-3p    | 1.466E-02 | 0.12 |
| mmu-mir-330-3p    | 6.471E-03 | 0.11 |
| mmu-mir-139-5p    | 2.483E-02 | 0.11 |
| mmu-mir-206-3p    | 5.260E-06 | 0.11 |
| mmu-mir-1249-3p   | 2.178E-03 | 0.10 |
| mmu-mir-1247-5p   | 4.958E-06 | 0.09 |
| mmu-mir-342-3p    | 1.233E-02 | 0.08 |
| mmu-mir-34b-3p    | 6.789E-06 | 0.08 |
| mmu-mir-1981-3p   | 1.934E-08 | 0.06 |
| mmu-mir-181a-2-3p | 1.610E-03 | 0.06 |
| mmu-mir-204-5p    | 8.508E-07 | 0.02 |
| mmu-mir-133a-3p   | 4.105E-05 | 0.00 |



SCC-vs-CHR

| <b>microRNA</b>   | <b>p-value SCC vs CHR</b> | <b>fold change SCC/CHR</b> |
|-------------------|---------------------------|----------------------------|
| mmu-mir-451a      | 7.492E-04                 | 15.94                      |
| mmu-mir-138-5p    | 4.681E-05                 | 13.24                      |
| mmu-mir-335-3p    | 3.793E-07                 | 10.45                      |
| mmu-mir-20a-5p    | 2.912E-06                 | 7.99                       |
| mmu-mir-21a-5p    | 8.097E-06                 | 7.69                       |
| mmu-mir-31-5p     | 8.006E-05                 | 6.57                       |
| mmu-mir-21a-3p    | 1.557E-05                 | 6.55                       |
| mmu-mir-106b-5p   | 1.722E-05                 | 6.04                       |
| mmu-mir-31-3p     | 2.506E-04                 | 5.77                       |
| mmu-mir-98-5p     | 4.038E-03                 | 5.67                       |
| mmu-mir-141-5p    | 1.127E-04                 | 5.38                       |
| mmu-mir-17-5p     | 8.055E-05                 | 5.33                       |
| mmu-mir-210-3p    | 8.736E-06                 | 5.25                       |
| mmu-mir-205-3p    | 5.494E-04                 | 5.03                       |
| mmu-mir-434-5p    | 1.583E-02                 | 4.95                       |
| mmu-mir-421-3p    | 6.121E-03                 | 4.93                       |
| mmu-mir-200a-3p   | 2.010E-02                 | 4.04                       |
| mmu-mir-15a-5p    | 3.021E-03                 | 3.96                       |
| mmu-mir-322-5p    | 5.395E-03                 | 3.74                       |
| mmu-mir-582-3p    | 6.692E-04                 | 3.74                       |
| mmu-mir-92a-1-5p  | 1.695E-03                 | 3.60                       |
| mmu-mir-22-3p     | 3.549E-03                 | 3.50                       |
| mmu-mir-1983      | 1.209E-03                 | 3.44                       |
| mmu-mir-126-5p    | 9.144E-03                 | 3.35                       |
| mmu-mir-411-5p    | 1.180E-02                 | 3.35                       |
| mmu-mir-200a-5p   | 1.743E-02                 | 3.33                       |
| mmu-mir-141-3p    | 1.232E-02                 | 3.29                       |
| mmu-mir-340-5p    | 1.125E-02                 | 3.20                       |
| mmu-mir-19b-3p    | 7.404E-03                 | 3.19                       |
| mmu-mir-872-3p    | 2.232E-03                 | 3.16                       |
| mmu-mir-708-5p    | 1.305E-02                 | 3.11                       |
| mmu-mir-182-5p    | 5.419E-05                 | 3.00                       |
| mmu-mir-142-5p    | 7.634E-03                 | 2.88                       |
| mmu-mir-410-3p    | 3.007E-02                 | 2.76                       |
| mmu-mir-300-3p    | 4.404E-02                 | 2.75                       |
| mmu-mir-192-5p    | 4.536E-05                 | 2.73                       |
| mmu-mir-345-5p    | 1.910E-02                 | 2.71                       |
| mmu-mir-126-3p    | 1.060E-03                 | 2.64                       |
| mmu-mir-224-5p    | 3.205E-02                 | 2.59                       |
| mmu-mir-30e-5p    | 5.767E-04                 | 2.57                       |
| mmu-mir-16-5p     | 1.022E-03                 | 2.54                       |
| mmu-mir-186-5p    | 1.303E-05                 | 2.46                       |
| mmu-mir-148b-5p   | 1.327E-02                 | 2.46                       |
| mmu-mir-125b-1-3p | 1.118E-02                 | 2.39                       |
| mmu-mir-429-3p    | 1.972E-02                 | 2.38                       |
| mmu-mir-872-5p    | 3.555E-02                 | 2.34                       |
| mmu-mir-130a-3p   | 1.414E-03                 | 2.34                       |



|                  |           |      |
|------------------|-----------|------|
| mmu-mir-93-5p    | 3.944E-04 | 2.17 |
| mmu-mir-15b-3p   | 3.006E-02 | 2.13 |
| mmu-mir-24-2-5p  | 2.634E-02 | 2.13 |
| mmu-mir-26b-5p   | 4.135E-05 | 2.06 |
| mmu-mir-148a-3p  | 1.558E-02 | 2.04 |
| mmu-mir-1843a-5p | 3.739E-02 | 2.04 |
| mmu-mir-96-5p    | 1.123E-02 | 2.04 |
| mmu-mir-148a-5p  | 4.330E-02 | 2.02 |
| mmu-mir-28c      | 8.492E-04 | 1.94 |
| mmu-mir-28a-5p   | 8.492E-04 | 1.94 |
| mmu-mir-25-3p    | 4.623E-03 | 1.90 |
| mmu-mir-27b-3p   | 1.384E-02 | 1.88 |
| mmu-let-7f-5p    | 4.279E-03 | 1.88 |
| mmu-mir-210-5p   | 4.768E-02 | 1.85 |
| mmu-mir-200b-3p  | 2.431E-02 | 1.83 |
| mmu-mir-28a-3p   | 5.943E-03 | 1.80 |
| mmu-mir-27a-3p   | 2.616E-02 | 1.76 |
| mmu-mir-26a-5p   | 4.281E-03 | 1.69 |
| mmu-let-7g-5p    | 4.052E-03 | 1.59 |
| mmu-mir-18a-5p   | 4.957E-02 | 1.56 |
| mmu-let-7i-5p    | 5.166E-03 | 1.52 |
| mmu-mir-103-3p   | 1.153E-03 | 1.50 |
| mmu-mir-361-3p   | 7.704E-03 | 0.63 |
| mmu-mir-219-1-3p | 2.661E-02 | 0.61 |
| mmu-mir-674-3p   | 3.001E-03 | 0.59 |
| mmu-mir-99a-5p   | 4.506E-02 | 0.58 |
| mmu-mir-30a-3p   | 4.397E-03 | 0.56 |
| mmu-mir-378a-5p  | 7.152E-03 | 0.55 |
| mmu-mir-128-3p   | 1.037E-02 | 0.54 |
| mmu-mir-667-3p   | 5.446E-03 | 0.53 |
| mmu-mir-125b-5p  | 1.097E-02 | 0.52 |
| mmu-mir-100-5p   | 2.837E-02 | 0.51 |
| mmu-let-7e-3p    | 2.706E-02 | 0.50 |
| mmu-mir-1198-5p  | 4.911E-03 | 0.50 |
| mmu-mir-423-5p   | 1.039E-02 | 0.50 |
| mmu-mir-99b-5p   | 5.140E-03 | 0.50 |
| mmu-mir-615-3p   | 2.758E-04 | 0.49 |
| mmu-let-7d-3p    | 2.533E-03 | 0.48 |
| mmu-mir-378a-3p  | 3.764E-04 | 0.48 |
| mmu-mir-149-5p   | 1.020E-02 | 0.45 |
| mmu-mir-351-5p   | 3.412E-03 | 0.45 |
| mmu-mir-350-5p   | 6.088E-03 | 0.44 |
| mmu-mir-320-3p   | 1.269E-03 | 0.44 |
| mmu-mir-365-1-5p | 3.812E-02 | 0.43 |
| mmu-mir-324-3p   | 4.697E-02 | 0.43 |
| mmu-mir-193b-5p  | 2.479E-02 | 0.43 |
| mmu-mir-744-5p   | 1.707E-03 | 0.43 |
| mmu-mir-486-5p   | 2.172E-02 | 0.41 |
| mmu-mir-3107-5p  | 2.172E-02 | 0.41 |



|                   |           |      |
|-------------------|-----------|------|
| mmu-mir-34c-3p    | 1.744E-02 | 0.41 |
| mmu-mir-1247-5p   | 4.904E-02 | 0.41 |
| mmu-mir-676-3p    | 3.682E-02 | 0.41 |
| mmu-mir-484       | 1.266E-03 | 0.40 |
| mmu-mir-378c      | 1.414E-03 | 0.40 |
| mmu-mir-139-5p    | 5.735E-03 | 0.39 |
| mmu-mir-181c-3p   | 3.030E-02 | 0.37 |
| mmu-mir-1306-5p   | 8.817E-03 | 0.37 |
| mmu-mir-222-3p    | 3.161E-04 | 0.37 |
| mmu-mir-193b-3p   | 2.690E-03 | 0.36 |
| mmu-let-7b-3p     | 2.348E-03 | 0.36 |
| mmu-let-7i-3p     | 6.211E-03 | 0.36 |
| mmu-mir-125a-5p   | 3.706E-04 | 0.36 |
| mmu-mir-501-3p    | 1.813E-03 | 0.35 |
| mmu-mir-6406      | 1.123E-02 | 0.31 |
| mmu-mir-218-1-3p  | 1.328E-03 | 0.31 |
| mmu-mir-339-5p    | 1.138E-02 | 0.31 |
| mmu-mir-532-3p    | 7.485E-04 | 0.30 |
| mmu-mir-700-5p    | 2.851E-02 | 0.30 |
| mmu-mir-671-3p    | 2.711E-07 | 0.30 |
| mmu-mir-145a-5p   | 1.012E-02 | 0.29 |
| mmu-mir-511-5p    | 2.506E-03 | 0.28 |
| mmu-mir-211-5p    | 2.449E-02 | 0.27 |
| mmu-mir-574-3p    | 9.400E-05 | 0.26 |
| mmu-mir-652-3p    | 6.913E-04 | 0.24 |
| mmu-mir-5107-3p   | 5.928E-04 | 0.22 |
| mmu-mir-3102-3p   | 1.101E-04 | 0.21 |
| mmu-mir-150-5p    | 4.739E-04 | 0.20 |
| mmu-mir-1943-5p   | 5.415E-04 | 0.19 |
| mmu-mir-326-3p    | 2.921E-04 | 0.18 |
| mmu-mir-328-3p    | 7.706E-07 | 0.18 |
| mmu-mir-92b-3p    | 8.311E-05 | 0.18 |
| mmu-mir-664-3p    | 8.346E-04 | 0.17 |
| mmu-mir-5107-5p   | 4.489E-04 | 0.16 |
| mmu-mir-1981-3p   | 1.069E-04 | 0.15 |
| mmu-mir-342-3p    | 6.551E-05 | 0.14 |
| mmu-mir-34b-3p    | 4.741E-05 | 0.12 |
| mmu-mir-486-3p    | 4.033E-03 | 0.12 |
| mmu-mir-330-3p    | 4.990E-04 | 0.11 |
| mmu-mir-3107-3p   | 2.939E-03 | 0.11 |
| mmu-mir-1843b-3p  | 7.533E-07 | 0.10 |
| mmu-mir-1249-3p   | 1.050E-06 | 0.10 |
| mmu-mir-181a-2-3p | 3.113E-06 | 0.07 |
| mmu-mir-204-5p    | 1.493E-04 | 0.06 |



SCC-vs-PAP

| <b>microRNA</b>   | <b>p-value SCC vs PAP</b> | <b>fold change SCC/PAP</b> |
|-------------------|---------------------------|----------------------------|
| mmu-mir-133a-3p   | 7.739E-03                 | 113.12                     |
| mmu-mir-669o-3p   | 9.036E-04                 | 8.46                       |
| mmu-mir-669a-3p   | 9.036E-04                 | 8.46                       |
| mmu-mir-126-5p    | 1.333E-03                 | 7.18                       |
| mmu-mir-199a-5p   | 4.092E-02                 | 6.83                       |
| mmu-mir-206-3p    | 4.440E-03                 | 6.16                       |
| mmu-mir-199b-3p   | 3.022E-03                 | 6.15                       |
| mmu-mir-199a-3p   | 3.022E-03                 | 6.15                       |
| mmu-mir-142-5p    | 1.345E-05                 | 5.79                       |
| mmu-mir-133b-3p   | 2.637E-03                 | 5.73                       |
| mmu-mir-195a-5p   | 1.431E-02                 | 5.47                       |
| mmu-mir-497-5p    | 2.365E-02                 | 5.36                       |
| mmu-mir-10b-5p    | 2.314E-04                 | 5.27                       |
| mmu-mir-214-5p    | 3.123E-02                 | 4.51                       |
| mmu-mir-195a-3p   | 7.376E-03                 | 4.40                       |
| mmu-mir-34a-5p    | 3.388E-03                 | 4.40                       |
| mmu-mir-1247-5p   | 5.404E-03                 | 4.34                       |
| mmu-mir-34c-5p    | 2.463E-02                 | 4.16                       |
| mmu-mir-1843b-5p  | 4.816E-03                 | 4.12                       |
| mmu-mir-10a-5p    | 3.566E-02                 | 4.11                       |
| mmu-mir-143-3p    | 7.699E-03                 | 3.94                       |
| mmu-mir-322-5p    | 5.435E-03                 | 3.88                       |
| mmu-mir-22-3p     | 1.524E-03                 | 3.67                       |
| mmu-mir-21a-5p    | 3.069E-03                 | 3.45                       |
| mmu-mir-340-3p    | 5.953E-03                 | 3.39                       |
| mmu-mir-199b-5p   | 5.143E-03                 | 3.13                       |
| mmu-mir-300-3p    | 2.193E-02                 | 3.12                       |
| mmu-mir-134-5p    | 6.731E-03                 | 3.02                       |
| mmu-mir-126-3p    | 9.269E-04                 | 3.01                       |
| mmu-mir-146a-5p   | 1.703E-02                 | 3.00                       |
| mmu-mir-148b-5p   | 6.094E-03                 | 2.96                       |
| mmu-mir-181a-1-3p | 4.184E-02                 | 2.70                       |
| mmu-mir-337-5p    | 3.150E-02                 | 2.69                       |
| mmu-mir-1843a-5p  | 4.388E-03                 | 2.65                       |
| mmu-mir-224-5p    | 4.143E-02                 | 2.52                       |
| mmu-mir-218-1-3p  | 4.308E-03                 | 2.40                       |
| mmu-mir-1981-3p   | 1.174E-02                 | 2.34                       |
| mmu-mir-148a-3p   | 2.000E-03                 | 2.29                       |
| mmu-mir-15a-5p    | 9.127E-03                 | 2.24                       |
| mmu-mir-145a-3p   | 2.152E-02                 | 2.22                       |
| mmu-mir-96-5p     | 4.134E-03                 | 2.15                       |
| mmu-mir-101a-3p   | 4.765E-02                 | 1.88                       |
| mmu-mir-101c      | 4.765E-02                 | 1.88                       |
| mmu-mir-301a-3p   | 3.530E-02                 | 1.85                       |
| mmu-mir-152-3p    | 4.946E-02                 | 1.84                       |
| mmu-let-7f-5p     | 2.954E-02                 | 1.79                       |
| mmu-mir-192-5p    | 1.094E-02                 | 1.79                       |



|                 |           |      |
|-----------------|-----------|------|
| mmu-mir-26a-5p  | 5.685E-03 | 1.56 |
| mmu-mir-18a-5p  | 4.957E-02 | 1.56 |
| mmu-mir-15b-5p  | 2.935E-03 | 0.66 |
| mmu-mir-125b-5p | 1.360E-02 | 0.62 |
| mmu-let-7d-3p   | 4.084E-02 | 0.60 |
| mmu-mir-361-3p  | 2.745E-02 | 0.59 |
| mmu-mir-210-3p  | 4.268E-02 | 0.59 |
| mmu-mir-484     | 1.991E-02 | 0.58 |
| mmu-mir-532-3p  | 3.805E-02 | 0.55 |
| mmu-mir-99b-5p  | 1.744E-02 | 0.55 |
| mmu-mir-744-5p  | 3.593E-02 | 0.54 |
| mmu-mir-320-3p  | 1.013E-02 | 0.54 |
| mmu-mir-423-5p  | 1.504E-02 | 0.50 |
| mmu-let-7b-5p   | 3.061E-03 | 0.49 |
| mmu-mir-210-5p  | 3.491E-02 | 0.47 |
| mmu-mir-200b-5p | 4.684E-02 | 0.46 |
| mmu-mir-106b-3p | 1.417E-02 | 0.45 |
| mmu-mir-193b-3p | 2.477E-02 | 0.45 |
| mmu-mir-1198-5p | 3.259E-03 | 0.42 |
| mmu-mir-328-3p  | 5.232E-03 | 0.41 |
| mmu-mir-331-3p  | 1.965E-02 | 0.40 |
| mmu-mir-200c-3p | 1.013E-03 | 0.37 |
| mmu-mir-149-5p  | 7.326E-03 | 0.35 |
| mmu-mir-664-3p  | 1.966E-02 | 0.35 |
| mmu-mir-486-5p  | 4.723E-03 | 0.28 |
| mmu-mir-3107-5p | 4.723E-03 | 0.28 |
| mmu-mir-6406    | 2.729E-02 | 0.26 |
| mmu-mir-6243    | 4.734E-02 | 0.15 |
| mmu-mir-5109    | 4.239E-02 | 0.06 |
| mmu-mir-6240    | 1.646E-02 | 0.05 |



## Appendix 10.

### Significant microRNA-mRNA functional pairs



| miRNA      | Gene    | AK-NS miRNA-mRNA enrichment, -log10(q-value) | SCC-AK miRNA-mRNA enrichment, -log10(q-value) | SCC-NS miRNA-mRNA enrichment, -log10(q-value) | PAP-CHR miRNA-mRNA enrichment, -log10(q-value) | SCC-CHR miRNA-mRNA enrichment, -log10(q-value) | miRNA-mRNA enrichment, -log10(q-value) | miRNA-mRNA enrichment recurrence human | miRNA-mRNA enrichment recurrence mouse | microRNA AK-over-NS log2(fold-change) | microRNA SCC-over-AK log2(fold-change) | microRNA SCC-over-NS log2(fold-change) | microRNA PAP-over-CHR log2(fold-change) | microRNA SCC-over-CHR log2(fold-change) | miRNA AK-over-NS log2(fold-change) | miRNA SCC-over-AK log2(fold-change) | miRNA SCC-over-NS log2(fold-change) | miRNA PAP-over-CHR log2(fold-change) | miRNA SCC-over-CHR log2(fold-change) |
|------------|---------|--|---|---|--|--|--|--|--|---------------------------------------|--|--|---|---|------------------------------------|-------------------------------------|-------------------------------------|--------------------------------------|--------------------------------------|
| let-7f-5p  | FBXO32  | 1.92   | 13.15   | 20.00   | 20.00  | 2  | 1                                      | 0.64                                   | 0.65                                   | 0.66                                  | -0.79                                  | -1.39                                  | -2.37                                   | -2.03                                   | -0.79                              | -1.05                               | -1.90                               | -1.27                                | -1.09                                |
| let-7f-5p  | RORC    | 1.92   | 13.15   | 20.00   | 20.00  | 2  | 1                                      | 0.64                                   | 0.65                                   | 0.66                                  | -1.05                                  | -1.90                                  | -1.27                                   | -1.09                                   | -1.05                              | -1.34                               | -1.90                               | -0.98                                | -1.14                                |
| let-7f-5p  | GHR     | 1.92   | 13.15   | 20.00   | 20.00  | 2  | 1                                      | 0.64                                   | 0.65                                   | 0.66                                  | -1.34                                  | -2.05                                  | -1.10                                   | -0.74                                   | -1.34                              | -2.05                               | -1.10                               | -0.74                                | -0.74                                |
| let-7f-5p  | CGN11   | 1.92   | 13.15   | 20.00   | 20.00  | 2  | 1                                      | 0.64                                   | 0.65                                   | 0.66                                  | -1.23                                  | -2.02                                  | -1.27                                   | -1.26                                   | -1.23                              | -2.02                               | -1.27                               | -1.26                                | -1.26                                |
| let-7f-5p  | EGR3    | 1.92   | 13.15   | 20.00   | 20.00  | 2  | 1                                      | 0.64                                   | 0.65                                   | 0.66                                  | -0.72                                  | -0.89                                  | -1.24                                   | -0.71                                   | -0.89                              | -1.24                               | -0.71                               | -0.71                                | -0.71                                |
| let-7f-5p  | LRI1    | 1.92   | 13.15   | 20.00   | 20.00  | 2  | 1                                      | 0.64                                   | 0.65                                   | 0.66                                  | -0.92                                  | -1.45                                  | -0.95                                   | -0.71                                   | -1.45                              | -0.95                               | -0.71                               | -0.71                                | -0.71                                |
| let-7f-5p  | SLC25A4 | 1.92   | 13.15   | 20.00   | 20.00  | 2  | 1                                      | 0.64                                   | 0.65                                   | 0.66                                  | -0.80                                  | -1.72                                  | -0.67                                   | -1.09                                   | -1.72                              | -0.67                               | -1.09                               | -1.09                                | -1.09                                |
| miR-17-5p  | ATP1A2  | 3.93   | 13.86   | 20.00   | 20.00  | 2  | 2                                      | 0.77                                   | 1.15                                   | 2.32                                  | 2.41                                   | -2.39                                  | -2.83                                   | -5.74                                   | -2.39                              | -2.83                               | -5.74                               | -2.39                                | -2.39                                |
| miR-17-5p  | RORC    | 3.93   | 13.86   | 20.00   | 20.00  | 2  | 2                                      | 0.77                                   | 1.15                                   | 2.32                                  | 2.41                                   | -1.05                                  | -1.90                                   | -1.27                                   | -1.05                              | -1.90                               | -1.27                               | -1.09                                | -1.09                                |
| miR-17-5p  | EGR2    | 3.93   | 13.86   | 20.00   | 20.00  | 2  | 2                                      | 0.77                                   | 1.15                                   | 2.32                                  | 2.41                                   | -1.20                                  | -2.05                                   | -2.57                                   | -1.20                              | -2.05                               | -2.57                               | -2.38                                | -2.38                                |
| miR-17-5p  | EGR3    | 3.93   | 13.86   | 20.00   | 20.00  | 2  | 2                                      | 0.77                                   | 1.15                                   | 2.32                                  | 2.41                                   | -1.23                                  | -2.02                                   | -1.27                                   | -1.23                              | -2.02                               | -1.27                               | -1.26                                | -1.26                                |
| miR-17-5p  | LRI1    | 3.93   | 13.86   | 20.00   | 20.00  | 2  | 2                                      | 0.77                                   | 1.15                                   | 2.32                                  | 2.41                                   | -0.72                                  | -0.89                                   | -1.24                                   | -0.72                              | -0.89                               | -1.24                               | -1.26                                | -1.26                                |
| miR-17-5p  | TNSI    | 3.93   | 13.86   | 20.00   | 20.00  | 2  | 2                                      | 0.77                                   | 1.15                                   | 2.32                                  | 2.41                                   | -0.89                                  | -1.38                                   | -2.26                                   | -0.89                              | -1.38                               | -2.26                               | -1.50                                | -1.50                                |
| miR-17-5p  | SH3BP5  | 3.93   | 13.86   | 20.00   | 20.00  | 2  | 2                                      | 0.77                                   | 1.15                                   | 2.32                                  | 2.41                                   | -0.98                                  | -1.39                                   | -0.81                                   | -0.98                              | -1.39                               | -0.81                               | -0.81                                | -0.81                                |
| miR-17-5p  | SYNM    | 3.93   | 13.86   | 20.00   | 20.00  | 2  | 2                                      | 0.77                                   | 1.15                                   | 2.32                                  | 2.41                                   | -1.96                                  | -2.48                                   | -2.40                                   | -1.96                              | -2.48                               | -2.40                               | -1.92                                | -1.92                                |
| miR-17-5p  | CH2     | 3.93   | 13.86   | 20.00   | 20.00  | 2  | 2                                      | 0.77                                   | 1.15                                   | 2.32                                  | 2.41                                   | -0.82                                  | -0.91                                   | -0.76                                   | -0.82                              | -0.91                               | -0.76                               | -0.76                                | -0.76                                |
| miR-17-5p  | NFIB    | 3.93   | 13.86   | 20.00   | 20.00  | 2  | 2                                      | 0.77                                   | 1.15                                   | 2.32                                  | 2.41                                   | -1.04                                  | -1.04                                   | -0.81                                   | -1.04                              | -1.04                               | -0.81                               | -0.81                                | -0.81                                |
| miR-21-3p  | TIMP3   | 5.33   | 13.07   | 15.30   | 15.30  | 2  | 1                                      | 1.29                                   | 2.75                                   | 2.71                                  | -1.07                                  | -1.48                                  | -1.86                                   | -1.02                                   | -1.07                              | -1.48                               | -1.86                               | -1.02                                | -1.02                                |
| miR-21-3p  | TIMP3   | 5.33   | 13.07   | 15.30   | 15.30  | 2  | 2                                      | 0.97                                   | 1.59                                   | 2.56                                  | -1.07                                  | -1.38                                  | -2.26                                   | -1.50                                   | -1.07                              | -1.38                               | -2.26                               | -1.50                                | -1.50                                |
| miR-21-3p  | EGR3    | 5.33   | 13.07   | 15.30   | 15.30  | 2  | 1                                      | 1.29                                   | 2.75                                   | 2.71                                  | -1.23                                  | -2.02                                  | -1.86                                   | -1.02                                   | -1.23                              | -2.02                               | -1.86                               | -1.02                                | -1.02                                |
| miR-21-3p  | EGR3    | 5.33   | 13.07   | 15.30   | 15.30  | 2  | 1                                      | 1.29                                   | 2.75                                   | 2.71                                  | -0.66                                  | -1.50                                  | -2.57                                   | -2.38                                   | -0.66                              | -1.50                               | -2.57                               | -2.38                                | -2.38                                |
| miR-21-5p  | AE1L    | 5.33   | 13.07   | 15.30   | 15.30  | 1  | 1                                      | 1.29                                   | 2.75                                   | 2.71                                  | -0.66                                  | -1.50                                  | -2.57                                   | -2.38                                   | -0.66                              | -1.50                               | -2.57                               | -2.38                                | -2.38                                |
| miR-21-5p  | AE1L    | 5.33   | 13.07   | 15.30   | 15.30  | 2  | 2                                      | 0.97                                   | 1.59                                   | 2.56                                  | -1.07                                  | -1.38                                  | -2.26                                   | -1.50                                   | -1.07                              | -1.38                               | -2.26                               | -1.50                                | -1.50                                |
| miR-21-5p  | TNSI    | 5.33   | 13.07   | 15.30   | 15.30  | 2  | 2                                      | 0.97                                   | 1.59                                   | 2.56                                  | -0.89                                  | -1.38                                  | -2.26                                   | -1.50                                   | -0.89                              | -1.38                               | -2.26                               | -1.50                                | -1.50                                |
| miR-21-5p  | NFIB    | 5.33   | 13.07   | 15.30   | 15.30  | 2  | 2                                      | 0.97                                   | 1.59                                   | 2.56                                  | -1.04                                  | -1.04                                  | -0.81                                   | -0.99                                   | -1.04                              | -1.04                               | -0.81                               | -0.99                                | -0.99                                |
| miR-21-5p  | NFIB    | 5.33   | 13.07   | 15.30   | 15.30  | 2  | 2                                      | 0.97                                   | 1.59                                   | 2.56                                  | -1.04                                  | -1.04                                  | -0.81                                   | -0.99                                   | -1.04                              | -1.04                               | -0.81                               | -0.99                                | -0.99                                |
| miR-224-5f | RELN    | 2.02   | 6.06  | 4.02  | 4.02   | 2  | 1                                      | 0.99                                   | 1.20                                   | 1.37                                  | -1.26                                  | -2.05                                  | -2.57                                   | -2.38                                   | -1.26                              | -2.05                               | -2.57                               | -2.38                                | -2.38                                |
| miR-224-5f | EGR2    | 2.02   | 6.06  | 4.02  | 4.02   | 2  | 1                                      | 0.99                                   | 1.20                                   | 1.37                                  | -1.26                                  | -2.05                                  | -2.57                                   | -2.38                                   | -1.26                              | -2.05                               | -2.57                               | -2.38                                | -2.38                                |
| miR-224-5f | CBX7    | 2.02   | 6.06  | 4.02  | 4.02   | 2  | 1                                      | 0.99                                   | 1.20                                   | 1.37                                  | -0.80                                  | -1.00                                  | -1.22                                   | -1.33                                   | -0.80                              | -1.00                               | -1.22                               | -1.33                                | -1.33                                |
| miR-224-5f | NFIB    | 2.02   | 6.06  | 4.02  | 4.02   | 2  | 1                                      | 0.99                                   | 1.20                                   | 1.37                                  | -1.04                                  | -1.97                                  | -0.81                                   | -0.99                                   | -1.04                              | -1.97                               | -0.81                               | -0.99                                | -0.99                                |
| miR-25-3p  | EDNRB   | 3.65   | 14.34   | 20.00   | 20.00  | 2  | 2                                      | 0.71                                   | 0.64                                   | 0.93                                  | -0.86                                  | -1.18                                  | -1.72                                   | -2.03                                   | -0.86                              | -1.18                               | -1.72                               | -2.03                                | -2.03                                |
| miR-25-3p  | FBXO32  | 3.65   | 14.34   | 20.00   | 20.00  | 2  | 2                                      | 0.71                                   | 0.64                                   | 0.93                                  | -0.79                                  | -1.39                                  | -2.37                                   | -2.03                                   | -0.79                              | -1.39                               | -2.37                               | -2.03                                | -2.03                                |
| miR-25-3p  | AXL     | 3.65   | 14.34   | 20.00   | 20.00  | 2  | 1                                      | 0.71                                   | 0.64                                   | 0.93                                  | -0.89                                  | -1.03                                  | -0.92                                   | -0.88                                   | -0.89                              | -1.03                               | -0.92                               | -0.88                                | -0.88                                |
| miR-25-3p  | MSRB3   | 3.65   | 14.34   | 20.00   | 20.00  | 1  | 2                                      | 0.71                                   | 0.64                                   | 0.93                                  | -0.76                                  | -0.93                                  | -2.26                                   | -0.61                                   | -0.76                              | -0.93                               | -2.26                               | -0.61                                | -0.61                                |
| miR-25-3p  | TACC2   | 3.65   | 14.34   | 20.00   | 20.00  | 2  | 1                                      | 0.71                                   | 0.64                                   | 0.93                                  | -0.62                                  | -0.93                                  | -2.57                                   | -2.38                                   | -0.62                              | -0.93                               | -2.57                               | -2.38                                | -2.38                                |
| miR-25-3p  | EGR2    | 3.65   | 14.34   | 20.00   | 20.00  | 2  | 2                                      | 0.71                                   | 0.64                                   | 0.93                                  | -1.20                                  | -2.05                                  | -2.57                                   | -2.38                                   | -1.20                              | -2.05                               | -2.57                               | -2.38                                | -2.38                                |
| miR-25-3p  | INSIG1  | 3.65   | 14.34   | 20.00   | 20.00  | 2  | 1                                      | 0.71                                   | 0.64                                   | 0.93                                  | -1.20                                  | -2.05                                  | -2.57                                   | -2.38                                   | -1.20                              | -2.05                               | -2.57                               | -2.38                                | -2.38                                |
| miR-25-3p  | CH2     | 3.65   | 14.34   | 20.00   | 20.00  | 2  | 2                                      | 0.71                                   | 0.64                                   | 0.93                                  | -0.82                                  | -0.91                                  | -0.76                                   | -0.99                                   | -0.82                              | -0.91                               | -0.76                               | -0.99                                | -0.99                                |
| miR-25-3p  | NFIB    | 3.65   | 14.34   | 20.00   | 20.00  | 2  | 2                                      | 0.71                                   | 0.64                                   | 0.93                                  | -1.04                                  | -1.97                                  | -0.81                                   | -0.99                                   | -1.04                              | -1.97                               | -0.81                               | -0.99                                | -0.99                                |
| miR-25-3p  | NFIB    | 3.65   | 14.34   | 20.00   | 20.00  | 2  | 2                                      | 0.71                                   | 0.64                                   | 0.93                                  | -1.04                                  | -1.97                                  | -0.81                                   | -0.99                                   | -1.04                              | -1.97                               | -0.81                               | -0.99                                | -0.99                                |
| miR-25-3p  | NFIB    | 3.65   | 14.34   | 20.00   | 20.00  | 2  | 2                                      | 0.71                                   | 0.64                                   | 0.93                                  | -1.04                                  | -1.97                                  | -0.81                                   | -0.99                                   | -1.04                              | -1.97                               | -0.81                               | -0.99                                | -0.99                                |
| miR-22b-3f | FBXO32  | 9.00   | 19.97   | 20.00   | 20.00  | 2  | 2                                      | 0.75                                   | 0.86                                   | 1.05                                  | -0.79                                  | -1.39                                  | -2.37                                   | -2.03                                   | -0.79                              | -1.39                               | -2.37                               | -2.03                                | -2.03                                |
| miR-27b-3f | ATF3    | 9.00   | 19.97   | 20.00   | 20.00  | 2  | 2                                      | 0.75                                   | 0.86                                   | 1.05                                  | -0.91                                  | -1.71                                  | -2.14                                   | -2.04                                   | -0.91                              | -1.71                               | -2.14                               | -2.04                                | -2.04                                |
| miR-27b-3f | FBIN5   | 9.00   | 19.97   | 20.00   | 20.00  | 2  | 1                                      | 0.75                                   | 0.86                                   | 1.05                                  | -0.95                                  | -0.97                                  | -0.94                                   | -1.10                                   | -0.95                              | -0.97                               | -0.94                               | -1.10                                | -1.10                                |
| miR-27b-3f | RELN    | 9.00   | 19.97   | 20.00   | 20.00  | 2  | 1                                      | 0.75                                   | 0.86                                   | 1.05                                  | -1.23                                  | -2.02                                  | -1.27                                   | -1.27                                   | -1.23                              | -2.02                               | -1.27                               | -1.26                                | -1.26                                |
| miR-27b-3f | EGR3    | 9.00   | 19.97   | 20.00   | 20.00  | 2  | 2                                      | 0.75                                   | 0.86                                   | 1.05                                  | -1.69                                  | -1.45                                  | -1.55                                   | -2.25                                   | -1.69                              | -1.45                               | -1.55                               | -2.25                                | -2.25                                |
| miR-27b-3f | SEMA3B  | 9.00   | 19.97   | 20.00   | 20.00  | 2  | 2                                      | 0.75                                   | 0.86                                   | 1.05                                  | -0.82                                  | -1.20                                  | -1.08                                   | -2.25                                   | -0.82                              | -1.20                               | -1.08                               | -2.25                                | -2.25                                |
| miR-27b-3f | POU3F3  | 9.00   | 19.97   | 20.00   | 20.00  | 2  | 2                                      | 0.75                                   | 0.86                                   | 1.05                                  | -0.91                                  | -1.43                                  | -1.92                                   | -2.11                                   | -0.91                              | -1.43                               | -1.92                               | -2.11                                | -2.11                                |
| miR-27b-3f | NCALD   | 9.00   | 19.97   | 20.00   | 20.00  | 2  | 2                                      | 0.75                                   | 0.86                                   | 1.05                                  | -1.16                                  | -2.08                                  | -5.42                                   | -0.71                                   | -1.16                              | -2.08                               | -5.42                               | -0.71                                | -0.71                                |
| miR-27b-3f | LPL     | 9.00   | 19.97   | 20.00   | 20.00  | 2  | 2                                      | 0.75                                   | 0.86                                   | 1.05                                  | -1.13                                  | -2.08                                  | -5.42                                   | -0.71                                   | -1.13                              | -2.08                               | -5.42                               | -0.71                                | -0.71                                |
| miR-27b-3f | HMGC51  | 9.00   | 19.97   | 20.00   | 20.00  | 2  | 1                                      | 0.75                                   | 0.86                                   | 1.05                                  | -0.91                                  | -1.43                                  | -1.92                                   | -2.11                                   | -0.91                              | -1.43                               | -1.92                               | -2.11                                | -2.11                                |
| miR-27b-3f | RCAN2   | 9.00   | 19.97   | 20.00   | 20.00  | 2  | 2                                      | 0.75                                   | 0.86                                   | 1.05                                  | -1.05                                  | -1.97                                  | -1.56                                   | -0.99                                   | -1.05                              | -1.97                               | -1.56                               | -0.99                                | -0.99                                |
| miR-27b-3f | NFIB    | 9.00   | 19.97   | 20.00   | 20.00  | 2  | 2                                      | 0.75                                   | 0.86                                   | 1.05                                  | -1.04                                  | -1.97                                  | -1.56                                   | -0.99                                   | -1.04                              | -1.97                               | -1.56                               | -0.99                                | -0.99                                |
| miR-31-5p  | RORC    | 4.08   | 6.31  | 7.46  | 7.46   | 2  | 2                                      | 1.80                                   | 2.60                                   | 3.21                                  | -1.05                                  | -1.90                                  | -1.27                                   | -1.09                                   | -1.05                              | -1.34                               | -1.90                               | -1.27                                | -1.09                                |
| miR-31-5p  | TACC2   | 4.08   | 6.31  | 7.46  | 7.46   | 2  | 1                                      | 1.80                                   | 2.60                                   | 3.21                                  | -0.62                                  | -0.93                                  | -2.26                                   | -1.50                                   | -0.62                              | -0.93                               | -2.26                               | -1.50                                | -1.50                                |
| miR-31-5p  | TNSI    | 4.08   | 6.31  | 7.46  | 7.46   | 2  | 2                                      | 1.80                                   | 2.60                                   | 3.21                                  | -0.89                                  | -1.38                                  | -2.26                                   | -1.50                                   | -0.89                              | -1.38                               | -2.26                               | -1.50                                | -1.50                                |



|                      |      |       |       |       |       |   |   |       |      |      |      |       |       |       |       |
|----------------------|------|-------|-------|-------|-------|---|---|-------|------|------|------|-------|-------|-------|-------|
| miR-31-5p            | 1134 | 4.08  | 6.31  | 7.16  | 7.46  | 2 | 2 | 1.80  | 2.60 | 3.21 | 2.72 | -0.73 | -1.54 | -1.19 | -1.01 |
| miR-31-5p PREP       |      | 4.08  | 6.31  | 7.16  | 7.46  | 2 | 2 | 1.80  | 2.60 | 3.21 | 2.72 | -1.15 | -1.61 | -1.34 | -1.59 |
| miR-141-5f CREB4     |      |       |       |       |       | 1 | 2 |       |      |      |      | -0.59 | -0.62 | -1.12 | -0.95 |
| miR-141-5f AD03      | 1.58 |       |       | 14.34 | 16.82 | 1 | 2 |       | 1.07 | 1.02 | 2.43 | -0.80 | -0.92 | -1.09 | -0.89 |
| miR-15b-3f MCF2L     | 1.58 |       |       | 14.34 | 16.82 | 1 | 2 |       | 1.07 | 1.02 | 2.43 | -0.80 | -0.92 | -1.09 | -0.89 |
| miR-15b-3f RASGEF1B  | 2.47 | 18.49 |       |       | 19.85 | 1 | 1 |       | 0.77 | 1.17 | 1.09 | -0.92 | -1.72 | -1.12 | -1.31 |
| miR-15b-3f NOTCH2    | 2.47 | 18.49 |       |       | 19.85 | 2 | 1 |       | 0.77 | 1.17 | 1.09 | -0.89 | -1.06 | -0.67 | -0.71 |
| miR-15b-3f CD69      | 2.47 | 18.49 |       |       | 19.85 | 2 | 1 |       | 0.77 | 1.17 | 1.09 | -1.57 | -1.38 | -0.92 | -1.02 |
| miR-15b-3f CCDC64    | 2.47 | 18.49 |       |       | 19.85 | 2 | 1 |       | 0.77 | 1.17 | 1.09 | -0.95 | -1.03 | -0.92 | -0.71 |
| miR-15b-3f CAS21     | 2.47 | 18.49 |       |       | 19.85 | 2 | 1 |       | 0.77 | 1.17 | 1.09 | -0.80 | -1.34 | -0.63 | -1.13 |
| miR-20a-5f MCF2L     | 2.59 | 13.86 | 20.00 |       | 20.00 | 2 | 2 |       | 0.79 | 1.10 | 3.00 | -0.92 | -1.72 | -0.67 | -1.09 |
| miR-20a-5f CD69      | 2.59 | 13.86 | 20.00 |       | 20.00 | 2 | 2 |       | 0.79 | 1.10 | 3.00 | -1.57 | -1.38 | -0.92 | -0.71 |
| miR-18a-5f NOTCH2    | 1.53 |       |       |       | 6.31  | 1 | 1 |       | 0.79 |      | 0.64 | -0.89 | -1.06 | -0.67 | -0.89 |
| miR-18a-5f AD03      | 1.53 |       |       |       | 6.31  | 1 | 1 |       | 0.79 |      | 0.64 | -0.62 | -1.12 | -1.12 | -0.89 |
| miR-21-3p SECISBP2L  | 1.98 | 13.07 |       |       | 15.30 | 2 | 1 | 1.29  | 2.75 |      | 2.71 | -0.78 | -1.02 | -1.34 | -1.13 |
| miR-21-5p SECISBP2L  | 1.98 | 13.07 | 7.56  |       | 15.30 | 2 | 2 | 0.97  | 2.56 | 1.15 | 2.94 | -0.78 | -1.02 | -1.34 | -1.13 |
| miR-21-3p CD69       | 1.98 | 13.07 |       |       | 15.30 | 2 | 1 | 1.29  | 2.56 |      | 2.71 | -1.57 | -1.38 | -0.92 | -0.71 |
| miR-21-5p CD69       | 1.98 | 13.07 | 7.56  |       | 15.30 | 2 | 2 | 0.97  | 2.56 | 1.15 | 2.94 | -1.57 | -1.38 | -0.92 | -0.71 |
| miR-22-3p OGN        | 2.30 | 5.46  |       |       | 8.48  | 2 | 1 |       | 0.86 | 1.10 | 1.81 | -1.21 | -3.11 | -3.42 | -2.07 |
| miR-22-3p SNX30      | 2.30 | 5.46  |       |       | 8.48  | 2 | 1 |       | 0.86 | 1.10 | 1.81 | -0.73 | -0.64 | -1.07 | -0.74 |
| miR-30e-5f MCF2L     | 4.13 |       | 20.00 |       | 20.00 | 1 | 2 |       | 0.67 | 0.82 | 1.36 | -0.92 | -1.72 | -0.67 | -1.09 |
| miR-30e-5f CREB4     | 4.13 |       | 20.00 |       | 20.00 | 1 | 2 |       | 0.67 | 0.82 | 1.36 | -0.59 | -0.92 | -1.10 | -0.95 |
| miR-30e-5f PLEKHA3   | 4.13 |       | 20.00 |       | 20.00 | 1 | 2 |       | 0.67 | 0.82 | 1.36 | -0.75 | -1.14 | -1.14 | -0.80 |
| miR-30e-5f GATM      | 4.13 |       | 20.00 |       | 20.00 | 1 | 1 |       | 0.67 | 0.82 | 1.36 | -0.97 | -1.24 | -1.46 | -0.74 |
| miR-30e-5f SMX30     | 4.13 |       | 20.00 |       | 20.00 | 1 | 2 |       | 0.67 | 0.82 | 1.36 | -0.73 | -0.64 | -1.07 | -0.86 |
| miR-30e-5f MFSO6     | 4.13 |       |       |       | 20.00 | 1 | 1 |       | 0.67 | 0.82 | 1.36 | -0.60 | -1.02 | -1.10 | -0.95 |
| miR-340-5f CREB4     | 2.54 |       |       |       | 20.00 | 1 | 1 |       | 1.36 | 1.84 | 1.68 | -0.59 | -1.02 | -1.10 | -0.95 |
| miR-340-5f SECISBP2L | 2.54 |       | 13.01 |       | 20.00 | 2 | 1 |       | 1.36 | 1.84 | 1.68 | -0.78 | -1.02 | -1.34 | -1.13 |
| miR-340-5f PLEKHA3   | 2.54 |       |       |       | 20.00 | 2 | 1 |       | 1.36 | 1.84 | 1.68 | -0.75 | -1.38 | -0.92 | -0.71 |
| miR-340-5f CD69      | 2.54 |       | 13.01 |       | 20.00 | 2 | 1 |       | 1.36 | 1.84 | 1.68 | -1.57 | -1.38 | -0.92 | -0.71 |
| miR-340-5f AF3       | 2.54 |       |       |       | 20.00 | 2 | 1 |       | 1.36 | 1.84 | 1.68 | -0.97 | -1.38 | -0.92 | -0.80 |
| miR-340-5f CCDC64    | 2.54 |       | 13.01 |       | 20.00 | 2 | 1 |       | 1.36 | 1.84 | 1.68 | -0.95 | -1.03 | -1.02 | -1.02 |
| miR-340-5f CAS21     | 2.54 |       | 13.01 |       | 20.00 | 2 | 1 |       | 1.36 | 1.84 | 1.68 | -0.80 | -1.34 | -0.63 | -1.13 |
| miR-411-5f CREB4     | 1.83 |       |       |       | 1.84  | 2 | 1 |       | 0.92 | 0.92 | 1.74 | -0.59 | -1.10 | -1.10 | -0.95 |
| miR-411-5f CD200     | 1.83 |       |       |       | 1.84  | 2 | 1 |       | 0.92 | 0.92 | 1.74 | -0.81 | -1.52 | -1.34 | -1.09 |
| let-7f-5p SECISBP2L  | 1.18 | 13.15 |       |       | 20.00 | 1 | 1 | 0.64  | 0.65 | 0.83 | 0.91 | -0.78 | -1.02 | -1.34 | -1.13 |
| let-7f-5p SECISBP2L  |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.65 | 0.83 | 0.91 | -0.66 | -1.02 | -1.34 | -1.13 |
| let-7f-5p SECISBP2L  |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.65 | 0.83 | 0.91 | -0.78 | -1.02 | -1.34 | -1.13 |
| let-7f-5p BTG2       |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.65 | 0.83 | 0.91 | -1.54 | -1.54 | -0.59 | -0.59 |
| let-7f-5p BTG2       |      | 13.15 |       |       | 20.00 | 1 | 1 | 0.64  | 0.65 | 0.82 | 0.66 | -1.54 | -1.54 | -0.59 | -0.59 |
| let-7f-5p NOVA1      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.65 | 0.82 | 0.66 | -1.63 | -1.63 | -4.29 | -1.97 |
| let-7f-5p NOVA1      |      | 13.15 |       |       | 20.00 | 1 | 1 | 0.64  | 0.65 | 0.82 | 0.66 | -1.63 | -1.63 | -4.29 | -1.97 |
| let-7f-5p NOVA1      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.65 | 0.82 | 0.66 | -1.63 | -1.63 | -4.29 | -1.97 |
| let-7f-5p NOVA1      |      | 13.15 |       |       | 20.00 | 1 | 1 | 0.64  | 0.65 | 0.82 | 0.66 | -1.63 | -1.63 | -4.29 | -1.97 |
| let-7f-5p SCAR3      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.65 | 0.82 | 0.66 | -0.94 | -0.94 | -3.53 | -1.23 |
| let-7f-5p SCAR3      |      | 13.15 |       |       | 20.00 | 1 | 1 | 0.64  | 0.65 | 0.82 | 0.66 | -0.94 | -0.94 | -3.53 | -1.23 |
| let-7f-5p FBXO32     |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.83 | 0.91 | 0.91 | -1.39 | -1.39 | -2.03 | -2.03 |
| let-7f-5p FBXO32     |      | 13.15 |       |       | 20.00 | 1 | 1 | -0.79 | 0.82 | 0.91 | 0.60 | -1.39 | -1.39 | -2.37 | -2.37 |
| let-7f-5p LPH        |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.83 | 0.91 | 0.60 | -1.61 | -2.48 | -1.53 | -1.53 |
| let-7f-5p LPH        |      | 13.15 |       |       | 20.00 | 1 | 1 | 0.64  | 0.65 | 0.83 | 0.66 | -1.61 | -2.48 | -1.53 | -1.53 |
| let-7f-5p LPH        |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.65 | 0.82 | 0.60 | -1.61 | -2.48 | -1.53 | -1.53 |
| let-7f-5p LPH        |      | 13.15 |       |       | 20.00 | 1 | 1 | -1.61 | 0.82 | 0.91 | 0.60 | -1.61 | -2.48 | -1.53 | -1.53 |
| let-7f-5p ADCY9      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.83 | 0.91 | 0.60 | -0.71 | -1.01 | -1.01 | -1.01 |
| let-7f-5p ADCY9      |      | 13.15 |       |       | 20.00 | 1 | 1 | 0.64  | 0.65 | 0.82 | 0.66 | -0.71 | -1.01 | -1.01 | -1.01 |
| let-7f-5p ADCY9      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.82 | 0.91 | 0.60 | -0.71 | -1.01 | -1.01 | -1.01 |
| let-7f-5p ADCY9      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.82 | 0.91 | 0.60 | -0.71 | -1.01 | -1.01 | -1.01 |
| let-7f-5p MLT14      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.83 | 0.91 | 0.60 | -0.63 | -1.01 | -1.01 | -0.90 |
| let-7f-5p MLT14      |      | 13.15 |       |       | 20.00 | 1 | 1 | 0.64  | 0.65 | 0.83 | 0.66 | -0.63 | -1.01 | -1.01 | -0.90 |
| let-7f-5p MLT14      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.82 | 0.91 | 0.60 | -0.63 | -1.01 | -1.01 | -0.90 |
| let-7f-5p MLT14      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.82 | 0.91 | 0.60 | -0.63 | -1.01 | -1.01 | -0.90 |
| let-7f-5p RORC       |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.82 | 0.91 | 0.60 | -1.05 | -1.27 | -1.09 | -1.09 |
| let-7f-5p RORC       |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.82 | 0.91 | 0.60 | -1.05 | -1.27 | -1.09 | -1.09 |
| let-7f-5p RORC       |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.82 | 0.91 | 0.60 | -1.05 | -1.27 | -1.09 | -1.09 |
| let-7f-5p RORC       |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.82 | 0.91 | 0.60 | -1.05 | -1.27 | -1.09 | -1.09 |
| let-7f-5p THRSBP     |      | 13.15 |       |       | 20.00 | 1 | 1 | 0.64  | 0.65 | 0.83 | 0.66 | -2.83 | -2.83 | -5.69 | -4.42 |
| let-7f-5p THRSBP     |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.65 | 0.83 | 0.66 | -2.83 | -2.83 | -5.69 | -4.42 |
| let-7f-5p THRSBP     |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.65 | 0.83 | 0.66 | -2.83 | -2.83 | -5.69 | -4.42 |
| let-7f-5p THRSBP     |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.65 | 0.83 | 0.66 | -2.83 | -2.83 | -5.69 | -4.42 |
| let-7f-5p DTX4       |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.83 | 0.91 | 0.60 | -1.30 | -2.71 | -1.14 | -1.14 |
| let-7f-5p DTX4       |      | 13.15 |       |       | 20.00 | 1 | 1 | 0.64  | 0.65 | 0.83 | 0.66 | -1.30 | -2.71 | -1.14 | -1.14 |
| let-7f-5p DTX4       |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.82 | 0.91 | 0.60 | -1.30 | -2.71 | -1.14 | -1.14 |
| let-7f-5p DTX4       |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.82 | 0.91 | 0.60 | -1.30 | -2.71 | -1.14 | -1.14 |
| let-7f-5p CGNL1      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.83 | 0.91 | 0.60 | -1.34 | -2.05 | -1.10 | -0.74 |
| let-7f-5p CGNL1      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.83 | 0.91 | 0.60 | -1.34 | -2.05 | -1.10 | -0.74 |
| let-7f-5p CGNL1      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.83 | 0.91 | 0.60 | -1.34 | -2.05 | -1.10 | -0.74 |
| let-7f-5p CGNL1      |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.83 | 0.91 | 0.60 | -1.34 | -2.05 | -1.10 | -0.74 |
| let-7f-5p EGK3       |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.83 | 0.91 | 0.60 | -1.23 | -2.02 | -1.27 | -1.27 |
| let-7f-5p EGK3       |      | 13.15 |       |       | 20.00 | 1 | 1 |       | 0.83 | 0.91 | 0.60 | -1.23 | -2.02 | -1.27 | -1.27 |







|                      |       |       |   |   |      |     |      |      |       |       |
|----------------------|-------|-------|---|---|------|-----|------|------|-------|-------|
| miR-141-5f-PGRMC2    | 17.36 | 16.82 | 1 | 1 | 1.07 | 102 | 1.65 | 2.43 | -1.05 | -0.69 |
| miR-200a-5f-PGRMC2   | 17.36 | 16.82 | 1 | 1 | 1.07 | 108 | 2.51 | 1.74 | -1.05 | -0.69 |
| miR-141-5f-CXCL12    | 17.36 | 16.82 | 1 | 2 | 1.07 | 102 | 1.65 | 2.43 | -1.01 | -4.64 |
| miR-200a-5f-CXCL12   | 17.36 | 16.82 | 1 | 2 | 1.07 | 108 | 2.51 | 1.74 | -1.01 | -2.18 |
| miR-141-5f-ATP6V1C2  | 17.36 | 16.82 | 1 | 2 | 1.07 | 102 | 1.65 | 2.43 | -0.96 | -4.64 |
| miR-200a-5f-ATP6V1C2 | 17.36 | 16.82 | 1 | 2 | 1.07 | 108 | 2.51 | 1.74 | -0.96 | -2.34 |
| miR-141-5f-PDZD2     | 17.36 | 16.82 | 1 | 1 | 1.07 | 102 | 1.65 | 2.43 | -1.11 | -3.33 |
| miR-200a-5f-PDZD2    | 17.36 | 16.82 | 1 | 1 | 1.07 | 108 | 2.51 | 1.74 | -1.11 | -0.71 |
| miR-141-5f-TNFS1     | 17.36 | 16.82 | 1 | 2 | 1.07 | 102 | 1.65 | 2.43 | -1.38 | -0.71 |
| miR-200a-5f-TNFS1    | 17.36 | 16.82 | 1 | 2 | 1.07 | 108 | 2.51 | 1.74 | -1.38 | -1.50 |
| miR-141-5f-TRIM2     | 17.36 | 16.82 | 1 | 2 | 1.07 | 102 | 1.65 | 2.43 | -0.92 | -2.26 |
| miR-200a-5f-TRIM2    | 17.36 | 16.82 | 1 | 2 | 1.07 | 108 | 2.51 | 1.74 | -0.92 | -1.50 |
| miR-141-5f-28TRB20   | 17.36 | 16.82 | 1 | 2 | 1.07 | 102 | 1.65 | 2.43 | -0.92 | -1.06 |
| miR-200a-5f-28TRB20  | 17.36 | 16.82 | 1 | 2 | 1.07 | 108 | 2.51 | 1.74 | -0.97 | -1.32 |
| miR-141-5f-GPD1      | 17.36 | 16.82 | 1 | 2 | 1.07 | 102 | 1.65 | 2.43 | -3.05 | -5.28 |
| miR-200a-5f-GPD1     | 17.36 | 16.82 | 1 | 2 | 1.07 | 108 | 2.51 | 1.74 | -3.05 | -3.18 |
| miR-141-5f-FOXK1     | 17.36 | 16.82 | 1 | 1 | 1.07 | 108 | 2.51 | 2.43 | -2.45 | -1.22 |
| miR-200a-5f-FOXK1    | 17.36 | 16.82 | 1 | 1 | 1.07 | 108 | 2.51 | 1.74 | -2.45 | -1.22 |
| miR-141-5f-HMGC51    | 17.36 | 16.82 | 1 | 1 | 1.07 | 102 | 1.65 | 2.43 | -2.08 | -0.71 |
| miR-200a-5f-HMGC51   | 17.36 | 16.82 | 1 | 1 | 1.07 | 108 | 2.51 | 1.74 | -2.08 | -0.71 |
| miR-141-5f-KALRN     | 17.36 | 16.82 | 1 | 1 | 1.07 | 102 | 1.65 | 2.43 | -0.72 | -1.25 |
| miR-200a-5f-KALRN    | 17.36 | 16.82 | 1 | 1 | 1.07 | 108 | 2.51 | 1.74 | -0.72 | -1.25 |
| miR-141-5f-CCDC80    | 17.36 | 16.82 | 1 | 1 | 1.07 | 102 | 1.65 | 2.43 | -1.79 | -1.83 |
| miR-200a-5f-CCDC80   | 17.36 | 16.82 | 1 | 1 | 1.07 | 108 | 2.51 | 1.74 | -1.79 | -1.83 |
| miR-141-5f-PPARA     | 17.36 | 16.82 | 1 | 2 | 1.07 | 102 | 1.65 | 2.43 | -1.14 | -2.09 |
| miR-200a-5f-PPARA    | 17.36 | 16.82 | 1 | 2 | 1.07 | 108 | 2.51 | 1.74 | -1.14 | -2.09 |
| miR-141-5f-SEMA6A    | 17.36 | 16.82 | 1 | 2 | 1.07 | 102 | 1.65 | 2.43 | -1.07 | -2.17 |
| miR-200a-5f-SEMA6A   | 17.36 | 16.82 | 1 | 2 | 1.07 | 108 | 2.51 | 1.74 | -1.07 | -2.17 |
| miR-15a-5f-MCF2L     | 18.49 | 19.85 | 1 | 1 | 1.07 | 149 | 1.99 | 1.34 | -1.72 | -2.05 |
| miR-16-5f-MCF2L      | 18.49 | 19.85 | 1 | 1 | 1.07 | 107 | 1.65 | 2.43 | -0.67 | -1.09 |
| miR-15a-5f-PDK4      | 18.49 | 19.85 | 1 | 1 | 1.07 | 149 | 1.99 | 1.34 | -2.07 | -1.09 |
| miR-16-5f-PDK4       | 18.49 | 19.85 | 1 | 1 | 1.07 | 107 | 1.65 | 2.43 | -2.07 | -2.19 |
| miR-15b-3f-PDK4      | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -2.07 | -2.19 |
| miR-15a-5f-8T62      | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -1.54 | -0.59 |
| miR-16-5f-8T62       | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -1.54 | -0.59 |
| miR-15b-3f-8T62      | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -1.54 | -0.59 |
| miR-15a-5f-LUPE      | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -1.91 | -1.21 |
| miR-16-5f-LUPE       | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -1.91 | -1.21 |
| miR-15b-3f-LUPE      | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -1.91 | -1.21 |
| miR-15a-5f-G0S2      | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -2.59 | -1.15 |
| miR-16-5f-G0S2       | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -2.59 | -1.15 |
| miR-15b-3f-G0S2      | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -2.59 | -1.15 |
| miR-15a-5f-SVEP1     | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -1.76 | -2.36 |
| miR-16-5f-SVEP1      | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -1.76 | -0.97 |
| miR-15b-3f-SVEP1     | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -1.76 | -0.97 |
| miR-15a-5f-NOTCH2    | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -1.06 | -0.67 |
| miR-16-5f-NOTCH2     | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -1.06 | -0.67 |
| miR-15b-3f-NOTCH2    | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -1.06 | -0.67 |
| miR-15a-5f-CD69      | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -1.38 | -0.92 |
| miR-16-5f-CD69       | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -1.38 | -0.92 |
| miR-15b-3f-CD69      | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -1.38 | -0.92 |
| miR-15a-5f-PDCD4     | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -0.76 | -0.77 |
| miR-16-5f-PDCD4      | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -0.76 | -0.77 |
| miR-15b-3f-PDCD4     | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -0.76 | -0.77 |
| miR-15a-5f-CACNB1    | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -0.87 | -0.77 |
| miR-16-5f-CACNB1     | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -0.87 | -0.77 |
| miR-15b-3f-CACNB1    | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -0.87 | -0.77 |
| miR-15a-5f-TACC1     | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -0.96 | -0.93 |
| miR-16-5f-TACC1      | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -0.96 | -0.93 |
| miR-15b-3f-TACC1     | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -0.96 | -0.93 |
| miR-15a-5f-KDSR      | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -0.66 | -0.93 |
| miR-16-5f-KDSR       | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -0.66 | -0.93 |
| miR-15b-3f-KDSR      | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -0.66 | -0.93 |
| miR-15a-5f-ADAMTS13  | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -1.51 | -1.75 |
| miR-16-5f-ADAMTS13   | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -1.51 | -1.75 |
| miR-15b-3f-ADAMTS13  | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -1.51 | -1.75 |
| miR-15a-5f-SEMA3D    | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -1.68 | -1.84 |
| miR-16-5f-SEMA3D     | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -1.68 | -1.84 |
| miR-15b-3f-SEMA3D    | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -1.68 | -1.84 |
| miR-15a-5f-FASN      | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -2.20 | -0.70 |
| miR-16-5f-FASN       | 18.49 | 19.85 | 1 | 1 | 0.77 | 107 | 1.65 | 2.43 | -2.20 | -0.70 |
| miR-15b-3f-FASN      | 18.49 | 19.85 | 1 | 1 | 0.77 | 117 | 1.17 | 1.09 | -2.20 | -0.70 |
| miR-15a-5f-GABARAP1  | 18.49 | 19.85 | 1 | 1 | 0.77 | 149 | 1.99 | 1.34 | -1.27 | -1.50 |



|            |           |       |       |   |   |   |      |      |       |       |       |       |
|------------|-----------|-------|-------|---|---|---|------|------|-------|-------|-------|-------|
| mir-1b-5p  | GABARAPL1 | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -0.89 | -1.27 | -1.53 | -1.50 |
| mir-15b-3f | GABARAPL1 | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -0.89 | -1.27 | -1.53 | -1.50 |
| mir-15a-5f | REIN      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.26 | -1.50 | -1.53 | -1.50 |
| mir-16-5p  | REIN      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.26 | -1.50 | -1.50 | -1.10 |
| mir-15a-5f | LRIG1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.34 | -0.72 | -1.50 | -1.26 | -1.10 |
| mir-16-5p  | LRIG1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -0.89 | -1.26 | -1.24 | -1.26 |
| mir-15b-3f | LRIG1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -0.72 | -0.89 | -1.24 | -1.26 |
| mir-15a-5f | RNF125    | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -0.89 | -1.24 | -1.24 | -1.24 |
| mir-16-5p  | RNF125    | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -0.62 | -1.59 | -0.62 | -1.59 |
| mir-15b-3f | RNF125    | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -0.81 | -1.59 | -0.81 | -1.59 |
| mir-15a-5f | FRY       | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -0.81 | -1.59 | -0.81 | -1.59 |
| mir-16-5p  | FRY       | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -0.89 | -0.72 | -1.08 | -0.72 |
| mir-15b-3f | FRY       | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.07 | -0.89 | -0.72 | -1.08 | -0.72 |
| mir-15a-5f | PDI1      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.34 | -1.12 | -0.92 | -2.62 | -1.12 |
| mir-16-5p  | PDI1      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -0.92 | -1.03 | -1.02 | -1.03 |
| mir-15b-3f | PDI1      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -0.95 | -1.03 | -1.02 | -1.03 |
| mir-15a-5f | CCDC64    | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.60 | -1.60 | -0.89 | -0.89 |
| mir-16-5p  | CCDC64    | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.77 | -1.77 | -0.82 | -0.82 |
| mir-15a-5f | LMOD1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.60 | -1.60 | -0.89 | -0.89 |
| mir-16-5p  | LMOD1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.77 | -1.77 | -0.89 | -0.89 |
| mir-15b-3f | LMOD1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -0.82 | -0.92 | -2.62 | -1.40 |
| mir-15a-5f | TRIM2     | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.60 | -1.60 | -1.06 | -1.06 |
| mir-16-5p  | TRIM2     | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -0.92 | -1.50 | -1.06 | -1.06 |
| mir-15b-3f | TRIM2     | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -0.92 | -1.50 | -1.06 | -1.06 |
| mir-15a-5f | TGFB3     | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.86 | -1.88 | -1.27 | -1.88 |
| mir-16-5p  | TGFB3     | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.86 | -1.88 | -1.27 | -1.88 |
| mir-15b-3f | TGFB3     | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.27 | -1.88 | -1.27 | -1.88 |
| mir-15a-5f | PANK1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.75 | -1.75 | -1.56 | -1.56 |
| mir-16-5p  | PANK1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -0.92 | -1.50 | -1.06 | -1.06 |
| mir-15b-3f | PANK1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -0.92 | -1.50 | -1.06 | -1.06 |
| mir-15a-5f | PREP      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.85 | -1.85 | -1.85 | -1.85 |
| mir-16-5p  | PREP      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.59 | -1.61 | -3.24 | -1.59 |
| mir-15b-3f | PREP      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.61 | -1.61 | -3.24 | -1.61 |
| mir-15a-5f | ACSL1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.59 | -1.34 | -3.24 | -1.59 |
| mir-16-5p  | ACSL1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.42 | -1.18 | -1.42 | -1.42 |
| mir-15b-3f | ACSL1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.09 | -1.18 | -1.42 | -1.42 |
| mir-15a-5f | FFCAB4A   | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.81 | -1.81 | -1.81 | -1.81 |
| mir-16-5p  | FFCAB4A   | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.19 | -1.81 | -1.81 | -1.81 |
| mir-15b-3f | FFCAB4A   | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.34 | -1.81 | -1.81 | -1.81 |
| mir-15a-5f | FFCAB4A   | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.13 | -1.63 | -0.63 | -0.63 |
| mir-16-5p  | CASZ1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.34 | -1.34 | -0.63 | -0.63 |
| mir-15a-5f | CASZ1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.34 | -1.34 | -0.63 | -0.63 |
| mir-16-5p  | CASZ1     | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.34 | -1.34 | -0.63 | -0.63 |
| mir-15a-5f | GRAMD3    | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -0.62 | -1.00 | -0.62 | -0.80 |
| mir-16-5p  | GRAMD3    | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -0.62 | -1.00 | -0.62 | -0.80 |
| mir-15b-3f | GRAMD3    | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15a-5f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.46 | -1.32 | -1.46 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.46 | -1.32 | -1.46 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.46 | -1.32 | -1.46 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.07 | 1.34 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.17 | 1.09 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-16-5p  | USP2      | 18.49 | 19.85 | 1 | 1 | 1 | 1.49 | 1.99 | -1.32 | -1.32 | -1.32 | -1.32 |
| mir-15b-3f | USP2      |       |       |   |   |   |      |      |       |       |       |       |



|                    |       |       |       |   |   |      |      |      |      |       |       |       |
|--------------------|-------|-------|-------|---|---|------|------|------|------|-------|-------|-------|
| miR-93-5p USP54    | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.66 | 1.54 | 1.12 | -0.86 | -0.87 | -0.92 |
| miR-106b-1 USP54   | 13.86 |       | 20.00 | 1 | 1 |      | 0.98 |      | 2.59 | -0.86 | -0.87 | -0.92 |
| miR-17-5p TACCT    | 13.86 | 20.00 | 20.00 | 1 | 2 | 0.77 | 1.15 | 2.32 | 2.41 | -0.96 | -1.96 | -0.93 |
| miR-20a-5f TACCT   | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 1.10 | 1.90 | 3.00 | -0.96 | -1.96 | -0.93 |
| miR-93-5p TACCT    | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.66 | 1.54 | 1.12 | -0.96 | -1.96 | -0.93 |
| miR-106b-1 TACCT   | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 0.98 |      | 2.59 | -0.96 | -1.96 | -0.93 |
| miR-17-5p ITPKB    | 13.86 | 20.00 | 20.00 | 1 | 2 | 0.77 | 1.15 | 2.32 | 2.41 | -0.68 | -1.46 | -1.33 |
| miR-20a-5f ITPKB   | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 1.10 | 1.90 | 3.00 | -0.68 | -1.46 | -1.33 |
| miR-93-5p ITPKB    | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.66 | 1.54 | 1.12 | -0.68 | -1.46 | -1.33 |
| miR-106b-1 ITPKB   | 13.86 |       | 20.00 | 1 | 1 |      | 0.98 |      | 2.59 | -0.68 | -1.46 | -1.33 |
| miR-17-5p LRP4     | 13.86 |       | 20.00 | 1 | 1 | 0.77 | 1.15 | 2.32 | 2.41 | -1.24 | -0.76 | -0.76 |
| miR-20a-5f LRP4    | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 1.10 | 1.90 | 3.00 | -1.24 | -0.76 | -0.76 |
| miR-93-5p LRP4     | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 0.66 | 1.54 | 1.12 | -1.24 | -0.76 | -0.76 |
| miR-106b-1 LRP4    | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 0.98 |      | 2.59 | -1.24 | -0.76 | -0.76 |
| miR-17-5p CACD2    | 13.86 | 20.00 | 20.00 | 1 | 2 | 0.77 | 1.15 | 2.32 | 2.41 | -0.79 | -0.66 | -1.29 |
| miR-20a-5f CACD2   | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 1.10 | 1.90 | 3.00 | -0.79 | -0.66 | -1.29 |
| miR-93-5p CACD2    | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.66 | 1.54 | 1.12 | -0.79 | -0.66 | -1.29 |
| miR-106b-1 CACD2   | 13.86 | 20.00 | 20.00 | 1 | 1 | 1.59 | 0.98 |      | 2.59 | -0.79 | -0.66 | -1.29 |
| miR-20a-5f EGR2    | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 1.10 | 1.90 | 3.00 | -2.05 | -2.57 | -2.38 |
| miR-93-5p EGR2     | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.66 | 1.54 | 1.12 | -2.05 | -2.57 | -2.38 |
| miR-106b-1 EGR2    | 13.86 |       | 20.00 | 1 | 1 |      | 0.98 |      | 2.59 | -2.05 | -2.57 | -2.38 |
| miR-20a-5f EGR3    | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 1.10 | 1.90 | 3.00 | -2.02 | -1.27 | -1.27 |
| miR-93-5p EGR3     | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 0.66 | 1.54 | 1.12 | -2.02 | -1.27 | -1.27 |
| miR-106b-1 EGR3    | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 0.98 |      | 2.59 | -2.02 | -1.27 | -1.27 |
| miR-20a-5f LRG1    | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 1.10 | 1.90 | 3.00 | -0.89 | -1.24 | -1.26 |
| miR-93-5p LRG1     | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.66 | 1.54 | 1.12 | -0.89 | -1.24 | -1.26 |
| miR-106b-1 LRG1    | 13.86 | 20.00 | 20.00 | 1 | 1 | 0.77 | 0.98 |      | 2.59 | -0.89 | -1.24 | -1.26 |
| miR-17-5p GPR133   | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 1.15 | 2.32 | 2.41 | -1.86 | -3.08 | -1.25 |
| miR-20a-5f GPR133  | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 1.10 | 1.90 | 3.00 | -1.86 | -3.08 | -1.25 |
| miR-93-5p GPR133   | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.66 | 1.54 | 1.12 | -1.86 | -3.08 | -1.25 |
| miR-106b-1 GPR133  | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 0.98 |      | 2.59 | -1.86 | -3.08 | -1.25 |
| miR-20a-5f TNF1    | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 1.10 | 1.90 | 3.00 | -1.86 | -3.08 | -1.25 |
| miR-93-5p TNF1     | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.66 | 1.54 | 1.12 | -1.86 | -3.08 | -1.25 |
| miR-106b-1 TNF1    | 13.86 |       | 20.00 | 1 | 1 |      | 0.98 |      | 2.59 | -1.86 | -3.08 | -1.25 |
| miR-20a-5f SH3BP5  | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 1.10 | 1.90 | 3.00 | -1.39 | -0.81 | -0.81 |
| miR-17-5p SH3BP5   | 13.86 | 20.00 | 20.00 | 1 | 1 | 0.77 | 1.15 | 2.32 | 2.41 | -1.11 | -0.75 | -0.75 |
| miR-20a-5f PARAC18 | 13.86 |       | 20.00 | 1 | 1 |      | 0.66 | 1.54 | 1.12 | -1.11 | -0.75 | -0.75 |
| miR-93-5p PARAC18  | 13.86 |       | 20.00 | 1 | 1 |      | 0.98 |      | 2.59 | -1.11 | -0.75 | -0.75 |
| miR-106b-1 PARAC18 | 13.86 | 20.00 | 20.00 | 1 | 1 | 0.77 | 1.15 | 2.32 | 2.41 | -1.14 | -2.09 | -1.84 |
| miR-17-5p PARAC18  | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 1.10 | 1.90 | 3.00 | -1.14 | -2.09 | -1.84 |
| miR-20a-5f PARAC18 | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.66 | 1.54 | 1.12 | -1.14 | -2.09 | -1.84 |
| miR-93-5p PARAC18  | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.98 |      | 2.59 | -1.14 | -2.09 | -1.84 |
| miR-106b-1 PARAC18 | 13.86 | 20.00 | 20.00 | 1 | 1 | 0.77 | 1.15 | 2.32 | 2.41 | -1.31 | -0.99 | -1.35 |
| miR-17-5p SLC6A3   | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 1.10 | 1.90 | 3.00 | -1.31 | -0.99 | -1.35 |
| miR-20a-5f SLC6A3  | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.66 | 1.54 | 1.12 | -1.31 | -0.99 | -1.35 |
| miR-93-5p SLC6A3   | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.98 |      | 2.59 | -1.31 | -0.99 | -1.35 |
| miR-106b-1 SLC6A3  | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 1.10 | 1.90 | 3.00 | -2.48 | -2.40 | -1.92 |
| miR-20a-5f SYNM1   | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.66 | 1.54 | 1.12 | -2.48 | -2.40 | -1.92 |
| miR-93-5p SYNM1    | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.98 |      | 2.59 | -2.48 | -2.40 | -1.92 |
| miR-106b-1 SYNM1   | 13.86 |       | 20.00 | 1 | 1 | 0.77 | 1.15 | 2.32 | 2.41 | -0.81 | -1.76 | -1.76 |
| miR-17-5p FAM13A   | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 1.10 | 1.90 | 3.00 | -0.81 | -1.76 | -1.76 |
| miR-20a-5f FAM13A  | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 0.66 | 1.54 | 1.12 | -0.81 | -1.76 | -1.76 |
| miR-93-5p FAM13A   | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 0.98 |      | 2.59 | -0.81 | -1.76 | -1.76 |
| miR-106b-1 FAM13A  | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 1.10 | 1.90 | 3.00 | -0.81 | -1.76 | -1.76 |
| miR-20a-5f CH2     | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 0.66 | 1.54 | 1.12 | -0.82 | -0.76 | -0.76 |
| miR-93-5p CH2      | 13.86 | 20.00 | 20.00 | 1 | 1 |      | 1.10 | 1.90 | 3.00 | -0.82 | -0.76 | -0.76 |
| miR-20a-5f NF18    | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.66 | 1.54 | 1.12 | -1.97 | -0.81 | -0.99 |
| miR-93-5p NF18     | 13.86 | 20.00 | 20.00 | 1 | 2 |      | 0.98 |      | 2.59 | -1.97 | -0.81 | -0.99 |
| miR-106b-1 NF18    | 13.86 |       | 20.00 | 1 | 1 |      | 1.10 | 1.90 | 3.00 | -1.97 | -0.81 | -0.99 |
| miR-192-5f ALCAM   | 0.87  |       | 1.14  | 1 | 1 |      | 0.98 |      | 2.59 | -1.04 | -3.06 | -2.26 |
| miR-192-5f ALCAM   | 0.87  |       | 1.14  | 1 | 1 |      | 1.10 | 1.90 | 3.00 | -0.91 | -0.76 | -0.76 |
| miR-21-3p PTEN14   | 13.07 | 7.56  | 15.30 | 1 | 1 | 1.29 | 2.75 | 1.15 | 2.71 | -0.94 | -0.81 | -0.79 |
| miR-21-3p PTEN14   | 13.07 | 7.56  | 15.30 | 1 | 2 | 0.97 | 2.56 | 1.15 | 2.94 | -0.94 | -0.81 | -0.79 |
| miR-21-3p B7G2     | 13.07 |       | 15.30 | 1 | 1 | 1.29 | 2.75 | 1.15 | 2.71 | -1.54 | -0.59 | -0.59 |
| miR-21-3p B7G2     | 13.07 |       | 15.30 | 1 | 1 | 1.29 | 2.75 | 1.15 | 2.94 | -1.54 | -0.59 | -0.59 |
| miR-21-3p B7G2     | 13.07 |       | 15.30 | 1 | 1 | 0.97 | 2.56 | 1.15 | 2.71 | -0.76 | -0.77 | -0.77 |
| miR-21-3p B7G2     | 13.07 |       | 15.30 | 1 | 1 | 1.29 | 2.75 | 1.15 | 2.94 | -0.76 | -0.77 | -0.77 |
| miR-21-3p PDCD4    | 13.07 | 7.56  | 15.30 | 1 | 2 | 0.97 | 2.56 | 1.15 | 2.71 | -0.80 | -1.16 | -0.99 |
| miR-21-3p PDCD4    | 13.07 | 7.56  | 15.30 | 1 | 2 | 0.97 | 2.56 | 1.15 | 2.94 | -0.80 | -1.16 | -0.99 |
| miR-21-3p ARHGAP24 | 13.07 | 7.56  | 15.30 | 1 | 2 | 0.97 | 2.56 | 1.15 | 2.94 | -0.80 | -1.16 | -0.99 |
| miR-21-3p ARHGAP24 | 13.07 | 7.56  | 15.30 | 1 | 2 | 0.97 | 2.56 | 1.15 | 2.94 | -0.80 | -1.16 | -0.99 |
| miR-21-3p MEGF9    | 13.07 |       | 15.30 | 1 | 1 | 1.29 | 2.75 | 1.15 | 2.71 | -0.89 | -0.65 | -0.65 |
| miR-21-3p MEGF9    | 13.07 |       | 15.30 | 1 | 1 | 0.97 | 2.56 | 1.15 | 2.94 | -0.89 | -0.65 | -0.65 |



|                    |       |       |   |   |      |      |      |      |       |       |
|--------------------|-------|-------|---|---|------|------|------|------|-------|-------|
| miR-21-3p PGRMC2   | 13.07 | 15.30 | 1 | 1 | 1.29 | 1.45 | 2.75 | 2.71 | -1.05 | -0.69 |
| miR-21-5p PGRMC2   | 13.07 | 15.30 | 1 | 1 | 0.97 | 1.59 | 2.56 | 2.94 | -1.05 | -0.69 |
| miR-21-3p PDZD2    | 13.07 | 15.30 | 1 | 1 | 1.29 | 1.45 | 2.75 | 2.71 | -1.11 | -0.71 |
| miR-21-5p PDZD2    | 13.07 | 15.30 | 1 | 1 | 0.97 | 1.59 | 2.56 | 2.94 | -1.11 | -0.71 |
| miR-21-3p UFR      | 13.07 | 15.30 | 1 | 1 | 1.29 | 1.45 | 2.75 | 2.71 | -1.23 | -1.46 |
| miR-21-5p UFR      | 13.07 | 15.30 | 1 | 1 | 0.97 | 1.59 | 2.56 | 2.94 | -1.23 | -1.46 |
| miR-21-5p SESTD1   | 13.07 | 7.56  | 1 | 1 | 0.97 | 1.59 | 2.56 | 2.94 | -0.73 | -1.02 |
| miR-21-3p SESTD1   | 13.07 | 7.56  | 1 | 1 | 1.29 | 1.45 | 2.75 | 2.71 | -1.14 | -1.84 |
| miR-21-5p PPARG    | 13.07 | 15.30 | 1 | 2 | 0.97 | 1.59 | 2.56 | 2.94 | -0.62 | -2.09 |
| miR-21-3p PPARG    | 13.07 | 15.30 | 1 | 1 | 0.97 | 1.59 | 2.56 | 2.94 | -0.62 | -2.09 |
| miR-21-5p PPARG    | 13.07 | 15.30 | 1 | 1 | 1.29 | 1.45 | 2.75 | 2.71 | -0.81 | -1.76 |
| miR-21-3p FAM13A   | 13.07 | 15.30 | 1 | 1 | 0.97 | 1.59 | 2.56 | 2.94 | -0.81 | -1.76 |
| miR-21-5p FAM13A   | 13.07 | 15.30 | 1 | 1 | 1.29 | 1.45 | 2.75 | 2.71 | -1.14 | -1.84 |
| miR-22-3p NTRK2    | 5.46  | 8.48  | 1 | 1 | 0.86 | 1.10 | 1.81 | 1.81 | -1.80 | -2.52 |
| miR-22-3p MLT4     | 5.46  | 8.48  | 1 | 1 | 0.86 | 1.10 | 1.81 | 1.81 | -1.63 | -1.01 |
| miR-22-3p RGS2     | 5.46  | 8.48  | 1 | 1 | 0.86 | 1.10 | 1.81 | 1.81 | -1.63 | -1.28 |
| miR-22-3p PPARGC1B | 5.46  | 8.48  | 1 | 1 | 0.86 | 1.10 | 1.81 | 1.81 | -1.11 | -0.75 |
| miR-22-3p PPARG    | 5.46  | 8.48  | 1 | 1 | 0.86 | 1.10 | 1.81 | 1.81 | -1.14 | -2.09 |
| miR-22-3p NFIB     | 5.46  | 8.48  | 1 | 1 | 0.86 | 1.10 | 1.81 | 1.81 | -1.97 | -0.81 |
| miR-22-4-5f ISM1   | 6.06  | 4.02  | 1 | 1 | 0.99 | 1.20 | 1.37 | 1.37 | -1.53 | -2.46 |
| miR-22-4-5f FENNA3 | 6.06  | 4.02  | 1 | 1 | 0.99 | 1.20 | 1.37 | 1.37 | -0.73 | -1.55 |
| miR-22-4-5f RFX2   | 6.06  | 4.02  | 1 | 1 | 0.99 | 1.20 | 1.37 | 1.37 | -0.61 | -1.20 |
| miR-22-4-5f SORF   | 6.06  | 4.02  | 1 | 1 | 0.99 | 1.20 | 1.37 | 1.37 | -1.39 | -0.66 |
| miR-22-4-5f SYNGR1 | 6.06  | 4.02  | 1 | 1 | 0.99 | 1.20 | 1.37 | 1.37 | -0.83 | -0.93 |
| miR-24-3p SCAR3    | 7.42  | 17.04 | 1 | 1 |      |      |      |      | -0.94 | -3.53 |
| miR-24-3p AXL      | 7.42  | 17.04 | 1 | 1 |      |      |      |      | -1.03 | -0.92 |
| miR-24-3p CMT      | 7.42  | 17.04 | 1 | 1 |      |      |      |      | -2.11 | -2.11 |
| miR-24-3p PRSS8    | 7.42  | 17.04 | 1 | 1 |      |      |      |      | -0.74 | -1.37 |
| miR-24-3p TNSI     | 7.42  | 17.04 | 1 | 1 |      |      |      |      | -1.38 | -2.26 |
| miR-24-3p SNX30    | 7.42  | 17.04 | 1 | 1 |      |      |      |      | -0.64 | -1.07 |
| miR-24-3p NCALD    | 7.42  | 17.04 | 1 | 1 |      |      |      |      | -1.68 | -1.92 |
| miR-24-3p INSIG1   | 7.42  | 17.04 | 1 | 1 |      |      |      |      | -2.67 | -0.78 |
| miR-24-3p CMMK2B   | 7.42  | 17.04 | 1 | 1 |      |      |      |      | -1.90 | -2.93 |
| miR-24-3p PPARG    | 7.42  | 17.04 | 1 | 1 |      |      |      |      | -1.14 | -1.84 |
| miR-24-3p SEMA6A   | 7.42  | 17.04 | 1 | 1 |      |      |      |      | -1.07 | -2.17 |
| miR-24-3p USP2     | 7.42  | 17.04 | 1 | 1 |      |      |      |      | -0.80 | -1.32 |
| miR-25-3p DENND4C  | 14.34 | 20.00 | 1 | 2 | 0.71 | 0.64 | 0.93 | 0.93 | -0.89 | -0.81 |
| miR-25-3p PTPN14   | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -0.94 | -0.79 |
| miR-25-3p BTG2     | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -1.54 | -0.59 |
| miR-25-3p BCAT2    | 14.34 | 20.00 | 1 | 2 | 0.71 | 0.64 | 0.93 | 0.93 | -1.64 | -1.52 |
| miR-25-3p NOV41    | 14.34 | 20.00 | 1 | 2 | 0.71 | 0.64 | 0.93 | 0.93 | -1.63 | -1.29 |
| miR-25-3p CD69     | 14.34 | 20.00 | 1 | 2 | 0.71 | 0.64 | 0.93 | 0.93 | -1.38 | -4.29 |
| miR-25-3p GPT2     | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -1.41 | -0.92 |
| miR-25-3p ADAMTSL3 | 14.34 | 20.00 | 1 | 2 | 0.71 | 0.64 | 0.93 | 0.93 | -1.51 | -2.03 |
| miR-25-3p PEX3     | 14.34 | 20.00 | 1 | 2 | 0.71 | 0.64 | 0.93 | 0.93 | -0.66 | -1.16 |
| miR-25-3p ITPR1    | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -0.96 | -0.79 |
| miR-25-3p FRV      | 14.34 | 20.00 | 1 | 2 | 0.71 | 0.64 | 0.93 | 0.93 | -0.89 | -1.11 |
| miR-25-3p PDZD2    | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -1.11 | -1.08 |
| miR-25-3p IQGAP2   | 14.34 | 20.00 | 1 | 2 | 0.71 | 0.64 | 0.93 | 0.93 | -1.22 | -0.71 |
| miR-25-3p SNX30    | 14.34 | 20.00 | 1 | 2 | 0.71 | 0.64 | 0.93 | 0.93 | -0.64 | -1.95 |
| miR-25-3p MTF      | 14.34 | 20.00 | 1 | 2 | 0.71 | 0.64 | 0.93 | 0.93 | -0.88 | -1.07 |
| miR-25-3p PPARGC1B | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -1.11 | -1.96 |
| miR-25-3p CXKC5    | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -0.71 | -0.75 |
| miR-25-3p DBT      | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -0.80 | -0.61 |
| miR-25-3p SESTD1   | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -0.73 | -0.64 |
| miR-25-3p KALRN    | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -0.72 | -1.02 |
| miR-25-3p KLF2     | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -0.72 | -1.25 |
| miR-25-3p IDH1     | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -1.30 | -1.22 |
| miR-25-3p ELOVL4   | 14.34 | 20.00 | 1 | 2 | 0.71 | 0.64 | 0.93 | 0.93 | -1.15 | -0.61 |
| miR-25-3p GRAMD3   | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -1.61 | -2.03 |
| miR-25-3p SNZ      | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -0.62 | -1.77 |
| miR-25-3p PDE4D    | 14.34 | 20.00 | 1 | 1 | 0.71 | 0.64 | 0.93 | 0.93 | -0.92 | -1.50 |
| miR-27a-3f GCNT2   | 19.97 | 20.00 | 1 | 1 |      |      |      |      | -1.17 | -0.61 |
| miR-27b-3f GCNT2   | 19.97 | 20.00 | 1 | 1 |      |      |      |      | -1.17 | -0.61 |
| miR-27a-3f GCNT2   | 19.97 | 20.00 | 1 | 1 |      |      |      |      | -2.07 | -0.61 |
| miR-27a-3f PDK4    | 19.97 | 20.00 | 1 | 2 |      |      |      |      | -2.07 | -2.19 |
| miR-27a-3f PDK4    | 19.97 | 20.00 | 1 | 2 |      |      |      |      | -2.07 | -3.16 |
| miR-27a-3f BTG2    | 19.97 | 20.00 | 1 | 1 |      |      |      |      | -1.54 | -0.59 |
| miR-27b-3f BTG2    | 19.97 | 20.00 | 1 | 1 |      |      |      |      | -1.54 | -0.59 |
| miR-27a-3f NOV41   | 19.97 | 20.00 | 1 | 2 |      |      |      |      | -1.63 | -4.29 |
| miR-27b-3f NOV41   | 19.97 | 20.00 | 1 | 2 |      |      |      |      | -1.63 | -1.97 |
| miR-27a-3f FBXO32  | 19.97 | 20.00 | 1 | 2 |      |      |      |      | -1.63 | -2.03 |



|                     |       |       |       |   |   |      |      |      |      |       |       |       |       |
|---------------------|-------|-------|-------|---|---|------|------|------|------|-------|-------|-------|-------|
| miR-27a-3f-ATF3     | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.71 | -3.33 | -2.14 | -2.04 |
| miR-27a-3f-GP12     | 19.97 | 20.00 |       | 1 | 1 |      | 0.86 | 0.95 | 0.82 |       | -1.41 | -2.03 |       |
| miR-27a-3f-EEP1     | 19.97 | 20.00 | 20.00 | 1 | 1 | 0.75 | 0.86 | 1.05 | 0.91 | -1.41 | -2.03 |       |       |
| miR-27b-3f-EEP1     | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -0.67 | -1.45 | -1.20 |       |
| miR-27a-3f-ADAMTS13 | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -0.67 | -1.45 | -1.20 |       |
| miR-27b-3f-ADAMTS13 | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.51 | -1.16 | -1.75 |       |
| miR-27a-3f-DTX4     | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -1.16 | -1.75 | -1.75 |       |
| miR-27b-3f-DTX4     | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.30 | -2.71 | -1.14 |       |
| miR-27a-3f-FBLN5    | 19.97 | 20.00 |       | 1 | 1 | 0.75 | 0.86 | 1.05 | 0.91 | -0.95 | -0.97 | -0.94 |       |
| miR-27a-3f-FALGAPA2 | 19.97 |       | 20.00 | 1 | 1 |      | 0.86 | 0.95 | 0.82 | -0.81 | -0.69 | -0.64 |       |
| miR-27b-3f-FALGAPA2 | 19.97 | 20.00 | 20.00 | 1 | 1 | 0.75 | 0.86 | 1.05 | 0.91 | -0.81 | -0.69 | -0.64 |       |
| miR-27a-3f-FENNA3   | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -0.73 | -1.55 | -2.04 |       |
| miR-27b-3f-FENNA3   | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -0.73 | -1.55 | -2.04 |       |
| miR-27a-3f-CACD2    | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -0.79 | -0.66 | -1.29 |       |
| miR-27b-3f-CACD2    | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -0.79 | -0.66 | -1.29 |       |
| miR-27a-3f-REIN     | 19.97 |       | 20.00 | 1 | 1 |      | 0.86 | 0.95 | 0.82 | -1.26 |       |       |       |
| miR-27a-3f-FEG3     | 19.97 | 20.00 | 20.00 | 1 | 1 |      | 0.86 | 0.95 | 0.82 | -1.23 |       |       |       |
| miR-27b-3f-MEGF9    | 19.97 | 20.00 | 20.00 | 1 | 1 | 0.75 | 0.86 | 1.05 | 0.91 |       |       |       |       |
| miR-27a-3f-MEGF9    | 19.97 | 20.00 | 20.00 | 1 | 1 |      | 0.86 | 0.95 | 0.82 |       |       |       |       |
| miR-27b-3f-FAM173B  | 19.97 |       | 20.00 | 1 | 1 |      | 0.86 | 0.95 | 0.82 | -0.87 | -0.87 | -0.62 |       |
| miR-27a-3f-FAM173B  | 19.97 | 20.00 | 20.00 | 1 | 1 | 0.75 | 0.86 | 1.05 | 0.91 | -0.87 | -0.87 | -0.62 |       |
| miR-27b-3f-GPR133   | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.86 | -3.08 | -1.25 |       |
| miR-27a-3f-GPR133   | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -1.86 | -3.08 | -1.25 |       |
| miR-27a-3f-SEMA3B   | 19.97 | 20.00 |       | 1 | 1 |      | 0.86 | 0.95 | 0.82 | -1.69 |       |       |       |
| miR-27b-3f-TRIM2    | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -0.92 | -1.50 | -1.06 |       |
| miR-27a-3f-CSF1     | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -0.73 | -1.06 | -0.74 |       |
| miR-27b-3f-CSF1     | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -0.73 | -1.06 | -0.74 |       |
| miR-27a-3f-TGFB3    | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.86 | -1.88 | -1.27 |       |
| miR-27b-3f-TGFB3    | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -1.86 | -1.88 | -1.27 |       |
| miR-27a-3f-PANK1    | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.75 | -1.56 | -1.85 |       |
| miR-27b-3f-PANK1    | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -1.75 | -1.56 | -1.85 |       |
| miR-27a-3f-POU2F3   | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -0.82 | -1.20 | -1.08 |       |
| miR-27a-3f-NCALD    | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.68 | -1.92 | -2.11 |       |
| miR-27b-3f-MITF     | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -0.88 | -2.66 | -1.96 |       |
| miR-27b-3f-MITF     | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -0.88 | -2.66 | -1.96 |       |
| miR-27a-3f-LPL      | 19.97 | 20.00 |       | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.20 | -5.42 | -3.12 |       |
| miR-27a-3f-PPARGC1B | 19.97 |       | 20.00 | 1 | 1 |      | 0.86 | 0.95 | 0.82 | -1.11 | -0.75 | -0.75 |       |
| miR-27b-3f-PPARGC1B | 19.97 | 20.00 | 20.00 | 1 | 1 | 0.75 | 0.86 | 1.05 | 0.91 | -1.11 | -0.75 | -0.75 |       |
| miR-27a-3f-GPD1     | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -3.05 | -5.28 | -3.18 |       |
| miR-27b-3f-GPD1     | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -3.05 | -5.28 | -3.18 |       |
| miR-27a-3f-LIFR     | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.23 | -1.46 | -1.50 |       |
| miR-27b-3f-LIFR     | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -1.23 | -1.46 | -1.50 |       |
| miR-27a-3f-HMGCS1   | 19.97 | 20.00 | 20.00 | 1 | 1 |      | 0.86 | 0.95 | 0.82 | -1.13 | -0.71 | -0.71 |       |
| miR-27a-3f-PPARG    | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -2.38 | -3.76 | -2.92 |       |
| miR-27b-3f-PPARG    | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -2.38 | -3.76 | -2.92 |       |
| miR-27a-3f-PPARA    | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.14 | -2.09 | -1.84 |       |
| miR-27b-3f-PPARA    | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -1.14 | -2.09 | -1.84 |       |
| miR-27a-3f-LPIN1    | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.40 | -1.59 | -1.59 |       |
| miR-27b-3f-LPIN1    | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -1.40 | -1.59 | -1.59 |       |
| miR-27a-3f-SEMA6A   | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.07 | -2.17 | -2.05 |       |
| miR-27b-3f-SEMA6A   | 19.97 | 20.00 | 20.00 | 1 | 2 | 0.75 | 0.86 | 1.05 | 0.91 | -1.07 | -2.17 | -2.05 |       |
| miR-27a-3f-ANK2     | 19.97 | 20.00 |       | 1 | 1 | 0.75 | 0.86 | 0.95 | 0.82 | -1.83 | -1.30 |       |       |
| miR-27b-3f-ANK2     | 19.97 | 20.00 |       | 1 | 1 |      | 0.86 | 0.95 | 0.82 | -1.83 | -1.30 |       |       |
| miR-27a-3f-RCAN2    | 19.97 | 20.00 |       | 1 | 1 |      | 0.86 | 0.95 | 0.82 | -0.86 | -1.56 |       |       |
| miR-27b-3f-FAM13A   | 19.97 |       | 20.00 | 1 | 1 |      | 0.86 | 0.95 | 0.82 | -0.81 | -1.76 | -1.76 |       |
| miR-27a-3f-FAM13A   | 19.97 | 20.00 | 20.00 | 1 | 1 | 0.75 | 0.86 | 1.05 | 0.91 | -0.81 | -1.76 | -1.76 |       |
| miR-27a-3f-ENPP1    | 19.97 | 20.00 |       | 1 | 1 |      | 0.86 | 0.95 | 0.82 | -0.80 | -2.11 |       |       |
| miR-27b-3f-ENPP1    | 19.97 | 20.00 |       | 1 | 1 | 0.75 | 0.86 | 1.05 | 0.91 | -0.80 | -2.11 |       |       |
| miR-27a-3f-NFIB     | 19.97 | 20.00 |       | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.04 | -0.81 | -0.99 |       |
| miR-27b-3f-NFIB     | 19.97 | 20.00 | 20.00 | 1 | 2 |      | 0.86 | 0.95 | 0.82 | -1.04 | -0.81 | -0.99 |       |
| miR-708-5f-ITPKB    | 1.81  | 2.28  |       | 1 | 1 |      | 0.91 | 1.64 |      | -0.68 | -1.46 | -1.33 |       |
| miR-31-3p-FAM134B   | 6.31  | 7.46  | 7.46  | 1 | 1 |      | 2.65 | 2.53 |      | -0.73 | -1.06 | -0.74 |       |
| miR-31-3p-FAM134B   | 6.31  | 7.46  | 7.46  | 1 | 2 | 1.80 | 2.65 | 3.21 | 2.72 | -1.31 | -1.39 | -1.44 |       |
| miR-31-3p-PTPN14    | 6.31  | 7.46  | 7.46  | 1 | 2 |      | 2.60 | 2.65 | 2.53 | -0.94 | -0.81 | -0.79 |       |
| miR-31-3p-PTPN14    | 6.31  | 7.46  | 7.46  | 1 | 2 | 1.80 | 2.60 | 3.21 | 2.72 | -0.94 | -0.81 | -0.79 |       |
| miR-31-3p-DHCR24    | 6.31  | 7.46  | 7.46  | 1 | 2 |      | 2.60 | 2.65 | 2.53 | -1.29 | -1.71 | -1.80 |       |
| miR-31-3p-DHCR24    | 6.31  | 7.46  | 7.46  | 1 | 2 | 1.80 | 2.60 | 3.21 | 2.72 | -1.29 | -1.71 | -1.80 |       |
| miR-31-3p-RORC      | 6.31  | 7.46  | 7.46  | 1 | 2 |      | 2.60 | 2.65 | 2.53 | -1.90 | -1.27 | -1.09 |       |
| miR-31-3p-TACC1     | 6.31  | 7.46  | 7.46  | 1 | 2 |      | 2.65 | 2.53 | 2.53 | -0.96 | -1.96 | -0.93 |       |



|                     |       |       |       |   |   |      |      |      |      |       |       |       |       |
|---------------------|-------|-------|-------|---|---|------|------|------|------|-------|-------|-------|-------|
| miR-31-5p TACC1     | 6.31  | 7.16  | 7.46  | 1 | 2 | 1.80 | 1.57 | 2.60 | 3.21 | 2.72  | -0.96 | -1.96 | -0.93 |
| miR-31-3p TACC2     | 6.31  | 7.16  | 7.46  | 1 | 2 | 1.80 | 1.57 | 2.20 | 2.65 | 2.53  | -0.93 | -0.61 | -0.93 |
| miR-31-3p PRSS8     | 6.31  | 7.16  | 7.46  | 1 | 2 | 1.80 | 1.57 | 2.20 | 2.65 | 2.53  | -0.74 | -0.96 | -1.37 |
| miR-31-5p PRSS8     | 6.31  | 7.16  | 7.46  | 1 | 2 | 1.80 | 1.57 | 2.60 | 3.21 | 2.72  | -0.74 | -0.96 | -1.37 |
| miR-31-3p TNF1      | 6.31  | 7.16  | 7.46  | 1 | 2 | 1.80 | 1.57 | 2.20 | 2.65 | 2.53  | -1.38 | -2.26 | -1.50 |
| miR-31-3p IL34      | 6.31  | 7.16  | 7.46  | 1 | 2 | 1.80 | 1.57 | 2.20 | 2.65 | 2.53  | -1.54 | -1.19 | -1.01 |
| miR-31-3p CREG1     | 6.31  | 7.16  | 7.46  | 1 | 2 | 1.80 | 1.57 | 2.20 | 2.65 | 2.53  | -1.27 | -2.96 | -2.00 |
| miR-31-5p CREG1     | 6.31  | 7.16  | 7.46  | 1 | 2 | 1.80 | 1.57 | 2.60 | 3.21 | 2.72  | -1.27 | -2.96 | -2.00 |
| miR-31-3p PRELP     | 6.31  | 7.16  | 7.46  | 1 | 2 | 1.80 | 1.57 | 2.20 | 2.65 | 2.53  | -1.61 | -3.24 | -1.59 |
| miR-31-3p SVN2      | 6.31  | 7.16  | 7.46  | 1 | 1 | 1.80 | 1.57 | 2.20 | 2.65 | 2.53  | -1.61 | -1.50 | -1.50 |
| miR-31-5p SVN2      | 6.31  | 7.16  | 7.46  | 1 | 1 | 1.80 | 1.57 | 2.60 | 3.21 | 2.72  | -1.61 | -1.50 | -1.50 |
| miR-31-3p PDE4D     | 6.31  | 7.16  | 7.46  | 1 | 1 | 1.80 | 1.57 | 2.20 | 2.65 | 2.53  | -0.92 | -0.64 | -0.64 |
| miR-31-5p PDE4D     | 6.31  | 7.16  | 7.46  | 1 | 1 | 1.80 | 1.57 | 2.60 | 3.21 | 2.72  | -0.92 | -0.64 | -0.64 |
| miR-340-5f PTPN14   | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.55 | -6.76 | -3.37 |
| miR-340-5f PTPN14   | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -0.94 | -0.81 | -0.79 |
| miR-340-5f PDK4     | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -2.07 | -3.16 | -2.19 |
| miR-340-5f GULP1    | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -0.91 | -1.99 | -0.83 |
| miR-340-5f EDNRB    | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.18 | -1.72 | -0.87 |
| miR-340-5f RORC     | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.90 | -1.27 | -1.09 |
| miR-340-5f KIT      | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.08 | -1.34 | -0.95 |
| miR-340-5f PDCD4    | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -0.76 | -0.77 | -0.70 |
| miR-340-5f ALCAM    | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -0.88 | -3.06 | -2.26 |
| miR-340-5f ARHGAP24 | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -0.80 | -1.16 | -0.99 |
| miR-340-5f LPHN3    | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -2.38 | -2.53 | -1.50 |
| miR-340-5f SCN7A    | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -3.55 | -4.82 | -2.11 |
| miR-340-5f ATP1B1   | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.01 | -2.29 | -2.31 |
| miR-340-5f EGFR3    | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -2.02 | -1.24 | -1.27 |
| miR-340-5f IGF1     | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -0.89 | -1.26 | -1.26 |
| miR-340-5f RNF125   | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -0.81 | -1.59 | -0.62 |
| miR-340-5f DLG2     | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.12 | -1.37 | -1.37 |
| miR-340-5f TNF1     | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.38 | -2.26 | -1.50 |
| miR-340-5f TGFBR3   | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.86 | -1.88 | -1.27 |
| miR-340-5f PRARGC1B | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.11 | -0.75 | -0.75 |
| miR-340-5f LIFR     | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.23 | -1.46 | -1.50 |
| miR-340-5f ACSL1    | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -2.52 | -1.18 | -1.42 |
| miR-340-5f COBL     | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -0.95 | -2.33 | -2.41 |
| miR-340-5f GKS      | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.48 | -0.96 | -0.96 |
| miR-340-5f FA2H     | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.86 | -5.13 | -4.33 |
| miR-340-5f GLUT1    | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -0.90 | -3.09 | -1.75 |
| miR-340-5f NFB      | 13.01 | 20.00 | 20.00 | 1 | 1 | 1.36 | 1.84 | 1.84 | 1.68 | 1.68  | -1.97 | -0.81 | -0.99 |
| miR-411-5f SCNA5    | 1.18  | 1.84  | 1.84  | 1 | 1 | 0.73 | 0.92 | 0.92 | 1.74 | -1.92 | -3.07 | -7.70 | -2.99 |



| miRNA               | Gene     | AK-NS miRNA-mRNA enrichment, -log10(q-value) | SCC-AK miRNA-mRNA enrichment, -log10(q-value) | SCC-NS miRNA-mRNA enrichment, -log10(q-value) | PAP-CHR miRNA-mRNA enrichment, -log10(q-value) | SCC-CHR miRNA-mRNA enrichment, -log10(q-value) | miRNA-mRNA enrichment, -log10(q-value) | miRNA-mRNA enrichment recurrence human | miRNA-mRNA enrichment recurrence mouse | microRNA AK-over-NS log2(fold-change) | microRNA SCC-over-AK log2(fold-change) | microRNA SCC-over-NS log2(fold-change) | microRNA PAP-over-CHR log2(fold-change) | microRNA SCC-over-CHR log2(fold-change) | mRNA AK-over-NS log2(fold-change) | mRNA SCC-over-AK log2(fold-change) | mRNA SCC-over-NS log2(fold-change) | mRNA PAP-over-CHR log2(fold-change) | mRNA SCC-over-CHR log2(fold-change) |
|---------------------|----------|--|---|---|--|--|--|--|--|---------------------------------------|--|--|---|---|-----------------------------------|------------------------------------|------------------------------------|-------------------------------------|-------------------------------------|
| let-7d-3p           | RRM2     | 3.80   | 4.33  | 4.33  | 10.72  | 2  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -0.82                                  | -1.05                                  | 0.92                                    | 1.09                                    | 1.46                              | 1.37                               |                                    |                                     |                                     |
| let-7e-3p           | RRM2     | 3.80   | 4.33  | 4.33  | 10.72  | 2  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  | 0.92                                   | 1.09                                    | 1.46                                    | 1.37                              |                                    |                                    |                                     |                                     |
| let-7d-3p           | DSG3     | 3.80   | 4.33  | 4.33  | 10.72  | 2  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -1.05                                  | 1.58                                   | 1.68                                    | 1.97                                    | 1.43                              |                                    |                                    |                                     |                                     |
| let-7e-3p           | DSG3     | 3.80   | 4.33  | 4.33  | 10.72  | 2  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  | 1.58                                   | 1.68                                    | 1.97                                    | 1.43                              |                                    |                                    |                                     |                                     |
| let-7d-3p           | CASP3    | 3.80   | 4.33  | 4.33  | 10.72  | 2  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -1.05                                  | 0.72                                   | 0.67                                    | 0.65                                    | 0.87                              | 1.43                               |                                    |                                     |                                     |
| let-7e-3p           | CASP3    | 3.80   | 4.33  | 4.33  | 10.72  | 2  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  | 0.72                                   | 0.67                                    | 0.65                                    | 0.87                              | 1.43                               |                                    |                                     |                                     |
| let-7d-3p           | ENTPD7   | 3.80   |   |   | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -1.05                                  | 0.92                                   |   | 0.85                                    | 0.70                              |                                    |                                    |                                     |                                     |
| let-7e-3p           | ENTPD7   | 3.80   |   |   | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  | 0.92                                   |   | 0.85                                    | 0.70                              |                                    |                                    |                                     |                                     |
| miR-30a-3f-E2F7     |          | 8.17   | 6.03  | 6.03  | 20.00  | 1  | 1                                      | -0.86                                  |  | -1.20                                 | -0.84                                  | 1.74                                   |   | 3.09                                    | 2.60                              |                                    |                                    |                                     |                                     |
| miR-30a-3f-PIK2B    |          | 8.17   | 6.03  | 6.03  | 20.00  | 2  | 1                                      | -0.86                                  |  | -1.20                                 | -0.84                                  | 0.70                                   |   | 0.71                                    | 0.89                              | 0.78                               |                                    |                                     |                                     |
| miR-30a-3f-PDE7A    |          | 8.17   | 6.03  | 6.03  | 20.00  | 1  | 1                                      | -0.86                                  |  | -1.20                                 | -0.84                                  | 0.92                                   |   | 0.70                                    | 1.12                              | 0.89                               | 0.76                               |                                     |                                     |
| miR-30a-3f-TFDP1    |          | 8.17   | 6.03  | 6.03  | 20.00  | 2  | 1                                      | -0.86                                  |  | -1.20                                 | -0.84                                  | 0.75                                   |   | 0.66                                    | 1.13                              | 0.72                               |                                    |                                     |                                     |
| miR-30a-3f-CDC47    |          | 8.17   | 6.03  | 6.03  | 20.00  | 2  | 1                                      | -0.86                                  |  | -1.20                                 | -0.84                                  | 0.59                                   |   | 1.35                                    | 0.95                              | 0.95                               |                                    |                                     |                                     |
| miR-30a-3f-CDC7     |          | 8.17   | 6.03  | 6.03  | 20.00  | 2  | 1                                      | -0.86                                  |  | -1.20                                 | -0.84                                  | 0.95                                   |   | 1.43                                    | 1.32                              | 1.19                               | 1.36                               |                                     |                                     |
| let-7d-3p           | MDFI     | 1.52   | 4.33  | 4.33  | 10.72  | 2  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -1.05                                  |  | 0.99                                    | 1.43                                    | 1.32                              | 1.19                               | 1.36                               |                                     |                                     |
| let-7d-3p           | CD276    | 1.52   | 4.33  | 4.33  | 10.72  | 2  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -1.05                                  |  | 0.73                                    | 0.77                                    | 1.08                              | 1.36                               | 1.36                               |                                     |                                     |
| miR-125b-5-LIMK1    |          | 1.11   | 2.42  | 2.42  | 3.98   | 2  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -0.95                                  |  | 0.60                                    | 0.74                                    | 1.32                              | 0.97                               | 1.36                               |                                     |                                     |
| miR-193b-5-LAMC2    |          | 0.62   | 2.47  | 2.47  | 1.34   | 2  | 1                                      | -0.64                                  | -0.64                                  | -0.68                                 | -1.46                                  |  | 1.84                                    | 2.52                                    | 2.03                              | 1.73                               | 0.93                               |                                     |                                     |
| let-7b-3p           | AURKB    | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -0.77                                 | -1.46                                  |  |   | 1.16                                    | 1.74                              | 1.40                               | 1.40                               |                                     |                                     |
| let-7d-3p           | AURKB    | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -1.05                                  |  |   | 1.16                                    | 1.74                              | 1.40                               | 1.40                               |                                     |                                     |
| let-7e-3p           | AURKB    | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  |  |   | 1.16                                    | 1.74                              | 1.40                               | 1.40                               |                                     |                                     |
| let-7b-3p           | VSNI1    | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -0.77                                 | -1.46                                  |  |   | 0.97                                    | 2.25                              | 2.21                               | 2.21                               |                                     |                                     |
| let-7d-3p           | VSNI1    | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -1.05                                  |  |   | 0.97                                    | 2.25                              | 2.21                               | 2.21                               |                                     |                                     |
| let-7e-3p           | VSNI1    | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  |  |   | 0.97                                    | 2.25                              | 2.21                               | 2.21                               |                                     |                                     |
| let-7b-3p           | RRM2     | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -0.77                                 | -1.46                                  | 0.92                                   |   | 1.09                                    | 1.46                              | 1.37                               | 1.37                               |                                     |                                     |
| let-7d-3p           | RRM2     | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -0.77                                 | -1.46                                  |  |   | 1.36                                    | 1.83                              | 1.61                               | 1.61                               |                                     |                                     |
| let-7e-3p           | RRM2     | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -0.77                                 | -1.46                                  |  |   | 1.36                                    | 1.83                              | 1.61                               | 1.61                               |                                     |                                     |
| let-7b-3p           | CDCA8    | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  |  |   | 1.36                                    | 1.83                              | 1.61                               | 1.61                               |                                     |                                     |
| let-7d-3p           | CDCA8    | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  |  |   | 1.36                                    | 1.83                              | 1.61                               | 1.61                               |                                     |                                     |
| let-7e-3p           | CDCA8    | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  |  |   | 1.36                                    | 1.83                              | 1.61                               | 1.61                               |                                     |                                     |
| let-7b-3p           | DSG3     | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -0.77                                 | -1.46                                  | 1.58                                   |   | 1.68                                    | 1.97                              | 1.43                               | 1.43                               |                                     |                                     |
| let-7d-3p           | DSG3     | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -0.77                                 | -1.46                                  | 0.72                                   |   | 0.67                                    | 0.87                              | 0.87                               | 0.87                               |                                     |                                     |
| let-7e-3p           | DSG3     | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -0.77                                 | -1.46                                  |  |   | 0.67                                    | 0.87                              | 0.87                               | 0.87                               |                                     |                                     |
| let-7b-3p           | SIC25A24 | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -0.77                                 | -1.46                                  |  |   | 0.60                                    | 0.88                              | 0.88                               | 0.88                               |                                     |                                     |
| let-7d-3p           | SIC25A24 | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -0.77                                 | -1.46                                  |  |   | 0.60                                    | 0.88                              | 0.88                               | 0.88                               |                                     |                                     |
| let-7e-3p           | SIC25A24 | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  |  |   | 0.60                                    | 0.88                              | 0.88                               | 0.88                               |                                     |                                     |
| let-7b-3p           | SIC25A24 | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  |  |   | 0.60                                    | 0.88                              | 0.88                               | 0.88                               |                                     |                                     |
| let-7e-3p           | HMGGA2   | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -0.77                                 | -1.46                                  |  |   | 3.42                                    | 2.63                              | 2.63                               | 2.63                               |                                     |                                     |
| let-7d-3p           | HMGGA2   | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -1.05                                  |  |   | 3.42                                    | 2.63                              | 2.63                               | 2.63                               |                                     |                                     |
| let-7e-3p           | HMGGA2   | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.77                                 | -1.46                                  |  |   | 3.42                                    | 2.63                              | 2.63                               | 2.63                               |                                     |                                     |
| let-7b-3p           | SIC1A4   | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -1.05                                  |  |   | 0.76                                    | 1.16                              | 1.23                               | 1.23                               |                                     |                                     |
| let-7d-3p           | SIC1A4   | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -1.05                                  |  |   | 0.76                                    | 1.16                              | 1.23                               | 1.23                               |                                     |                                     |
| let-7e-3p           | SIC1A4   | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -0.59                                  | -0.61                                  | -1.20                                 | -1.05                                  |  |   | 0.76                                    | 1.16                              | 1.23                               | 1.23                               |                                     |                                     |
| let-7b-3p           | MDFI     | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.77                                 | -1.46                                  | 0.99                                   |   | 1.43                                    | 1.32                              | 1.19                               | 1.19                               |                                     |                                     |
| let-7d-3p           | MDFI     | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.77                                 | -1.46                                  | 0.99                                   |   | 1.43                                    | 1.32                              | 1.19                               | 1.19                               |                                     |                                     |
| let-7e-3p           | MDFI     | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.77                                 | -1.46                                  | 0.99                                   |   | 1.43                                    | 1.32                              | 1.19                               | 1.19                               |                                     |                                     |
| let-7b-3p           | CD276    | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  |  |   | 0.77                                    | 1.08                              | 1.36                               | 1.36                               |                                     |                                     |
| let-7d-3p           | CD276    | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  |  |   | 0.77                                    | 1.08                              | 1.36                               | 1.36                               |                                     |                                     |
| let-7e-3p           | CD276    | 4.33   | 4.33  | 4.33  | 10.72  | 1  | 1                                      | -1.49                                  | -0.61                                  | -0.82                                 | -0.99                                  |  |   | 0.77                                    | 1.08                              | 1.36                               | 1.36                               |                                     |                                     |
| miR-125b-5-PCGF6    |          | 2.42   | 2.42  | 2.42  | 3.98   | 1  | 1                                      | -0.69                                  | -0.69                                  | -1.21                                 | -0.95                                  |  |   | 1.39                                    | 1.04                              | 1.02                               | 1.02                               |                                     |                                     |
| miR-125b-5-E1F4EBP1 |          | 2.42   | 2.42  | 2.42  | 3.98   | 1  | 1                                      | -0.69                                  | -0.69                                  | -1.21                                 | -0.95                                  |  |   | 1.16                                    | 1.33                              | 0.93                               | 0.93                               |                                     |                                     |



|                   |      |       |   |   |       |       |       |       |      |      |      |      |
|-------------------|------|-------|---|---|-------|-------|-------|-------|------|------|------|------|
| miR-125b-5-PIAK2B | 2.42 | 3.98  | 1 | 1 |       | -0.69 | -1.21 | -0.95 | 0.70 | 0.71 | 0.89 | 0.78 |
| miR-125b-5-SEMA4B | 2.42 | 3.98  | 1 | 1 |       | -0.69 | -1.21 | -0.95 |      | 0.97 | 0.92 | 0.74 |
| miR-30a-3f-MYBL2  | 6.03 | 20.00 | 1 | 1 | -0.86 |       | -1.20 | -0.84 |      | 1.37 | 1.54 | 1.49 |
| miR-30a-3f-CCNE2  | 6.03 | 20.00 | 1 | 1 | -0.86 |       | -1.20 | -0.84 |      | 1.15 | 1.44 | 1.31 |
| miR-30a-3f-POP1   | 6.03 | 20.00 | 1 | 1 | -0.86 |       | -1.20 | -0.84 |      | 0.76 | 1.35 | 0.97 |
| miR-30a-3f-COT11  | 6.03 | 20.00 | 1 | 1 | -0.86 |       | -1.20 | -0.84 |      | 0.90 |      | 0.80 |
| miR-30a-3f-ENAH   | 6.03 | 20.00 | 1 | 1 | -0.86 |       | -1.20 | -0.84 |      | 1.56 | 1.54 | 1.86 |



## Appendix 11.

### GSEA analysis of cuSCC signatures across TCGA cancers



| Gene | 12379364 | 12380394 | 12380933 | 12381432 | 12381929 | 12382427 | 12382926 | 12383425 | 12383924 | 12384423 | 12384922 | 12385421 | 12385920 | 12386419 | 12386918 | 12387417 | 12387916 | 12388415 | 12388914 | 12389413 | 12389912 | 12390411 | 12390910 | 12391409 | 12391908 | 12392407 | 12392906 | 12393405 | 12393904 | 12394403 | 12394902 | 12395401 | 12395900 | 12396399 | 12396898 | 12397397 | 12397896 | 12398395 | 12398894 | 12399393 | 12399892 | 12400391 | 12400890 | 12401389 | 12401888 | 12402387 | 12402886 | 12403385 | 12403884 | 12404383 | 12404882 | 12405381 | 12405880 | 12406379 | 12406878 | 12407377 | 12407876 | 12408375 | 12408874 | 12409373 | 12409872 | 12410371 | 12410870 | 12411369 | 12411868 | 12412367 | 12412866 | 12413365 | 12413864 | 12414363 | 12414862 | 12415361 | 12415860 | 12416359 | 12416858 | 12417357 | 12417856 | 12418355 | 12418854 | 12419353 | 12419852 | 12420351 | 12420850 | 12421349 | 12421848 | 12422347 | 12422846 | 12423345 | 12423844 | 12424343 | 12424842 | 12425341 | 12425840 | 12426339 | 12426838 | 12427337 | 12427836 | 12428335 | 12428834 | 12429333 | 12429832 | 12430331 | 12430830 | 12431329 | 12431828 | 12432327 | 12432826 | 12433325 | 12433824 | 12434323 | 12434822 | 12435321 | 12435820 | 12436319 | 12436818 | 12437317 | 12437816 | 12438315 | 12438814 | 12439313 | 12439812 | 12440311 | 12440810 | 12441309 | 12441808 | 12442307 | 12442806 | 12443305 | 12443804 | 12444303 | 12444802 | 12445301 | 12445800 | 12446299 | 12446798 | 12447297 | 12447796 | 12448295 | 12448794 | 12449293 | 12449792 | 12450291 | 12450790 | 12451289 | 12451788 | 12452287 | 12452786 | 12453285 | 12453784 | 12454283 | 12454782 | 12455281 | 12455780 | 12456279 | 12456778 | 12457277 | 12457776 | 12458275 | 12458774 | 12459273 | 12459772 | 12460271 | 12460770 | 12461269 | 12461768 | 12462267 | 12462766 | 12463265 | 12463764 | 12464263 | 12464762 | 12465261 | 12465760 | 12466259 | 12466758 | 12467257 | 12467756 | 12468255 | 12468754 | 12469253 | 12469752 | 12470251 | 12470750 | 12471249 | 12471748 | 12472247 | 12472746 | 12473245 | 12473744 | 12474243 | 12474742 | 12475241 | 12475740 | 12476239 | 12476738 | 12477237 | 12477736 | 12478235 | 12478734 | 12479233 | 12479732 | 12480231 | 12480730 | 12481229 | 12481728 | 12482227 | 12482726 | 12483225 | 12483724 | 12484223 | 12484722 | 12485221 | 12485720 | 12486219 | 12486718 | 12487217 | 12487716 | 12488215 | 12488714 | 12489213 | 12489712 | 12490211 | 12490710 | 12491209 | 12491708 | 12492207 | 12492706 | 12493205 | 12493704 | 12494203 | 12494702 | 12495201 | 12495700 | 12496199 | 12496698 | 12497197 | 12497696 | 12498195 | 12498694 | 12499193 | 12499692 | 12500191 | 12500690 | 12501189 | 12501688 | 12502187 | 12502686 | 12503185 | 12503684 | 12504183 | 12504682 | 12505181 | 12505680 | 12506179 | 12506678 | 12507177 | 12507676 | 12508175 | 12508674 | 12509173 | 12509672 | 12510171 | 12510670 | 12511169 | 12511668 | 12512167 | 12512666 | 12513165 | 12513664 | 12514163 | 12514662 | 12515161 | 12515660 | 12516159 | 12516658 | 12517157 | 12517656 | 12518155 | 12518654 | 12519153 | 12519652 | 12520151 | 12520650 | 12521149 | 12521648 | 12522147 | 12522646 | 12523145 | 12523644 | 12524143 | 12524642 | 12525141 | 12525640 | 12526139 | 12526638 | 12527137 | 12527636 | 12528135 | 12528634 | 12529133 | 12529632 | 12530131 | 12530630 | 12531129 | 12531628 | 12532127 | 12532626 | 12533125 | 12533624 | 12534123 | 12534622 | 12535121 | 12535620 | 12536119 | 12536618 | 12537117 | 12537616 | 12538115 | 12538614 | 12539113 | 12539612 | 12540111 | 12540610 | 12541109 | 12541608 | 12542107 | 12542606 | 12543105 | 12543604 | 12544103 | 12544602 | 12545101 | 12545600 | 12546099 | 12546598 | 12547097 | 12547596 | 12548095 | 12548594 | 12549093 | 12549592 | 12550091 | 12550590 | 12551089 | 12551588 | 12552087 | 12552586 | 12553085 | 12553584 | 12554083 | 12554582 | 12555081 | 12555580 | 12556079 | 12556578 | 12557077 | 12557576 | 12558075 | 12558574 | 12559073 | 12559572 | 12560071 | 12560570 | 12561069 | 12561568 | 12562067 | 12562566 | 12563065 | 12563564 | 12564063 | 12564562 | 12565061 | 12565560 | 12566059 | 12566558 | 12567057 | 12567556 | 12568055 | 12568554 | 12569053 | 12569552 | 12570051 | 12570550 | 12571049 | 12571548 | 12572047 | 12572546 | 12573045 | 12573544 | 12574043 | 12574542 | 12575041 | 12575540 | 12576039 | 12576538 | 12577037 | 12577536 | 12578035 | 12578534 | 12579033 | 12579532 | 12580031 | 12580530 | 12581029 | 12581528 | 12582027 | 12582526 | 12583025 | 12583524 | 12584023 | 12584522 | 12585021 | 12585520 | 12586019 | 12586518 | 12587017 | 12587516 | 12588015 | 12588514 | 12589013 | 12589512 | 12590011 | 12590510 | 12591009 | 12591508 | 12592007 | 12592506 | 12593005 | 12593504 | 12594003 | 12594502 | 12595001 | 12595500 | 12596000 | 12596499 | 12596998 | 12597497 | 12597996 | 12598495 | 12598994 | 12599493 | 12599992 | 12600491 | 12600990 | 12601489 | 12601988 | 12602487 | 12602986 | 12603485 | 12603984 | 12604483 | 12604982 | 12605481 | 12605980 | 12606479 | 12606978 | 12607477 | 12607976 | 12608475 | 12608974 | 12609473 | 12609972 | 12610471 | 12610970 | 12611469 | 12611968 | 12612467 | 12612966 | 12613465 | 12613964 | 12614463 | 12614962 | 12615461 | 12615960 | 12616459 | 12616958 | 12617457 | 12617956 | 12618455 | 12618954 | 12619453 | 12619952 | 12620451 | 12620950 | 12621449 | 12621948 | 12622447 | 12622946 | 12623445 | 12623944 | 12624443 | 12624942 | 12625441 | 12625940 | 12626439 | 12626938 | 12627437 | 12627936 | 12628435 | 12628934 | 12629433 | 12629932 | 12630431 | 12630930 | 12631429 | 12631928 | 12632427 | 12632926 | 12633425 | 12633924 | 12634423 | 12634922 | 12635421 | 12635920 | 12636419 | 12636918 | 12637417 | 12637916 | 12638415 | 12638914 | 12639413 | 12639912 | 12640411 | 12640910 | 12641409 | 12641908 | 12642407 | 12642906 | 12643405 | 12643904 | 12644403 | 12644902 | 12645401 | 12645900 | 12646399 | 12646898 | 12647397 | 12647896 | 12648395 | 12648894 | 12649393 | 12649892 | 12650391 | 12650890 | 12651389 | 12651888 | 12652387 | 12652886 | 12653385 | 12653884 | 12654383 | 12654882 | 12655381 | 12655880 | 12656379 | 12656878 | 12657377 | 12657876 | 12658375 | 12658874 | 12659373 | 12659872 | 12660371 | 12660870 | 12661369 | 12661868 | 12662367 | 12662866 | 12663365 | 12663864 | 12664363 | 12664862 | 12665361 | 12665860 | 12666359 | 12666858 | 12667357 | 12667856 | 12668355 | 12668854 | 12669353 | 12669852 | 12670351 | 12670850 | 12671349 | 12671848 | 12672347 | 12672846 | 12673345 | 12673844 | 12674343 | 12674842 | 12675341 | 12675840 | 12676339 | 12676838 | 12677337 | 12677836 | 12678335 | 12678834 | 12679333 | 12679832 | 12680331 | 12680830 | 12681329 | 12681828 | 12682327 | 12682826 | 12683325 | 12683824 | 12684323 | 12684822 | 12685321 | 12685820 | 12686319 | 12686818 | 12687317 | 12687816 | 12688315 | 12688814 | 12689313 | 12689812 | 12690311 | 12690810 | 12691309 | 12691808 | 12692307 | 12692806 | 12693305 | 12693804 | 12694303 | 12694802 | 12695301 | 12695800 | 12696299 | 12696798 | 12697297 | 12697796 | 12698295 | 12698794 | 12699293 | 12699792 | 12700291 | 12700790 | 12701289 | 12701788 | 12702287 | 12702786 | 12703285 | 12703784 | 12704283 | 12704782 | 12705281 | 12705780 | 12706279 | 12706778 | 12707277 | 12707776 | 12708275 | 12708774 | 12709273 | 12709772 | 12710271 | 12710770 | 12711269 | 12711768 | 12712267 | 12712766 | 12713265 | 12713764 | 12714263 | 12714762 | 12715261 | 12715760 | 12716259 | 12716758 | 12717257 | 12717756 | 12718255 | 12718754 | 12719253 | 12719752 | 12720251 | 12720750 | 12721249 | 12721748 | 12722247 | 12722746 | 12723245 | 12723744 | 12724243 | 12724742 | 12725241 | 12725740 | 12726239 | 12726738 | 12727237 | 12727736 | 12728235 | 12728734 | 12729233 | 12729732 | 12730231 | 12730730 | 12731229 | 12731728 | 12732227 | 12732726 | 12733225 | 12733724 | 12734223 | 12734722 | 12735221 | 12735720 | 12736219 | 12736718 | 12737217 | 12737716 | 12738215 | 12738714 | 12739213 | 12739712 | 12740211 | 12740710 | 12741209 | 12741708 | 12742207 | 12742706 | 12743205 | 12743704 | 12744203 | 12744702 | 12745201 | 12745700 | 12746199 | 12746698 | 12747197 | 12747696 | 12748195 | 12748694 | 12749193 | 12749692 | 12750191 | 12750690 | 12751189 | 12751688 | 12752187 | 12752686 | 12753185 | 12753684 | 12754183 | 12754682 | 12755181 | 12755680 | 12756179 | 12756678 | 12757177 | 12757676 | 12758175 | 12758674 | 12759173 | 12759672 | 12760171 | 12760670 | 12761169 | 12761668 | 12762167 | 12762666 | 12763165 | 12763664 | 12764163 | 12764662 | 12765161 | 12765660 | 12766159 | 12766658 | 12767157 | 12767656 | 12768155 | 12768654 | 12769153 | 12769652 | 12770151 | 12770650 | 12771149 | 12771648 | 12772147 | 12772646 | 12773145 | 12773644 | 12774143 | 12774642 | 12775141 | 12775640 | 12776139 | 12776638 | 12777137 | 12777636 | 12778135 | 12778634 | 12779133 | 12779632 | 12780131 | 12780630 | 12781129 | 12781628 | 12782127 | 12782626 | 12783125 | 12783624 | 12784123 | 12784622 | 12785121 | 12785620 | 12786119 | 12786618 | 12787117 | 12787616 | 12788115 | 12788614 | 12789113 | 12789612 | 12790111 | 12790610 | 12791109 | 12791608 | 12792107 | 12792606 | 12793105 | 12793604 | 12794103 | 12794602 | 12795101 | 12795600 | 12796099 | 12796598 | 12797097 | 12797596 | 12798095 | 12798594 | 12799093 | 12799592 | 12800091 | 12800590 | 12801089 | 12801588 | 12802087 | 12802586 | 12803085 | 12803584 | 12804083 | 12804582 | 12805081 | 12805580 | 12806079 | 12806578 | 12807077 | 12807576 | 12808075 | 12808574 | 12809073 | 12809572 | 12810071 | 12810570 | 12811069 | 12811568 | 12812067 | 12812566 | 12813065 | 12813564 | 12814063 | 12814562 | 12815061 | 12815560 | 12816059 | 12816558 | 12817057 | 12817556 | 12818055 | 12818554 | 12819053 | 12819552 | 12820051 | 12820550 | 12821049 | 12821548 | 12822047 | 12822546 | 12823045 | 12823544 | 12824043 | 12824542 | 12825041 | 12825540 | 12826039 | 12826538 | 12827037 | 12827536 | 12828035 | 12828534 | 12829033 | 12829532 | 12830031 | 12830530 | 12831029 | 12831528 | 12832027 | 12832526 | 12833025 | 12833524 | 12834023 | 12834522 | 12835021 | 12835520 | 12836019 | 12836518 | 12837017 | 12837516 | 12838015 | 12838514 | 12839013 | 12839512 | 12840011 | 12840510 | 12841009 | 12841508 | 12842007 | 12842506 | 12843005 | 12843504 | 12844003 | 12844502 | 12845001 | 12845500 | 12846000 | 12846499 | 12846998 | 12847497 | 12847996 | 12848495 | 12848994 | 12849493 | 12849992 | 12850491 | 12850990 | 12851489 | 12851988 | 12852487 | 12852986 | 1285348 |
|------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|---------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## Appendix 12.

Survival prediction data for  
TP53-mutant TCGA HNSCC



HNSC-mouse-SCC-over-PAP.TCGA-HN

| Bottom (%) | Top (%) | Log-rank  | Log-rank (rl Coxph | Best survival           |
|------------|---------|-----------|--------------------|-------------------------|
| 5          | 5       | 0.3187838 | 0.3645128          | 0.3214318 Indicator=Top |
| 5          | 95      | 0.3475293 | 0.1009875          | 0.3745425 Indicator=Top |
| 10         | 10      | 0.0409866 | 0.0399659          | 0.0420946 Indicator=Top |
| 10         | 90      | 0.1045503 | 0.03385            | 0.1325953 Indicator=Top |
| 15         | 15      | 0.0212875 | 0.0473271          | 0.0197838 Indicator=Top |
| 15         | 85      | 0.2321723 | 0.091233           | 0.2546976 Indicator=Top |
| 20         | 20      | 0.1997678 | 0.529446           | 0.1976131 Indicator=Top |
| 20         | 80      | 0.2763875 | 0.2025731          | 0.2918611 Indicator=Top |
| 25         | 25      | 0.226503  | 0.5897846          | 0.2263111 Indicator=Top |
| 25         | 75      | 0.4289247 | 0.5475913          | 0.4390869 Indicator=Top |
| 30         | 30      | 0.1770369 | 0.5857882          | 0.1768857 Indicator=Top |
| 30         | 70      | 0.2892019 | 0.6516331          | 0.300876 Indicator=Top  |
| 33         | 33      | 0.0554678 | 0.304117           | 0.055798 Indicator=Top  |
| 33         | 67      | 0.2025123 | 0.5675084          | 0.2133244 Indicator=Top |
| 35         | 35      | 0.0579495 | 0.2419539          | 0.0585103 Indicator=Top |
| 35         | 65      | 0.1960189 | 0.5391701          | 0.2059744 Indicator=Top |
| 40         | 40      | 0.2600917 | 0.7925596          | 0.2608568 Indicator=Top |
| 40         | 60      | 0.3399396 | 0.6894966          | 0.3473322 Indicator=Top |
| 45         | 45      | 0.3459078 | 0.9228188          | 0.3439016 Indicator=Top |
| 45         | 55      | 0.2915686 | 0.7294477          | 0.2946856 Indicator=Top |
| 50         | 50      | 0.3733032 | 0.8703815          | 0.3722463 Indicator=Top |
| 50         | 50      | 0.3733032 | 0.8703815          | 0.3722463 Indicator=Top |
| 50         | 50      | 0.3733032 | 0.8703815          | 0.3722463 Indicator=Top |
| 55         | 45      | 0.4316961 | 0.9060461          | 0.4281667 Indicator=Top |
| 60         | 40      | 0.2369561 | 0.8834165          | 0.2314015 Indicator=Top |
| 65         | 35      | 0.0356475 | 0.1807718          | 0.0310022 Indicator=Top |
| 67         | 33      | 0.0334915 | 0.2572848          | 0.0281114 Indicator=Top |
| 70         | 30      | 0.2458407 | 0.6162881          | 0.2353601 Indicator=Top |
| 75         | 25      | 0.3124499 | 0.7629028          | 0.3010815 Indicator=Top |
| 80         | 20      | 0.4724769 | 0.985625           | 0.4611655 Indicator=Top |
| 85         | 15      | 0.0614355 | 0.1247923          | 0.0420209 Indicator=Top |
| 90         | 10      | 0.1021747 | 0.1548087          | 0.0721424 Indicator=Top |
| 95         | 5       | 0.2553183 | 0.4125004          | 0.2054738 Indicator=Top |



## HNSCp53-conservedMiRNATargetsTC

| Bottom (%) | Top (%) | Log-rank  | Coxph     | Best survival    |
|------------|---------|-----------|-----------|------------------|
| 5          | 5       | 0.0093789 | 0.0034754 | Indicator=Bottom |
| 5          | 95      | 0.0509548 | 0.0067214 | Indicator=Bottom |
| 10         | 10      | 0.0014574 | 0.0011361 | Indicator=Bottom |
| 10         | 90      | 0.1122139 | 0.0795362 | Indicator=Bottom |
| 15         | 15      | 0.0482942 | 0.0453155 | Indicator=Bottom |
| 15         | 85      | 0.1384682 | 0.1091451 | Indicator=Bottom |
| 20         | 20      | 0.0736256 | 0.0698724 | Indicator=Bottom |
| 20         | 80      | 0.0530023 | 0.0373205 | Indicator=Bottom |
| 25         | 25      | 0.0352241 | 0.0322021 | Indicator=Bottom |
| 25         | 75      | 0.0481203 | 0.0354634 | Indicator=Bottom |
| 30         | 30      | 0.0791468 | 0.0765966 | Indicator=Bottom |
| 30         | 70      | 0.0818816 | 0.0706005 | Indicator=Bottom |
| 33         | 33      | 0.0564799 | 0.0546501 | Indicator=Bottom |
| 33         | 67      | 0.0394102 | 0.0325201 | Indicator=Bottom |
| 35         | 35      | 0.0418639 | 0.0402756 | Indicator=Bottom |
| 35         | 65      | 0.0340632 | 0.0285636 | Indicator=Bottom |
| 40         | 40      | 0.1225039 | 0.1220287 | Indicator=Bottom |
| 40         | 60      | 0.0750768 | 0.0703589 | Indicator=Bottom |
| 45         | 45      | 0.1618737 | 0.1606265 | Indicator=Bottom |
| 45         | 55      | 0.1181952 | 0.1156982 | Indicator=Bottom |
| 50         | 50      | 0.2341659 | 0.2308364 | Indicator=Bottom |
| 50         | 50      | 0.2341659 | 0.2308364 | Indicator=Bottom |
| 50         | 50      | 0.2341659 | 0.2308364 | Indicator=Bottom |
| 55         | 45      | 0.287311  | 0.2855945 | Indicator=Bottom |
| 60         | 40      | 0.296842  | 0.2982933 | Indicator=Bottom |
| 65         | 35      | 0.1487812 | 0.1545286 | Indicator=Bottom |
| 67         | 33      | 0.2737115 | 0.2783949 | Indicator=Bottom |
| 70         | 30      | 0.2627322 | 0.2694111 | Indicator=Bottom |
| 75         | 25      | 0.2298974 | 0.2416386 | Indicator=Bottom |
| 80         | 20      | 0.5922409 | 0.5936933 | Indicator=Bottom |
| 85         | 15      | 0.1879759 | 0.205419  | Indicator=Bottom |
| 90         | 10      | 0.0046487 | 0.013122  | Indicator=Bottom |
| 95         | 5       | 0.186126  | 0.2258997 | Indicator=Bottom |



## Appendix 13.

### Ingenuity Pathway Analysis of differentially expressed genes in NS to AK transition





Analysis Name: IPA early transition human data only-Only NS to AK transit - 2015-06-13 11:33 AM

Analysis Creation Date: 2015-06-13

Build version: 346717M

Content version: 23814503 (Release Date: 2015-03-22)

#### Analysis Settings

Reference set: Ingenuity Knowledge Base (Genes Only)

Relationship to include: Direct and Indirect

Does not Include Endogenous Chemicals

Optional Analyses: My Pathways My List

#### Filter Summary:

Consider only molecules and/or relationships where

(species = Human) AND

(confidence = Experimentally Observed)



Top Canonical Pathways

| Name  | p-value  | Overlap       |
|---|----------|---------------|
| Mitotic Roles of Polo-Like Kinase                 | 1.92E-09 | 28.6 % 18/63  |
| Cell Cycle Control of Chromosomal Replication     | 3.15E-09 | 44.4 % 12/27  |
| Cell Cycle: G2/M DNA Damage Checkpoint Regulation | 5.77E-06 | 24.5 % 12/49  |
| Hereditary Breast Cancer Signaling                | 7.97E-06 | 15.9 % 20/126 |
| Role of BRCA1 in DNA Damage Response              | 4.48E-05 | 17.9 % 14/78  |

Top Upstream Regulators

| Upstream Regulator | p-value of overlap | Predicted Activation |
|--------------------|--------------------|----------------------|
| E2F4               | 1.00E-31           | Activated            |
| RABL6              | 2.58E-25           |                      |
| ERBB2              | 1.42E-18           |                      |
| TP53               | 1.16E-15           | Inhibited            |
| E2F1               | 1.99E-15           |                      |

Top Diseases and Bio Functions

| Diseases and Disorders              |                     |            |
|-------------------------------------|---------------------|------------|
| Name                                | p-value             | #Molecules |
| Cancer                              | 4.90E-03 - 5.38E-18 | 858        |
| Organismal Injury and Abnormalities | 4.90E-03 - 5.38E-18 | 862        |
| Reproductive System Disease         | 4.90E-03 - 5.38E-18 | 466        |
| Gastrointestinal Disease            | 4.82E-03 - 2.77E-08 | 643        |
| Cardiovascular Disease              | 4.82E-03 - 9.61E-06 | 136        |

Molecular and Cellular Functions



Summary of Analysis - IPA early transition human data only-Only NS to AK transit - 2015-06-13 11:33 AM

| Name                                       | p-value             | #Molecules |
|--|---------------------|------------|
| Cell Cycle                                 | 4.82E-03 - 5.96E-23 | 182        |
| Cellular Assembly and Organization         | 4.77E-03 - 1.50E-18 | 154        |
| DNA Replication, Recombination, and Repair | 4.82E-03 - 1.50E-18 | 145        |
| Cell Death and Survival                    | 4.82E-03 - 4.76E-16 | 266        |
| Cellular Growth and Proliferation          | 4.22E-03 - 1.28E-14 | 268        |

Physiological System Development and Function

| Name   | p-value             | #Molecules |
|--|---------------------|------------|
| Renal and Urological System Development and Function | 2.38E-07 - 2.38E-07 | 24         |
| Hair and Skin Development and Function               | 1.84E-03 - 3.21E-06 | 29         |
| Embryonic Development                                | 4.22E-03 - 1.22E-05 | 34         |
| Humoral Immune Response                              | 2.71E-03 - 4.83E-05 | 14         |
| Cardiovascular System Development and Function       | 4.82E-03 - 6.71E-05 | 37         |

Top Tox Functions

Assays: Clinical Chemistry and Hematology

| Name                                     | p-value             | #Molecules |
|--|---------------------|------------|
| Increased Levels of LDH                  | 3.13E-01 - 7.86E-03 | 3          |
| Increased Levels of Alkaline Phosphatase | 1.51E-01 - 1.51E-01 | 3          |

Cardiotoxicity

| Name                   | p-value             | #Molecules |
|------------------------|---------------------|------------|
| Pulmonary Hypertension | 1.48E-01 - 1.44E-02 | 7          |
| Cardiac Dysfunction    | 9.25E-02 - 2.73E-02 | 3          |
| Cardiac Infarction     | 5.75E-01 - 3.67E-02 | 14         |
| Cardiac Arrythmia      | 5.35E-01 - 4.98E-02 | 14         |



|                |                     |   |
|----------------|---------------------|---|
| Cardiac Damage | 5.21E-02 - 5.21E-02 | 1 |
|----------------|---------------------|---|

Hepatotoxicity

| Name                                 | p-value             | #Molecules |
|--------------------------------------|---------------------|------------|
| Liver Hyperplasia/Hyperproliferation | 2.75E-01 - 4.92E-04 | 362        |
| Hepatocellular Carcinoma             | 1.09E-01 - 3.42E-03 | 44         |
| Liver Steatosis                      | 3.39E-01 - 1.15E-02 | 8          |
| Liver Inflammation/Hepatitis         | 1.00E00 - 5.21E-02  | 8          |
| Liver Proliferation                  | 4.15E-01 - 9.34E-02 | 3          |

Nephrotoxicity

| Name                      | p-value             | #Molecules |
|---------------------------|---------------------|------------|
| Renal Proliferation       | 2.38E-07 - 2.38E-07 | 24         |
| Renal Necrosis/Cell Death | 5.39E-01 - 5.19E-02 | 24         |
| Nephrosis                 | 4.74E-01 - 5.21E-02 | 3          |
| Renal Inflammation        | 1.00E00 - 5.21E-02  | 5          |
| Renal Nephritis           | 1.00E00 - 5.21E-02  | 5          |

| Top Regulator Effect Networks |                                    |   |
|-------------------------------|------------------------------------|---|
| ID                            | Regulators                         | Diseases & Functions                              |
| 1                             | CDKN1A,FOXO1,KDM5B,RABL6,RB1,TRAF2 | cytokinesis,M phase of tumor cell lines (+1 more) |
| 2                             | FOXO1,TP53                         | alignment of chromosomes (+1 more)                |
| 3                             | TP53                               | apoptosis of cervical cancer cell lines           |
| 4                             | E2f                                | apoptosis of cervical cancer cell lines           |
| 5                             | RB1                                | apoptosis of squamous cell carcinoma cell lines   |
|                               |                                    | Consistency Score                                 |
|                               |                                    | 5.421   |
|                               |                                    | 3.333   |
|                               |                                    | -2.111  |
|                               |                                    | -6.261  |
|                               |                                    | -7.5  |



Top Networks

| ID | Associated Network Functions   | Score |
|----|--|-------|
| 1  | Cellular Assembly and Organization, Cell Cycle, DNA Replication, Recombination, and Repair | 43    |
| 2  | Cell Cycle, Cancer, Organismal Injury and Abnormalities                                    | 35    |
| 3  | Cell Cycle, DNA Replication, Recombination, and Repair, Cellular Growth and Proliferation  | 33    |
| 4  | DNA Replication, Recombination, and Repair, Cancer, Organismal Injury and Abnormalities    | 31    |
| 5  | Cancer, Organismal Injury and Abnormalities, Cell-To-Cell Signaling and Interaction        | 29    |

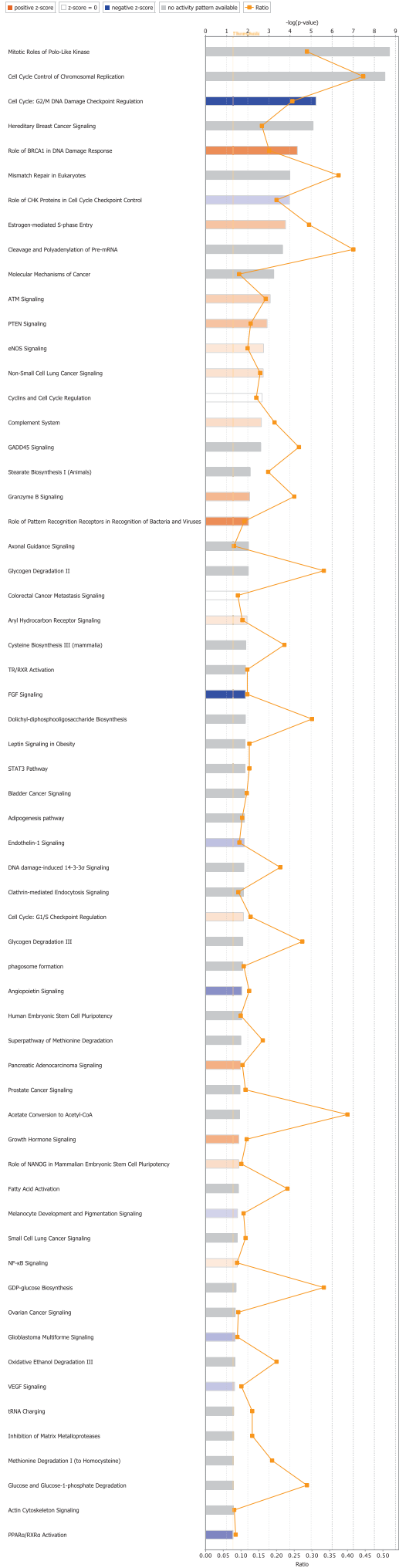
Top Tox Lists

| Name  | p-value  | Overlap       |
|---|----------|---------------|
| Cardiac Necrosis/Cell Death                       | 2.94E-06 | 12.5 % 33/264 |
| Cell Cycle: G2/M DNA Damage Checkpoint Regulation | 9.02E-06 | 23.5 % 12/51  |
| Cardiac Hypertrophy                               | 5.97E-04 | 9.3 % 36/388  |
| Renal Necrosis/Cell Death                         | 2.55E-03 | 8.3 % 40/482  |
| Increases Renal Proliferation                     | 3.18E-03 | 11.5 % 15/130 |

Top My Lists

| Name                  | p-value  | Overlap        |
|-----------------------|----------|----------------|
| 12.3.13 cell adhesion | 2.56E-05 | 7.6 % 116/1534 |









Analysis Name: IPA early transition Mouse data only-Only pap vs Chonic uv - 2015-06-13 11:35 AM

Analysis Creation Date: 2015-06-13

Build version: 346717M

Content version: 23814503 (Release Date: 2015-03-22)

#### Analysis Settings

Reference set: Ingenuity Knowledge Base (Genes Only)

Relationship to include: Direct and Indirect

Does not Include Endogenous Chemicals

Optional Analyses: My Pathways My List

Filter Summary:

Consider only molecules and/or relationships where

(species = Human) AND

(confidence = Experimentally Observed)



Top Canonical Pathways

| Name  | p-value  | Overlap       |
|---|----------|---------------|
| Cell Cycle Control of Chromosomal Replication     | 3.19E-09 | 44.4 % 12/27  |
| Mitotic Roles of Polo-Like Kinase                 | 1.42E-08 | 27.0 % 17/63  |
| Hereditary Breast Cancer Signaling                | 2.85E-05 | 15.1 % 19/126 |
| Cell Cycle: G2/M DNA Damage Checkpoint Regulation | 3.45E-05 | 22.4 % 11/49  |
| Role of BRCA1 in DNA Damage Response              | 4.53E-05 | 17.9 % 14/78  |

Top Upstream Regulators

| Upstream Regulator | p-value of overlap | Predicted Activation |
|--------------------|--------------------|----------------------|
| E2F4               | 1.06E-31           | Activated            |
| RABL6              | 5.21E-24           |                      |
| ERBB2              | 9.64E-18           |                      |
| TP53               | 4.02E-15           | Inhibited            |
| CDK4               | 4.09E-15           |                      |

Top Diseases and Bio Functions

| Diseases and Disorders              |                     |            |
|-------------------------------------|---------------------|------------|
| Name                                | p-value             | #Molecules |
| Cancer                              | 5.36E-03 - 2.24E-17 | 857        |
| Organismal Injury and Abnormalities | 5.36E-03 - 2.24E-17 | 861        |
| Reproductive System Disease         | 4.94E-03 - 2.24E-17 | 465        |
| Gastrointestinal Disease            | 4.84E-03 - 5.13E-08 | 642        |
| Cardiovascular Disease              | 4.84E-03 - 9.88E-06 | 136        |

Molecular and Cellular Functions



Summary of Analysis - IPA early transition Mouse data only-Only pap vs Chonic uv - 2015-06-13 11:35 AM

| Name                                       | p-value             | #Molecules |
|--|---------------------|------------|
| Cell Cycle                                 | 4.84E-03 - 3.11E-22 | 181        |
| Cellular Assembly and Organization         | 5.08E-03 - 1.52E-17 | 153        |
| DNA Replication, Recombination, and Repair | 5.43E-03 - 1.52E-17 | 151        |
| Cell Death and Survival                    | 4.84E-03 - 1.09E-15 | 265        |
| Cellular Growth and Proliferation          | 4.24E-03 - 2.68E-14 | 267        |

Physiological System Development and Function

| Name   | p-value             | #Molecules |
|--|---------------------|------------|
| Renal and Urological System Development and Function | 2.43E-07 - 2.43E-07 | 24         |
| Hair and Skin Development and Function               | 1.85E-03 - 3.27E-06 | 29         |
| Embryonic Development                                | 4.23E-03 - 1.24E-05 | 34         |
| Humoral Immune Response                              | 2.72E-03 - 4.86E-05 | 14         |
| Cardiovascular System Development and Function       | 4.84E-03 - 6.78E-05 | 37         |

Top Tox Functions

Assays: Clinical Chemistry and Hematology

| Name                                     | p-value             | #Molecules |
|--|---------------------|------------|
| Increased Levels of LDH                  | 3.13E-01 - 7.87E-03 | 3          |
| Increased Levels of Alkaline Phosphatase | 1.52E-01 - 1.52E-01 | 3          |

Cardiotoxicity

| Name                   | p-value             | #Molecules |
|------------------------|---------------------|------------|
| Pulmonary Hypertension | 1.48E-01 - 1.45E-02 | 7          |
| Cardiac Dysfunction    | 9.26E-02 - 2.73E-02 | 3          |
| Cardiac Infarction     | 5.76E-01 - 3.70E-02 | 14         |
| Cardiac Arrythmia      | 5.36E-01 - 5.01E-02 | 14         |



|                |                     |   |
|----------------|---------------------|---|
| Cardiac Damage | 5.22E-02 - 5.22E-02 | 1 |
|----------------|---------------------|---|

Hepatotoxicity

| Name                                 | p-value             | #Molecules |
|--------------------------------------|---------------------|------------|
| Liver Hyperplasia/Hyperproliferation | 2.75E-01 - 6.83E-04 | 361        |
| Hepatocellular Carcinoma             | 1.09E-01 - 5.77E-03 | 43         |
| Liver Steatosis                      | 3.39E-01 - 1.15E-02 | 8          |
| Liver Inflammation/Hepatitis         | 1.00E00 - 5.22E-02  | 8          |
| Liver Proliferation                  | 4.15E-01 - 9.36E-02 | 3          |

Nephrotoxicity

| Name                      | p-value             | #Molecules |
|---------------------------|---------------------|------------|
| Renal Proliferation       | 2.43E-07 - 2.43E-07 | 24         |
| Nephrosis                 | 4.74E-01 - 5.22E-02 | 3          |
| Renal Inflammation        | 1.00E00 - 5.22E-02  | 5          |
| Renal Nephritis           | 1.00E00 - 5.22E-02  | 5          |
| Renal Necrosis/Cell Death | 5.40E-01 - 5.23E-02 | 24         |

| Top Regulator Effect Networks |                                   |   |
|-------------------------------|-----------------------------------|---|
| ID                            | Regulators                        | Diseases & Functions                              |
| 1                             | FOXN1,HCAR2,NGFR,STUB1,TRAF2,YAP1 | amplification of centrosome,apoptosis (+4 more)   |
| 2                             | E2f,FOXO1,RABL6,TP53,TRAF2        | alignment of chromosomes (+4 more)                |
| 3                             | CDKN1A,RABL6,TP53                 | cell death of cancer cells                        |
| 4                             | AURKB,E2F6,FOXN1,RABL6,YAP1       | amplification of centrosome,cytokinesis (+1 more) |
| 5                             | KDM5B,RABL6,TP63                  | M phase of tumor cell lines                       |
|                               |                                   | Consistency Score                                 |
|                               |                                   | 14.5  |
|                               |                                   | 7.201   |
|                               |                                   | 5.669   |
|                               |                                   | 4.707   |
|                               |                                   | 2.111   |



Top Networks

| ID | Associated Network Functions   | Score |
|----|--|-------|
| 1  | Cell Cycle, Cellular Assembly and Organization, DNA Replication, Recombination, and Repair | 43    |
| 2  | Cell Cycle, Cancer, Organismal Injury and Abnormalities                                    | 38    |
| 3  | Cell Cycle, DNA Replication, Recombination, and Repair, Cellular Growth and Proliferation  | 33    |
| 4  | Molecular Transport, Nucleic Acid Metabolism, Small Molecule Biochemistry                  | 31    |
| 5  | Cell-mediated Immune Response, Cellular Development, Cellular Function and Maintenance     | 31    |

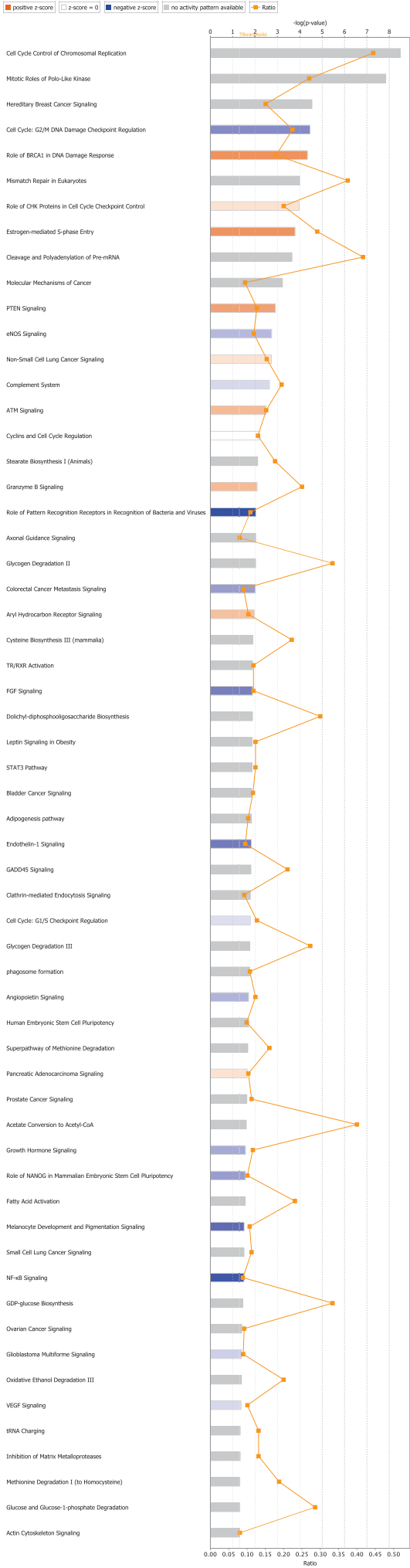
Top Tox Lists

| Name  | p-value  | Overlap       |
|---|----------|---------------|
| Cardiac Necrosis/Cell Death                       | 3.00E-06 | 12.5 % 33/264 |
| Cell Cycle: G2/M DNA Damage Checkpoint Regulation | 5.12E-05 | 21.6 % 11/51  |
| Cardiac Hypertrophy                               | 6.08E-04 | 9.3 % 36/388  |
| Increases Renal Proliferation                     | 3.21E-03 | 11.5 % 15/130 |
| Renal Necrosis/Cell Death                         | 4.49E-03 | 8.1 % 39/482  |

Top My Lists

| Name                  | p-value  | Overlap        |
|-----------------------|----------|----------------|
| 12.3.13 cell adhesion | 2.68E-05 | 7.6 % 116/1534 |







## Appendix 14.

### Information for TGFBR3-miRNA 3' UTR target clones



## Information for HmiT066530b-MT05 and TGFBR3-miRNA 3' UTR target clones

### HmiT066530a-MT05

aaccagcttttctgtacaaagtgggttcgatctagaatggctagttcagagcagacatgat  
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acgtcatggccttcgcgcgctgcctggagccctacaccgcctgcgacctggcgccccccg  
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